Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO molecular function
GO biological process
GO cellular component

JOB ID: a8f1689c20233851980ac74699c7dad4
Results URL: http://sbi.imim.es/BIPS.php?jobID=a8f1689c20233851980ac74699c7dad4

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner
3: Query homolog sequence (multiple names can appear if the proteins share the same sequence)
4: Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)
5: Query-Template Blast E-value
6: Predicted partner-Template Blast E-value
7: Joint e-value
8: Query-Template identities
9: Predicted partner-Template identities
10: Joint identities
11: Pfam domain-domain interactions found (0: False, 1: True)
12: Sharing GO terms found (0: False, 1: True)
13: Interaction found directly in database. (0: False, 1: True)
14: Interacting Pfam domains
15: Template interaction detection method
16: Template interaction source database

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|A5U2D9|PGK_MYCTA Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pgk P	KPYM_HUMAN	PGK1_HUMAN	KPYM_HUMAN	4,00E-68	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A5U521|A5U521_MYCTA Malate oxidoreductase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=mez	MAOX_HUMAN	MAOM_HUMAN	MAOM_HUMAN	5,00E-91	0	0	36	55	44,4972	1	1	0	malic:Mali	in vitro	hprd
sp|A5U0Y6|G6PI_MYCTA Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GI	B4DE36_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
sp|A5U0Y6|G6PI_MYCTA Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GI	B4DVJ0_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	89	61,8628	1	1	0	-	in vitro	hprd
sp|A5U0Y6|G6PI_MYCTA Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GI	G6PI_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	100	65,5744	0	1	0	-	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A0SD91_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A1DTJ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A1DTL0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A1DTV1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A1DUU4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A1DV22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A3RM82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A4ZLD6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A4ZLI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A4ZLS9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A4ZMF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A4ZMW5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6YW19_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6YWQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6YX95_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6YZY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z2T0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z460_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z708_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z809_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z8G5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z8Z7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z9Q7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z9S0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZB50_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZBW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZC77_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZDK7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZFQ8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A7LDP6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A7LFE4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A7XTZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A8JLT5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A8WFB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B0EWB5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B0EWB5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B0Z6N9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B0Z745_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B0Z7E9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B1NVE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B1W6U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B1W7S8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2CB40_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-109	7,07E-103	42	90	61,4817	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2CB92_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-111	7,07E-104	42	91	61,8223	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2KLD8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2WRF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XEK5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XEN1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XFT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XGB4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XMF0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XNQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XNX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2YAW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2Z5S5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2Z642_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2ZNN0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B3DE35_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B3VEA5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B4YBC2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B4YCG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B4YGV7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B5M8C0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B7TMW4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B8RFL3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B8X4N0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B8XZS7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B9ECT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B9EE11_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B9EEE1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B9EEI0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B9EF90_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C4PK82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C4RU97_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5MM24_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C7B321_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C7B3W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-111	7,07E-104	42	96	63,498	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C7SJU6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C7SKT4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C8XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C8Y3W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C8Y5S3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C8YGY6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C9D5W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D0V1V1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D1GI28_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D3K5V4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D6BZS8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D6C3F2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D6N462_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D6N765_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D7NV03_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D7P622_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D7P661_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E0Y4D8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E1B320_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E2FQB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E2J0C2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5DY67_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5DYD2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5E0U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5E1D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5E1I7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5EY89_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5LFL6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0G899_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0VXC5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0Z7D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0Z7G1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0ZFF5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q15H46_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q15HG3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q15II8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q15IP0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q19MP4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q27H55_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q2HJS3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q2HKH0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q2HKI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q2HKT7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q305I0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q305K6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q305X3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q3S961_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4EWP5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4EXJ4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4EZD1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4F0P9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4F0T8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4F1I5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4F2A8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4F2U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4G6P4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4G6V9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4G7C8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4G9U9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GBF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GC16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GFE9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GG20_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GI22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GIA0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GIY4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GMA4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GPI4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GPN6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GSY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GU59_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GV60_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4VFD0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4ZEA6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4ZED2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4ZEF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4ZF68_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5SAG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5SB31_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XSC1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZI2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZI9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZK9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZL8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZP7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZR9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZT6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XZY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y011_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y065_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y070_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y078_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y0E5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y0F3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y0G2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y0H4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5Y0J7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6R0Q1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6R0W6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6RLY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6RMU0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6RPE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6RRW7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VH99_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VHA9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VIB9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VIH5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VIM0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VJ16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VK16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VKA3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VLN4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6WQA1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6WQG6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7Y664_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7YCC7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7YCE0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7YCE5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7YCF3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7YEF1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q85KW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q85KW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q85KZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q85L04_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q85L10_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q8HNQ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q8WCY1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q9B1S4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q9B1S6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q9B2U6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q9B2W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q9B2X0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	COX3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A0S0W7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A0S2P1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A0S3T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A0SA07_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A1Z455_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A1Z4V2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A4ZKZ0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6YW54_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6YWD1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6YXV0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z3M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6Z6E8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZEU4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZF47_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZFK3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A6ZHA9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A7LDC6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A7LF11_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	A7LFA2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B0Z6W4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B1W855_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2CB37_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-107	7,07E-102	42	95	63,1664	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2WRY8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XHF9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XHT9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XIR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XL43_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XP28_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B2XPS3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B3DE06_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B3GUF3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	B5M7M0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6K5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-109	7,07E-103	42	96	63,498	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6K6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6K7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6L3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6M4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6M7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C5H6M8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C8XWJ6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C8Y3G4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C8Y3Q5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C8YBL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	C9D661_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D1G421_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D2IKF4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D2K1G3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D3YPT7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D5M8T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	D7NUN3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E0AF97_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E2DTL8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E2JFC4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E2JJS5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5DZN4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5E079_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5E1A6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5E1V1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5EWG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5EWL4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5EWR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	E5FWC0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q06TE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q09U41_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0Z7D8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0Z7F1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0Z7J0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0Z7K3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q0Z7S0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q15HH9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q19MP7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q305H0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4EYL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4EZD4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4F4V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4F6A2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GCC3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GCG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GCZ4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GHE1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GQP0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GVP5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q4GW12_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5S971_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5SA98_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5SAP1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5SB08_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q5XRW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6R0V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6RKW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6RNN7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6RQ80_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VIG7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VJD8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q6VJJ3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7Y626_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7Y6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7Y6N0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7YCE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q7YEH2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q85KS0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q8HNR1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q8HNR6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q8HQB7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q8WCW3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q9B138_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q9B1F9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q9B2U8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	COX2_YEAST	COX1_HUMAN	COX2_HUMAN	5,00E-96	3,00E-47	1,22E-71	42	42	42	1	1	0	COX1:COX	in vivo	hprd
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	COX2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|A5U1T8|MDH_MYCTA Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=mdh P	MDHC_HUMAN	MDHC_HUMAN	MDHC_HUMAN	3,00E-88	0	0	51	100	71,4143	1	1	0	Ldh_1_C:L	in vitro	hprd
sp|A5U315|ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ar	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	intact
sp|A5U315|ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ar	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	biogrid
sp|A5U315|ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ar	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	hprd
sp|A5U315|ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ar	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	intact
sp|A5U315|ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ar	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	biogrid
sp|A5U315|ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ar	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	hprd
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	blue native	intact
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	blue native	intact
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	in vitro	hprd
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	in vitro	hprd
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	in vitro	hprd
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
tr|A5U6S1|A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37R	B4DDS7_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54_N:S	x-ray cryst	biogrid
tr|A5U6S1|A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37R	B4DDS7_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54_N:S	in vitro	hprd
tr|A5U6S1|A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37R	SRP54_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54:SRP	x-ray cryst	biogrid
tr|A5U6S1|A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37R	SRP54_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54:SRP	in vitro	hprd
tr|A5U6S1|A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37R	SRP19_HUMAN	SRP54_HUMAN	SRP19_HUMAN	2,00E-57	0	0	30	100	54,7723	0	1	0	-	in vitro	hprd
sp|A5U090|RL2_MYCTA 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=rplB P	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|A5U090|RL2_MYCTA 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=rplB P	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|A5U090|RL2_MYCTA 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=rplB P	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|A5U090|RL2_MYCTA 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=rplB P	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP7C_HUMAN	GRP78_HUMAN	HSP71_HUMAN	1,00E-148	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP7C_HUMAN	GRP78_HUMAN	HSP71_HUMAN	1,00E-148	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP71_HUMAN	GRP78_HUMAN	HSP71_HUMAN	1,00E-148	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP71_HUMAN	GRP78_HUMAN	HSP71_HUMAN	1,00E-148	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in databas e. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	TBB2C_HUMAN	GRP78_HUMAN	TBB5_HUMAN	1,00E-148	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP71_HUMAN	GRP78_HUMAN	HSP7C_HUMAN	1,00E-148	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP7C_HUMAN	GRP78_HUMAN	HSP7C_HUMAN	1,00E-148	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP78_HUMAN	ACTH_HUMAN	1,00E-148	0	0	49	93	67,5056	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	1,00E-148	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP78_HUMAN	ACTG_HUMAN	1,00E-148	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	TBB2C_HUMAN	GRP78_HUMAN	TBB4_HUMAN	1,00E-148	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	CH60_HUMAN	GRP78_HUMAN	CH60_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ENPL_HUMAN	GRP78_HUMAN	ENPL_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP71_HUMAN	GRP78_HUMAN	HS71L_HUMAN	1,00E-148	0	0	49	89	66,0379	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP7C_HUMAN	GRP78_HUMAN	HS71L_HUMAN	1,00E-148	0	0	49	82	63,3877	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ENPL_HUMAN	GRP78_HUMAN	HS90A_HUMAN	1,00E-148	1,00E-151	3,16E-150	49	46	47,4763	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HS90B_HUMAN	GRP78_HUMAN	HS90A_HUMAN	1,00E-148	0	0	49	85	64,5368	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HS90A_HUMAN	GRP78_HUMAN	HS90A_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	A8K9K1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	77	49,6387	1	1	0	Cation_AT	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	A8MYK9_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	76	49,3153	1	1	0	Cation_AT	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	AT2C1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	1,00E-129	3,16E-126	32	34	32,9848	1	1	0	Cation_AT	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	B7ZA13_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	1,00E-117	3,16E-120	32	32	32	1	1	0	Cation_AT	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	AT2C2_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	1,00E-114	1,00E-118	32	31	31,496	1	1	0	Cation_AT	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	Q7Z6E5_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	84	51,8459	1	1	0	Cation_AT	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	AT2A1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	84	51,8459	1	1	0	Cation_AT	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	AT2A3_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	76	49,3153	1	1	0	Cation_AT	in vivo	hprd
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25	AT2A2_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	100	56,5685	1	1	0	Cation_AT	in vivo	hprd
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	blue nativ	intact
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	blue nativ	intact
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	in vitro	hprd
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	blue nativ	intact
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	blue nativ	intact
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	1,00E-157	0	0	54	100	73,4847	0	1	0	-	blue nativ	intact
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=at	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	1,00E-157	0	0	54	100	73,4847	0	1	0	-	blue nativ	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-105	0	0	41	86	59,3801	0	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-105	0	0	41	86	59,3801	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	SMAD3_HUMAN	CH60_HUMAN	SMAD2_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	display ted	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	TBB2C_HUMAN	CH60_HUMAN	TBB5_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-105	0	0	41	86	59,3801	0	1	0	-	molecular	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	TBB2C_HUMAN	CH60_HUMAN	TBA1A_HUMAN	1,00E-119	2,00E-99	1,41E-109	46	40	42,8952	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ACTB_HUMAN	CH60_HUMAN	ACTH_HUMAN	1,00E-119	0	0	46	93	65,4064	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ACTB_HUMAN	CH60_HUMAN	ACTG_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	cross-linki	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	biochemic	biogrid
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	cross-linki	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	biochemic	biogrid

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	cross-linki	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	biochemic	biogrid
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	cross-linki	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	biochemic	biogrid
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-119	0	0	46	64	54,2586	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-119	0	0	46	65	54,6809	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-105	0	0	41	64	51,225	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-105	0	0	41	65	51,6236	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	95	66,106	1	1	0	-	in vitro	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	87	63,2614	0	1	0	-	in vitro	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	CH60_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	-	in vitro	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-105	0	0	41	95	62,4099	1	1	0	-	in vitro	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-105	0	0	41	87	59,7244	0	1	0	-	in vitro	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	83	58,3352	0	1	0	-	molecular	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	83	58,3352	0	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	83	58,3352	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	80	57,2713	0	1	0	-	molecular	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	80	57,2713	0	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	80	57,2713	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	molecular	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	94	65,7571	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	ENPL_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	1,00E-156	3,16E-138	46	48	46,9894	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	HS90B_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-105	0	0	41	98	63,3877	0	1	0	-	molecular	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-105	0	0	41	94	62,0806	0	1	0	-	molecular	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-105	0	0	41	86	59,3801	0	1	0	-	molecular	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	1,00E-60	3,16E-90	46	31	37,7624	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	1,00E-59	1,00E-89	46	31	37,7624	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-58	7,07E-89	46	30	37,1484	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	85	62,53	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	1,00E-60	3,16E-83	41	31	35,6511	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	5,00E-57	2,24E-81	41	30	35,0714	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	1,00E-59	1,00E-82	41	31	35,6511	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	5,00E-58	7,07E-82	41	30	35,0714	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	5,00E-57	2,24E-81	41	30	35,0714	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	85	59,0339	1	1	0	-	surface pla	intact
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	-	surface pla	intact
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	92	65,0538	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 P	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	92	61,4166	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 P	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|A5U630|DCUP_MYCTA Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q53ZP6_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	99	60,5227	0	1	0	-	x-ray cryst	biogrid
sp|A5U630|DCUP_MYCTA Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	Q53ZP6_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	99	60,5227	0	1	0	-	in vitro	hprd
sp|A5U630|DCUP_MYCTA Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	DCUP_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	100	60,8276	0	1	0	-	x-ray cryst	biogrid
sp|A5U630|DCUP_MYCTA Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra)	DCUP_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	100	60,8276	0	1	0	-	in vitro	hprd
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B2R5P6_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B2R5P6_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B4DMK9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	95	57,6628	1	1	0	Pyr_redox	x-ray cryst	intact
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B4DMK9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	95	57,6628	1	1	0	Pyr_redox	in vivo	hprd
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B4DT69_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	90	56,1249	1	1	0	Pyr_redox	x-ray cryst	intact
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B4DT69_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	90	56,1249	1	1	0	Pyr_redox	in vivo	hprd
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B7Z2S5_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B7Z2S5_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	E2QRB9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	4,00E-47	1,55E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	E2QRB9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	4,00E-47	1,55E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:	fluorescen	mint
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:	in vitro	hprd
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	1,00E-134	2,45E-107	50	68	58,3095	1	1	0	Gp_dh_N:	fluorescen	mint
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	1,00E-134	2,45E-107	50	68	58,3095	1	1	0	Gp_dh_N:	in vitro	hprd
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_C:	fluorescen	mint
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_C:	in vitro	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP7C_HUMAN	GRP75_HUMAN	HSP71_HUMAN	1,00E-166	0	0	54	86	68,1469	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP7C_HUMAN	GRP75_HUMAN	HSP71_HUMAN	1,00E-166	0	0	54	86	68,1469	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP71_HUMAN	GRP75_HUMAN	HSP71_HUMAN	1,00E-166	0	0	54	100	73,4847	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP71_HUMAN	GRP75_HUMAN	HSP71_HUMAN	1,00E-166	0	0	54	100	73,4847	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP75_HUMAN	ACTB_HUMAN	1,00E-166	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP75_HUMAN	ACTH_HUMAN	1,00E-166	0	0	54	93	70,8661	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP75_HUMAN	ACTB_HUMAN	1,00E-166	0	0	54	98	72,7461	0	1	0	-	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ACTB_HUMAN	GRP75_HUMAN	ACTG_HUMAN	1,00E-166	0	0	54	98	72,7461	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP71_HUMAN	GRP75_HUMAN	GRP78_HUMAN	1,00E-166	0	0	54	64	58,7878	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP71_HUMAN	GRP75_HUMAN	GRP78_HUMAN	1,00E-166	0	0	54	64	58,7878	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP7C_HUMAN	GRP75_HUMAN	GRP78_HUMAN	1,00E-166	0	0	54	65	59,2453	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HSP7C_HUMAN	GRP75_HUMAN	GRP78_HUMAN	1,00E-166	0	0	54	65	59,2453	1	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	CH60_HUMAN	GRP75_HUMAN	CH60_HUMAN	1,00E-166	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ENPL_HUMAN	GRP75_HUMAN	ENPL_HUMAN	1,00E-166	0	0	54	100	73,4847	0	1	0	-	in vitro	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	ENPL_HUMAN	GRP75_HUMAN	HS90A_HUMAN	1,00E-166	1,00E-151	3,16E-159	54	46	49,8397	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HS90B_HUMAN	GRP75_HUMAN	HS90A_HUMAN	1,00E-166	0	0	54	85	67,7495	0	1	0	-	in vivo	hprd
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK	HS90A_HUMAN	GRP75_HUMAN	HS90A_HUMAN	1,00E-166	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	PPIA_HUMAN	HS90A_HUMAN	PPIA_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TBB2C_HUMAN	HS90A_HUMAN	TBB5_HUMAN	1,00E-114	0	0	38	98	61,0246	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TBB2C_HUMAN	HS90A_HUMAN	TBB5_HUMAN	1,00E-114	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TBB2C_HUMAN	HS90A_HUMAN	TBA1A_HUMAN	1,00E-114	2,00E-99	4,47E-107	38	40	38,9872	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	ACTB_HUMAN	HS90A_HUMAN	ACTH_HUMAN	1,00E-114	0	0	38	93	59,4475	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	1,00E-114	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	ACTB_HUMAN	HS90A_HUMAN	ACTG_HUMAN	1,00E-114	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90A_HUMAN	GRP78_HUMAN	1,00E-114	0	0	38	64	49,3153	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90A_HUMAN	GRP78_HUMAN	1,00E-114	0	0	38	65	49,6991	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	AIPL1_HUMAN	HS90A_HUMAN	AIP_HUMAN	1,00E-114	1,00E-93	3,16E-104	38	49	43,1509	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	AIPL1_HUMAN	HS90A_HUMAN	AIP_HUMAN	1,00E-114	1,00E-93	3,16E-104	38	49	43,1509	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	95	60,0833	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	95	60,0833	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	95	60,0833	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	87	57,4978	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	87	57,4978	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	87	57,4978	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	CRYAB_HUMAN	HS90A_HUMAN	CRYAB_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	A8K4T2_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	two hybrid	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	Q59EH7_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	two hybrid	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	DNJC7_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	two hybrid	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	83	56,1605	1	1	0	HATPase_	two hybrid	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	83	56,1605	1	1	0	HATPase_	two hybrid	mint

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	83	56,1605	1	1	0	HATPase_	two hybrid	biogrid
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	83	56,1605	1	1	0	HATPase_	in vitro	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	80	55,1362	1	1	0	HATPase_	two hybrid	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	80	55,1362	1	1	0	HATPase_	two hybrid	mint
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	80	55,1362	1	1	0	HATPase_	two hybrid	biogrid
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	80	55,1362	1	1	0	HATPase_	in vitro	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	100	61,6441	1	1	0	HATPase_	two hybrid	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	100	61,6441	1	1	0	HATPase_	two hybrid	mint
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	100	61,6441	1	1	0	HATPase_	two hybrid	biogrid
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	100	61,6441	1	1	0	HATPase_	in vitro	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	94	59,7662	1	1	0	HATPase_	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	94	59,7662	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	94	59,7662	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	94	59,7662	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	1,00E-114	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	1,00E-114	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	1,00E-114	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	A1JUI8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	A8K2X8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	1,00E-60	1,00E-87	38	31	34,322	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	A8K3C3_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	5,00E-57	7,07E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B2R9K8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DDU6_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	1,00E-59	3,16E-87	38	31	34,322	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DPJ8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DX08_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	5,00E-58	2,24E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	Q59ET3_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TCPD_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	5,00E-57	7,07E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TCPW_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	85	56,8331	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TCPZ_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	surface pla	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90B_HUMAN	HSP71_HUMAN	1,00E-117	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90B_HUMAN	HSP71_HUMAN	1,00E-117	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	ACTB_HUMAN	HS90B_HUMAN	ACTB_HUMAN	1,00E-117	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TBB2C_HUMAN	HS90B_HUMAN	TBB5_HUMAN	1,00E-117	0	0	38	98	61,0246	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP71_HUMAN	HS90B_HUMAN	HSP7C_HUMAN	1,00E-117	0	0	38	86	57,1664	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HSP7C_HUMAN	HS90B_HUMAN	HSP7C_HUMAN	1,00E-117	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TBB2C_HUMAN	HS90B_HUMAN	TBA1A_HUMAN	1,00E-117	2,00E-99	1,41E-108	38	40	38,9872	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	ACTB_HUMAN	HS90B_HUMAN	ACTG_HUMAN	1,00E-117	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z4F6_HUMAN	HS90B_HUMAN	CH60_HUMAN	1,00E-117	0	0	38	95	60,0833	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z5E7_HUMAN	HS90B_HUMAN	CH60_HUMAN	1,00E-117	0	0	38	87	57,4978	0	1	0	-	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS74L_HUMAN	HS90B_HUMAN	HS105_HUMAN	1,00E-117	0	0	38	60	47,7493	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	molecular	intact
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DGL0_HUMAN	HS90B_HUMAN	HS90B_HUMAN	1,00E-117	0	0	38	98	61,0246	1	1	0	HATPase_	in vitro	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DMA2_HUMAN	HS90B_HUMAN	HS90B_HUMAN	1,00E-117	0	0	38	94	59,7662	1	1	0	HATPase_	in vitro	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	HS90A_HUMAN	HS90B_HUMAN	HS90B_HUMAN	1,00E-117	0	0	38	86	57,1664	1	1	0	HATPase_	in vitro	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	A8K2X8_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-66	4,47E-92	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	A8K3C3_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-68	3,16E-93	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	A8K402_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-73	1,41E-95	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DDU6_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	8,00E-66	8,94E-92	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DEM7_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-61	1,00E-89	38	31	34,322	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DX08_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-65	1,41E-91	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B4DXI1_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-54	3,16E-86	38	30	33,7639	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B5BTY7_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	5,00E-74	7,07E-96	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z243_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-66	4,47E-92	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B7Z7K4_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-66	3,16E-92	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	B8ZZC9_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	5,00E-64	7,07E-91	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	Q2TU64_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	3,00E-73	1,73E-95	38	33	35,4119	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	Q53HU0_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-61	1,00E-89	38	31	34,322	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	Q53HV2_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-78	3,16E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TCPG_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	4,00E-74	6,32E-96	38	33	35,4119	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TCPG_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	4,00E-63	2,00E-90	38	31	34,322	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	Q6IBT3_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	5,00E-79	2,24E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TCPB_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	4,00E-74	6,32E-96	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TCPD_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	8,00E-69	2,83E-93	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG	TCPH_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-79	1,41E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3	PGK2_HUMAN	KPYM_HUMAN	PGK1_HUMAN	3,00E-73	0	0	36	87	55,9643	0	1	0	-	in vivo	hprd
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3	PGK1_HUMAN	KPYM_HUMAN	PGK1_HUMAN	3,00E-73	0	0	36	100	60	0	1	0	-	in vivo	hprd
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3	B4DRT3_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	91	57,2364	1	1	0	PK:PK_C P	in vitro	hprd
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3	KPYR_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	71	50,5569	1	1	0	PK:PK_C P	in vitro	hprd
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3	KPYM_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	100	60	1	1	0	PK:PK_C P	in vitro	hprd
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) G	A8K455_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	99	73,1163	1	1	0	S-AdoMet	inferred by	intact
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) G	A8K455_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	99	73,1163	1	1	0	S-AdoMet	inferred by	intact
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) G	METK2_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	84	67,3498	1	1	0	S-AdoMet	inferred by	intact
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) G	METK2_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	84	67,3498	1	1	0	S-AdoMet	inferred by	intact
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) G	METK1_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	100	73,4847	1	1	0	S-AdoMet	inferred by	intact
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) G	METK1_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	100	73,4847	1	1	0	S-AdoMet	inferred by	intact
tr|A5TZM9|A5TZM9_MYCTA Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37R	P5CR2_HUMAN	P5CR3_HUMAN	P5CR3_HUMAN	3,00E-28	3,00E-54	3,00E-41	31	46	37,7624	1	1	0	-	two hybrid	hprd
sp|A5TZ84|PURA_MYCTA Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	B4E1L0_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	78	58,5833	1	1	0	-	in vitro	hprd
sp|A5TZ84|PURA_MYCTA Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=	PURA1_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	100	66,3325	1	1	0	-	in vitro	hprd
sp|A5U7S2|SAHH_MYCTA Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ahc	SAHH_HUMAN	SAHH_HUMAN	SAHH_HUMAN	1,00E-143	0	0	55	100	74,162	1	1	0	-	in vitro	hprd

#Finished correctly

Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO molecular function
GO biological process
GO cellular component

JOB ID: ea44adcd48655a7c447d8815c4a11073
Results URL: http://sbi.imim.es/BIPS.php?jobID=ea44adcd48655a7c447d8815c4a11073

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner

Query protein	Predicted partner
sp|P9WID1|PGK_MYCTU Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pgk PE=1 SV=1	KPYM_HUMAN
sp|P9WK25|MAOX_MYCTU Putative malate oxidoreductase [NAD] OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mez PE=1 SV=1	MAOX_HUMAN
sp|P9WN69|G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pgi PE=1 SV=1	B4DE36_HUMAN
sp|P9WN69|G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pgi PE=1 SV=1	B4DVJ0_HUMAN
sp|P9WN69|G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pgi PE=1 SV=1	G6PI_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A0SD91_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A1DTJ7_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A1DTL0_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A1DTV1_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A1DUU4_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A1DV22_HUMAN

Query protein	Predicted partner
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A3RM82_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A4ZLD6_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A4ZLI8_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A4ZLS9_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A4ZMF9_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A4ZMW5_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6YW19_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6YWQ1_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6YX95_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6YZY0_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6Z2T0_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6Z460_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6Z708_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6Z809_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6Z8G5_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6Z8Z7_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6Z9Q7_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6Z9S0_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	A6ZB50_HUMAN
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q4GCC3_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q4GCG2_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q4GCZ4_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q4GHE1_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q4GQP0_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q4GVP5_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q4GW12_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q5S971_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q5SA98_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q5SAP1_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q5SB08_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q5XRW8_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q6R0V6_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q6RKW8_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q6RNN7_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q6RQ80_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q6VIG7_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q6VJD8_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q6VJJ3_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q7Y626_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q7Y6M3_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q7Y6N0_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q7YCE6_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q7YEH2_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q85KS0_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q8HNR1_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q8HNR6_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q8HQB7_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q8WCW3_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q9B138_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q9B1F9_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Q9B2U8_HUMAN
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	COX2_YEAST
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	COX2_HUMAN
sp|P9WK13|MDH_MYCTU Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mdh PE=1 SV=1	MDHC_HUMAN

Query protein	Predicted partner
sp|P9WPW7|ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=argG PE=1 SV=1	A8KAP9_HUMAN
sp|P9WPW7|ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=argG PE=1 SV=1	ASSY_HUMAN
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpG PE=1 SV=1	B4DY56_HUMAN
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpG PE=1 SV=1	ATPA_HUMAN
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpG PE=1 SV=1	ATPB_HUMAN
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpG PE=1 SV=1	ATPD_HUMAN
sp|P9WGD7|SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ffh PE=1 SV=1	B4DDS7_HUMAN
sp|P9WGD7|SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ffh PE=1 SV=1	SRP54_HUMAN
sp|P9WGD7|SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ffh PE=1 SV=1	SRP19_HUMAN
sp|P9WHA5|RL2_MYCTU 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rplB PE=1 SV=1	RL6_HUMAN
sp|P9WHA5|RL2_MYCTU 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rplB PE=1 SV=1	RL30_HUMAN
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	HSP7C_HUMAN
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	HSP71_HUMAN
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	ACTB_HUMAN
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	TBB2C_HUMAN
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	CH60_HUMAN
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	ENPL_HUMAN
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	HS90B_HUMAN
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	HS90A_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	A8K9K1_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	A8MYK9_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	AT2C1_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	B7ZA13_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	AT2C2_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	Q7Z6E5_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	AT2A1_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	AT2A3_HUMAN
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	AT2A2_HUMAN
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpA PE=1 SV=1	ATPG_HUMAN
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpA PE=1 SV=1	ATPB_HUMAN
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpA PE=1 SV=1	ATPD_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	HSP7C_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	HSP71_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	HSP7C_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	HSP71_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	ACTB_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	SMAD3_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	TBB2C_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	Q9UNM1_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	CH10_HUMAN

Query protein	Predicted partner
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	Q9UNM1_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	CH10_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B7Z4F6_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B7Z5E7_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	CH60_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B7Z4F6_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B7Z5E7_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B4DGL0_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B4DMA2_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	ENPL_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	HS90B_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	HS90A_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B4DGL0_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B4DMA2_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	HS90A_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	A1JUI8_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	A8K2X8_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	A8K3C3_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B2R9K8_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B4DDU6_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B4DPJ8_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B4DX08_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	Q59ET3_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	TCPD_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	TCPW_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	TCPZ_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	A1JUI8_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	A8K2X8_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	A8K3C3_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B2R9K8_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B4DDU6_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B4DPJ8_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B4DX08_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	Q59ET3_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	TCPD_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	TCPW_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	TCPZ_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	B4DR68_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	Q53FS6_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	Q53G55_HUMAN

Query protein	Predicted partner
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	Q59EK6_HUMAN
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	Q9BV61_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	B4DR68_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	Q53FS6_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	Q53G55_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	Q59EK6_HUMAN
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	Q9BV61_HUMAN
sp|P9WFE1|DCUP_MYCTU Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=hemE PE=1 SV=1	Q53ZP6_HUMAN
sp|P9WFE1|DCUP_MYCTU Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=hemE PE=1 SV=1	DCUP_HUMAN
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpdC PE=1 SV=1	B2R5P6_HUMAN
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpdC PE=1 SV=1	B4DMK9_HUMAN
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpdC PE=1 SV=1	B4DT69_HUMAN
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpdC PE=1 SV=1	B7Z2S5_HUMAN
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpdC PE=1 SV=1	E2QRB9_HUMAN
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=gap PE=1 SV=1	Q2TSD0_HUMAN
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=gap PE=1 SV=1	G3PT_HUMAN
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=gap PE=1 SV=1	G3P_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	PPIA_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	HSP7C_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	HSP71_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	ACTB_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	TBB2C_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	AIPL1_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B7Z4F6_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B7Z5E7_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	CRYAB_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	A8K4T2_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	Q59EH7_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	DNJC7_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B4DGL0_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B4DMA2_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	HS90A_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	HS74L_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	A1JUI8_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	A8K2X8_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	A8K3C3_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B2R9K8_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B4DDU6_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B4DPJ8_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B4DX08_HUMAN

Query protein	Predicted partner
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	Q59ET3_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	TCPD_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	TCPW_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	TCPZ_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	A8K402_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B4DEM7_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B4DXI1_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B5BTY7_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B7Z243_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B7Z7K4_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	B8ZZC9_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	Q2TU64_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	Q53HU0_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	Q53HV2_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	TCPG_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	TCPG_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	Q6IBT3_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	TCPB_HUMAN
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	TCPH_HUMAN
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pyk PE=1 SV=1	PGK2_HUMAN
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pyk PE=1 SV=1	PGK1_HUMAN
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pyk PE=1 SV=1	B4DRT3_HUMAN
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pyk PE=1 SV=1	KPYR_HUMAN
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pyk PE=1 SV=1	KPYM_HUMAN
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=metK PE=1 SV=1	A8K455_HUMAN
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=metK PE=1 SV=1	METK2_HUMAN
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=metK PE=1 SV=1	METK1_HUMAN
sp|P9WHU7|P5CR_MYCTU Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=proC PE=1 SV=1	P5CR2_HUMAN
sp|P9WHN3|PURA_MYCTU Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=purA PE=1 SV=1	B4E1L0_HUMAN
sp|P9WHN3|PURA_MYCTU Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=purA PE=1 SV=1	PURA1_HUMAN
sp|P9WGV3|SAHH_MYCTU Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ahcY PE=1 SV=1	SAHH_HUMAN
#Finished correctly	

COLUMNS
1: Query protein
2: Predicted partner
3: Query homolog sequence (multiple names can appear if the proteins share the same sequence)
4: Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)
5: Query-template blast E-value
6: Predicted partner-template blast E-value
7: Joint e-value
8: Query-template identities
9: Predicted partner-template identities
10: Joint identities
11: Pfam domain-domain interactions found (0: false, 1: true)
12: Sharing GO terms found (0: false, 1: true)
13: Interaction found directly in database (0: false, 1: true)
14: Interacting Pfam domains
15: Template interaction detection method
16: Template interaction source database

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WID1|PGK_MYCTU Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC	KPYM_HUMAN	PGK1_HUMAN	KPYM_HUMAN	4,00E-68	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WK25|MAOX_MYCTU Putative malate oxidoreductase [NAD] OS=Mycobacterium tuberculo	MAOX_HUMAN	MAOM_HUMAN	MAOM_HUMAN	5,00E-91	0	0	36	55	44,4972	1	1	0	malic:Mali	in vitro	hprd
sp|P9WN69|G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strai	B4DE36_HUMAN	G6PI_HUMAN	G6PI_HUMAN	########	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
sp|P9WN69|G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strai	B4DVJ0_HUMAN	G6PI_HUMAN	G6PI_HUMAN	########	0	0	43	89	61,8628	1	1	0	-	in vitro	hprd
sp|P9WN69|G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strai	G6PI_HUMAN	G6PI_HUMAN	G6PI_HUMAN	########	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A0SD91_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WN69|G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strai	G6PI_HUMAN	G6PI_HUMAN	G6PI_HUMAN	########	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A0SD91_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A1DTJ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A1DTL0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A1DTV1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A1DUU4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A1DV22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A3RM82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A4ZLD6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A4ZLI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A4ZLS9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A4ZMF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A4ZMW5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6YW19_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6YWQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6YX95_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6YZY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z2T0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z460_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z708_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z809_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z8G5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z8Z7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z9Q7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z9S0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZB50_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZBW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZC77_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZDK7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZFQ8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A7LDP6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A7LFE4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A7XTZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A8JLT5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A8WFB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B0EWB5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B0Z6N9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B0Z745_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B0Z7E9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B1NVE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B1W6U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B1W7S8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2CB40_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	90	61,4817	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2CB92_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	91	61,8223	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2KLD8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2WRF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XEK5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XEN1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XFT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XGB4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XMF0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XNQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XNX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2YAW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2Z5S5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2Z642_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2ZNN0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B3DE35_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B3VEA5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B4YBC2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B4YCG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B4YGV7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B5M8C0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B7TMW4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B8RFL3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B8X4N0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B8XZS7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B9ECT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B9EE11_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B9EEE1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B9EEI0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B9EF90_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C4PK82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C4RU97_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5MM24_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C7B321_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C7B3W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	96	63,498	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C7SJU6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C7SKT4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C8XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C8Y3W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C8Y5S3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C8YGY6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C9D5W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D0V1V1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D1GI28_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D3K5V4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D6BZS8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D6C3F2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D6N462_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D6N765_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D7NV03_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D7P622_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D7P661_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E0Y4D8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E1B320_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E2FQB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E2J0C2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5DY67_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5DYD2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5E0U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5E1D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5E1I7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5EY89_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5LFL6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0G899_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0VXC5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0Z7D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0Z7G1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0ZFF5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q15H46_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q15HG3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q15II8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q15IP0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q19MP4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q27H55_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q2HJS3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q2HKH0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q2HKI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q2HKT7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q305I0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q305K6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q305X3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q3S961_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4EWP5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4EXJ4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4EZD1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4F0P9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4F0T8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4F1I5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4F2A8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4F2U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4G6P4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4G6V9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4G7C8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4G9U9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GBF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GC16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GFE9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GG20_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GI22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GIA0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GIY4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GMA4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GPI4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GPN6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GSY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GU59_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GV60_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4VFD0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4ZEA6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4ZED2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4ZEF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4ZF68_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5SAG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5SB31_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XSC1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZI2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZI9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZK9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZL8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZP7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZR9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZT6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XZY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y011_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y065_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y070_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y078_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y0E5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y0F3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y0G2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y0H4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5Y0J7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6R0Q1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6R0W6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6RLY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6RMU0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6RPE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6RRW7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VH99_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VHA9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VIB9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VIH5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VIM0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VJ16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VK16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VKA3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VLN4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6WQA1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6WQG6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7Y664_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7YCC7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7YCE0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7YCE5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7YCF3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7YEF1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q85KW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q85KW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q85KZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q85L04_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q85L10_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q8HNQ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q8WCY1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q9B1S4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q9B1S6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q9B2U6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q9B2W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q9B2X0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	COX3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A0S0W7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A0S2P1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A0S3T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A0SA07_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A1Z455_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A1Z4V2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A4ZKZ0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6YW54_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6YWD1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6YXV0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z3M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6Z6E8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZEU4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZF47_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZFK3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A6ZHA9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A7LDC6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A7LF11_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	A7LFA2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B0Z6W4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B1W855_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2CB37_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	95	63,1664	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2WRY8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XHF9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XHT9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XIR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XL43_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XP28_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B2XPS3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B3DE06_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B3GUF3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	B5M7M0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6K5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	96	63,498	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6K6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6K7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6L3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6M4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6M7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C5H6M8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C8XWJ6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C8Y3G4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C8Y3Q5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C8YBL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	C9D661_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D1G421_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D2IKF4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D2K1G3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D3YPT7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D5M8T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	D7NUN3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E0AF97_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E2DTL8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E2JFC4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E2JJS5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5DZN4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5E079_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5E1A6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5E1V1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5EWG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5EWL4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5EWR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	E5FWC0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q06TE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q09U41_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0Z7D8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0Z7F1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0Z7J0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0Z7K3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q0Z7S0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q15HH9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q19MP7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q305H0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4EYL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4EZD4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4F4V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4F6A2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GCC3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GCG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GCZ4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GHE1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GQP0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GVP5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q4GW12_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5S971_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5SA98_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5SAP1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5SB08_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q5XRW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6R0V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6RKW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6RNN7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6RQ80_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VIG7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VJD8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q6VJJ3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7Y626_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7Y6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7Y6N0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7YCE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q7YEH2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q85KS0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q8HNR1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q8HNR6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q8HQB7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q8WCW3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q9B138_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q9B1F9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	Q9B2U8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	COX2_YEAST	COX1_HUMAN	COX2_HUMAN	5,00E-96	3,00E-47	1,22E-71	42	42	42	1	1	0	COX1:CO	in vivo	hprd
sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tubercul	COX2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:CO	in vivo	hprd
sp|P9WK13|MDH_MYCTU Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC	MDHC_HUMAN	MDHC_HUMAN	MDHC_HUMAN	3,00E-88	0	0	51	100	71,4143	1	1	0	Ldh_1_C:	in vitro	hprd
sp|P9WPW7|ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain A	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	intact
sp|P9WPW7|ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain A	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	biogrid
sp|P9WPW7|ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain A	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	hprd
sp|P9WPW7|ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain A	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	intact
sp|P9WPW7|ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain A	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	biogrid
sp|P9WPW7|ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain A	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	hprd
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:	blue native	intact
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:	blue native	intact
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:	in vitro	hprd
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:	blue native	intact
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:	blue native	intact
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:	in vitro	hprd
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:	blue native	intact
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:	blue native	intact
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:	in vitro	hprd
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:	blue native	intact
sp|P9WPU9|ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain A	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:	blue native	intact
sp|P9WGD7|SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (s	B4DDS7_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54_N	x-ray cryst	biogrid
sp|P9WGD7|SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (s	B4DDS7_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54_N	in vitro	hprd
sp|P9WGD7|SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (s	SRP54_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54:SR	x-ray cryst	biogrid
sp|P9WGD7|SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (s	SRP54_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54:SR	in vitro	hprd
sp|P9WGD7|SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (s	SRP19_HUMAN	SRP54_HUMAN	SRP19_HUMAN	2,00E-57	0	0	30	100	54,7723	0	1	0	-	in vitro	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WHA5|RL2_MYCTU 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATC	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|P9WHA5|RL2_MYCTU 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATC	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|P9WHA5|RL2_MYCTU 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATC	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|P9WHA5|RL2_MYCTU 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATC	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP7C_HUMAN	GRP78_HUMAN	HSP71_HUMAN	########	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP7C_HUMAN	GRP78_HUMAN	HSP71_HUMAN	########	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP71_HUMAN	GRP78_HUMAN	HSP71_HUMAN	########	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP71_HUMAN	GRP78_HUMAN	HSP71_HUMAN	########	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	TBB2C_HUMAN	GRP78_HUMAN	TBB5_HUMAN	########	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP71_HUMAN	GRP78_HUMAN	HSP7C_HUMAN	########	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP7C_HUMAN	GRP78_HUMAN	HSP7C_HUMAN	########	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP78_HUMAN	ACTH_HUMAN	########	0	0	49	93	67,5056	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	########	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP78_HUMAN	ACTG_HUMAN	########	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	TBB2C_HUMAN	GRP78_HUMAN	TBB4_HUMAN	########	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	CH60_HUMAN	GRP78_HUMAN	CH60_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ENPL_HUMAN	GRP78_HUMAN	ENPL_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP71_HUMAN	GRP78_HUMAN	HS71L_HUMAN	########	0	0	49	89	66,0379	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP7C_HUMAN	GRP78_HUMAN	HS71L_HUMAN	########	0	0	49	82	63,3877	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ENPL_HUMAN	GRP78_HUMAN	HS90A_HUMAN	########	########	########	49	46	47,4763	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HS90B_HUMAN	GRP78_HUMAN	HS90A_HUMAN	########	0	0	49	85	64,5368	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HS90A_HUMAN	GRP78_HUMAN	HS90A_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	A8K9K1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	0	0	32	77	49,6387	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	A8MYK9_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	0	0	32	76	49,3153	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	AT2C1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	########	########	32	34	32,9848	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	B7ZA13_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	########	########	32	32	32	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	AT2C2_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	########	########	32	31	31,496	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	Q7Z6E5_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	0	0	32	84	51,8459	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	AT2A1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	0	0	32	84	51,8459	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	AT2A3_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	0	0	32	76	49,3153	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS9|CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculos	AT2A2_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	########	0	0	32	100	56,5685	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain A	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt	blue native	intact
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain A	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt	blue native	intact
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain A	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt	in vitro	hprd
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain A	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt	blue native	intact
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain A	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt	blue native	intact
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain A	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	blue native	intact
sp|P9WPU7|ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain A	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	blue native	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	46	86	62,8967	0	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	46	86	62,8967	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	41	86	59,3801	0	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	41	86	59,3801	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	SMAD3_HUMAN	CH60_HUMAN	SMAD2_HUMAN	########	0	0	46	83	61,79	0	1	0	-	display tec	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	TBB2C_HUMAN	CH60_HUMAN	TBB5_HUMAN	########	0	0	46	98	67,1416	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 2	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	########	0	0	46	86	62,8967	0	1	0	-	molecular	intact

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	########	0	0	41	86	59,3801	0	1	0	-	molecular	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	TBB2C_HUMAN	CH60_HUMAN	TBA1A_HUMAN	########	2,00E-99	########	46	40	42,8952	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	ACTB_HUMAN	CH60_HUMAN	ACTH_HUMAN	########	0	0	46	93	65,4064	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	########	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	ACTB_HUMAN	CH60_HUMAN	ACTG_HUMAN	########	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	cross-linki	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	biochemic	biogrid
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TC	cross-linki	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TC	biochemic	biogrid
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	cross-linki	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	biochemic	biogrid
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TC	cross-linki	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TC	biochemic	biogrid
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	########	0	0	46	64	54,2586	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	########	0	0	46	65	54,6809	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	########	0	0	41	64	51,225	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	########	0	0	41	65	51,6236	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	46	95	66,106	1	1	0	-	in vitro	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	46	87	63,2614	0	1	0	-	in vitro	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	CH60_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	46	100	67,8233	1	1	0	-	in vitro	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	41	95	62,4099	1	1	0	-	in vitro	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	41	87	59,7244	0	1	0	-	in vitro	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	83	61,79	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	83	61,79	0	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	83	61,79	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	80	60,663	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	80	60,663	0	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	80	60,663	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	########	########	46	46	46	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	########	########	46	46	46	0	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	########	########	46	46	46	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	85	62,53	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	85	62,53	0	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	85	62,53	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	molecular	intact

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	83	58,3352	0	1	0	-	molecular	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	83	58,3352	0	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	83	58,3352	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	80	57,2713	0	1	0	-	molecular	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	80	57,2713	0	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	80	57,2713	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	molecular	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	46	98	67,1416	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	46	94	65,7571	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	ENPL_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	########	########	46	48	46,9894	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	46	86	62,8967	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	HS90B_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	41	98	63,3877	0	1	0	-	molecular	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	41	94	62,0806	0	1	0	-	molecular	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	41	86	59,3801	0	1	0	-	molecular	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	1,00E-60	3,16E-90	46	31	37,7624	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	1,00E-59	1,00E-89	46	31	37,7624	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-58	7,07E-89	46	30	37,1484	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	85	62,53	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	100	67,8233	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	1,00E-60	3,16E-83	41	31	35,6511	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-57	2,24E-81	41	30	35,0714	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	1,00E-59	1,00E-82	41	31	35,6511	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-58	7,07E-82	41	30	35,0714	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-57	2,24E-81	41	30	35,0714	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	85	59,0339	1	1	0	-	surface pla	intact
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	100	64,0312	1	1	0	-	surface pla	intact
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	92	65,0538	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|P9WPE7|CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	92	61,4166	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|P9WPE9|CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|P9WFE1|DCUP_MYCTU Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (str	Q53ZP6_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	99	60,5227	0	1	0	-	x-ray cryst	biogrid
sp|P9WFE1|DCUP_MYCTU Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (str	Q53ZP6_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	99	60,5227	0	1	0	-	in vitro	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WFE1|DCUP_MYCTU Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (str	DCUP_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	100	60,8276	0	1	0	-	x-ray cryst	biogrid
sp|P9WFE1|DCUP_MYCTU Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (str	DCUP_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	100	60,8276	0	1	0	-	in vitro	hprd
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	B2R5P6_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	B2R5P6_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	B4DMK9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	95	57,6628	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	B4DMK9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	95	57,6628	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	B4DT69_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	90	56,1249	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	B4DT69_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	90	56,1249	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	B7Z2S5_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	B7Z2S5_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	E2QRB9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	4,00E-47	1,55E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain	E2QRB9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	4,00E-47	1,55E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tubercu	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:	fluorescen	mint
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tubercu	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:	in vitro	hprd
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tubercu	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	########	########	50	68	58,3095	1	1	0	Gp_dh_N:	fluorescen	mint
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tubercu	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	########	########	50	68	58,3095	1	1	0	Gp_dh_N:	in vitro	hprd
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tubercu	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_C:	fluorescen	mint
sp|P9WN83|G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tubercu	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_C:	in vitro	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP7C_HUMAN	GRP75_HUMAN	HSP71_HUMAN	########	0	0	54	86	68,1469	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP7C_HUMAN	GRP75_HUMAN	HSP71_HUMAN	########	0	0	54	86	68,1469	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP71_HUMAN	GRP75_HUMAN	HSP71_HUMAN	########	0	0	54	100	73,4847	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP71_HUMAN	GRP75_HUMAN	HSP71_HUMAN	########	0	0	54	100	73,4847	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP75_HUMAN	ACTB_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP75_HUMAN	ACTH_HUMAN	########	0	0	54	93	70,8661	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP75_HUMAN	ACTB_HUMAN	########	0	0	54	98	72,7461	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ACTB_HUMAN	GRP75_HUMAN	ACTG_HUMAN	########	0	0	54	98	72,7461	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP71_HUMAN	GRP75_HUMAN	GRP78_HUMAN	########	0	0	54	64	58,7878	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP71_HUMAN	GRP75_HUMAN	GRP78_HUMAN	########	0	0	54	64	58,7878	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP7C_HUMAN	GRP75_HUMAN	GRP78_HUMAN	########	0	0	54	65	59,2453	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HSP7C_HUMAN	GRP75_HUMAN	GRP78_HUMAN	########	0	0	54	65	59,2453	1	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	CH60_HUMAN	GRP75_HUMAN	CH60_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ENPL_HUMAN	GRP75_HUMAN	ENPL_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	in vitro	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	ENPL_HUMAN	GRP75_HUMAN	HS90A_HUMAN	########	########	########	54	46	49,8397	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HS90B_HUMAN	GRP75_HUMAN	HS90A_HUMAN	########	0	0	54	85	67,7495	0	1	0	-	in vivo	hprd
sp|P9WMJ9|DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain AT	HS90A_HUMAN	GRP75_HUMAN	HS90A_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	PPIA_HUMAN	HS90A_HUMAN	PPIA_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TBB2C_HUMAN	HS90A_HUMAN	TBB5_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TBB2C_HUMAN	HS90A_HUMAN	TBB5_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TBB2C_HUMAN	HS90A_HUMAN	TBA1A_HUMAN	########	2,00E-99	########	38	40	38,9872	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	ACTB_HUMAN	HS90A_HUMAN	ACTH_HUMAN	########	0	0	38	93	59,4475	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	ACTB_HUMAN	HS90A_HUMAN	ACTG_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90A_HUMAN	GRP78_HUMAN	########	0	0	38	64	49,3153	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90A_HUMAN	GRP78_HUMAN	########	0	0	38	65	49,6991	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	AIPL1_HUMAN	HS90A_HUMAN	AIP_HUMAN	########	1,00E-93	########	38	49	43,1509	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	AIPL1_HUMAN	HS90A_HUMAN	AIP_HUMAN	########	1,00E-93	########	38	49	43,1509	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	95	60,0833	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	95	60,0833	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	95	60,0833	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	87	57,4978	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	87	57,4978	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	87	57,4978	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	CRYAB_HUMAN	HS90A_HUMAN	CRYAB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	A8K4T2_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	two hybrid	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	Q59EH7_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	two hybrid	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	DNJC7_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	two hybrid	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase	two hybrid	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase	two hybrid	mint
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase	two hybrid	biogrid
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase	in vitro	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase	two hybrid	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase	two hybrid	mint
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase	two hybrid	biogrid
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase	in vitro	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase	two hybrid	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase	two hybrid	mint
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase	two hybrid	biogrid
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase	in vitro	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	########	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	########	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	########	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	A1JUI8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	A8K2X8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	1,00E-60	1,00E-87	38	31	34,322	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	A8K3C3_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	5,00E-57	7,07E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B2R9K8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DDU6_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	1,00E-59	3,16E-87	38	31	34,322	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DPJ8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DX08_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	5,00E-58	2,24E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	Q59ET3_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TCPD_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	5,00E-57	7,07E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TCPW_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	85	56,8331	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TCPZ_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	surface pla	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90B_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90B_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	ACTB_HUMAN	HS90B_HUMAN	ACTB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TBB2C_HUMAN	HS90B_HUMAN	TBB5_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP71_HUMAN	HS90B_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HSP7C_HUMAN	HS90B_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TBB2C_HUMAN	HS90B_HUMAN	TBA1A_HUMAN	########	2,00E-99	########	38	40	38,9872	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	ACTB_HUMAN	HS90B_HUMAN	ACTG_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z4F6_HUMAN	HS90B_HUMAN	CH60_HUMAN	########	0	0	38	95	60,0833	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z5E7_HUMAN	HS90B_HUMAN	CH60_HUMAN	########	0	0	38	87	57,4978	0	1	0	-	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS74L_HUMAN	HS90B_HUMAN	HS105_HUMAN	########	0	0	38	60	47,7493	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase	molecular	intact
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DGL0_HUMAN	HS90B_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase	in vitro	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DMA2_HUMAN	HS90B_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase	in vitro	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	HS90A_HUMAN	HS90B_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase	in vitro	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	A8K2X8_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-66	4,47E-92	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	A8K3C3_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-68	3,16E-93	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	A8K402_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-73	1,41E-95	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DDU6_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	8,00E-66	8,94E-92	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DEM7_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-61	1,00E-89	38	31	34,322	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DX08_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-65	1,41E-91	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B4DXI1_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-54	3,16E-86	38	30	33,7639	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B5BTY7_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	5,00E-74	7,07E-96	38	35	36,4692	0	1	0	-	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence (multiple names can appear if the proteins share the same sequence)	Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)	Query-template blast E-value	Predicted partner-template blast E-value	Joint e-value	Query-template identities	Predicted partner-template identities	Joint identities	Pfam domain-domain interactions found (0: false, 1: true)	Sharing GO terms found (0: false, 1: true)	Interaction found directly in database. (0: false, 1: true)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z243_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-66	4,47E-92	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B7Z7K4_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-66	3,16E-92	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	B8ZZC9_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	5,00E-64	7,07E-91	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	Q2TU64_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	3,00E-73	1,73E-95	38	33	35,4119	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	Q53HU0_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-61	1,00E-89	38	31	34,322	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	Q53HV2_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-78	3,16E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TCPG_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	4,00E-74	6,32E-96	38	33	35,4119	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TCPG_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	4,00E-63	2,00E-90	38	31	34,322	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	Q6IBT3_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	5,00E-79	2,24E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TCPB_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	4,00E-74	6,32E-96	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TCPD_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	8,00E-69	2,83E-93	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ7|HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATC	TCPH_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-79	1,41E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618	PGK2_HUMAN	KPYM_HUMAN	PGK1_HUMAN	3,00E-73	0	0	36	87	55,9643	0	1	0	-	in vivo	hprd
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618	PGK1_HUMAN	KPYM_HUMAN	PGK1_HUMAN	3,00E-73	0	0	36	100	60	0	1	0	-	in vivo	hprd
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618	B4DRT3_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	91	57,2364	1	1	0	PK:PK_C	in vitro	hprd
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618	KPYR_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	71	50,5569	1	1	0	PK:PK_C	in vitro	hprd
sp|P9WKE5|KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618	KPYM_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	100	60	1	1	0	PK:PK_C	in vitro	hprd
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (stra	A8K455_HUMAN	METK1_HUMAN	METK1_HUMAN	########	0	0	54	99	73,1163	1	1	0	S-AdoMet	inferred by	intact
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (stra	A8K455_HUMAN	METK1_HUMAN	METK1_HUMAN	########	0	0	54	99	73,1163	1	1	0	S-AdoMet	inferred by	intact
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (stra	METK2_HUMAN	METK1_HUMAN	METK1_HUMAN	########	0	0	54	84	67,3498	1	1	0	S-AdoMet	inferred by	intact
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (stra	METK2_HUMAN	METK1_HUMAN	METK1_HUMAN	########	0	0	54	84	67,3498	1	1	0	S-AdoMet	inferred by	intact
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (stra	METK1_HUMAN	METK1_HUMAN	METK1_HUMAN	########	0	0	54	100	73,4847	1	1	0	S-AdoMet	inferred by	intact
sp|P9WGV1|METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (stra	METK1_HUMAN	METK1_HUMAN	METK1_HUMAN	########	0	0	54	100	73,4847	1	1	0	S-AdoMet	inferred by	intact
sp|P9WHU7|P5CR_MYCTU Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (st	P5CR2_HUMAN	P5CR3_HUMAN	P5CR3_HUMAN	3,00E-28	3,00E-54	3,00E-41	31	46	37,7624	1	1	0	-	two hybrid	hprd
sp|P9WHN3|PURA_MYCTU Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain	B4E1L0_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	78	58,5833	1	1	0	-	in vitro	hprd
sp|P9WHN3|PURA_MYCTU Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain	PURA1_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	100	66,3325	1	1	0	-	in vitro	hprd
sp|P9WGV3|SAHH_MYCTU Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain AT	SAHH_HUMAN	SAHH_HUMAN	SAHH_HUMAN	########	0	0	55	100	74,162	1	1	0	-	in vitro	hprd

#Finished correctly.

Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO molecular function
GO biological process
GO cellular component

JOB ID: a8f1689c20233851980ac74699c7dad4
Results URL: http://sbi.imim.es/BIPS.php?jobID=a8f1689c20233851980ac74699c7dad4

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner

Query protein	Predicted partner
sp|A5U2D9|PGK_MYCTA Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pgk PE=3 SV=1	KPYM_HUMAN
tr|A5U521|A5U521_MYCTA Malate oxidoreductase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=mez PE=3 SV=1	MAOX_HUMAN
sp|A5U0Y6|G6PI_MYCTA Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pgi PE=3 SV=1	B4DE36_HUMAN
sp|A5U0Y6|G6PI_MYCTA Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pgi PE=3 SV=1	B4DVJ0_HUMAN
sp|A5U0Y6|G6PI_MYCTA Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pgi PE=3 SV=1	G6PI_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A0SD91_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A1DTJ7_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A1DTL0_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A1DTV1_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A1DUU4_HUMAN

Query protein	Predicted partner
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A1DV22_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A3RM82_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A4ZLD6_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A4ZLI8_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A4ZLS9_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A4ZMF9_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A4ZMW5_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6YW19_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6YWQ1_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6YX95_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6YZY0_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6Z2T0_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6Z460_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6Z708_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6Z809_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6Z8G5_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6Z8Z7_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6Z9Q7_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6Z9S0_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6ZB50_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6ZBW0_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6ZC77_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6ZDK7_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A6ZFQ8_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A7LDP6_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A7LFE4_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A7XTZ1_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A8JLT5_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	A8WFB7_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B0EWB5_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B0Z6N9_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B0Z745_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B0Z7E9_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B1NVE6_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B1W6U0_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B1W7S8_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2CB40_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2CB92_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2KLD8_HUMAN

Query protein	Predicted partner
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2WRF9_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2XEK5_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2XEN1_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2XFT2_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2XGB4_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2XMF0_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2XNQ1_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2XNX9_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2YAW2_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2Z5S5_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2Z642_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B2ZNN0_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B3DE35_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	B3VEA5_HUMAN
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	Q8WCW3_HUMAN
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tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	Q9B2U8_HUMAN
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	COX2_YEAST
tr|A5U757|A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	COX2_HUMAN
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sp|A5U315|ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=argG PE=3 SV=1	A8KAP9_HUMAN
sp|A5U315|ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=argG PE=3 SV=1	ASSY_HUMAN
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpG PE=3 SV=1	B4DY56_HUMAN
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpG PE=3 SV=1	ATPA_HUMAN
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpG PE=3 SV=1	ATPB_HUMAN
sp|A5U208|ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpG PE=3 SV=1	ATPD_HUMAN
tr|A5U6S1|A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ffh PE=3 SV=1	B4DDS7_HUMAN
tr|A5U6S1|A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ffh PE=3 SV=1	SRP54_HUMAN
tr|A5U6S1|A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ffh PE=3 SV=1	SRP19_HUMAN
sp|A5U090|RL2_MYCTA 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=rplB PE=3 SV=1	RL6_HUMAN
sp|A5U090|RL2_MYCTA 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=rplB PE=3 SV=1	RL30_HUMAN
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	HSP7C_HUMAN
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	HSP71_HUMAN
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	ACTB_HUMAN
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	TBB2C_HUMAN
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	CH60_HUMAN
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	ENPL_HUMAN
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	HS90B_HUMAN
sp|A5TZ77|DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	HS90A_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	A8K9K1_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	A8MYK9_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	AT2C1_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	B7ZA13_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	AT2C2_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	Q7Z6E5_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	AT2A1_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	AT2A3_HUMAN
tr|A5U422|A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	AT2A2_HUMAN
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpA PE=3 SV=1	ATPG_HUMAN
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpA PE=3 SV=1	ATPB_HUMAN

Query protein	Predicted partner
sp|A5U207|ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpA PE=3 SV=1	ATPD_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	HSP7C_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	HSP71_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	HSP7C_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	HSP71_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	ACTB_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	SMAD3_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	TBB2C_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	Q9UNM1_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	CH10_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	Q9UNM1_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	CH10_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B7Z4F6_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B7Z5E7_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	CH60_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B7Z4F6_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B7Z5E7_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B4DGL0_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B4DMA2_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	ENPL_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	HS90B_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	HS90A_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B4DGL0_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B4DMA2_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	HS90A_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	A1JUI8_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	A8K2X8_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	A8K3C3_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B2R9K8_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B4DDU6_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B4DPJ8_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B4DX08_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	Q59ET3_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	TCPD_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	TCPW_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	TCPZ_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	A1JUI8_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	A8K2X8_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	A8K3C3_HUMAN

Query protein	Predicted partner
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B2R9K8_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B4DDU6_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B4DPJ8_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B4DX08_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	Q59ET3_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	TCPD_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	TCPW_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	TCPZ_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	B4DR68_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	Q53FS6_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	Q53G55_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	Q59EK6_HUMAN
sp|A5TZG6|CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	Q9BV61_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	B4DR68_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	Q53FS6_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	Q53G55_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	Q59EK6_HUMAN
sp|A5U892|CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	Q9BV61_HUMAN
sp|A5U630|DCUP_MYCTA Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=hemE PE=3 SV=1	Q53ZP6_HUMAN
sp|A5U630|DCUP_MYCTA Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=hemE PE=3 SV=1	DCUP_HUMAN
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=lpd PE=3 SV=1	B2R5P6_HUMAN
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=lpd PE=3 SV=1	B4DMK9_HUMAN
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=lpd PE=3 SV=1	B4DT69_HUMAN
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=lpd PE=3 SV=1	B7Z2S5_HUMAN
tr|A5TZI9|A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=lpd PE=3 SV=1	E2QRB9_HUMAN
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=gap PE=3 SV=1	Q2TSD0_HUMAN
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=gap PE=3 SV=1	G3PT_HUMAN
tr|A5U2D8|A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=gap PE=3 SV=1	G3P_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	PPIA_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	HSP7C_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	HSP71_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	ACTB_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	TBB2C_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	AIPL1_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B7Z4F6_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B7Z5E7_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	CRYAB_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	A8K4T2_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	Q59EH7_HUMAN

Query protein	Predicted partner
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	DNJC7_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B4DGL0_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B4DMA2_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	HS90A_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	HS74L_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	A1JUI8_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	A8K2X8_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	A8K3C3_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B2R9K8_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B4DDU6_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B4DPJ8_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B4DX08_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	Q59ET3_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	TCPD_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	TCPW_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	TCPZ_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	A8K402_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B4DEM7_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B4DXI1_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B5BTY7_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B7Z243_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B7Z7K4_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	B8ZZC9_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	Q2TU64_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	Q53HU0_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	Q53HV2_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	TCPG_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	TCPG_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	Q6IBT3_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	TCPB_HUMAN
sp|A5U4Y2|HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	TCPH_HUMAN
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3 SV=1	PGK2_HUMAN
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3 SV=1	PGK1_HUMAN
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3 SV=1	B4DRT3_HUMAN
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3 SV=1	KPYR_HUMAN
tr|A5U2X3|A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3 SV=1	KPYM_HUMAN
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=metK PE=3 SV=1	A8K455_HUMAN
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=metK PE=3 SV=1	METK2_HUMAN
sp|A5U294|METK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=metK PE=3 SV=1	METK1_HUMAN

Query protein	Predicted partner
tr|A5TZM9|A5TZM9_MYCTA Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=proC PE=3 SV=1	P5CR2_HUMAN
sp|A5TZ84|PURA_MYCTA Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=purA PE=3 SV=1	B4E1L0_HUMAN
sp|A5TZ84|PURA_MYCTA Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=purA PE=3 SV=1	PURA1_HUMAN
sp|A5U7S2|SAHH_MYCTA Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ahcY PE=3 SV=1	SAHH_HUMAN
#Finished correctly	

Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO molecular function
GO biological process
GO cellular component

JOB ID: e9326d3da362e33dc7a016e01eb8427b
Results URL: http://sbi.imim.es/BIPS.php?jobID=e9326d3da362e33dc7a016e01eb8427b

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner

Query protein	Predicted partner
sp|P9WID0|PGK_MYCTO Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pgk PE=3 SV=1	KPYM_HUMAN
sp|P9WK24|MAOX_MYCTO Putative malate oxidoreductase [NAD] OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=mez PE=3 SV=1	MAOX_HUMAN
sp|P9WN68|G6PI_MYCTO Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pgi PE=3 SV=1	B4DE36_HUMAN
sp|P9WN68|G6PI_MYCTO Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pgi PE=3 SV=1	B4DVJ0_HUMAN
sp|P9WN68|G6PI_MYCTO Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pgi PE=3 SV=1	G6PI_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A0SD91_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A1DTJ7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A1DTL0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A1DTV1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A1DUU4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A1DV22_HUMAN

Query protein	Predicted partner
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A3RM82_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A4ZLD6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A4ZLI8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A4ZLS9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A4ZMF9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A4ZMW5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6YW19_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6YWQ1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6YX95_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6YZY0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6Z2T0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6Z460_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6Z708_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6Z809_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6Z8G5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6Z8Z7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6Z9Q7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6Z9S0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6ZB50_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6ZBW0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6ZC77_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6ZDK7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A6ZFQ8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A7LDP6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A7LFE4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A7XTZ1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A8JLT5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	A8WFB7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B0EWB5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B0Z6N9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B0Z745_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B0Z7E9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B1NVE6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B1W6U0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B1W7S8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2CB40_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2CB92_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2KLD8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2WRF9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2XEK5_HUMAN

Query protein	Predicted partner
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2XEN1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2XFT2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2XGB4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2XMF0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2XNQ1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2XNX9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2YAW2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2Z5S5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2Z642_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B2ZNN0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B3DE35_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B3VEA5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B4YBC2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B4YCG0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B4YGV7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B5M8C0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B7TMW4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B8RFL3_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B8X4N0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B8XZS7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B9ECT2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B9EE11_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B9EEE1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B9EEI0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	B9EF90_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C4PK82_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C4RU97_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C5MM24_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C7B321_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C7B3W9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C7SJU6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C7SKT4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C8XZH6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C8Y3W0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C8Y5S3_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C8YGY6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C9D5W0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D0V1V1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D1GI28_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D3K5V4_HUMAN

Query protein	Predicted partner
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D6BZS8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D6C3F2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D6N462_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D6N765_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D7NV03_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D7P622_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D7P661_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E0Y4D8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E1B320_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E2FQB7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E2J0C2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5DY67_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5DYD2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5E0U0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5E1D5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5E1I7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5EY89_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5LFL6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0G899_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0VXC5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0Z7D5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0Z7G1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0ZFF5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q15H46_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q15HG3_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q15II8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q15IP0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q19MP4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q27H55_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q2HJS3_HUMAN
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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Query protein	Predicted partner
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sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C5H6M5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C5H6M7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C5H6M8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C8XWJ6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C8Y3G4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C8Y3Q5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C8YBL1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	C9D661_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D1G421_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D2IKF4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D2K1G3_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D3YPT7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D5M8T1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	D7NUN3_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E0AF97_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E2DTL8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E2JFC4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E2JJS5_HUMAN
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sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5E079_HUMAN
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sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	E5FWC0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q06TE6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q09U41_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0Z7D8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0Z7F1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0Z7J0_HUMAN
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sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q0Z7S0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q15HH9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q19MP7_HUMAN

Query protein	Predicted partner
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q305H0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4EYL1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4EZD4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4F4V6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4F6A2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4GCC3_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4GCG2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4GCZ4_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4GHE1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4GQP0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4GVP5_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q4GW12_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q5S971_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q5SA98_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q5SAP1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q5SB08_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q5XRW8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q6R0V6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q6RKW8_HUMAN
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sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q6RQ80_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q6VIG7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q6VJD8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q6VJJ3_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q7Y626_HUMAN
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sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q7Y6N0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q7YCE6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q7YEH2_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q85KS0_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q8HNR1_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q8HNR6_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q8HQB7_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q8WCW3_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q9B138_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q9B1F9_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Q9B2U8_HUMAN
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	COX2_YEAST
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	COX2_HUMAN
sp|P9WK12|MDH_MYCTO Malate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=mdh PE=3 SV=1	MDHC_HUMAN

Query protein	Predicted partner
sp|P9WPW6|ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=argG PE=3 SV=1	A8KAP9_HUMAN
sp|P9WPW6|ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=argG PE=3 SV=1	ASSY_HUMAN
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpG PE=3 SV=1	B4DY56_HUMAN
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpG PE=3 SV=1	ATPA_HUMAN
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpG PE=3 SV=1	ATPB_HUMAN
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpG PE=3 SV=1	ATPD_HUMAN
sp|P9WGD6|SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ffh PE=3 SV=1	B4DDS7_HUMAN
sp|P9WGD6|SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ffh PE=3 SV=1	SRP54_HUMAN
sp|P9WGD6|SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ffh PE=3 SV=1	SRP19_HUMAN
sp|P9WHA4|RL2_MYCTO 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=rplB PE=3 SV=1	RL6_HUMAN
sp|P9WHA4|RL2_MYCTO 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=rplB PE=3 SV=1	RL30_HUMAN
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	HSP7C_HUMAN
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	HSP71_HUMAN
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	ACTB_HUMAN
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	TBB2C_HUMAN
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	CH60_HUMAN
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	ENPL_HUMAN
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	HS90B_HUMAN
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	HS90A_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	A8K9K1_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	A8MYK9_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	AT2C1_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	B7ZA13_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	AT2C2_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	Q7Z6E5_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	AT2A1_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	AT2A3_HUMAN
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	AT2A2_HUMAN
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpA PE=3 SV=1	ATPG_HUMAN
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpA PE=3 SV=1	ATPB_HUMAN
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpA PE=3 SV=1	ATPD_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	HSP7C_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	HSP71_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	HSP7C_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	HSP71_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	ACTB_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	SMAD3_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	TBB2C_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	Q9UNM1_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	CH10_HUMAN

Query protein	Predicted partner
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	Q9UNM1_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	CH10_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B7Z4F6_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B7Z5E7_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	CH60_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B7Z4F6_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B7Z5E7_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B4DGL0_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B4DMA2_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	ENPL_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	HS90B_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	HS90A_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B4DGL0_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B4DMA2_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	HS90A_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	A1JUI8_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	A8K2X8_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	A8K3C3_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B2R9K8_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B4DDU6_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B4DPJ8_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B4DX08_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	Q59ET3_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	TCPD_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	TCPW_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	TCPZ_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	A1JUI8_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	A8K2X8_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	A8K3C3_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B2R9K8_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B4DDU6_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B4DPJ8_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B4DX08_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	Q59ET3_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	TCPD_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	TCPW_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	TCPZ_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	B4DR68_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	Q53FS6_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	Q53G55_HUMAN

Query protein	Predicted partner
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	Q59EK6_HUMAN
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	Q9BV61_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	B4DR68_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	Q53FS6_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	Q53G55_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	Q59EK6_HUMAN
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	Q9BV61_HUMAN
sp|P9WFE0|DCUP_MYCTO Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=hemE PE=3 SV=1	Q53ZP6_HUMAN
sp|P9WFE0|DCUP_MYCTO Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=hemE PE=3 SV=1	DCUP_HUMAN
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=lpdC PE=3 SV=1	B2R5P6_HUMAN
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=lpdC PE=3 SV=1	B4DMK9_HUMAN
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=lpdC PE=3 SV=1	B4DT69_HUMAN
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=lpdC PE=3 SV=1	B7Z2S5_HUMAN
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=lpdC PE=3 SV=1	E2QRB9_HUMAN
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=gap PE=3 SV=1	Q2TSD0_HUMAN
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=gap PE=3 SV=1	G3PT_HUMAN
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=gap PE=3 SV=1	G3P_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	PPIA_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	HSP7C_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	HSP71_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	ACTB_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	TBB2C_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	AIPL1_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B7Z4F6_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B7Z5E7_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	CRYAB_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	A8K4T2_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	Q59EH7_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	DNJC7_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B4DGL0_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B4DMA2_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	HS90A_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	HS74L_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	A1JUI8_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	A8K2X8_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	A8K3C3_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B2R9K8_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B4DDU6_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B4DPJ8_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B4DX08_HUMAN

Query protein	Predicted partner
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	Q59ET3_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	TCPD_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	TCPW_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	TCPZ_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	A8K402_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B4DEM7_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B4DXI1_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B5BTY7_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B7Z243_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B7Z7K4_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	B8ZZC9_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	Q2TU64_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	Q53HU0_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	Q53HV2_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	TCPG_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	TCPG_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	Q6IBT3_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	TCPB_HUMAN
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	TCPH_HUMAN
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 SV=1	PGK2_HUMAN
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 SV=1	PGK1_HUMAN
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 SV=1	B4DRT3_HUMAN
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 SV=1	KPYR_HUMAN
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 SV=1	KPYM_HUMAN
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=metK PE=3 SV=1	A8K455_HUMAN
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=metK PE=3 SV=1	METK2_HUMAN
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=metK PE=3 SV=1	METK1_HUMAN
sp|P9WHU6|P5CR_MYCTO Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=proC PE=3 SV=1	P5CR2_HUMAN
sp|P9WHN2|PURA_MYCTO Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=purA PE=3 SV=1	B4E1L0_HUMAN
sp|P9WHN2|PURA_MYCTO Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=purA PE=3 SV=1	PURA1_HUMAN
sp|P9WGV2|SAHH_MYCTO Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ahcY PE=3 SV=1	SAHH_HUMAN

#Finished correctly

Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO molecular function
GO biological process
GO cellular component

JOB ID: e9326d3da362e33dc7a016e01eb8427b
Results URL: http://sbi.imim.es/BIPS.php?jobID=e9326d3da362e33dc7a016e01eb8427b

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner
3: Query homolog sequence (multiple names can appear if the proteins share the same sequence)
4: Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)
5: Query-Template Blast E-value
6: Predicted partner-Template Blast E-value
7: Joint e-value
8: Query-Template identities
9: Predicted partner-Template identities
10: Joint identities
11: Pfam domain-domain interactions found (0: False, 1: True)
12: Sharing GO terms found (0: False, 1: True)
13: Interaction found directly in database. (0: False, 1: True)
14: Interacting Pfam domains
15: Template interaction detection method
16: Template interaction source database

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WID0|PGK_MYCTO Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pgk	KPYM_HUMAN	PGK1_HUMAN	KPYM_HUMAN	4,00E-68	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WK24|MAOX_MYCTO Putative malate oxidoreductase [NAD] OS=Mycobacterium tuberculosis (strain CDC 1551 / C	MAOX_HUMAN	MAOM_HUMAN	MAOM_HUMAN	5,00E-91	0	0	36	55	44,4972	1	1	0	malic:Mali	in vitro	hprd
sp|P9WN68|G6PI_MYCTO Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh	B4DE36_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
sp|P9WN68|G6PI_MYCTO Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh	B4DVJ0_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	89	61,8628	1	1	0	-	in vitro	hprd
sp|P9WN68|G6PI_MYCTO Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh	G6PI_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	100	65,5744	0	1	0	-	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A0SD91_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A1DTJ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A1DTL0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A1DTV1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A1DUU4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A1DV22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A3RM82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A4ZLD6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A4ZLI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A4ZLS9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A4ZMF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A4ZMW5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6YW19_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6YWQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6YX95_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6YZY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z2T0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z460_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z708_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z809_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z8G5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z8Z7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z9Q7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z9S0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZB50_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZBW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZC77_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZDK7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZFQ8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A7LDP6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A7LFE4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A7XTZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A8JLT5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A8WFB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B0EWB5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B0Z6N9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B0Z745_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B0Z7E9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B1NVE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B1W6U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B1W7S8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2CB40_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-109	7,07E-103	42	90	61,4817	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2CB92_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-111	7,07E-104	42	91	61,8223	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2KLD8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2WRF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XEK5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XEN1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XFT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XGB4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XMF0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XNQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XNX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2YAW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2Z5S5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2Z642_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2ZNN0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B3DE35_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B3VEA5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B4YBC2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B4YCG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B4YGV7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B5M8C0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B7TMW4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B8RFL3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B8X4N0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B8XZS7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B9ECT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B9EE11_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B9EEE1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B9EEI0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B9EF90_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C4PK82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C4RU97_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5MM24_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C7B321_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C7B3W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-111	7,07E-104	42	96	63,498	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C7SJU6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C7SKT4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C8XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C8Y3W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C8Y5S3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C8YGY6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C9D5W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D0V1V1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D1GI28_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D3K5V4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D6BZS8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D6C3F2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D6N462_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D6N765_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D7NV03_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D7P622_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D7P661_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E0Y4D8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E1B320_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E2FQB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E2J0C2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5DY67_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5DYD2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5E0U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5E1D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5E1I7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5EY89_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5LFL6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0G899_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0VXC5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0Z7D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0Z7G1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0ZFF5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q15H46_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q15HG3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q15II8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q15IP0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q19MP4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q27H55_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q2HJS3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q2HKH0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q2HKI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q2HKT7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q305I0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q305K6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q305X3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q3S961_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4EWP5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4EXJ4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4EZD1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4F0P9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4F0T8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4F1I5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4F2A8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4F2U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4G6P4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4G6V9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4G7C8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4G9U9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GBF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GC16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GFE9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GG20_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GI22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GIA0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GIY4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GMA4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GPI4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GPN6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GSY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GU59_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GV60_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4VFD0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4ZEA6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4ZED2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4ZEF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4ZF68_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5SAG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5SB31_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XSC1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZI2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZI9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZK9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZL8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZP7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZR9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZT6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XZY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y011_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y065_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y070_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y078_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y0E5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y0F3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y0G2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y0H4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5Y0J7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6R0Q1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6R0W6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6RLY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6RMU0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6RPE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6RRW7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VH99_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VHA9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VIB9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VIH5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VIM0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VJ16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VK16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VKA3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VLN4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6WQA1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6WQG6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7Y664_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7YCC7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7YCE0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7YCE5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7YCF3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7YEF1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q85KW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q85KW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q85KZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q85L04_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q85L10_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q8HNQ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q8WCY1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q9B1S4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q9B1S6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q9B2U6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q9B2W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q9B2X0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	COX3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A0S0W7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A0S2P1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A0S3T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A0SA07_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A1Z455_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A1Z4V2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A4ZKZ0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6YW54_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6YWD1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6YXV0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z3M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6Z6E8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZEU4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZF47_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZFK3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A6ZHA9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A7LDC6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A7LF11_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	A7LFA2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B0Z6W4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B1W855_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2CB37_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-107	7,07E-102	42	95	63,1664	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2WRY8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XHF9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XHT9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XIR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XL43_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XP28_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B2XPS3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B3DE06_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B3GUF3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	B5M7M0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6K5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-109	7,07E-103	42	96	63,498	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6K6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6K7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6L3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6M4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6M7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C5H6M8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C8XWJ6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C8Y3G4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C8Y3Q5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C8YBL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	C9D661_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D1G421_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D2IKF4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D2K1G3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D3YPT7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D5M8T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	D7NUN3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E0AF97_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E2DTL8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E2JFC4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E2JJS5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5DZN4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5E079_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5E1A6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5E1V1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5EWG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5EWL4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5EWR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	E5FWC0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q06TE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q09U41_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0Z7D8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0Z7F1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0Z7J0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0Z7K3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	98	64,1561	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q0Z7S0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q15HH9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q19MP7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q305H0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4EYL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4EZD4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4F4V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4F6A2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GCC3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GCG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GCZ4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GHE1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GQP0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GVP5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q4GW12_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5S971_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5SA98_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5SAP1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5SB08_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q5XRW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6R0V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6RKW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6RNN7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6RQ80_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VIG7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VJD8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q6VJJ3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7Y626_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7Y6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7Y6N0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7YCE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q7YEH2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q85KS0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q8HNR1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q8HNR6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q8HQB7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q8WCW3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q9B138_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q9B1F9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	Q9B2U8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	COX2_YEAST	COX1_HUMAN	COX2_HUMAN	5,00E-96	3,00E-47	1,22E-71	42	42	42	1	1	0	COX1:COX	in vivo	hprd
sp|P9WP70|COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 /	COX2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:COX	in vivo	hprd
sp|P9WK12|MDH_MYCTO Malate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=md	MDHC_HUMAN	MDHC_HUMAN	MDHC_HUMAN	3,00E-88	0	0	51	100	71,4143	1	1	0	Ldh_1_C:L	in vitro	hprd
sp|P9WPW6|ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	intact
sp|P9WPW6|ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	biogrid
sp|P9WPW6|ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	hprd
sp|P9WPW6|ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	intact
sp|P9WPW6|ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	biogrid
sp|P9WPW6|ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	hprd
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	blue native	intact
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	blue native	intact
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	in vitro	hprd
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	in vitro	hprd
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	in vitro	hprd
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|P9WPU8|ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
sp|P9WGD6|SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshk	B4DDS7_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54_N:S	x-ray cryst	biogrid
sp|P9WGD6|SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshk	B4DDS7_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54_N:S	in vitro	hprd
sp|P9WGD6|SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshk	SRP54_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54:SRP	x-ray cryst	biogrid
sp|P9WGD6|SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshk	SRP54_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54:SRP	in vitro	hprd
sp|P9WGD6|SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshk	SRP19_HUMAN	SRP54_HUMAN	SRP19_HUMAN	2,00E-57	0	0	30	100	54,7723	0	1	0	-	in vitro	hprd
sp|P9WHA4|RL2_MYCTO 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=rpl	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|P9WHA4|RL2_MYCTO 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=rpl	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|P9WHA4|RL2_MYCTO 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=rpl	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|P9WHA4|RL2_MYCTO 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=rpl	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP7C_HUMAN	GRP78_HUMAN	HSP71_HUMAN	1,00E-148	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP7C_HUMAN	GRP78_HUMAN	HSP71_HUMAN	1,00E-148	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP71_HUMAN	GRP78_HUMAN	HSP71_HUMAN	1,00E-148	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP71_HUMAN	GRP78_HUMAN	HSP71_HUMAN	1,00E-148	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in databas. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	TBB2C_HUMAN	GRP78_HUMAN	TBB5_HUMAN	1,00E-148	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP71_HUMAN	GRP78_HUMAN	HSP7C_HUMAN	1,00E-148	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP7C_HUMAN	GRP78_HUMAN	HSP7C_HUMAN	1,00E-148	0	0	49	100	70	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ACTH_HUMAN	GRP78_HUMAN	ACTH_HUMAN	1,00E-148	0	0	49	93	67,5056	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	1,00E-148	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ACTB_HUMAN	GRP78_HUMAN	ACTG_HUMAN	1,00E-148	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	TBB2C_HUMAN	GRP78_HUMAN	TBB4_HUMAN	1,00E-148	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	CH60_HUMAN	GRP78_HUMAN	CH60_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ENPL_HUMAN	GRP78_HUMAN	ENPL_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP71_HUMAN	GRP78_HUMAN	HS71L_HUMAN	1,00E-148	0	0	49	89	66,0379	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP7C_HUMAN	GRP78_HUMAN	HS71L_HUMAN	1,00E-148	0	0	49	82	63,3877	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ENPL_HUMAN	GRP78_HUMAN	HS90A_HUMAN	1,00E-148	1,00E-151	3,16E-150	49	46	47,4763	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HS90B_HUMAN	GRP78_HUMAN	HS90A_HUMAN	1,00E-148	0	0	49	85	64,5368	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HS90A_HUMAN	GRP78_HUMAN	HS90A_HUMAN	1,00E-148	0	0	49	100	70	0	1	0	-	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	A8K9K1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	77	49,6387	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	A8MYK9_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	76	49,3153	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	AT2C1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	1,00E-129	3,16E-126	32	34	32,9848	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	B7ZA13_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	1,00E-117	3,16E-120	32	32	32	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	AT2C2_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	1,00E-114	1,00E-118	32	31	31,496	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	Q7Z6E5_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	84	51,8459	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	AT2A1_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	84	51,8459	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	AT2A3_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	76	49,3153	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Os	AT2A2_HUMAN	AT2A2_HUMAN	AT2A2_HUMAN	1,00E-122	0	0	32	100	56,5685	1	1	0	Cation_AT	in vivo	hprd
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	blue nativ	intact
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	blue nativ	intact
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	in vitro	hprd
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	blue nativ	intact
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_	blue nativ	intact
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	1,00E-157	0	0	54	100	73,4847	0	1	0	-	blue nativ	intact
sp|P9WPU6|ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	1,00E-157	0	0	54	100	73,4847	0	1	0	-	blue nativ	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-105	0	0	41	86	59,3801	0	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-105	0	0	41	86	59,3801	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	SMAD3_HUMAN	CH60_HUMAN	SMAD2_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	display tec	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	TBB2C_HUMAN	CH60_HUMAN	TBB5_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-105	0	0	41	86	59,3801	0	1	0	-	molecular	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	TBB2C_HUMAN	CH60_HUMAN	TBA1A_HUMAN	1,00E-119	2,00E-99	1,41E-109	46	40	42,8952	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ACTB_HUMAN	CH60_HUMAN	ACTH_HUMAN	1,00E-119	0	0	46	93	65,4064	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ACTB_HUMAN	CH60_HUMAN	ACTG_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	cross-linki	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	biochemic	biogrid
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	cross-linki	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	biochemic	biogrid

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TC	two hybrid	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	cross-linki	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	biochemic	biogrid
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	cross-linki	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	biochemic	biogrid
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	biogrid
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	Cpn60_TC	two hybrid	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-119	0	0	46	64	54,2586	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-119	0	0	46	65	54,6809	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-105	0	0	41	64	51,225	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-105	0	0	41	65	51,6236	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	95	66,106	1	1	0	-	in vitro	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	87	63,2614	0	1	0	-	in vitro	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	CH60_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	-	in vitro	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-105	0	0	41	95	62,4099	1	1	0	-	in vitro	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-105	0	0	41	87	59,7244	0	1	0	-	in vitro	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	83	58,3352	0	1	0	-	molecular	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	83	58,3352	0	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	83	58,3352	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	80	57,2713	0	1	0	-	molecular	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	80	57,2713	0	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	80	57,2713	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	molecular	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-105	0	0	41	100	64,0312	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	94	65,7571	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	ENPL_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	1,00E-156	3,16E-138	46	48	46,9894	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90B_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-105	0	0	41	98	63,3877	0	1	0	-	molecular	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-105	0	0	41	94	62,0806	0	1	0	-	molecular	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-105	0	0	41	86	59,3801	0	1	0	-	molecular	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	1,00E-60	3,16E-90	46	31	37,7624	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	1,00E-59	1,00E-89	46	31	37,7624	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-58	7,07E-89	46	30	37,1484	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	85	62,53	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	1,00E-60	3,16E-83	41	31	35,6511	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	5,00E-57	2,24E-81	41	30	35,0714	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	1,00E-59	1,00E-82	41	31	35,6511	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	5,00E-58	7,07E-82	41	30	35,0714	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	99	63,7103	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	5,00E-57	2,24E-81	41	30	35,0714	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	85	59,0339	1	1	0	-	surface pla	intact
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-105	0	0	41	100	64,0312	1	1	0	-	surface pla	intact
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	92	65,0538	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|P9WPE6|CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	92	61,4166	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|P9WPE8|CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groE	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-105	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
sp|P9WFE0|DCUP_MYCTO Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkos	Q53ZP6_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	99	60,5227	0	1	0	-	x-ray cryst	biogrid
sp|P9WFE0|DCUP_MYCTO Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkos	Q53ZP6_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	99	60,5227	0	1	0	-	in vitro	hprd
sp|P9WFE0|DCUP_MYCTO Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkos	DCUP_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	100	60,8276	0	1	0	-	x-ray cryst	biogrid
sp|P9WFE0|DCUP_MYCTO Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkos	DCUP_HUMAN	DCUP_HUMAN	DCUP_HUMAN	3,00E-53	0	0	37	100	60,8276	0	1	0	-	in vitro	hprd
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B2R5P6_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B2R5P6_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B4DMK9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	95	57,6628	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B4DMK9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	95	57,6628	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B4DT69_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	90	56,1249	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B4DT69_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	90	56,1249	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B7Z2S5_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B7Z2S5_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	E2QRB9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	4,00E-47	1,55E-59	35	30	32,4037	1	1	0	Pyr_redox	x-ray cryst	intact
sp|P9WHH8|DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	E2QRB9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	4,00E-47	1,55E-59	35	30	32,4037	1	1	0	Pyr_redox	in vivo	hprd
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 155	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:	fluorescen	mint
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 155	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:	in vitro	hprd
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 155	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	1,00E-134	2,45E-107	50	68	58,3095	1	1	0	Gp_dh_N:	fluorescen	mint
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 155	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	1,00E-134	2,45E-107	50	68	58,3095	1	1	0	Gp_dh_N:	in vitro	hprd
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 155	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_C:	fluorescen	mint
sp|P9WN82|G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 155	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_C:	in vitro	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=c	HSP7C_HUMAN	GRP75_HUMAN	HSP71_HUMAN	1,00E-166	0	0	54	86	68,1469	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=c	HSP7C_HUMAN	GRP75_HUMAN	HSP71_HUMAN	1,00E-166	0	0	54	86	68,1469	1	1	0	-	in vitro	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=c	HSP71_HUMAN	GRP75_HUMAN	HSP71_HUMAN	1,00E-166	0	0	54	100	73,4847	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=c	HSP71_HUMAN	GRP75_HUMAN	HSP71_HUMAN	1,00E-166	0	0	54	100	73,4847	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=c	ACTB_HUMAN	GRP75_HUMAN	ACTB_HUMAN	1,00E-166	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=c	ACTB_HUMAN	GRP75_HUMAN	ACTH_HUMAN	1,00E-166	0	0	54	93	70,8661	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=c	ACTB_HUMAN	GRP75_HUMAN	ACTB_HUMAN	1,00E-166	0	0	54	98	72,7461	0	1	0	-	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ACTB_HUMAN	GRP75_HUMAN	ACTG_HUMAN	1,00E-166	0	0	54	98	72,7461	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP71_HUMAN	GRP75_HUMAN	GRP78_HUMAN	1,00E-166	0	0	54	64	58,7878	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP71_HUMAN	GRP75_HUMAN	GRP78_HUMAN	1,00E-166	0	0	54	64	58,7878	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP7C_HUMAN	GRP75_HUMAN	GRP78_HUMAN	1,00E-166	0	0	54	65	59,2453	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HSP7C_HUMAN	GRP75_HUMAN	GRP78_HUMAN	1,00E-166	0	0	54	65	59,2453	1	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	CH60_HUMAN	GRP75_HUMAN	CH60_HUMAN	1,00E-166	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ENPL_HUMAN	GRP75_HUMAN	ENPL_HUMAN	1,00E-166	0	0	54	100	73,4847	0	1	0	-	in vitro	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	ENPL_HUMAN	GRP75_HUMAN	HS90A_HUMAN	1,00E-166	1,00E-151	3,16E-159	54	46	49,8397	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HS90B_HUMAN	GRP75_HUMAN	HS90A_HUMAN	1,00E-166	0	0	54	85	67,7495	0	1	0	-	in vivo	hprd
sp|P9WMJ8|DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=d	HS90A_HUMAN	GRP75_HUMAN	HS90A_HUMAN	1,00E-166	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	PPIA_HUMAN	HS90A_HUMAN	PPIA_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TBB2C_HUMAN	HS90A_HUMAN	TBB5_HUMAN	1,00E-114	0	0	38	98	61,0246	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TBB2C_HUMAN	HS90A_HUMAN	TBB5_HUMAN	1,00E-114	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TBB2C_HUMAN	HS90A_HUMAN	TBA1A_HUMAN	1,00E-114	2,00E-99	4,47E-107	38	40	38,9872	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	ACTB_HUMAN	HS90A_HUMAN	ACTH_HUMAN	1,00E-114	0	0	38	93	59,4475	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	1,00E-114	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	ACTB_HUMAN	HS90A_HUMAN	ACTG_HUMAN	1,00E-114	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90A_HUMAN	GRP78_HUMAN	1,00E-114	0	0	38	64	49,3153	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90A_HUMAN	GRP78_HUMAN	1,00E-114	0	0	38	65	49,6991	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	AIPL1_HUMAN	HS90A_HUMAN	AIP_HUMAN	1,00E-114	1,00E-93	3,16E-104	38	49	43,1509	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	AIPL1_HUMAN	HS90A_HUMAN	AIP_HUMAN	1,00E-114	1,00E-93	3,16E-104	38	49	43,1509	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	95	60,0833	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	95	60,0833	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	95	60,0833	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	87	57,4978	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	87	57,4978	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	1,00E-114	0	0	38	87	57,4978	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	CRYAB_HUMAN	HS90A_HUMAN	CRYAB_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	A8K4T2_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	two hybrid	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	Q59EH7_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	two hybrid	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	DNJC7_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	two hybrid	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	83	56,1605	1	1	0	HATPase_	two hybrid	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	83	56,1605	1	1	0	HATPase_	two hybrid	mint

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	83	56,1605	1	1	0	HATPase_	two hybrid	biogrid
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	83	56,1605	1	1	0	HATPase_	in vitro	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	80	55,1362	1	1	0	HATPase_	two hybrid	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	80	55,1362	1	1	0	HATPase_	two hybrid	mint
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	80	55,1362	1	1	0	HATPase_	two hybrid	biogrid
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	80	55,1362	1	1	0	HATPase_	in vitro	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	100	61,6441	1	1	0	HATPase_	two hybrid	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	100	61,6441	1	1	0	HATPase_	two hybrid	mint
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	100	61,6441	1	1	0	HATPase_	two hybrid	biogrid
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	1,00E-114	0	0	38	100	61,6441	1	1	0	HATPase_	in vitro	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	98	61,0246	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	94	59,7662	1	1	0	HATPase_	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	94	59,7662	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	94	59,7662	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	94	59,7662	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	1,00E-114	0	0	38	86	57,1664	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	1,00E-114	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	1,00E-114	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	1,00E-114	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	A1JUI8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	A8K2X8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	1,00E-60	1,00E-87	38	31	34,322	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	A8K3C3_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	5,00E-57	7,07E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B2R9K8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DDU6_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	1,00E-59	3,16E-87	38	31	34,322	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DPJ8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DX08_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	5,00E-58	2,24E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	Q59ET3_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	99	61,3351	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TCPD_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	5,00E-57	7,07E-86	38	30	33,7639	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TCPW_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	85	56,8331	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TCPZ_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	1,00E-114	0	0	38	100	61,6441	0	1	0	-	surface pla	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90B_HUMAN	HSP71_HUMAN	1,00E-117	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90B_HUMAN	HSP71_HUMAN	1,00E-117	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	ACTB_HUMAN	HS90B_HUMAN	ACTB_HUMAN	1,00E-117	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TBB2C_HUMAN	HS90B_HUMAN	TBB5_HUMAN	1,00E-117	0	0	38	98	61,0246	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP71_HUMAN	HS90B_HUMAN	HSP7C_HUMAN	1,00E-117	0	0	38	86	57,1664	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HSP7C_HUMAN	HS90B_HUMAN	HSP7C_HUMAN	1,00E-117	0	0	38	100	61,6441	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TBB2C_HUMAN	HS90B_HUMAN	TBA1A_HUMAN	1,00E-117	2,00E-99	1,41E-108	38	40	38,9872	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	ACTB_HUMAN	HS90B_HUMAN	ACTG_HUMAN	1,00E-117	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z4F6_HUMAN	HS90B_HUMAN	CH60_HUMAN	1,00E-117	0	0	38	95	60,0833	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z5E7_HUMAN	HS90B_HUMAN	CH60_HUMAN	1,00E-117	0	0	38	87	57,4978	0	1	0	-	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS74L_HUMAN	HS90B_HUMAN	HS105_HUMAN	1,00E-117	0	0	38	60	47,7493	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	83	56,1605	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	80	55,1362	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	molecular	intact
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	1,00E-117	0	0	38	100	61,6441	1	1	0	HATPase_	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DGL0_HUMAN	HS90B_HUMAN	HS90B_HUMAN	1,00E-117	0	0	38	98	61,0246	1	1	0	HATPase_	in vitro	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DMA2_HUMAN	HS90B_HUMAN	HS90B_HUMAN	1,00E-117	0	0	38	94	59,7662	1	1	0	HATPase_	in vitro	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	HS90A_HUMAN	HS90B_HUMAN	HS90B_HUMAN	1,00E-117	0	0	38	86	57,1664	1	1	0	HATPase_	in vitro	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	A8K2X8_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-66	4,47E-92	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	A8K3C3_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-68	3,16E-93	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	A8K402_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-73	1,41E-95	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DDU6_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	8,00E-66	8,94E-92	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DEM7_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-61	1,00E-89	38	31	34,322	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DX08_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-65	1,41E-91	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B4DXI1_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-54	3,16E-86	38	30	33,7639	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B5BTY7_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	5,00E-74	7,07E-96	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z243_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-66	4,47E-92	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B7Z7K4_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-66	3,16E-92	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	B8ZZC9_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	5,00E-64	7,07E-91	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	Q2TU64_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	3,00E-73	1,73E-95	38	33	35,4119	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	Q53HU0_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-61	1,00E-89	38	31	34,322	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	Q53HV2_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	1,00E-78	3,16E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TCPG_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	4,00E-74	6,32E-96	38	33	35,4119	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TCPG_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	4,00E-63	2,00E-90	38	31	34,322	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	Q6IBT3_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	5,00E-79	2,24E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TCPB_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	4,00E-74	6,32E-96	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TCPD_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	8,00E-69	2,83E-93	38	32	34,8712	0	1	0	-	in vivo	hprd
sp|P9WMJ6|HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=h	TCPH_HUMAN	HS90B_HUMAN	TCPA_HUMAN	1,00E-117	2,00E-79	1,41E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 S	PGK2_HUMAN	KPYM_HUMAN	PGK1_HUMAN	3,00E-73	0	0	36	87	55,9643	0	1	0	-	in vivo	hprd
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 S	PGK1_HUMAN	KPYM_HUMAN	PGK1_HUMAN	3,00E-73	0	0	36	100	60	0	1	0	-	in vivo	hprd
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 S	B4DRT3_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	91	57,2364	1	1	0	PK:PK_C P	in vitro	hprd
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 S	KPYR_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	71	50,5569	1	1	0	PK:PK_C P	in vitro	hprd
sp|P9WKE4|KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 S	KPYM_HUMAN	KPYM_HUMAN	KPYM_HUMAN	3,00E-73	0	0	36	100	60	1	1	0	PK:PK_C P	in vitro	hprd
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosl	A8K455_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	99	73,1163	1	1	0	S-AdoMet	inferred b	intact
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosl	A8K455_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	99	73,1163	1	1	0	S-AdoMet	inferred b	intact
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosl	METK2_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	84	67,3498	1	1	0	S-AdoMet	inferred b	intact
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosl	METK2_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	84	67,3498	1	1	0	S-AdoMet	inferred b	intact
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosl	METK1_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	100	73,4847	1	1	0	S-AdoMet	inferred b	intact
sp|P9WGV0|METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosl	METK1_HUMAN	METK1_HUMAN	METK1_HUMAN	1,00E-103	0	0	54	100	73,4847	1	1	0	S-AdoMet	inferred b	intact
sp|P9WHU6|P5CR_MYCTO Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshko	P5CR2_HUMAN	P5CR3_HUMAN	P5CR3_HUMAN	3,00E-28	3,00E-54	3,00E-41	31	46	37,7624	1	1	0	-	two hybrid	hprd
sp|P9WHN2|PURA_MYCTO Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	B4E1L0_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	78	58,5833	1	1	0	-	in vitro	hprd
sp|P9WHN2|PURA_MYCTO Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (	PURA1_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	100	66,3325	1	1	0	-	in vitro	hprd
sp|P9WGV2|SAHH_MYCTO Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=	SAHH_HUMAN	SAHH_HUMAN	SAHH_HUMAN	1,00E-143	0	0	55	100	74,162	1	1	0	-	in vitro	hprd
#Finished correctly															

Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO m
GO bi
GO ce

JOB ID: 1eee6e7d1f9228500250ff09fb75b9c3
Results URL: http://sbi.imim.es/BIPS.php?jobID=1eee6e7d1f9228500250ff09fb75b9c3

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner

Query protein	P
tr|A0A0H3L9H4|A0A0H3L9H4_MYCTE Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=pgk PE=3 SV=1	KPYM
tr|A0A0H3LI71|A0A0H3LI71_MYCTE Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=mez PE=3 SV=1	MAO
tr|A0A0H3L7U3|A0A0H3L7U3_MYCTE Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=pgi PE=3 SV=1	B4DE
tr|A0A0H3L7U3|A0A0H3L7U3_MYCTE Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=pgi PE=3 SV=1	B4DV
tr|A0A0H3L7U3|A0A0H3L7U3_MYCTE Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=pgi PE=3 SV=1	G6PI_
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A0SD
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DT
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DT
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DT
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DU
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DV
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A3RM

Query protein	P
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZLD
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZLI
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZLS
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZM
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZM
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YW
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YW
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YX
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YZ
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z2
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z4
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z7
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z8
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z8
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z8
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z9
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z9
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZB
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZB
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZC
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZD
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZF
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7LD
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7LFE
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7XT
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A8JLT
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A8WF
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0EW
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0Z6
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0Z7
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0Z7
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B1NV
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B1W6
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B1W7
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2CB
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2CB
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2KL
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2WF
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XEI
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XEI
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XF

Query protein	P
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XG
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XM
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XN
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XN
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2YA
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2Z5
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2Z6
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2ZN
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B3DE
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B3VE
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B4YB
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B4YC
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B4YG
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B5M8
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B7TM
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B8RF
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B8X4
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B8XZ
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9EC
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9EE
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9EE
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9EE
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C4PK
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C4RU
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5MM
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C7B3
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C7B3
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Query protein	P
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tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4G9
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tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZK
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Query protein	P
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Query protein	P
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tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5S9
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5SA
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5SA
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5SB
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XR
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6R0
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RK
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RN
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RC
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VI
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VJI
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VJJ
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7Y6
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7Y6
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7Y6
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YC
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YE
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q85K
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8HN
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8HN
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8HC
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8W
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B1
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B1
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B2
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	COX2
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	COX2
tr|A0A0H3L7V8|A0A0H3L7V8_MYCTE Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=mdh PE=3 SV=1	MDH
tr|A0A0H3L910|A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=argG PE=3 SV=1	A8KA
tr|A0A0H3L910|A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=argG PE=3 SV=1	ASSY
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	B4DY
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPA
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPB
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPD
tr|A0A0H3LD73|A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ffh PE=3 SV=1	B4DD
tr|A0A0H3LD73|A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ffh PE=3 SV=1	SRP54
tr|A0A0H3LD73|A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ffh PE=3 SV=1	SRP19

Query protein	P
tr|A0A0H3L6B9|A0A0H3L6B9_MYCTE 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=rplB PE=3 SV=1	RL6_
tr|A0A0H3L6B9|A0A0H3L6B9_MYCTE 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=rplB PE=3 SV=1	RL30_
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7(
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7:
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	TBB2(
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	CH60_
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ENPL_
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HS90I
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HS90/
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPG_
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPB_
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPD_
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7(
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7:
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7(
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7:
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ACTB_
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	SMAI
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TBB2(
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UN
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UN
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B7Z4F
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B7Z5E
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH60_
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B7Z4F
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B7Z5E
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DG
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DM
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ENPL_
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90I
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90/
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DG
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DM
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90/
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A1JUI
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A8K2:
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A8K3(
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B2R9I

Query protein	P
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DD
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DP
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DX
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q59E
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPD
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPW
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPZ
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A1JUI
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A8K2
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A8K3
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B2R9I
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DD
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DP
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DX
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q59E
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPD
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPW
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPZ
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DR
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q53F
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q53G
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q59E
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9BV
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DR
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q53F
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q53G
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q59E
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9BV
tr|A0A0H3LCK6|A0A0H3LCK6_MYCTE Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=hemE PE=3 SV=1	Q53Z
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B2R5I
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B4DM
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B4DT
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B7Z2S
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	E2QR
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	Q2TSI
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	G3PT
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	G3P
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	PPIA
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB

Query protein	P
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TBB2
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	AIPL1
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z4F
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z5E
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	CRYA
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K4
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q59E
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	DNJC
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DG
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DM
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS74I
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A1JUI
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K2
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K3
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B2R9I
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DD
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DP
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DX
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q59E
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPD
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPW
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPZ
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K4
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DE
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DX
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B5BT
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z2
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z7I
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B8ZZ
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q2TU
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q53H
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q53H
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPG
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPG
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q6IBT
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPB
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPH
tr|A0A0H3L5R1|A0A0H3L5R1_MYCTE Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=proC PE=3 SV=1	P5CR
tr|A0A0H3LC41|A0A0H3LC41_MYCTE Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=purA PE=3 SV=1	B4E1I
tr|A0A0H3LC41|A0A0H3LC41_MYCTE Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=purA PE=3 SV=1	PURA

Query protein	P
tr|A0A0H3LE62|A0A0H3LE62_MYCTE Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=sahH PE=3 SV=1	SAHH

#Finished correctly

Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO molecular function
GO biological process
GO cellular component

JOB ID: 1eee6e7d1f9228500250ff09fb75b9c3
Results URL: http://sbi.imim.es/BIPS.php?jobID=1eee6e7d1f9228500250ff09fb75b9c3

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner
3: Query homolog sequence (multiple names can appear if the proteins share the same sequence)
4: Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)
5: Query-Template Blast E-value
6: Predicted partner-Template Blast E-value
7: Joint e-value
8: Query-Template identities
9: Predicted partner-Template identities
10: Joint identities
11: Pfam domain-domain interactions found (0: False, 1: True)
12: Sharing GO terms found (0: False, 1: True)
13: Interaction found directly in database. (0: False, 1: True)
14: Interacting Pfam domains
15: Template interaction detection method
16: Template interaction source database

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3L9H4|A0A0H3L9H4_MYCTE Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=pgk PE=3 SV=1	KPYM_HUMAN	PGK1_HUMAN	KPYM_HUMAN	4,00E-68	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LI71|A0A0H3LI71_MYCTE Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=mez PE=3 SV=1	MAOX_HUMAN	MAOM_HUMAN	MAOM_HUMAN	5,00E-91	0	0	36	55	44,4972	1	1	0	malic:Malic_M	in vitro	hprd
tr|A0A0H3L7U3|A0A0H3L7U3_MYCTE Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=pgi PE=3 SV=1	B4DE36_HUMAN	G6PI_HUMAN	G6PI_HUMAN	########	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
tr|A0A0H3L7U3|A0A0H3L7U3_MYCTE Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=pgi PE=3 SV=1	B4DVJ0_HUMAN	G6PI_HUMAN	G6PI_HUMAN	########	0	0	43	89	61,8628	1	1	0	-	in vitro	hprd
tr|A0A0H3L7U3|A0A0H3L7U3_MYCTE Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=pgi PE=3 SV=1	G6PI_HUMAN	G6PI_HUMAN	G6PI_HUMAN	########	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A0SD91_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DTJ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DTL0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DTV1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DUU4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1DV22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A3RM82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZLD6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZLI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZLS9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZMF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZMW5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YW19_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YWQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YX95_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YZY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z2T0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z460_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z708_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z809_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z8G5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z8Z7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z9Q7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z9S0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZB50_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZBW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZC77_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZDK7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZFQ8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7LDP6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7LFE4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7XTZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A8JLT5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A8WFB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0EWB5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0Z6N9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0Z745_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0Z7E9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B1NVE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B1W6U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B1W7S8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2CB40_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	90	61,4817	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2CB92_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	91	61,8223	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2KLD8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2WRF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XEK5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XEN1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XFT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XGB4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XMF0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XNQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XNX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2YAW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2Z5S5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2Z642_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2ZNN0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B3DE35_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B3VEA5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B4YBC2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B4YCG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B4YGV7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B5M8C0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B7TMW4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B8RFL3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B8X4N0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B8XZS7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9ECT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9EE11_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9EEE1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9EEI0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B9EF90_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C4PK82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C4RU97_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5MM24_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C7B321_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C7B3W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	96	63,498	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C7SJU6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C7SKT4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C8XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C8Y3W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C8Y5S3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C8YGY6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C9D5W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D0V1V1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D1GI28_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D3K5V4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D6BZS8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D6C3F2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D6N462_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D6N765_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D7NV03_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D7P622_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D7P661_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E0Y4D8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E1B320_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E2FQB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E2J0C2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5DY67_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5DYD2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5E0U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5E1D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5E1I7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5EY89_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5LFL6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0G899_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0VXC5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0Z7D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0Z7G1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0ZFF5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q15H46_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q15HG3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q15II8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q15IP0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q19MP4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q27H55_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q2HJS3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q2HKH0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q2HKI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q2HKT7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q305I0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q305K6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q305X3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q3S961_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4EWP5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4EXJ4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4EZD1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4F0P9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4F0T8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4F1I5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4F2A8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4F2U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4G6P4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4G6V9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4G7C8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4G9U9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GBF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GC16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GFE9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GG20_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GI22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GIA0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GIY4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GMA4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GPI4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GPN6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GSY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GU59_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GV60_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4VFD0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4ZEA6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4ZED2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4ZEF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4ZF68_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5SAG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5SB31_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XSC1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZI2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZI9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZK9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZL8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZP7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZR9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZT6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XZY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y011_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y065_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y070_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y078_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y0E5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y0F3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y0G2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y0H4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5Y0J7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6R0Q1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6R0W6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RLY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RMU0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RPE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RRW7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VH99_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VHA9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VIB9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VIH5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VIM0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VJ16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VK16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VKA3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VLN4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6WQA1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6WQG6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7Y664_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YCC7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YCE0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YCE5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YCF3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YEF1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q85KW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q85KW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q85KZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q85L04_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q85L10_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8HNQ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8WCY1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B1S4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B1S6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B2U6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B2W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B2X0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	COX3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A0S0W7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A0S2P1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A0S3T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A0SA07_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1Z455_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A1Z4V2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A4ZKZ0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YW54_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YWD1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6YXV0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z3M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6Z6E8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZEU4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZF47_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZFK3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A6ZHA9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7LDC6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7LF11_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	A7LFA2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B0Z6W4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B1W855_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2CB37_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	95	63,1664	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2WRY8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XHF9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XHT9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XIR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XL43_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XP28_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B2XPS3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B3DE06_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B3GUF3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	B5M7M0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6K5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	96	63,498	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6K6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6K7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6L3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6M4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6M5_HUMAN	COX1_HUMAN

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6M7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C5H6M8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C8XWJ6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C8Y3G4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C8Y3Q5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C8YBL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	C9D661_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D1G421_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D2IKF4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D2K1G3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D3YPT7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D5M8T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	D7NUN3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E0AF97_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E2DTL8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E2JFC4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E2JJS5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5DZN4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5E079_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5E1A6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5E1V1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5EWG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5EWL4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5EWR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	E5FWC0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q06TE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q09U41_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0Z7D8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0Z7F1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0Z7J0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0Z7K3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	98	64,1561	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q0Z7S0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q15HH9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q19MP7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q305H0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4EYL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4EZD4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4F4V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4F6A2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GCC3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GCG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GCZ4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GHE1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GQP0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GVP5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q4GW12_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	100	64,8074	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5S971_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5SA98_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5SAP1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5SB08_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q5XRW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6R0V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RKW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RNN7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6RQ80_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VIG7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VJD8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q6VJJ3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7Y626_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7Y6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7Y6N0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YCE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q7YEH2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q85KS0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8HNR1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8HNR6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8HQB7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q8WCW3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B138_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B1F9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Q9B2U8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	########	########	42	99	64,4826	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	COX2_YEAST	COX1_HUMAN	COX2_HUMAN	5,00E-96	3,00E-47	1,22E-71	42	42	42	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3LHR0|A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	COX2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:COX2 CO	in vivo	hprd
tr|A0A0H3L7V8|A0A0H3L7V8_MYCTE Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=mdh PE=3 SV=1	MDHC_HUMAN	MDHC_HUMAN	MDHC_HUMAN	3,00E-88	0	0	51	100	71,4143	1	1	0	Ldh_1_C:Ldh_1	in vitro	hprd
tr|A0A0H3L910|A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tubercul

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3L910|A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=argG PE=3 SV=1	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	biogrid
tr|A0A0H3L910|A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=argG PE=3 SV=1	A8KAP9_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	99	61,3351	1	1	0	-	two hybrid	hprd
tr|A0A0H3L910|A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=argG PE=3 SV=1	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid po	intact
tr|A0A0H3L910|A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=argG PE=3 SV=1	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	biogrid
tr|A0A0H3L910|A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=argG PE=3 SV=1	ASSY_HUMAN	ASSY_HUMAN	ASSY_HUMAN	9,00E-70	0	0	38	100	61,6441	1	1	0	-	two hybrid	hprd
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:ATP-s	blue native pa	intact
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:ATP-s	blue native pa	intact
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:ATP-s	in vitro	hprd
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:ATP-s	blue native pa	intact
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:ATP-s	blue native pa	intact
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:ATP-s	in vitro	hprd
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:ATP-s	blue native pa	intact
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:ATP-s	blue native pa	intact
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:ATP-s	in vitro	hprd
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:ATP-s	blue native pa	intact
tr|A0A0H3L814|A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpG PE=3 SV=1	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:ATP-s	blue native pa	intact
tr|A0A0H3LD73|A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ffh PE=3 SV=1	B4DDS7_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54_N:SRP54	x-ray crystallo	biogrid
tr|A0A0H3LD73|A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ffh PE=3 SV=1	B4DDS7_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54_N:SRP54	in vitro	hprd
tr|A0A0H3LD73|A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ffh PE=3 SV=1	SRP54_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54:SRP54_N	x-ray crystallo	biogrid
tr|A0A0H3LD73|A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ffh PE=3 SV=1	SRP54_HUMAN	SRP54_HUMAN	SRP54_HUMAN	2,00E-57	0	0	30	100	54,7723	1	1	0	SRP54:SRP54_N	in vitro	hprd
tr|A0A0H3LD73|A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ffh PE=3 SV=1	SRP19_HUMAN	SRP54_HUMAN	SRP19_HUMAN	2,00E-57	0	0	30	100	54,7723	0	1	0	-	in vitro	hprd
tr|A0A0H3L6B9|A0A0H3L6B9_MYCTE 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=rplB PE=3 SV=1	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
tr|A0A0H3L6B9|A0A0H3L6B9_MYCTE 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=rplB PE=3 SV=1	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
tr|A0A0H3L6B9|A0A0H3L6B9_MYCTE 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=rplB PE=3 SV=1	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
tr|A0A0H3L6B9|A0A0H3L6B9_MYCTE 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=rplB PE=3 SV=1	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7C_HUMAN	GRP78_HUMAN	HSP71_HUMAN	########	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7C_HUMAN	GRP78_HUMAN	HSP71_HUMAN	########	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP71_HUMAN	GRP78_HUMAN	HSP71_HUMAN	########	0	0	49	100	70	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP71_HUMAN	GRP78_HUMAN	HSP71_HUMAN	########	0	0	49	100	70	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	TBB2C_HUMAN	GRP78_HUMAN	TBB5_HUMAN	########	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP71_HUMAN	GRP78_HUMAN	HSP7C_HUMAN	########	0	0	49	86	64,9153	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7C_HUMAN	GRP78_HUMAN	HSP7C_HUMAN	########	0	0	49	100	70	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP78_HUMAN	ACTH_HUMAN	########	0	0	49	93	67,5056	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP78_HUMAN	ACTB_HUMAN	########	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP78_HUMAN	ACTG_HUMAN	########	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	TBB2C_HUMAN	GRP78_HUMAN	TBB4_HUMAN	########	0	0	49	98	69,2965	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	CH60_HUMAN	GRP78_HUMAN	CH60_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ENPL_HUMAN	GRP78_HUMAN	ENPL_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP71_HUMAN	GRP78_HUMAN	HS71L_HUMAN	########	0	0	49	89	66,0379	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7C_HUMAN	GRP78_HUMAN	HS71L_HUMAN	########	0	0	49	82	63,3877	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ENPL_HUMAN	GRP78_HUMAN	HS90A_HUMAN	########	########	########	49	46	47,4763	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HS90B_HUMAN	GRP78_HUMAN	HS90A_HUMAN	########	0	0	49	85	64,5368	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HS90A_HUMAN	GRP78_HUMAN	HS90A_HUMAN	########	0	0	49	100	70	0	1	0	-	in vivo	hprd
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt_ab:AT	blue native pa	intact
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt_ab:AT	blue native pa	intact
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt_ab:AT	in vitro	hprd
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt_ab:AT	blue native pa	intact
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	########	0	0	54	100	73,4847	1	1	0	ATP-synt_ab:AT	blue native pa	intact
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	blue native pa	intact
tr|A0A0H3LEY6|A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=atpA PE=3 SV=1	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	blue native pa	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	46	86	62,8967	0	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	46	86	62,8967	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	41	86	59,3801	0	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	41	86	59,3801	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	SMAD3_HUMAN	CH60_HUMAN	SMAD2_HUMAN	########	0	0	46	83	61,79	0	1	0	-	display techn	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TBB2C_HUMAN	CH60_HUMAN	TBB5_HUMAN	########	0	0	46	98	67,1416	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	########	0	0	46	86	62,8967	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	molecular siev	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	########	0	0	41	86	59,3801	0	1	0	-	molecular siev	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TBB2C_HUMAN	CH60_HUMAN	TBA1A_HUMAN	########	2,00E-99	########	46	40	42,8952	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTH_HUMAN	########	0	0	46	93	65,4064	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	########	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTG_HUMAN	########	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	cross-linking s	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	biochemical	biogrid
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	two hybrid	biogrid

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	two hybrid	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	cross-linking s	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	biochemical	biogrid
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	two hybrid	biogrid
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	46	100	67,8233	1	1	0	Cpn60_TCP1:Cp	two hybrid	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	cross-linking s	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	biochemical	biogrid
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	two hybrid	biogrid
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	########	1,00E-38	3,16E-72	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	two hybrid	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	cross-linking s	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	biochemical	biogrid
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	two hybrid	biogrid
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	########	0	0	41	100	64,0312	1	1	0	Cpn60_TCP1:Cp	two hybrid	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	########	0	0	46	64	54,2586	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	########	0	0	46	65	54,6809	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	########	0	0	41	64	51,225	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	########	0	0	41	65	51,6236	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	46	95	66,106	1	1	0	-	in vitro	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	46	87	63,2614	0	1	0	-	in vitro	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	CH60_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	46	100	67,8233	1	1	0	-	in vitro	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	41	95	62,4099	1	1	0	-	in vitro	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	########	0	0	41	87	59,7244	0	1	0	-	in vitro	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	83	61,79	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	83	61,79	0	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	83	61,79	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	80	60,663	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	80	60,663	0	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	80	60,663	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	########	########	46	46	46	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	########	########	46	46	46	0	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	########	########	46	46	46	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	85	62,53	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	85	62,53	0	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	85	62,53	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	83	58,3352	0	1	0	-	molecular siev	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	83	58,3352	0	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	83	58,3352	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	80	57,2713	0	1	0	-	molecular siev	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	80	57,2713	0	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	80	57,2713	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	molecular siev	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	########	0	0	41	100	64,0312	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	46	98	67,1416	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	46	94	65,7571	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	ENPL_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	########	########	46	48	46,9894	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	46	86	62,8967	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90B_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	46	100	67,8233	0	1	0	-	molecular siev	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	41	98	63,3877	0	1	0	-	molecular siev	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	41	94	62,0806	0	1	0	-	molecular siev	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	########	0	0	41	86	59,3801	0	1	0	-	molecular siev	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	99	67,4833	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	1,00E-60	3,16E-90	46	31	37,7624	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	99	67,4833	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	1,00E-59	1,00E-89	46	31	37,7624	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	99	67,4833	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-58	7,07E-89	46	30	37,1484	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	99	67,4833	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	85	62,53	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	46	100	67,8233	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	99	63,7103	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	1,00E-60	3,16E-83	41	31	35,6511	1	1	0	-	surface plasm	intact

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-57	2,24E-81	41	30	35,0714	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	99	63,7103	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	1,00E-59	1,00E-82	41	31	35,6511	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	99	63,7103	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-58	7,07E-82	41	30	35,0714	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	99	63,7103	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	5,00E-57	2,24E-81	41	30	35,0714	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	85	59,0339	1	1	0	-	surface plasm	intact
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	########	0	0	41	100	64,0312	1	1	0	-	surface plasm	intact
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	92	65,0538	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
tr|A0A0H3LCC3|A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	92	61,4166	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
tr|A0A0H3LEL3|A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	########	0	0	41	99	63,7103	0	1	0	-	in vivo	hprd
tr|A0A0H3LCK6|A0A0H3LCK6_MYCTE Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=hemE PE=3 SV=1	Q53ZP6_HUMAN	DCUP_HUMAN	DCUP_HUMAN	2,00E-53	0	0	37	99	60,5227	0	1	0	-	x-ray crystallo	biogrid
tr|A0A0H3LCK6|A0A0H3LCK6_MYCTE Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=hemE PE=3 SV=1	Q53ZP6_HUMAN	DCUP_HUMAN	DCUP_HUMAN	2,00E-53	0	0	37	99	60,5227	0	1	0	-	in vitro	hprd
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B2R5P6_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox_2:Pv	x-ray crystallo	intact
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B2R5P6_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox_2:Pv	in vivo	hprd
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B4DMK9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	95	57,6628	1	1	0	Pyr_redox_2:Pv	x-ray crystallo	intact
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B4DMK9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	95	57,6628	1	1	0	Pyr_redox_2:Pv	in vivo	hprd
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B4DT69_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	90	56,1249	1	1	0	Pyr_redox_2:Pv	x-ray crystallo	intact
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B4DT69_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	0	0	35	90	56,1249	1	1	0	Pyr_redox_2:Pv	in vivo	hprd
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B7Z2S5_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox_2:Pv	x-ray crystallo	intact
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	B7Z2S5_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	1,00E-46	2,45E-59	35	30	32,4037	1	1	0	Pyr_redox_2:Pv	in vivo	hprd
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	E2QRB9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	4,00E-47	1,55E-59	35	30	32,4037	1	1	0	Pyr_redox_2:Pv	x-ray crystallo	intact
tr|A0A0H3L5N9|A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	E2QRB9_HUMAN	DLDH_HUMAN	DLDH_HUMAN	6,00E-72	4,00E-47	1,55E-59	35	30	32,4037	1	1	0	Pyr_redox_2:Pv	in vivo	hprd
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:Gp_d	fluorescent re	mint
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:Gp_d	in vitro	hprd
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	########	########	50	68	58,3095	1	1	0	Gp_dh_N:Gp_d	fluorescent re	mint
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	########	########	50	68	58,3095	1	1	0	Gp_dh_N:Gp_d	in vitro	hprd
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_C:Gp_d	fluorescent re	mint
tr|A0A0H3LCN1|A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=gap PE=3 SV=1	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_C:Gp_d	in vitro	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7C_HUMAN	GRP75_HUMAN	HSP71_HUMAN	########	0	0	54	86	68,1469	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7C_HUMAN	GRP75_HUMAN	HSP71_HUMAN	########	0	0	54	86	68,1469	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP71_HUMAN	GRP75_HUMAN	HSP71_HUMAN	########	0	0	54	100	73,4847	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP71_HUMAN	GRP75_HUMAN	HSP71_HUMAN	########	0	0	54	100	73,4847	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP75_HUMAN	ACTB_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP75_HUMAN	ACTH_HUMAN	########	0	0	54	93	70,8661	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP75_HUMAN	ACTB_HUMAN	########	0	0	54	98	72,7461	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ACTB_HUMAN	GRP75_HUMAN	ACTG_HUMAN	########	0	0	54	98	72,7461	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP71_HUMAN	GRP75_HUMAN	GRP78_HUMAN	########	0	0	54	64	58,7878	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP71_HUMAN	GRP75_HUMAN	GRP78_HUMAN	########	0	0	54	64	58,7878	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7C_HUMAN	GRP75_HUMAN	GRP78_HUMAN	########	0	0	54	65	59,2453	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HSP7C_HUMAN	GRP75_HUMAN	GRP78_HUMAN	########	0	0	54	65	59,2453	1	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	CH60_HUMAN	GRP75_HUMAN	CH60_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ENPL_HUMAN	GRP75_HUMAN	ENPL_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	in vitro	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	ENPL_HUMAN	GRP75_HUMAN	HS90A_HUMAN	########	########	########	54	46	49,8397	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HS90B_HUMAN	GRP75_HUMAN	HS90A_HUMAN	########	0	0	54	85	67,7495	0	1	0	-	in vivo	hprd
tr|A0A0H3L5C8|A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	HS90A_HUMAN	GRP75_HUMAN	HS90A_HUMAN	########	0	0	54	100	73,4847	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	PPIA_HUMAN	HS90A_HUMAN	PPIA_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TBB2C_HUMAN	HS90A_HUMAN	TBB5_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TBB2C_HUMAN	HS90A_HUMAN	TBB5_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	molecular siev	intact

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TBB2C_HUMAN	HS90A_HUMAN	TBA1A_HUMAN	########	2,00E-99	########	38	40	38,9872	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB_HUMAN	HS90A_HUMAN	ACTH_HUMAN	########	0	0	38	93	59,4475	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB_HUMAN	HS90A_HUMAN	ACTB_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB_HUMAN	HS90A_HUMAN	ACTG_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90A_HUMAN	GRP78_HUMAN	########	0	0	38	64	49,3153	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90A_HUMAN	GRP78_HUMAN	########	0	0	38	65	49,6991	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	AIPL1_HUMAN	HS90A_HUMAN	AIP_HUMAN	########	1,00E-93	########	38	49	43,1509	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	AIPL1_HUMAN	HS90A_HUMAN	AIP_HUMAN	########	1,00E-93	########	38	49	43,1509	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	95	60,0833	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	95	60,0833	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z4F6_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	95	60,0833	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	87	57,4978	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	87	57,4978	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z5E7_HUMAN	HS90A_HUMAN	CH60_HUMAN	########	0	0	38	87	57,4978	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	CRYAB_HUMAN	HS90A_HUMAN	CRYAB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K4T2_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	two hybrid	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q59EH7_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	two hybrid	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	DNJC7_HUMAN	HS90A_HUMAN	DNJC7_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	two hybrid	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase_c:HSP	two hybrid po	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase_c:HSP	two hybrid	mint
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase_c:HSP	two hybrid	biogrid
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase_c:HSP	in vitro	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase_c:HSP	two hybrid po	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase_c:HSP	two hybrid	mint
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase_c:HSP	two hybrid	biogrid
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase_c:HSP	in vitro	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	two hybrid po	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	two hybrid	mint
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	two hybrid	biogrid
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90A_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	in vitro	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase_c:HSP	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase_c:HSP	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase_c:HSP	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90A_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	########	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	########	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS74L_HUMAN	HS90A_HUMAN	HSP74_HUMAN	########	0	0	38	63	48,9285	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A1JUI8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K2X8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	1,00E-60	1,00E-87	38	31	34,322	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K3C3_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	5,00E-57	7,07E-86	38	30	33,7639	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B2R9K8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DDU6_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	1,00E-59	3,16E-87	38	31	34,322	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DPJ8_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DX08_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	5,00E-58	2,24E-86	38	30	33,7639	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q59ET3_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	99	61,3351	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPD_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	5,00E-57	7,07E-86	38	30	33,7639	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPW_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	85	56,8331	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPZ_HUMAN	HS90A_HUMAN	TCPZ_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	surface plasm	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90B_HUMAN	HSP71_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90B_HUMAN	HSP71_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB_HUMAN	HS90B_HUMAN	ACTB_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TBB2C_HUMAN	HS90B_HUMAN	TBB5_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP71_HUMAN	HS90B_HUMAN	HSP7C_HUMAN	########	0	0	38	86	57,1664	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HSP7C_HUMAN	HS90B_HUMAN	HSP7C_HUMAN	########	0	0	38	100	61,6441	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TBB2C_HUMAN	HS90B_HUMAN	TBA1A_HUMAN	########	2,00E-99	########	38	40	38,9872	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	ACTB_HUMAN	HS90B_HUMAN	ACTG_HUMAN	########	0	0	38	98	61,0246	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z4F6_HUMAN	HS90B_HUMAN	CH60_HUMAN	########	0	0	38	95	60,0833	0	1	0	-	molecular siev	intact

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z5E7_HUMAN	HS90B_HUMAN	CH60_HUMAN	########	0	0	38	87	57,4978	0	1	0	-	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS74L_HUMAN	HS90B_HUMAN	HS105_HUMAN	########	0	0	38	60	47,7493	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase_c:HSP	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	83	56,1605	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase_c:HSP	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	80	55,1362	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	molecular siev	intact
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90B_HUMAN	HS90A_HUMAN	########	0	0	38	100	61,6441	1	1	0	HATPase_c:HSP	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DGL0_HUMAN	HS90B_HUMAN	HS90B_HUMAN	########	0	0	38	98	61,0246	1	1	0	HATPase_c:HSP	in vitro	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DMA2_HUMAN	HS90B_HUMAN	HS90B_HUMAN	########	0	0	38	94	59,7662	1	1	0	HATPase_c:HSP	in vitro	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	HS90A_HUMAN	HS90B_HUMAN	HS90B_HUMAN	########	0	0	38	86	57,1664	1	1	0	HATPase_c:HSP	in vitro	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K2X8_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-66	4,47E-92	38	32	34,8712	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K3C3_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-68	3,16E-93	38	32	34,8712	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	A8K402_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-73	1,41E-95	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DDU6_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	8,00E-66	8,94E-92	38	32	34,8712	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DEM7_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-61	1,00E-89	38	31	34,322	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DX08_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-65	1,41E-91	38	32	34,8712	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B4DXI1_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-54	3,16E-86	38	30	33,7639	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B5BTY7_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	5,00E-74	7,07E-96	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z243_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-66	4,47E-92	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B7Z7K4_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-66	3,16E-92	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	B8ZZC9_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	5,00E-64	7,07E-91	38	32	34,8712	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q2TU64_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	3,00E-73	1,73E-95	38	33	35,4119	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q53HU0_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-61	1,00E-89	38	31	34,322	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q53HV2_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	1,00E-78	3,16E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPG_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	4,00E-74	6,32E-96	38	33	35,4119	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPG_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	4,00E-63	2,00E-90	38	31	34,322	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Q6IBT3_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	5,00E-79	2,24E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPB_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	4,00E-74	6,32E-96	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPD_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	8,00E-69	2,83E-93	38	32	34,8712	0	1	0	-	in vivo	hprd
tr|A0A0H3LFE0|A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	TCPH_HUMAN	HS90B_HUMAN	TCPA_HUMAN	########	2,00E-79	1,41E-98	38	35	36,4692	0	1	0	-	in vivo	hprd
tr|A0A0H3L5R1|A0A0H3L5R1_MYCTE Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=proC PE=3 SV=1	P5CR2_HUMAN	P5CR3_HUMAN	P5CR3_HUMAN	3,00E-28	3,00E-54	3,00E-41	31	46	37,7624	1	1	0	-	two hybrid	hprd
tr|A0A0H3LC41|A0A0H3LC41_MYCTE Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=purA PE=3 SV=1	B4E1L0_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	78	58,5833	1	1	0	-	in vitro	hprd
tr|A0A0H3LC41|A0A0H3LC41_MYCTE Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=purA PE=3 SV=1	PURA1_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	100	66,3325	1	1	0	-	in vitro	hprd
tr|A0A0H3LE62|A0A0H3LE62_MYCTE Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=sahH PE=3 SV=1	SAHH_HUMAN	SAHH_HUMAN	SAHH_HUMAN	########	0	0	55	100	74,162	1	1	0	-	in vitro	hprd
#Finished correctly															

Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO molecular function
GO biological process
GO cellular component

JOB ID: a6101ff07857dc9a9e8c30ef605118b2
Results URL: http://sbi.imim.es/BIPS.php?jobID=a6101ff07857dc9a9e8c30ef605118b2

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner

Query protein	Predicted partn
tr|R4M5K1|R4M5K1_MYCTX Phosphoglycerate kinase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgk PE=3 SV=1	KPYM_HUMAN
tr|R4MJZ1|R4MJZ1_MYCTX Malate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_16165 PE=3 SV=1	MAOX_HUMAN
tr|R4M485|R4M485_MYCTX Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgi PE=3 SV=1	B4DE36_HUMAN
tr|R4M485|R4M485_MYCTX Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgi PE=3 SV=1	B4DVJ0_HUMAN
tr|R4M485|R4M485_MYCTX Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgi PE=3 SV=1	G6PI_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A0SD91_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DTJ7_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DTL0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DTV1_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DUU4_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DV22_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A3RM82_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZLD6_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZLI8_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZLS9_HUMAN

Query protein	Predicted partn
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZMF9_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZMW5_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YW19_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YWQ1_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YX95_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YZY0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z2T0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z460_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z708_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z809_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z8G5_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z8Z7_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z9Q7_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z9S0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZB50_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZBW0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZC77_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZDK7_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZFQ8_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A7LDP6_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A7LFE4_HUMAN
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tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B0EWB5_HUMAN
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tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5E1D5_HUMAN
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Query protein	Predicted partn
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tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GPN6_HUMAN
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Query protein	Predicted partn
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tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7D8_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7F1_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7J0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7K3_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7S0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q15HH9_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q19MP7_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q305H0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4EYL1_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4EZD4_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F4V6_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F6A2_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GCC3_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GCG2_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GCZ4_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GHE1_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GQP0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GVP5_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GW12_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5S971_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5SA98_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5SAP1_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5SB08_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XRW8_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6R0V6_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RKW8_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RNN7_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RQ80_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VIG7_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VJD8_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VJJ3_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7Y626_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7Y6M3_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7Y6N0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YCE6_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YEH2_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q85KS0_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8HNR1_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8HNR6_HUMAN

Query protein	Predicted partn
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8HQB7_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8WCW3_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B138_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B1F9_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B2U8_HUMAN
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	COX2_YEAST
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	COX2_HUMAN
tr|R4MCD1|R4MCD1_MYCTX Malate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=mdh PE=3 SV=1	MDHC_HUMAN
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	B4DY56_HUMAN
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPA_HUMAN
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPB_HUMAN
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPD_HUMAN
tr|R4MFC5|R4MFC5_MYCTX 50S ribosomal protein L2 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=rplB PE=3 SV=1	RL6_HUMAN
tr|R4MFC5|R4MFC5_MYCTX 50S ribosomal protein L2 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=rplB PE=3 SV=1	RL30_HUMAN
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPG_HUMAN
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPB_HUMAN
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPD_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP7C_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP71_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ACTB_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	SMAD3_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TBB2C_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9UNM1_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH10_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B7Z4F6_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B7Z5E7_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH60_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DGL0_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DMA2_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ENPL_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90B_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90A_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	A1JUI8_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	A8K2X8_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	A8K3C3_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B2R9K8_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DDU6_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DPJ8_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DX08_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q59ET3_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TCPD_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TCPW_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TCPZ_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DR68_HUMAN

Query protein	Predicted partn
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q53FS6_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q53G55_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q59EK6_HUMAN
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9BV61_HUMAN
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	Q2TSD0_HUMAN
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	G3PT_HUMAN
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	G3P_HUMAN
tr|R4M2F9|R4M2F9_MYCTX Adenylosuccinate synthetase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=purA PE=3 SV=1	B4E1L0_HUMAN
tr|R4M2F9|R4M2F9_MYCTX Adenylosuccinate synthetase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=purA PE=3 SV=1	PURA1_HUMAN
#Finished correctly	

Homology Conditions
evalue: 1e-10
identities: 30
Query Sequence coverage: 80
Template Sequence coverage: 90
Joint e-value: 1e-10
Joint Identities: 30

Template Interactions
Exclude co-complex methods as TAP

Predicted partner
Partner taxonomy: 9606
Inferred interactions
Must share at level 3 (and):

GO molecular function
GO biological process
GO cellular component

JOB ID: a6101ff07857dc9a9e8c30ef605118b2
Results URL: http://sbi.imim.es/BIPS.php?jobID=a6101ff07857dc9a9e8c30ef605118b2

PREDICTIONS

COLUMNS
1: Query protein
2: Predicted partner
3: Query homolog sequence (multiple names can appear if the proteins share the same sequence)
4: Predicted partner homolog sequence (multiple names can appear if the proteins share the same sequence)
5: Query-Template Blast E-value
6: Predicted partner-Template Blast E-value
7: Joint e-value
8: Query-Template identities
9: Predicted partner-Template identities
10: Joint identities
11: Pfam domain-domain interactions found (0: False, 1: True)
12: Sharing GO terms found (0: False, 1: True)
13: Interaction found directly in database. (0: False, 1: True)
14: Interacting Pfam domains
15: Template interaction detection method
16: Template interaction source database

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|R4M5K1|R4M5K1_MYCTX Phosphoglycerate kinase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgk PE=3 SV=1	KPYM_HUMAN	PGK1_HUMAN	KPYM_HUMAN	4,00E-68	0	0	38	100	61,6441	0	1	0	-	in vivo	hprd
tr|R4MJZ1|R4MJZ1_MYCTX Malate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_16165 PE=3 SV=1	MAOX_HUMAN	MAOM_HUMAN	MAOM_HUMAN	5,00E-91	0	0	36	55	44,4972	1	1	0	malic:Malic	in vitro	hprd
tr|R4M485|R4M485_MYCTX Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgi PE=3 SV=1	B4DE36_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
tr|R4M485|R4M485_MYCTX Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgi PE=3 SV=1	B4DVJ0_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	89	61,8628	1	1	0	-	in vitro	hprd
tr|R4M485|R4M485_MYCTX Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgi PE=3 SV=1	G6PI_HUMAN	G6PI_HUMAN	G6PI_HUMAN	1,00E-129	0	0	43	100	65,5744	0	1	0	-	in vitro	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A0SD91_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DTJ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DTL0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DTV1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DUU4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1DV22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A3RM82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZLD6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZLI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZLS9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZMF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZMW5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YW19_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YWQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YX95_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YZY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z2T0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z460_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z708_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z809_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z8G5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z8Z7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z9Q7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z9S0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZB50_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZBW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZC77_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZDK7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZFQ8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A7LDP6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A7LFE4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A7XTZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A8JLT5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A8WFB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B0EWB5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B0Z6N9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B0Z745_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B0Z7E9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B1NVE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B1W6U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B1W7S8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2CB40_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-109	7,07E-103	42	90	61,4817	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2CB92_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-111	7,07E-104	42	91	61,8223	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2KLD8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2WRF9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XEK5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XEN1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XFT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XGB4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XMF0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XNQ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XNX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2YAW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2Z5S5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2Z642_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2ZNN0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B3DE35_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B3VEA5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B4YBC2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B4YCG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B4YGV7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B5M8C0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B7TMW4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B8RFL3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B8X4N0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B8XZS7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B9ECT2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B9EE11_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B9EEE1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B9EEI0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B9EF90_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C4PK82_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C4RU97_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5MM24_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C7B321_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C7B3W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-111	7,07E-104	42	96	63,498	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C7SJU6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C7SKT4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C8XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C8Y3W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C8Y5S3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C8YGY6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C9D5W0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D0V1V1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D1GI28_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D3K5V4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D6BZS8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D6C3F2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D6N462_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D6N765_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D7NV03_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D7P622_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D7P661_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E0Y4D8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E1B320_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E2FQB7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E2J0C2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5DY67_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5DYD2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5E0U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5E1D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5E1I7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5EY89_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5LFL6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0G899_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0VXC5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7D5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7G1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0ZFF5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q15H46_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q15HG3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q15II8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q15IP0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q19MP4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q27H55_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q2HJS3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q2HKH0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q2HKI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q2HKT7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q305I0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q305K6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q305X3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q3S961_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4EWP5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4EXJ4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4EZD1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F0P9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F0T8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F1I5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	98	64,1561	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F2A8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F2U0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4G6P4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4G6V9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4G7C8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4G9U9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GBF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GC16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GFE9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GG20_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GI22_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GIA0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GIY4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GMA4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GPI4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GPN6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GSY0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GU59_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GV60_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4VFD0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4ZEA6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4ZED2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4ZEF8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4ZF68_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5SAG0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5SB31_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XSC1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZH6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZI2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZI3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZI8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZI9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZK9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZL8_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZP7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZR9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZT6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZX9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XZY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y011_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y065_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y070_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y078_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y0E5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y0F3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y0G2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y0H4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5Y0J7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6R0Q1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6R0W6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RLY3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RMU0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RPE6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RRW7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VH99_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VHA9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VIB9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VIH5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VIM0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-116	2,24E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VJ16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VK16_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VKA3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VLN4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6WQA1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6WQG6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7Y664_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YCC7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YCE0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YCE5_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YCF3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YEF1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q85KW0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q85KW2_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q85KZ1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q85L04_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q85L10_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8HNQ7_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8WCY1_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B1S4_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B1S6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B2U6_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B2W9_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B2X0_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	1,00E-115	7,07E-106	42	99	64,4826	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	COX3_HUMAN	COX1_HUMAN	COX3_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:COX3	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A0S0W7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A0S2P1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A0S3T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A0SA07_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1Z455_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A1Z4V2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A4ZKZ0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YW54_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YWD1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6YXV0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z3M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6Z6E8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZEU4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZF47_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZFK3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A6ZHA9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A7LDC6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A7LF11_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	A7LFA2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B0Z6W4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B1W855_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2CB37_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-107	7,07E-102	42	95	63,1664	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2WRY8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XHF9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XHT9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XIR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XL43_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XP28_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B2XPS3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B3DE06_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B3GUF3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	B5M7M0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6K5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-109	7,07E-103	42	96	63,498	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6K6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6K7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	98	64,1561	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6L3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6M4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6M5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6M7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C5H6M8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C8XWJ6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C8Y3G4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C8Y3Q5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C8YBL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	C9D661_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D1G421_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D2IKF4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D2K1G3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D3YPT7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D5M8T1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	D7NUN3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E0AF97_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	100	64,8074	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E2DTL8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	100	64,8074	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E2JFC4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E2JJS5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5DZN4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5E079_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5E1A6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5E1V1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5EWG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5EWL4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5EWR3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	E5FWC0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q06TE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q09U41_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7D8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7F1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7J0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7K3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-112	2,24E-104	42	98	64,1561	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q0Z7S0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q15HH9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q19MP7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q305H0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4EYL1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4EZD4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F4V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4F6A2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GCC3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GCG2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GCZ4_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GHE1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GQP0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GVP5_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q4GW12_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	100	64,8074	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5S971_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5SA98_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5SAP1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5SB08_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q5XRW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6R0V6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RKW8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RNN7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6RQ80_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VIG7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VJD8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q6VJJ3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7Y626_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7Y6M3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7Y6N0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YCE6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q7YEH2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q85KS0_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8HNR1_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8HNR6_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8HQB7_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-113	7,07E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q8WCW3_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B138_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B1F9_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	Q9B2U8_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	1,00E-114	2,24E-105	42	99	64,4826	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	COX2_YEAST	COX1_HUMAN	COX2_HUMAN	5,00E-96	3,00E-47	1,22E-71	42	42	42	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MKL8|R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_21205 PE=3 SV=1	COX2_HUMAN	COX1_HUMAN	COX2_HUMAN	5,00E-96	0	0	42	100	64,8074	1	1	0	COX1:COX2	in vivo	hprd
tr|R4MCD1|R4MCD1_MYCTX Malate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=mdh PE=3 SV=1	MDHC_HUMAN	MDHC_HUMAN	MDHC_HUMAN	3,00E-88	0	0	51	100	71,4143	1	1	0	Ldh_1_N:Ld	in vitro	hprd
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	blue native	intact
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	blue native	intact
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	B4DY56_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	95	54,2679	1	1	0	ATP-synt:A	in vitro	hprd
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPA_HUMAN	ATPG_HUMAN	ATPA_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	in vitro	hprd
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPB_HUMAN	ATPG_HUMAN	ATPB_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	in vitro	hprd
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
tr|R4MCL4|R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	ATPD_HUMAN	ATPG_HUMAN	ATPD_HUMAN	7,00E-25	0	0	31	100	55,6776	1	1	0	ATP-synt:A	blue native	intact
tr|R4MFC5|R4MFC5_MYCTX 50S ribosomal protein L2 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=rplB PE=3 SV=1	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
tr|R4MFC5|R4MFC5_MYCTX 50S ribosomal protein L2 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=rplB PE=3 SV=1	RL6_HUMAN	RL8_HUMAN	RL6_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
tr|R4MFC5|R4MFC5_MYCTX 50S ribosomal protein L2 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=rplB PE=3 SV=1	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
tr|R4MFC5|R4MFC5_MYCTX 50S ribosomal protein L2 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=rplB PE=3 SV=1	RL30_HUMAN	RL8_HUMAN	RL30_HUMAN	3,00E-13	0	0	31	100	55,6776	0	1	0	-	in vivo	hprd
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_a	blue native	intact

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_a	blue native	intact
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPG_HUMAN	ATPA_HUMAN	ATPG_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_a	in vitro	hprd
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_a	blue native	intact
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPB_HUMAN	ATPA_HUMAN	ATPB_HUMAN	1,00E-157	0	0	54	100	73,4847	1	1	0	ATP-synt_a	blue native	intact
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	1,00E-157	0	0	54	100	73,4847	0	1	0	-	blue native	intact
tr|R4MH86|R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	ATPD_HUMAN	ATPA_HUMAN	ATPD_HUMAN	1,00E-157	0	0	54	100	73,4847	0	1	0	-	blue native	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP71_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	SMAD3_HUMAN	CH60_HUMAN	SMAD2_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	display tec	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TBB2C_HUMAN	CH60_HUMAN	TBB5_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	HSP7C_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TBB2C_HUMAN	CH60_HUMAN	TBA1A_HUMAN	1,00E-119	2,00E-99	1,41E-109	46	40	42,8952	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTH_HUMAN	1,00E-119	0	0	46	93	65,4064	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTB_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ACTB_HUMAN	CH60_HUMAN	ACTG_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP	cross-linkin	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP	biochemica	biogrid
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP	two hybrid	biogrid
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9UNM1_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	1,00E-38	3,16E-79	46	100	67,8233	1	1	0	Cpn60_TCP	two hybrid	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TCP	cross-linkin	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TCP	biochemica	biogrid
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TCP	two hybrid	biogrid
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TCP	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TCP	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH10_HUMAN	CH60_HUMAN	CH10_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	Cpn60_TCP	two hybrid	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP71_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-119	0	0	46	64	54,2586	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HSP7C_HUMAN	CH60_HUMAN	GRP78_HUMAN	1,00E-119	0	0	46	65	54,6809	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B7Z4F6_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	95	66,106	1	1	0	-	in vitro	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B7Z5E7_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	87	63,2614	0	1	0	-	in vitro	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	CH60_HUMAN	CH60_HUMAN	CH60_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	-	in vitro	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	83	61,79	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	80	60,663	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ENPL_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	1,00E-151	1,00E-135	46	46	46	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90B_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	85	62,53	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90A_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DGL0_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	98	67,1416	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DMA2_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	94	65,7571	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	ENPL_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	1,00E-156	3,16E-138	46	48	46,9894	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90A_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	86	62,8967	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	HS90B_HUMAN	CH60_HUMAN	HS90B_HUMAN	1,00E-119	0	0	46	100	67,8233	0	1	0	-	molecular s	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	A1JUI8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	A8K2X8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	1,00E-60	3,16E-90	46	31	37,7624	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	A8K3C3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B2R9K8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DDU6_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	1,00E-59	1,00E-89	46	31	37,7624	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DPJ8_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DX08_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-58	7,07E-89	46	30	37,1484	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q59ET3_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	99	67,4833	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TCPD_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	5,00E-57	2,24E-88	46	30	37,1484	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TCPW_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	85	62,53	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	TCPZ_HUMAN	CH60_HUMAN	TCPZ_HUMAN	1,00E-119	0	0	46	100	67,8233	1	1	0	-	surface pla	intact
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	B4DR68_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	92	65,0538	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q53FS6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q53G55_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q59EK6_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
tr|R4MDA5|R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Q9BV61_HUMAN	CH60_HUMAN	TRAP1_HUMAN	1,00E-119	0	0	46	99	67,4833	0	1	0	-	in vivo	hprd
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:G	fluorescent	mint
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	Q2TSD0_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	99	70,3562	1	1	0	Gp_dh_C:G	in vitro	hprd
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	1,00E-134	2,45E-107	50	68	58,3095	1	1	0	Gp_dh_N:G	fluorescent	mint
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	G3PT_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	1,00E-134	2,45E-107	50	68	58,3095	1	1	0	Gp_dh_N:G	in vitro	hprd
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_N:G	fluorescent	mint

Query protein	Predicted partner	Query homolog sequence	Predicted partner homolog sequence	Query-Template Blast E-value	Predicted partner-Template Blast E-value	Joint e-value	Query-Template identities	Predicted partner-Template identities	Joint identities	Pfam domain-domain interactions found (0: False, 1: True)	Sharing GO terms found (0: False, 1: True)	Interaction found directly in database. (0: False, 1: True)	Interacting Pfam domains	Template interaction detection method	Template interaction source database
tr|R4MD46|R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	G3P_HUMAN	G3P_HUMAN	G3P_HUMAN	6,00E-80	0	0	50	100	70,7107	1	1	0	Gp_dh_N:G	in vitro	hprd
tr|R4M2F9|R4M2F9_MYCTX Adenylosuccinate synthetase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=purA PE=3 SV=1	B4E1L0_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	78	58,5833	1	1	0	-	in vitro	hprd
tr|R4M2F9|R4M2F9_MYCTX Adenylosuccinate synthetase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=purA PE=3 SV=1	PURA1_HUMAN	PURA1_HUMAN	PURA1_HUMAN	4,00E-89	0	0	44	100	66,3325	1	1	0	-	in vitro	hprd
#Finished correctly															