

SeqID	Localization	Score
sp P9WFE1 DCUP_MYCTU Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) Cytoplasmic		7,5
sp P9WGD7 SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) Cytoplasmic	membrane or plasma membrane	8,78
sp P9WGV1 METH_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) Cytoplasmic		10
sp P9WGV3 SAHH_MYCTU Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ah Cytoplasmic		9,97
sp P9WHA5 RL2_MYCTU 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rplE Cytoplasmic		7,5
sp P9WHH9 DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=gdh Cytoplasmic		9,97
sp P9WHN3 PURA_MYCTU Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=adp Cytoplasmic		9,97
sp P9WHU7 P5CR_MYCTU Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pyr5 Cytoplasmic		9,67
sp P9WID1 PGK_MYCTU Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pgk1 Cytoplasmic		10
sp P9WK13 MDH_MYCTU Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mdh1 Cytoplasmic	Unknown	2,5
sp P9WK25 MAOX_MYCTU Putative malate oxidoreductase [NAD] OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mdh2 Cytoplasmic	membrane or plasma membrane	8,16
sp P9WKE5 KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pyk PE=1 Cytoplasmic		7,5
sp P9WMJ7 HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htp Cytoplasmic		9,97
sp P9WMJ9 DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK Cytoplasmic		9,97
sp P9WN69 G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=g6p Cytoplasmic		9,95
sp P9WN83 G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=g3p Cytoplasmic		10
sp P9WP71 COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=cox1 Cytoplasmic	membrane or plasma membrane	10
sp P9WPE9 CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL Cytoplasmic		9,97
sp P9WPE7 CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 Cytoplasmic		9,97
sp P9WPS9 CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpf Cytoplasmic	membrane or plasma membrane	10
sp P9WPU7 ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpA Cytoplasmic		9,97
sp P9WPU9 ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpG Cytoplasmic		7,5
sp P9WPW7 ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=argS Cytoplasmic		7,5
sp A5TZ77 DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK Cytoplasmic		9,97
sp A5TZ84 PURA_MYCTA Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=adp Cytoplasmic		9,97
sp A5TZG6 CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 Cytoplasmic		9,97
sp A5U090 RL2_MYCTA 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=rplB Cytoplasmic		7,5
sp A5U0Y6 G6PI_MYCTA Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=g6p Cytoplasmic		9,95
sp A5U1T8 MDH_MYCTA Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=mdh1 Cytoplasmic	Unknown	2,5
sp A5U207 ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpA Cytoplasmic		9,97
sp A5U208 ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpG Cytoplasmic		7,5
sp A5U294 METH_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ah Cytoplasmic		10
sp A5U2D9 PGK_MYCTA Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pgk1 Cytoplasmic		10
sp A5U315 ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=argS Cytoplasmic		7,5
sp A5U4Y2 HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htp Cytoplasmic		9,97
sp A5U630 DCUP_MYCTA Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dcuA Cytoplasmic		7,5
sp A5U7S2 SAHH_MYCTA Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ah Cytoplasmic		9,97
sp A5U892 CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 Cytoplasmic		9,97
tr A5TZI9 A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=gdh Cytoplasmic		9,97
tr A5TZM9 A5TZM9_MYCTA Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pyr5 Cytoplasmic		9,67
tr A5U2D8 A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=g3p Cytoplasmic		10
tr A5U2X3 A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=1 Cytoplasmic		7,5
tr A5U422 A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF Cytoplasmic	membrane or plasma membrane	10
tr A5U521 A5U521_MYCTA Malate oxidoreductase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=mdh2 Cytoplasmic	membrane or plasma membrane	8,16
tr A5U6S1 A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=srpA Cytoplasmic	membrane or plasma membrane	8,78
tr A5U757 A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=cox1 Cytoplasmic	membrane or plasma membrane	10
sp P9WFE0 DCUP_MYCTO Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dcuA Cytoplasmic		7,5
sp P9WGD6 SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=srpA Cytoplasmic	membrane or plasma membrane	8,78
sp P9WGV0 METH_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ah Cytoplasmic		10
sp P9WGV2 SAHH_MYCTO Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ah Cytoplasmic		9,97
sp P9WHA4 RL2_MYCTO 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=rplB Cytoplasmic		7,5
sp P9WHH8 DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=gdh Cytoplasmic		9,97
sp P9WHN2 PURA_MYCTO Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=adp Cytoplasmic		9,97
sp P9WHU6 P5CR_MYCTO Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyr5 Cytoplasmic		9,67
sp P9WID0 PGK_MYCTO Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pgk1 Cytoplasmic		10
sp P9WKI6 IMDH_MYCTO Inosine-5'-monophosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=mdh1 Cytoplasmic	Unknown	2,5
sp P9WK12 MDH_MYCTO Malate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=mdh1 Cytoplasmic	Unknown	2,5
sp P9WK24 MAOX_MYCTO Putative malate oxidoreductase [NAD] OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=mdh2 Cytoplasmic	membrane or plasma membrane	8,16
sp P9WKE4 KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 Cytoplasmic		7,5
sp P9WMJ6 HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htp Cytoplasmic		9,97
sp P9WMJ8 DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK Cytoplasmic		9,97
sp P9WN68 G6PI_MYCTO Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=g6p Cytoplasmic		9,95
sp P9WN82 G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=g3p Cytoplasmic		10
sp P9WP70 COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=cox1 Cytoplasmic	membrane or plasma membrane	10
sp P9WPE6 CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 Cytoplasmic		9,97
sp P9WPE8 CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 Cytoplasmic		9,97
sp P9WPS8 CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpf Cytoplasmic	membrane or plasma membrane	10
sp P9WPU6 ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpA Cytoplasmic		9,97
sp P9WPU8 ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpG Cytoplasmic		7,5
sp P9WPW6 ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=argS Cytoplasmic		7,5
tr A0A0H3L5C8 A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic		9,97
tr A0A0H3L5N9 A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic		9,97
tr A0A0H3L5R1 A0A0H3L5R1_MYCTE Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic		9,67
tr A0A0H3L6B9 A0A0H3L6B9_MYCTE 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic		7,5
tr A0A0H3L7U3 A0A0H3L7U3_MYCTE Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic		9,95
tr A0A0H3L7V8 A0A0H3L7V8_MYCTE Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic	Unknown	2,5
tr A0A0H3L814 A0A0H3L814_MYCTE ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic		7,5
tr A0A0H3L910 A0A0H3L910_MYCTE Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic		7,5
tr A0A0H3L9H4 A0A0H3L9H4_MYCTE Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM102) Cytoplasmic		10

SeqID	Localization	Score
tr A0A0H3LC41 A0A0H3LC41_MYCTE Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 35801 / Cytoplasmic		9,97
tr A0A0H3LCC3 A0A0H3LCC3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 10 Cytoplasmic		9,97
tr A0A0H3LCK6 A0A0H3LCK6_MYCTE Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 35 Cytoplasmic		7,5
tr A0A0H3LCN1 A0A0H3LCN1_MYCTE Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain Cytoplasmic		10
tr A0A0H3LD73 A0A0H3LD73_MYCTE Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 35 Cytoplasmic	membrane or plasma membrane	8,78
tr A0A0H3LE62 A0A0H3LE62_MYCTE Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM Cytoplasmic		9,97
tr A0A0H3LEL3 A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 Cytoplasmic		9,97
tr A0A0H3LEY6 A0A0H3LEY6_MYCTE ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 35801 / Cytoplasmic		9,97
tr A0A0H3LFE0 A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TM Cytoplasmic		9,97
tr A0A0H3LHR0 A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 358 Cytoplasmic	membrane or plasma membrane	10
tr A0A0H3LI71 A0A0H3LI71_MYCTE Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 10 Cytoplasmic	membrane or plasma membrane	8,16
tr R4M2F9 R4M2F9_MYCTX Adenylosuccinate synthetase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN Cytoplasmic		9,97
tr R4M485 R4M485_MYCTX Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 Cytoplasmic		9,95
tr R4M5K1 R4M5K1_MYCTX Phosphoglycerate kinase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=p Cytoplasmic		10
tr R4MCD1 R4MCD1_MYCTX Malate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=mc	Unknown	2,5
tr R4MCL4 R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN Cytoplasmic		7,5
tr R4MD46 R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 C Cytoplasmic		10
tr R4MDA5 R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL J Cytoplasmic		9,97
tr R4MFC5 R4MFC5_MYCTX 50S ribosomal protein L2 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=r Cytoplasmic		7,5
tr R4MH86 R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN Cytoplasmic		9,97
tr R4MJZ1 R4MJZ1_MYCTX Malate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113 Cytoplasmic	membrane or plasma membrane	8,16
tr R4MKL8 R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 Cytoplasmic	membrane or plasma membrane	10