

VICMpred

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Score of Different Functional Class

Protein ID	Cellular Process	Information Molecule	Metabolism	Virulence factors	Predicted Functional Class
DCUP_MYCTU	-3,4104556	-3,1159716	2,942717	-2,9097476	Metabolism Molecule
SRP54_MYCTU	-0,042314953	-2,7006337	0,049646604	-4,2457884	Metabolism Molecule
METK_MYCTU	-5,6361408	-6,6128921	4,2966992	-5,3134929	Metabolism Molecule
SAHH_MYCTU	-0,96370643	-1,6544067	0,2823385	1,7453249	Virulence factors
RL2_MYCTU	1,4549681	-2,4318072	-0,9536611	-0,79782661	Cellular Process
DLDH_MYCTU	-0,53241754	-3,2095259	-0,52659624	0,61592396	Virulence factors
PURA_MYCTU	1,6035135	-5,5485944	-0,5690321	-0,55826015	Cellular Process
P5CR_MYCTU	-2,9887364	-3,2379582	4,2833435	-5,2423082	Metabolism Molecule
PGK_MYCTU	-4,941717	-2,9775698	5,9982872	-6,3129286	Metabolism Molecule
MDH_MYCTU	-1,1951414	-2,0331561	0,052302819	1,8251424	Virulence factors
MAOX_MYCTU	0,83514064	-3,7499108	-0,13323144	-0,66625881	Cellular Process
KPYK_MYCTU	-3,3202981	0,22924209	0,27179099	0,48635621	Virulence factors
HTPG_MYCTU	1,7195179	-3,102554	-4,129728	0,70503559	Cellular Process
DNAK_MYCTU	0,12873883	-2,2247127	-3,1720472	3,122894	Virulence factors
G6PI_MYCTU	-1,6146975	-3,4022331	0,8029382	0,13665876	Metabolism Molecule
G3P_MYCTU	0,000345373	-3,8491643	0,18829626	0,25046761	Virulence factors
COX1_MYCTU	-1,4613637	-3,952077	3,791911	-3,920607	Metabolism Molecule
CH602_MYCTU	-1,8726251	-2,5468882	-0,5128164	-0,99790336	Metabolism Molecule
CH601_MYCTU	-3,7201349	-1,4580412	-0,13221619	-1,4837894	Metabolism Molecule
CTPF_MYCTU	-4,5960206	-0,89005506	-6,0889971	-2,0937964	Information Molecule
ATPA_MYCTU	-0,093256717	-2,5848745	-1,3083101	2,5287839	Virulence factors
ATPG_MYCTU	2,6522874	-3,0495733	-3,6873911	-1,0846351	Cellular Process
ASSY_MYCTU	-0,94847998	-6,9408646	2,3885113	-1,8042376	Metabolism Molecule
DNAK_MYCTA	0,12873883	-2,2247127	-3,1720472	3,122894	Virulence factors
PURA_MYCTA	1,6035135	-5,5485944	-0,5690321	-0,55826015	Cellular Process
CH601_MYCTA	-1,8726251	-2,5468882	-0,5128164	-0,99790336	Metabolism Molecule
RL2_MYCTA	1,4549681	-2,4318072	-0,9536611	-0,79782661	Cellular Process
G6PI_MYCTA	-1,6146975	-3,4022331	0,8029382	0,13665876	Metabolism Molecule
MDH_MYCTA	-1,1951414	-2,0331561	0,052302819	1,8251424	Virulence factors
ATPA_MYCTA	-0,093256717	-2,5848745	-1,3083101	2,5287839	Virulence factors
ATPG_MYCTA	2,6522874	-3,0495733	-3,6873911	-1,0846351	Cellular Process
METK_MYCTA	-5,6361408	-6,6128921	4,2966992	-5,3134929	Metabolism Molecule
PGK_MYCTA	-4,941717	-2,9775698	5,9982872	-6,3129286	Metabolism Molecule
ASSY_MYCTA	-0,94847998	-6,9408646	2,3885113	-1,8042376	Metabolism Molecule
HTPG_MYCTA	1,7195179	-3,102554	-4,129728	0,70503559	Cellular Process

Protein ID	Cellular Process	Information Molecule	Metabolism	Virulence factors	Predicted Functional Class
DCUP_MYCTA	-3,4104556	-3,1159716	2,942717	-2,9097476	Metabolism Molecule
SAHH_MYCTA	-0,96370643	-1,6544067	0,2823385	1,7453249	Virulence factors
CH602_MYCTA	-3,7201349	-1,4580412	-0,13221619	-1,4837894	Metabolism Molecule
A5TZI9_MYCTA	-0,53241754	-3,2095259	-0,52659624	0,61592396	Virulence factors
A5TzM9_MYCTA	-2,9887364	-3,2379582	4,2833435	-5,2423082	Metabolism Molecule
A5U2D8_MYCTA	0,000345373	-3,8491643	0,18829626	0,25046761	Virulence factors
A5U2X3_MYCTA	-3,3202981	0,22924209	0,27179099	0,48635621	Virulence factors
A5U422_MYCTA	-4,5960206	-0,89005506	-6,0889971	-2,0937964	Information Molecule
A5U521_MYCTA	0,83514064	-3,7499108	-0,13323144	-0,66625881	Cellular Process
A5U6S1_MYCTA	-0,042314953	-2,7006337	0,049646604	-4,2457884	Metabolism Molecule
A5U757_MYCTA	-1,4613637	-3,952077	3,791911	-3,920607	Metabolism Molecule
DCUP_MYCTO	-3,4104556	-3,1159716	2,942717	-2,9097476	Metabolism Molecule
SRP54_MYCTO	-0,042314953	-2,7006337	0,049646604	-4,2457884	Metabolism Molecule
METK_MYCTO	-5,6361408	-6,6128921	4,2966992	-5,3134929	Metabolism Molecule
SAHH_MYCTO	-0,96370643	-1,6544067	0,2823385	1,7453249	Virulence factors
RL2_MYCTO	1,4549681	-2,4318072	-0,9536611	-0,79782661	Cellular Process
DLDH_MYCTO	-0,53241754	-3,2095259	-0,52659624	0,61592396	Virulence factors
PURA_MYCTO	1,6035135	-5,5485944	-0,5690321	-0,55826015	Cellular Process
P5CR_MYCTO	-2,9887364	-3,2379582	4,2833435	-5,2423082	Metabolism Molecule
PGK_MYCTO	-4,941717	-2,9775698	5,9982872	-6,3129286	Metabolism Molecule
MDH_MYCTO	-1,1951414	-2,0331561	0,052302819	1,8251424	Virulence factors
MAOX_MYCTO	0,83514064	-3,7499108	-0,13323144	-0,66625881	Cellular Process
KPYK_MYCTO	-3,3202981	0,22924209	0,27179099	0,48635621	Virulence factors
HTPG_MYCTO	1,7195179	-3,102554	-4,129728	0,70503559	Cellular Process
DNAK_MYCTO	0,12873883	-2,2247127	-3,1720472	3,122894	Virulence factors
G6PI_MYCTO	-1,6146975	-3,4022331	0,8029382	0,13665876	Metabolism Molecule
G3P_MYCTO	0,000345373	-3,8491643	0,18829626	0,25046761	Virulence factors
COX1_MYCTO	-1,4613637	-3,952077	3,791911	-3,920607	Metabolism Molecule
CH602_MYCTO	-1,8726251	-2,5468882	-0,5128164	-0,99790336	Metabolism Molecule
CH601_MYCTO	-3,7201349	-1,4580412	-0,13221619	-1,4837894	Metabolism Molecule
CTPF_MYCTO	-4,5960206	-0,89005506	-6,0889971	-2,0937964	Information Molecule
ATPA_MYCTO	-0,093256717	-2,5848745	-1,3083101	2,5287839	Virulence factors
ATPG_MYCTO	2,6522874	-3,0495733	-3,6873911	-1,0846351	Cellular Process
ASSY_MYCTO	-0,94847998	-6,9408646	2,3885113	-1,8042376	Metabolism Molecule
A0A0H3L5C8_MYCTE	0,12873883	-2,2247127	-3,1720472	3,122894	Virulence factors
A0A0H3L5N9_MYCTE	-0,53241754	-3,2095259	-0,52659624	0,61592396	Virulence factors
A0A0H3L5R1_MYCTE	-2,9887364	-3,2379582	4,2833435	-5,2423082	Metabolism Molecule
A0A0H3L6B9_MYCTE	1,4549681	-2,4318072	-0,9536611	-0,79782661	Cellular Process
A0A0H3L7U3_MYCTE	-1,6146975	-3,4022331	0,8029382	0,13665876	Metabolism Molecule
A0A0H3L7V8_MYCTE	-1,1951414	-2,0331561	0,052302819	1,8251424	Virulence factors
A0A0H3L814_MYCTE	2,6522874	-3,0495733	-3,6873911	-1,0846351	Cellular Process

Protein ID	Cellular Process	Information Molecule	Metabolism	Virulence factors	Predicted Functional Class
A0A0H3L910_MYCTE	-0,94847998	-6,9408646	2,3885113	-1,8042376	Metabolism Molecule
A0A0H3L9H4_MYCTE	-4,941717	-2,9775698	5,9982872	-6,3129286	Metabolism Molecule
A0A0H3LC41_MYCTE	1,6035135	-5,5485944	-0,5690321	-0,55826015	Cellular Process
A0A0H3LCC3_MYCTE	-1,8726251	-2,5468882	-0,5128164	-0,99790336	Metabolism Molecule
A0A0H3LCK6_MYCTE	-2,9088984	-2,3930906	2,9844691	-2,676038	Metabolism Molecule
A0A0H3LCN1_MYCTE	0,000345373	-3,8491643	0,18829626	0,25046761	Virulence factors
A0A0H3LD73_MYCTE	-0,042314953	-2,7006337	0,049646604	-4,2457884	Metabolism Molecule
A0A0H3LE62_MYCTE	-0,96370643	-1,6544067	0,2823385	1,7453249	Virulence factors
A0A0H3LEL3_MYCTE	-3,7201349	-1,4580412	-0,13221619	-1,4837894	Metabolism Molecule
A0A0H3LEY6_MYCTE	-0,093256717	-2,5848745	-1,3083101	2,5287839	Virulence factors
A0A0H3LFE0_MYCTE	1,7195179	-3,102554	-4,129728	0,70503559	Cellular Process
A0A0H3LHR0_MYCTE	-1,4613637	-3,952077	3,791911	-3,920607	Metabolism Molecule
A0A0H3LI71_MYCTE	0,83514064	-3,7499108	-0,13323144	-0,66625881	Cellular Process
A0A051TU38_MYCTX	-0,51725556	-2,7817403	0,9888088	0,65311687	Metabolism Molecule
A0A051TUE3_MYCTX	-3,7615688	-6,3766579	3,2661261	-2,9696303	Metabolism Molecule
A0A051TUY3_MYCTX	-2,2856763	-1,0237191	-2,6386934	-1,4459337	Information Molecule
A0A051TVN9_MYCTX	-2,8332396	-3,0047122	1,675367	-0,5449572	Metabolism Molecule
R4M2F9_MYCTX	1,6035135	-5,5485944	-0,5690321	-0,55826015	Cellular Process
R4M485_MYCTX	-1,6146975	-3,4022331	0,8029382	0,13665876	Metabolism Molecule
R4M5K1_MYCTX	-4,941717	-2,9775698	5,9982872	-6,3129286	Metabolism Molecule
R4MCD1_MYCTX	-1,1951414	-2,0331561	0,052302819	1,8251424	Virulence factors
R4MCL4_MYCTX	2,6522874	-3,0495733	-3,6873911	-1,0846351	Cellular Process
R4MD46_MYCTX	0,000345373	-3,8491643	0,18829626	0,25046761	Virulence factors
R4MDA5_MYCTX	-1,8726251	-2,5468882	-0,5128164	-0,99790336	Metabolism Molecule
R4MFC5_MYCTX	1,4549681	-2,4318072	-0,9536611	-0,79782661	Cellular Process
R4MH86_MYCTX	-0,093256717	-2,5848745	-1,3083101	2,5287839	Virulence factors
R4MJZ1_MYCTX	0,83514064	-3,7499108	-0,13323144	-0,66625881	Cellular Process
R4MKL8_MYCTX	-1,4613637	-3,952077	3,791911	-3,920607	Metabolism Molecule

PREDICTION RESULTS OF VIRULENT PRED

S. no.	Protein name	Prediction results amino acid- composition-based	Predicted scores	Prediction results dipeptide-composition- based	Predicted scores	Prediction results higher order dipeptide- composition-based	Predicted scores	Prediction results similarity-based using PSI- BLAST	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores
1	>sp P9WFE1 DCUP_MYCTU Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=heme PE=1 SV=1	Non-Virulent	-0,599	Non-Virulent	-0,377	Non-Virulent	-0,614	No hits obtained	Zero	Non-Virulent	-0,591	No Hits obtained	Zero
2	>sp P9WGD7 SRP54_MYCTU Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ffh PE=1 SV=1	Non-Virulent	-0,958	Non-Virulent	-1,033	Non-Virulent	-1,391	Virulent	7,00E-75	Non-Virulent	-0,878	Non-Virulent	-0,98
3	>sp P9WGV1 METK_MYCTU S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=metK PE=1 SV=1	Non-Virulent	-1,426	Non-Virulent	-0,94	Non-Virulent	-1,349	Virulent	0	Non-Virulent	-1,481	Non-Virulent	-0,378
4	>sp P9WGV3 SAHH_MYCTU Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ahcY PE=1 SV=1	Non-Virulent	-1,946	Non-Virulent	-0,453	Non-Virulent	-1,216	No hits obtained	Zero	Non-Virulent	-1,275	Non-Virulent	-1,029
5	>sp P9WHA5 RL2_MYCTU 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rplB PE=1 SV=1	Virulent	0,9134	Virulent	0,2046	Virulent	0,0324	No hits obtained	Zero	Virulent	0,6771	Non-Virulent	-0,999
6	>sp P9WHH9 DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpdC PE=1 SV=1	Non-Virulent	-2,16	Non-Virulent	-1,78	Non-Virulent	-1,599	Virulent	e-180	Non-Virulent	-1,128	Virulent	0,9832
7	>sp P9WHN3 PURA_MYCTU Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=purA PE=1 SV=1	Non-Virulent	-1,074	Non-Virulent	-1,006	Non-Virulent	-1,41	Virulent	0	Non-Virulent	-0,907	Non-Virulent	-0,989
8	>sp P9WHU7 P5CR_MYCTU Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=proC PE=1 SV=1	Non-Virulent	-0,348	Virulent	0,928	Non-Virulent	-0,146	Virulent	e-130	Virulent	0,0265	Non-Virulent	-1,024
9	>sp P9WID1 PGK_MYCTU Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pgk PE=1 SV=1	Non-Virulent	-0,717	Non-Virulent	-0,749	Non-Virulent	-0,752	No hits obtained	Zero	Non-Virulent	-0,722	Virulent	1,0003
10	>sp P9WK13 MDH_MYCTU Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mdh PE=1 SV=1	Non-Virulent	-0,746	Non-Virulent	-0,727	Non-Virulent	-0,524	Virulent	3,00E-91	Non-Virulent	-0,871	Non-Virulent	-0,995

S. no.	Protein name	Prediction results amino acid- composition-based	Predicted scores	Prediction results diptide-composition- based	Predicted scores	Prediction results higher order diptide- composition-based	Predicted scores	Prediction results similarity-based using PSI- BLAST	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores
11	>sp P9WK25 MAOX_MYCTU Putative malate oxidoreductase [NAD] OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mez PE=1 SV=1	Non-Virulent	-1,247	Non-Virulent	-1,305	Non-Virulent	-1,574	No hits obtained	Zero	Non-Virulent	-1,226	Non-Virulent	-1,01
12	>sp P9WKE5 KPYK_MYCTU Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pyk PE=1 SV=1	Non-Virulent	-1,276	Non-Virulent	-0,914	Non-Virulent	-1,226	Virulent	0	Non-Virulent	-0,643	Non-Virulent	-1,077
13	>sp P9WMJ7 HTPG_MYCTU Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=htpG PE=1 SV=1	Non-Virulent	-1,069	Non-Virulent	-0,462	Non-Virulent	-0,978	Virulent	0	Non-Virulent	-1,349	Non-Virulent	-0,306
14	>sp P9WMJ9 DNAK_MYCTU Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1	Non-Virulent	-1,906	Non-Virulent	-0,977	Non-Virulent	-1,398	Virulent	0	Non-Virulent	-2,007	Non-Virulent	-1,004
15	>sp P9WN69 G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pgi PE=1 SV=1	Non-Virulent	-0,155	Non-Virulent	-0,055	Non-Virulent	-0,819	No hits obtained	Zero	Non-Virulent	-0,3	Non-Virulent	-1,043
16	>sp P9WN83 G3P_MYCTU Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=gap PE=1 SV=1	Non-Virulent	-0,528	Non-Virulent	-0,887	Non-Virulent	-0,241	Virulent	e-166	Non-Virulent	-1,059	Non-Virulent	-0,919
17	>sp P9WP71 COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1	Non-Virulent	-1,421	Non-Virulent	-2,042	Non-Virulent	-1,818	Virulent	0	Non-Virulent	-1,767	Non-Virulent	-1,067
18	>sp P9WPE9 CH601_MYCTU 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL1 PE=1 SV=1	Non-Virulent	-1,726	Non-Virulent	-1,488	Non-Virulent	-1,576	Virulent	0	Non-Virulent	-1,524	Non-Virulent	-1,062
19	>sp P9WPE7 CH602_MYCTU 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=groEL2 PE=1 SV=1	Non-Virulent	-1,691	Non-Virulent	-1,329	Non-Virulent	-2,671	Virulent	0	Non-Virulent	-1,83	Non-Virulent	-1,048
20	>sp P9WPS9 CTPF_MYCTU Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpF PE=1 SV=1	Non-Virulent	-1,376	Non-Virulent	-1,902	Non-Virulent	-1,748	Virulent	0	Non-Virulent	-1,077	Non-Virulent	-0,645
21	>sp P9WPU7 ATPA_MYCTU ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpA PE=1 SV=1	Non-Virulent	-2,125	Non-Virulent	-1,155	Non-Virulent	-1,761	Virulent	0	Non-Virulent	-1,488	Non-Virulent	-1,008

S. no.	Protein name	Prediction results amino acid- composition-based	Predicted scores	Prediction results dipeptide-composition- based	Predicted scores	Prediction results higher order dipeptide- composition-based	Predicted scores	Prediction results similarity-based using PSI- BLAST	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores
22	>sp P9WPU9 ATPG_MYCTU ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=atpG PE=1 SV=1	Non-Virulent	-0,22	Non-Virulent	-0,999	Virulent	0,0114	Virulent	e-127	Non-Virulent	-0,005	Non-Virulent	-1,017
23	>sp P9WPW7 ASSY_MYCTU Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=argG PE=1 SV=1	Non-Virulent	-1,821	Non-Virulent	-1,509	Non-Virulent	-1,427	No hits obtained	Zero	Non-Virulent	-1,166	Non-Virulent	-1
24	>sp A5TZ77 DNAK_MYCTA Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaK PE=3 SV=1	Non-Virulent	-1,906	Non-Virulent	-0,977	Non-Virulent	-1,398	Virulent	0	Non-Virulent	-2,007	Non-Virulent	-1,115
25	>sp A5TZ84 PURA_MYCTA Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=purA PE=3 SV=1	Non-Virulent	-1,074	Non-Virulent	-1,006	Non-Virulent	-1,41	Virulent	0	Non-Virulent	-0,907	Non-Virulent	-1,043
26	>sp A5TZG6 CH601_MYCTA 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL1 PE=3 SV=1	Non-Virulent	-1,691	Non-Virulent	-1,329	Non-Virulent	-2,671	Virulent	0	Non-Virulent	-1,83	Non-Virulent	-1,024
27	>sp A5U090 RL2_MYCTA 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=rpIB PE=3 SV=1	Virulent	0,9134	Virulent	0,2046	Virulent	0,0324	No hits obtained	Zero	Virulent	0,6771	Non-Virulent	-0,645
28	>sp A5U0Y6 G6PI_MYCTA Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pgi PE=3 SV=1	Non-Virulent	-0,155	Non-Virulent	-0,055	Non-Virulent	-0,819	No hits obtained	Zero	Non-Virulent	-0,3	Virulent	0,9832
29	>sp A5U1T8 MDH_MYCTA Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=mdh PE=3 SV=1	Non-Virulent	-0,746	Non-Virulent	-0,727	Non-Virulent	-0,524	Virulent	3,00E-91	Non-Virulent	-0,871	Non-Virulent	-0,919
30	>sp A5U207 ATPA_MYCTA ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpA PE=3 SV=1	Non-Virulent	-2,125	Non-Virulent	-1,155	Non-Virulent	-1,761	Virulent	0	Non-Virulent	-1,488	Non-Virulent	-1,01
31	>sp A5U208 ATPG_MYCTA ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=atpG PE=3 SV=1	Non-Virulent	-0,22	Non-Virulent	-0,999	Virulent	0,0114	Virulent	e-127	Non-Virulent	-0,005	Non-Virulent	-1,017
32	>sp A5U294 METHK_MYCTA S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=metK PE=3 SV=1	Non-Virulent	-1,426	Non-Virulent	-0,94	Non-Virulent	-1,349	Virulent	0	Non-Virulent	-1,481	Non-Virulent	-1

S. no.	Protein name	Prediction results amino acid- composition-based	Predicted scores	Prediction results dipeptide-composition- based	Predicted scores	Prediction results higher order dipeptide- composition-based	Predicted scores	Prediction results similarity-based using PSI- BLAST	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores
33	>sp A5U2D9 PGK_MYCTA Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pgk PE=3 SV=1	Non-Virulent	-0,717	Non-Virulent	-0,749	Non-Virulent	-0,752	No hits obtained	Zero	Non-Virulent	-0,722	Non-Virulent	-1,029
34	>sp A5U315 ASSY_MYCTA Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=argG PE=3 SV=1	Non-Virulent	-1,821	Non-Virulent	-1,509	Non-Virulent	-1,427	No hits obtained	Zero	Non-Virulent	-1,166	Non-Virulent	-0,995
35	>sp A5U4Y2 HTPG_MYCTA Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=htpG PE=3 SV=1	Non-Virulent	-1,069	Non-Virulent	-0,462	Non-Virulent	-0,978	Virulent	0	Non-Virulent	-1,349	Non-Virulent	-1,115
36	>sp A5U630 DCUP_MYCTA Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=heme PE=3 SV=1	Non-Virulent	-0,599	Non-Virulent	-0,377	Non-Virulent	-0,614	No hits obtained	Zero	Non-Virulent	-0,591	Non-Virulent	-1,004
37	>sp A5U7S2 SAHH_MYCTA Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ahcY PE=3 SV=1	Non-Virulent	-1,946	Non-Virulent	-0,453	Non-Virulent	-1,216	No hits obtained	Zero	Non-Virulent	-1,275	Non-Virulent	-0,98
38	>sp A5U892 CH602_MYCTA 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=groL2 PE=3 SV=1	Non-Virulent	-1,726	Non-Virulent	-1,488	Non-Virulent	-1,576	Virulent	0	Non-Virulent	-1,524	Non-Virulent	-0,999
39	>tr A5TZI9 A5TZI9_MYCTA Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=lpd PE=3 SV=1	Non-Virulent	-2,16	Non-Virulent	-1,78	Non-Virulent	-1,599	Virulent	e-180	Non-Virulent	-1,128	Non-Virulent	-1,048
40	>tr A5TZM9 A5TZM9_MYCTA Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=proC PE=3 SV=1	Non-Virulent	-0,348	Virulent	0,928	Non-Virulent	-0,146	Virulent	e-130	Virulent	0,0265	Non-Virulent	-0,989
41	>tr A5U2D8 A5U2D8_MYCTA Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=gap PE=3 SV=1	Non-Virulent	-0,528	Non-Virulent	-0,887	Non-Virulent	-0,241	Virulent	e-166	Non-Virulent	-1,059	Virulent	1,0003
42	>tr A5U2X3 A5U2X3_MYCTA Pyruvate kinase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=pykA PE=3 SV=1	Non-Virulent	-1,276	Non-Virulent	-0,914	Non-Virulent	-1,226	Virulent	0	Non-Virulent	-0,643	Non-Virulent	-1,067
43	>tr A5U422 A5U422_MYCTA Metal cation transporting P-type ATPase CtpF OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctpF PE=4 SV=1	Non-Virulent	-1,376	Non-Virulent	-1,902	Non-Virulent	-1,748	Virulent	0	Non-Virulent	-1,077	Non-Virulent	-0,306

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44	>tr A5U521 A5U521_MYCTA Malate oxidoreductase OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=mez PE=3 SV=1	Non-Virulent	-1,247	Non-Virulent	-1,305	Non-Virulent	-1,574	No hits obtained	Zero	Non-Virulent	-1,226	Non-Virulent	-1,008
45	>tr A5U6S1 A5U6S1_MYCTA Signal recognition particle protein OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ffh PE=3 SV=1	Non-Virulent	-0,958	Non-Virulent	-1,033	Non-Virulent	-1,391	Virulent	7,00E-75	Non-Virulent	-0,878	Non-Virulent	-1,077
46	>tr A5U757 A5U757_MYCTA Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ctaD PE=3 SV=1	Non-Virulent	-1,421	Non-Virulent	-2,042	Non-Virulent	-1,818	Virulent	0	Non-Virulent	-1,767	Non-Virulent	-0,378
47	>sp P9WFE0 DCUP_MYCTO Uroporphyrinogen decarboxylase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=heme PE=3 SV=1	Non-Virulent	-0,599	Non-Virulent	-0,377	Non-Virulent	-0,614	No hits obtained	Zero	Non-Virulent	-0,591	Non-Virulent	-1,062
48	>sp P9WGD6 SRP54_MYCTO Signal recognition particle protein OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ffh PE=3 SV=1	Non-Virulent	-0,958	Non-Virulent	-1,033	Non-Virulent	-1,391	Virulent	7,00E-75	Non-Virulent	-0,878	Non-Virulent	-0,98
49	>sp P9WGV0 METK_MYCTO S-adenosylmethionine synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=metK PE=3 SV=1	Non-Virulent	-1,426	Non-Virulent	-0,94	Non-Virulent	-1,349	Virulent	0	Non-Virulent	-1,481	Non-Virulent	-0,378
50	>sp P9WGV2 SAHH_MYCTO Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ahcY PE=3 SV=1	Non-Virulent	-1,946	Non-Virulent	-0,453	Non-Virulent	-1,216	No hits obtained	Zero	Non-Virulent	-1,275	Non-Virulent	-1,029
51	>sp P9WHA4 RL2_MYCTO 50S ribosomal protein L2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=rplB PE=3 SV=1	Virulent	0,9134	Virulent	0,2046	Virulent	0,0324	No hits obtained	Zero	Virulent	0,6771	Non-Virulent	-0,999
52	>sp P9WHH8 DLDH_MYCTO Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=lpdC PE=3 SV=1	Non-Virulent	-2,16	Non-Virulent	-1,78	Non-Virulent	-1,599	Virulent	e-180	Non-Virulent	-1,128	Virulent	0,9832
53	>sp P9WHN2 PURA_MYCTO Adenylosuccinate synthetase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=purA PE=3 SV=1	Non-Virulent	-1,203	Non-Virulent	-0,903	Non-Virulent	-1,326	Virulent	0	Non-Virulent	-0,957	Non-Virulent	-0,989
54	>sp P9WHU6 P5CR_MYCTO Pyrroline-5-carboxylate reductase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=proC PE=3 SV=1	Non-Virulent	-0,348	Virulent	0,928	Non-Virulent	-0,146	Virulent	e-130	Virulent	0,0265	Non-Virulent	-1,016

S. no.	Protein name	Prediction results amino acid- composition-based	Predicted scores	Prediction results dipeptide-composition- based	Predicted scores	Prediction results higher order dipeptide- composition-based	Predicted scores	Prediction results similarity-based using PSI- BLAST	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores	Prediction results PSI-BLAST created PSSM profiles	Predicted scores
55	>sp P9WID0 PGK_MYCTO Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pgk PE=3 SV=1	Non-Virulent	-0,717	Non-Virulent	-0,749	Non-Virulent	-0,752	No hits obtained	Zero	Non-Virulent	-0,722	Virulent	1,0003
56	>sp P9WKI6 IMDH_MYCTO Inosine-5'-monophosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=guaB PE=3 SV=1	Non-Virulent	-0,877	Non-Virulent	-0,494	Non-Virulent	-0,801	Virulent	8,00E-32	Non-Virulent	-0,967	Non-Virulent	-0,995
57	>sp P9WK12 MDH_MYCTO Malate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=mdh PE=3 SV=1	Non-Virulent	-0,746	Non-Virulent	-0,727	Non-Virulent	-0,524	Virulent	3,00E-91	Non-Virulent	-0,871	Virulent	0,1515
58	>sp P9WK24 MAOX_MYCTO Putative malate oxidoreductase [NAD] OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=mez PE=3 SV=1	Non-Virulent	-1,247	Non-Virulent	-1,305	Non-Virulent	-1,574	No hits obtained	Zero	Non-Virulent	-1,226	Non-Virulent	-1,01
59	>sp P9WKE4 KPYK_MYCTO Pyruvate kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pyk PE=3 SV=1	Non-Virulent	-1,276	Non-Virulent	-0,914	Non-Virulent	-1,226	Virulent	0	Non-Virulent	-0,643	Non-Virulent	-1,077
60	>sp P9WMJ6 HTPG_MYCTO Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=htpG PE=3 SV=1	Non-Virulent	-1,069	Non-Virulent	-0,462	Non-Virulent	-0,978	Virulent	0	Non-Virulent	-1,349	Non-Virulent	-0,306
61	>sp P9WMJ8 DNAK_MYCTO Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dnaK PE=3 SV=1	Non-Virulent	-1,906	Non-Virulent	-0,977	Non-Virulent	-1,398	Virulent	0	Non-Virulent	-2,007	Non-Virulent	-1,004
62	>sp P9WN68 G6PI_MYCTO Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pgi PE=3 SV=1	Non-Virulent	-0,155	Non-Virulent	-0,055	Non-Virulent	-0,819	No hits obtained	Zero	Non-Virulent	-0,3	Non-Virulent	-1,043
63	>sp P9WN82 G3P_MYCTO Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=gap PE=3 SV=1	Non-Virulent	-0,528	Non-Virulent	-0,887	Non-Virulent	-0,241	Virulent	e-166	Non-Virulent	-1,059	Non-Virulent	-0,919
64	>sp P9WP70 COX1_MYCTO Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctaD PE=3 SV=1	Non-Virulent	-1,421	Non-Virulent	-2,042	Non-Virulent	-1,818	Virulent	0	Non-Virulent	-1,767	Non-Virulent	-1,067
65	>sp P9WPE6 CH602_MYCTO 60 kDa chaperonin 2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL2 PE=3 SV=1	Non-Virulent	-1,691	Non-Virulent	-1,329	Non-Virulent	-2,671	Virulent	0	Non-Virulent	-1,83	Non-Virulent	-1,062

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66	>sp P9WPE8 CH601_MYCTO 60 kDa chaperonin 1 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=groEL1 PE=3 SV=1	Non-Virulent	-1,726	Non-Virulent	-1,488	Non-Virulent	-1,576	Virulent	0	Non-Virulent	-1,524	Non-Virulent	-0,645
67	>sp P9WPS8 CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1	Non-Virulent	-1,376	Non-Virulent	-1,902	Non-Virulent	-1,748	Virulent	0	Non-Virulent	-1,077	Non-Virulent	-1,048
68	>sp P9WPU6 ATPA_MYCTO ATP synthase subunit alpha OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpA PE=3 SV=1	Non-Virulent	-2,125	Non-Virulent	-1,155	Non-Virulent	-1,761	Virulent	0	Non-Virulent	-1,488	Non-Virulent	-1,008
69	>sp P9WPU8 ATPG_MYCTO ATP synthase gamma chain OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=atpG PE=3 SV=1	Non-Virulent	-0,22	Non-Virulent	-0,999	Virulent	0,0114	Virulent	e-127	Non-Virulent	-0,005	Non-Virulent	-1,017
70	>sp P9WPW6 ASSY_MYCTO Argininosuccinate synthase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=argG PE=3 SV=1	Non-Virulent	-1,821	Non-Virulent	-1,509	Non-Virulent	-1,427	No hits obtained	Zero	Non-Virulent	-1,166	Non-Virulent	-1
71	>tr A0A0H3L5C8 A0A0H3L5C8_MYCTE Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=dnaK PE=2 SV=1	Non-Virulent	-1,906	Non-Virulent	-0,977	Non-Virulent	-1,398	Virulent	0	Non-Virulent	-2,007	Non-Virulent	-1,115
72	>tr A0A0H3L5N9 A0A0H3L5N9_MYCTE Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=lpd PE=3 SV=1	Non-Virulent	-2,16	Non-Virulent	-1,78	Non-Virulent	-1,599	Virulent	e-180	Non-Virulent	-1,128	Non-Virulent	-1,043
73	>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	Non-Virulent	-0,348	Virulent	0,928	Non-Virulent	-0,146	Virulent	e-130	Virulent	0,0265	Non-Virulent	-0,989
74	>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	Virulent	0,9134	Virulent	0,2046	Virulent	0,0324	No hits obtained	Zero	Virulent	0,6771	Virulent	1,0003
75	>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	Non-Virulent	-0,155	Non-Virulent	-0,055	Non-Virulent	-0,819	No hits obtained	Zero	Non-Virulent	-0,3	Virulent	0,9832

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86	>tr A0A0H3LEL3 A0A0H3LEL3_MYCTE 60 kDa chaperonin OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=groEL PE=3 SV=1	Non-Virulent	-1,726	Non-Virulent	-1,488	Non-Virulent	-1,576	Virulent	0	Non-Virulent	-1,524	Non-Virulent	-0,999
87	>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	Non-Virulent	-2,125	Non-Virulent	-1,155	Non-Virulent	-1,761	Virulent	0	Non-Virulent	-1,488	Non-Virulent	-1,048
88	>tr A0A0H3LFE0 A0A0H3LFE0_MYCTE Chaperone protein HtpG OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=htpG PE=3 SV=1	Non-Virulent	-1,069	Non-Virulent	-0,462	Non-Virulent	-0,978	Virulent	0	Non-Virulent	-1,349	Non-Virulent	-1,017
89	>tr A0A0H3LHR0 A0A0H3LHR0_MYCTE Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=ctaD PE=3 SV=1	Non-Virulent	-1,421	Non-Virulent	-2,042	Non-Virulent	-1,818	Virulent	0	Non-Virulent	-1,767	Non-Virulent	-1,004
90	>tr A0A0H3LI71 A0A0H3LI71_MYCTE Malate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) OX=652616 GN=mez PE=3 SV=1	Non-Virulent	-1,247	Non-Virulent	-1,305	Non-Virulent	-1,574	No hits obtained	Zero	Non-Virulent	-1,226	Non-Virulent	-1,062
91	>tr R4M2F9 R4M2F9_MYCTX Adenylosuccinate synthetase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=purA PE=3 SV=1	Non-Virulent	-1,074	Non-Virulent	-1,006	Non-Virulent	-1,41	Virulent	0	Non-Virulent	-0,907	Non-Virulent	-1,077
92	>tr R4M485 R4M485_MYCTX Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgi PE=3 SV=1	Non-Virulent	-0,155	Non-Virulent	-0,055	Non-Virulent	-0,819	No hits obtained	Zero	Non-Virulent	-0,3	Non-Virulent	-1,024
93	>tr R4M5K1 R4M5K1_MYCTX Phosphoglycerate kinase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=pgk PE=3 SV=1	Non-Virulent	-0,717	Non-Virulent	-0,749	Non-Virulent	-0,752	No hits obtained	Zero	Non-Virulent	-0,722	Non-Virulent	-0,919
94	>tr R4MCD1 R4MCD1_MYCTX Malate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=mdh PE=3 SV=1	Non-Virulent	-0,746	Non-Virulent	-0,727	Non-Virulent	-0,524	Virulent	3,00E-91	Non-Virulent	-0,871	Non-Virulent	-0,995
95	>tr R4MCL4 R4MCL4_MYCTX ATP synthase gamma chain OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpG PE=3 SV=1	Non-Virulent	-0,22	Non-Virulent	-0,999	Virulent	0,0114	Virulent	e-127	Non-Virulent	-0,005	Non-Virulent	-1,01
96	>tr R4MD46 R4MD46_MYCTX Glyceraldehyde-3-phosphate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113_10015 PE=3 SV=1	Non-Virulent	-0,528	Non-Virulent	-0,887	Non-Virulent	-0,241	Virulent	e-166	Non-Virulent	-1,059	Non-Virulent	-1

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97	>tr R4MDA5 R4MDA5_MYCTX 60 kDa chaperonin OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=groL PE=3 SV=1	Non-Virulent	-1,691	Non-Virulent	-1,329	Non-Virulent	-2,671	Virulent	0	Non-Virulent	-1,83	Non-Virulent	-1,067
98	>tr R4MFC5 R4MFC5_MYCTX 50S ribosomal protein L2 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=rplB PE=3 SV=1	Virulent	0,9134	Virulent	0,2046	Virulent	0,0324	No hits obtained	Zero	Virulent	0,6771	Non-Virulent	-0,645
99	>tr R4MH86 R4MH86_MYCTX ATP synthase subunit alpha OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=atpA PE=3 SV=1	Non-Virulent	-2,125	Non-Virulent	-1,155	Non-Virulent	-1,761	Virulent	0	Non-Virulent	-1,488	Virulent	0,9832
100	>tr R4MJZ1 R4MJZ1_MYCTX Malate dehydrogenase OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113 16165 PE=3 SV=1	Non-Virulent	-1,247	Non-Virulent	-1,305	Non-Virulent	-1,574	No hits obtained	Zero	Non-Virulent	-1,226	Non-Virulent	-1,017
101	>tr R4MKL8 R4MKL8_MYCTX Cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis CAS/NITR204 OX=1310114 GN=J113 21205 PE=3 SV=1	Non-Virulent	-1,421	Non-Virulent	-2,042	Non-Virulent	-1,818	Virulent	0	Non-Virulent	-1,767	Non-Virulent	-1,077