

**Table S1.** Full length of sequence analysis of top 10 TB phage clones using NCBI BLAST

<b>Ran k</b>	<b>Clone and peptide size</b>	<b>Peptide sequences of mimotopes in-frame with T7 10B gene</b>	<b>Description of the sequences that mimotopes mimic</b>	<b>Region of similarity of peptide</b>
1	P51_BP3_38 (23aa)	S A C L Q S L R T Q L L T W A L V G D V G Q P	polyketide synthase, partial [Mycobacterium tuberculosis] Sequence ID: <a href="#">WP_072515331.1</a>	Id=8/9(89%) Gaps=1/9(11%) Length=894 Query 2 ACLQSLRTQ 10 AC QSLRTQ Sbjct 283 AC-QSLRTQ 290
2	P51_BP3_60 (17aa)	S S E R N G Q F P W P L K M F L T	hydrolase [Mycobacterium tuberculosis] Sequence ID: <a href="#">CFG62212.1</a>	Id=7/10 (70%) Gaps=0/10(0%) Length=280 Query 7 QFPWPLKMFL 16 Q WPL MFL Sbjct 46 QLRWPLRMFL 55
3	P51_BP3_72 (9aa)	I Q H Q H L G Q I	ferredoxin [Mycobacterium tuberculosis] Sequence ID: <a href="#">ref WP_00391835 8.1 </a>	Id=6/6 (88%) Gaps=0/6 (0%) Length=105 Query 2 QHQHLG 7 QHQLHG Sbjct 56 QHQHLG 61
4	P51_BP3_131 (14aa)	L Q A C F P Q I L R G S L A	dihydroxy-acid dehydratase IlvD [Mycobacterium tuberculosis TKK-01- 0051] Sequence ID: <a href="#">gb KBZ68064.1 </a>	Id=7/7(100%) Gaps=0/7(0%) Length=570 Query 8 ILRGLA 14 ILRGLA Sbjct 395 ILRGLA 401
5	P51_BP3_137 (17aa)	D L S S E V A T H Q P I I A C L P	transketolase [Mycobacterium tuberculosis] Sequence ID: ref WP_0167 21353.1  TetR family transcriptional	Id=5/5(100%) Gaps=0/10(0%) Length=651 Query 8 THQPI 12 THQPI Sbjct 453THQPI 457
6	P51_BP3_334 (18aa)	L P W S S G V C D I D L K W M V F S	regulator [Mycobacterium tuberculosis] Sequence ID: <a href="#">ref WP_01562873 9.1 </a>	Id=6/7 (86%) Gaps=0/7 (0%) Length=265 Query 6 GVCIDDL 12 GVCDDL Sbjct 250 GVCIDDL 256
7	P51_BP4_403 (11aa)	D C V V M T S G T L L	menaquinone biosynthesis protein MenD [Mycobacterium tuberculosis]	Id=7/8 (88%) Gaps=0/8 (0%) Length=486 Query 2 CVVMTSGT 9 CV MTSQT Sbjct 74 CVAMTSGT 81

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			Sequence ID: <a href="#">CKO35590.1</a> cobalamin biosynthesis protein CobN [Mycobacterium tuberculosis]	
8	P51_BP4_497 (6aa)	S G K N Y L	Sequence ID: <a href="#">ref WP_03165914</a> <a href="#">7.11</a>	Id=5/5 (100%) Gaps=0/5 (0%) Length=1174 Query 1 SGKNY 5 SGKNY Sbjct 22 SGKNY 26
9	P51_BP4_584 (18aa)	S V E R F I N E S N D S M N N A T F	5-oxoprolinase [Mycobacterium tuberculosis] Sequence ID: <a href="#">ref WP_00390632</a> <a href="#">1.11</a>	Id=6/11(55%) Gaps=0/11(0%) Length=383 Query 8 ESND SMNNATF 18 E MNN TF Sbjct 218 EGSGTMNNVTF 228
10	P197_BP4_107 8 (12aa)	H E Y A Q A S E E A R L	Signal peptidase I LepB [Mycobacterium tuberculosis] Sequence ID: <a href="#">CNI35074.1</a>	Id=7/10(70%) Gaps=0/10(0%) Length=384 Query 3 YAQASEEARL 12 Y QA EE RL Sbjct 153 YSQAQEEGRL 162

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