

Detection of Cystic Fibrosis Serological Biomarkers Using a T7 Phage Display Library

Harvinder Talwar¹, Samer Najeeb Hanoudi², Andreea Geamanu¹, Dana Kissner¹, Sorin Draghici^{2,3} and Lobelia Samavati^{1,4}

¹Department of Medicine, Division of Pulmonary, Critical Care and Sleep Medicine, Wayne State University School of Medicine and Detroit Medical Center, Detroit, MI 48201;

²Department of Computer Science, Wayne State University; ³Department of Obstetrics and Gynecology, Wayne State University; ⁴Center for Molecular Medicine and Genetics, Wayne State University School of Medicine, 540 E. Canfield, Detroit, MI 48201, USA.

Rank	Clone and Peptide size	Peptide Sequences of mimotopes in-frame with T7 10B gene	Description of the sequences that mimotopes mimic	Region of similarity of peptide
1	P51_BP3_25 (15aa)	L P R I F I E L A Q H Q A R V	histidine kinase [Pseudomonas sp. BRH_c35] Sequence ID: gb KJS26770.1 	Id=10/12(83%) Gaps=0/12(0%) Length=1238 Query 1 LPRIFIELAQHQ 12 L RIFIELA H+ Sbjct 960 LERIFIELARHE 971
2	P51_BP3_47 (134 aa)	S A K Y K E T R L K E K E D A L T R T E L E T L Q K Q K K V K K P K P E F P V Y T P L E T T Y I Q S Y D H G T S I E E I E E Q M D D W L E N R N R T Q K K Q A P E W T E E D L S Q L T R S M V K F P G G T P G R W E K I A H E L G R S V T D V T T K A K L A A A L E	dnaJ homolog subfamily C member 1 precursor [Homo sapiens] Sequence ID: NP_071760.2	Id= 123/127 (97%) Gaps=4/127 (3%) Length= 554 Query 2 AKYKETRLKEKEDALTRTELET LQKQKKVKKPKPEFPVYTPLETTYIQSYDHGTSIEEIE 61 AKYKETRLKEKEDALTRTELET LQKQKKVKKPKPEFPVYTPLETTYIQSYDHGTSIEEIE Sbjct 250 AKYKETRLKEKEDALTRTELET LQKQKKVKKPKPEFPVYTPLETTYIQSYDHGTSIEEIE 309 Query 62 EQMETDDWLENRNRTQKKQAPWTEEDLSQLTRSMETVKFPGGTPGRWEKIAHELGRSVT 121 EQM DDWLENRNRTQKKQAPWTEEDLSQLTRSM VKFPGGTPGRWEKIAHELGRSVT Sbjct 310 EQM-DDWLENRNRTQKKQAPWTEEDLSQLTRSM--VKFPGGTPGRWEKIAHELGRSVT 365 Query 122 DVTTKAK 128 DVTTKAK Sbjct 366 DVTTKAK 372

3	P51_BP3_104 (20 aa)	P Y V G M V A T T S P P S P P P A V T T	lytic transglycosylase [Burkholderia cepacia] Sequence ID: ref WP_059730606.1 	Id=9/10 (90%), Gaps=0/10 (0%) Length=412 Query 8 TTSPSPPPPA 17 TTSPPS PPA Sbjct 364 TTSPPSNPPA 373
4	P51_BP3_129 (16aa)	A G I S R E L V D K L A A A L E	Chain A, Pseudomonas Aeruginosa Metap, In Mn Form Sequence ID: pdb 4FO7 A	Id=11/11 (100%) Gaps=0/11(0%) Length=280 Query 6 ELVDKLAAALE 16 ELVDKLAAALE Sbjct 264 ELVDKLAAALE 274
5	P51_BP3_228 (23 aa)	R D P Q C W R W D L V R G V W V T G T D P S W	ABC transporter permease [Pseudomonas aeruginosa] Sequence ID: ref WP_033938298.1 	Id=7/10 (70%) Gaps=1/10 (10%) Length=377 Query 6 WRWDLVRGVW 15 WRWD V G W Sbjct 369 WRWDNVKG-W 377

6	P51_BP3_250 (16aa)	S R N C V N T W V F L N L M Q D	Beta-lactamase [Burkholderia cepacia GG4] Sequence ID: gb AFQ51711.1 	Id=7/10(70%) Gaps=0/10(0%) Length=301 Query 7 TWVFLNLMQD 16 T VF NL QD Sbjct 262 TLVFANLIQD 271
7	P51_BP3_252 (29 aa)	R D T G N S I F L S N G R R Y A L K F G W D T Q F S F I F	gamma- glutamyltranspeptidase [Pseudomonas fluorescens] Sequence ID: ref WP_042609239.1 	Id=10/12 (83%) Gaps=1/12 (8%) Length=575 Query 1 RDTGNSIFLSNG 12 RD G SIFLSNG Sbjct 189 RDSG-SIFLSNG 199
8	P51_BP3_254 (18aa)	G K Y N S T F T S S I I H N K N M K	porin [Burkholderia cepacia] Sequence ID: ref WP_060349386.1 	Id=8/11(72%) Gaps=0/11(0%) Length=399 Query 1 GKYNSTFTSSI 11 G Y+ TF SSI Sbjct 234 GSYDGTFASSI 244
9	P51_BP4_718 (66 aa)	V A T A Q T R L R S Y S C A S L R F S S A T M S D K P D M A E I E K F D K S K L K K T E T Q E K N P L P S K E T I E Q E K Q A G E S	TMSB4X protein, partial [Homo sapiens] Sequence ID: gb AAH61586.1 	Id=65/65 (100%) Gaps=0/65 (0%) Length=65 Query 2 ATAQTRLRSYSCASLRFSSATMSDKPDMAEIEKFDKSKLKKTTETQEKNPLPSKETI EQEK 61 ATAQTRLRSYSCASLRFSSATMSDKPDMAEIEKFDKSKLKKTTETQEKNPLPSKETI EQEK Sbjct 1 ATAQTRLRSYSCASLRFSSATMSDKPDMAEIEKFDKSKLKKTTETQEKNPLPSKETI EQEK 60 Query 62 QAGES 66 QAGES Sbjct 61 QAGES 65

10	P197_BP4_762 (9 aa)	I Q H Q H L G Q I	beta-ketoacyl-ACP reductase [Pseudomonas aeruginosa] Sequence ID: WP_034004244.1	Id=7/8 (88%) Gaps=1/8(12%) Length=247 Query 1 I Q H Q H L G Q 8 I Q Q H L G Q Sbjct 76 I Q - Q H L G Q 82
11	P197_BP4_775 (27 aa)	V D K S V L L S L G R K K Y G A V G S L S Q S T G G H	conjugal transfer protein [Pseudomonas aeruginosa] Sequence ID: WP_044265747.1	Id=10/14 (71%) Gaps=1/14 (7%) Length= 609 Query 2 D K S V L L S L G R K K Y G 15 D K S V L S L K Y G Sbjct 226 D K S V R L S L - T K N Y G 238
12	P197_BP4_805 (19 aa)	S L G A M V C L H S V P S H K A T W I	hemolysin D [Burkholderia cepacia] Sequence ID: ref WP_060377052.1 	Id= 7/12 (58%) Gaps=2/12 (16%) Length=402 Query 10 S V P S H K A T - - W I 19 S V P + A T W I Sbjct 299 S V P A Q N A T G N W I 310
13	P197_BP4_830 (8aa)	Y M C F S L P P	TetR family transcriptional regulator [Burkholderia cepacia] Sequence ID: ref WP_043185598.1 	Id=6/8(75%) Gaps=0/8(0%) Length=209 Query 1 Y M C F S L P P 8 Y M S L P P Sbjct 201 Y M S A S L P P 208

14	P197_BP4_834 (34aa)	G I T S A R L G T G T G E R L R S G C V Q G L V G M G R P V D R A C	AMP-dependent synthetase [Burkholderia cepacia] Sequence ID: ref WP_048244810.1 	Id=13/18(72%) Gaps=0/18(0%) Length=490 Query 14 RLRSGCVQGLVGMGRPVD 31 RL S C +G+V GRP+D Sbjct 305 RLDSYCFEGVVAPGRPID 322
15	P197_BP4_898 (17aa)	D L S S E V A T H Q P I I A C L P	AraC family transcriptional regulator [Burkholderia cepacia] Sequence ID: ref WP_059486090.1 	Id=7/8 (88%) Gaps=0/8 (0%) Length=342 Query 4 SEVATHQP 11 SEVATH P Sbjct 76 SEVATHPP 83
16	P197_BP4_925 (49aa)	D A P S P L P E T T E N V V C A L G L T V G L V G I I I G T I F I I K G V R K S N A A E R R G P L	HLA-DR alpha [Homo sapiens] Sequence ID: gb AAO23887.1 AF481359_1	Id=49/49(100%) Gaps=0/49(0%) Length=50 Query 1 DAPSPLPETTENVVICALGLTVGLVGIIIGTIFIIGVRRKSNAERRGPL 49 DAPSPLPETTENVVICALGLTVGLVGIIIGTIFIIG+RKSNAERRGPL Sbjct 2 DAPSPLPETTENVVICALGLTVGLVGIIIGTIFIIGLRKSNAERRGPL 50

17	P197_BP4_926 (16 aa)	V T L M R Q R V M M M G R H T T	Signal transduction histidine-protein kinase/phosphatase [Pseudomonas aeruginosa] Sequence ID: emb CRQ82296.1 	Id=7/9 (78%) Gaps=0/9(0%) Length=110 Query 4 MRQRVMMMG 12 MR+RV+MMG Sbjct 76 MRERVLMMG 84
18	P197_BP4_952 (12)	S A T S S L A V Y S I L	NADH dehydrogenase subunit 1 (mitochondrion) [Homo sapiens] Sequence ID: gb AFA28546.1 	Id=11/11(100%) Gaps=0/11(0%) Length=316 Query 2 ATSSLAVYSIL 12 ATSSLAVYSIL Sbjct 105 ATSSLAVYSIL 115
19	P197_BP4_1109 (213 aa)	K I D R L D G A H A P E L T K K V Q R H A S S G S F L P S A N E H L K E D L N L R L K K L T H A A P C M L F M K G T P Q E P R C G F S K Q M V E I L H K H N I Q F S S F D I F S D E E V R Q G L K A Y S S W P T Y P Q L Y V S G E L I G G L D I I K E L E A S E E L D T I C P K A P K L E E R L K V L T N K A S V M L F M K G N K Q E A K C G F S K Q I L E I L N S T G V E Y E T F D I L E D E E V R Q G L K A	Thioredoxin-like protein [Homo sapiens] Sequence ID: emb CAA09375.1 	Id=205/206 (99%) Gaps 206/206 (0%) Length=335 Query 1 KIDRLDGAHAPELTKKVQRHASSGSFLPSANEHLKEDLNLRLLKLTAAAPCMLFMKGTPQ 60 KIDRLDGAHAPELTKKVQRHASSGSFLPSANEHLKEDLNLRLLKLTAAAPCMLFMKGTPQ Sbjct 96 KIDRLDGAHAPELTKKVQRHASSGSFLPSANEHLKEDLNLRLLKLTAAAPCMLFMKGTPQ 155 Query 61 EPRCGFSKQMV EILHKHNIQFSSFDIFSDEEVRQGLKAYSSWPTY PQLYVSGELIGGLDI 120 EPRCGFSKQMV EILHKHNIQFSSFDIFSDEEVRQGLKAYSSWPTY PQLYVSGELIGGLDI Sbjct 156 EPRCGFSKQMV EILHKHNIQFSSFDIFSDEEVRQGLKAYSSWPTY PQLYVSGELIGGLDI 215 Query 121 IKELEASEELDTICPKAPKLEERLKVLTNKASVLMFMKGNKQEAACGFSKQILEILNSTG 180 IKELEASEELDTICPKAPKLEERLKVLTNKASVLMFMKGNKQEAACGFSKQILEILNSTG Sbjct 216 IKELEASEELDTICPKAPKLEERLKVLTNKASVLMFMKGNKQEAACGFSKQILEILNSTG 275

		Y S N W P S L R P H S S N		Query 181 VEYETFDILEDEEVRQGLKAYSNWPS 206 VEYETFDILEDEEVRQGLKAYSNWP+ Sbjct 276 VEYETFDILEDEEVRQGLKAYSNWPT 301
20	P197_BP4_1114 (29aa)	L R P P N N P P P N T N Y L T P T P H N H G K P T P L I Q	peptide ABC transporter substrate-binding protein [Burkholderia cepacia complex] Sequence ID: gb ALB12327.1 	Id=13/26(50%) Gaps=5/26(19%) Query 3 PPNNP-PPNT-NY---LTPTPHNHGK 23 P NP PPNT Y P PH+ K Sbjct 325 PATNPYPPNTWSYAKSIAPYPHDPK 350

Supplementary Table S1. Full length of sequence analysis of top 20 CF phage clones using NCBI BLAST.