Phyre^2

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Description	RVBD0755c_(PPE12)_848106_850043
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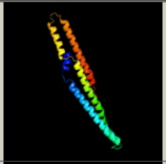
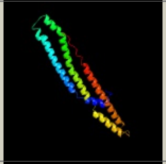
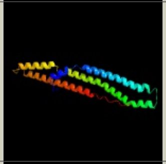
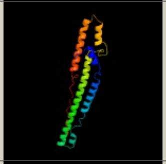
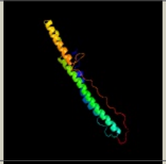
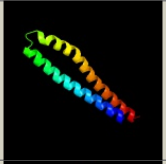
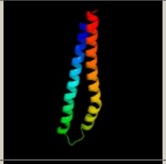
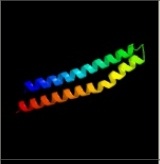
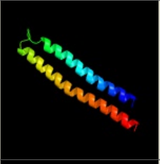
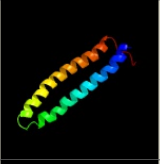
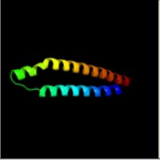
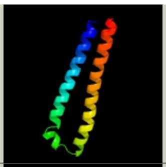
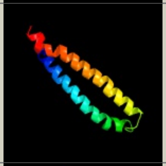
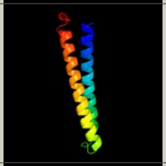
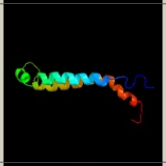
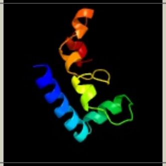
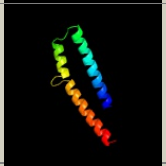
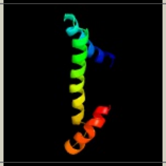
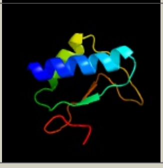
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	Alignment		100.0	49	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**ppe family protein ppe15; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
2	c2g38B_	Alignment		100.0	34	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ppe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	Alignment		100.0	34	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PPE
4	c4xy3A_	Alignment		100.0	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**esx-1 secretion-associated protein espb; **PDBTitle:** structure of esx-1 secreted protein espb
5	c4wj2A_	Alignment		98.9	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**antigen mtb48; **PDBTitle:** mycobacterial protein
6	c2vs0B_	Alignment		98.1	15	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	Alignment		97.9	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c3zbhC_	Alignment		97.8	14	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**esxa; **PDBTitle:** geobacillus thermodenitrificans esxa crystal form i
9	c4iogD_	Alignment		97.8	17	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**secreted protein esxb; **PDBTitle:** the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
10	d1wa8a1	Alignment		97.5	19	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
11	c4lwsA_	Alignment		96.5	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	Alignment		96.5	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		96.3	23	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
14	c4i0xA_	Alignment		95.3	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**esat-6-like protein mab_3112; **PDBTitle:** crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B_	Alignment		94.1	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**esat-6-like protein esxh; **PDBTitle:** structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	d1ui5a2	Alignment		69.6	24	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
17	c4i0xJ_	Alignment		65.4	27	**PDB header:**structural genomics, unknown function **Chain:** J: **PDB Molecule:**esat-6-like protein mab_3113; **PDBTitle:** crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
18	d1xkna_	Alignment		62.3	16	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
19	c2lyyB_	Alignment		31.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the protein nb7890a from shewanella sp
20	d2ewoa1	Alignment		27.6	28	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
21	c2kg7A_	Alignment	not modelled	24.4	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein esxg (pe family protein); **PDBTitle:** structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
22	d2jera1	Alignment	not modelled	23.9	26	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
23	c2iu1A_	Alignment	not modelled	23.5	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** crystal structure of eif5 c-terminal domain
24	d1vkpa_	Alignment	not modelled	22.6	24	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
25	c2jerG_	Alignment	not modelled	22.5	26	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**agmatine deiminase; **PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
26	c5frgA_	Alignment	not modelled	20.9	63	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**formin-binding protein 1-like; **PDBTitle:** the nmr structure of the cdc42-interacting region of toca1
27	c4yk2B_	Alignment	not modelled	19.3	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**bartonella effector protein (bep) substrate of virb t4ss; **PDBTitle:** crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
28	c2fulE_	Alignment	not modelled	18.7	39	**PDB header:**translation **Chain:** E: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** crystal structure of the c-terminal domain of s. cerevisiae eif5

29	c4yk3B_		Alignment	not modelled	18.2	23	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**bepe protein; **PDBTitle:** crystal structure of the bid domain of bepe from bartonella henselae
30	c3jywF_		Alignment	not modelled	17.6	48	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**60s ribosomal protein l7(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
31	c2l5bA_		Alignment	not modelled	17.5	53	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**activator of apoptosis harakiri; **PDBTitle:** solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
32	c1bkvA_		Alignment	not modelled	16.7	31	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**t3-785; **PDBTitle:** collagen
33	c1bkvB_		Alignment	not modelled	15.4	31	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**t3-785; **PDBTitle:** collagen
34	c1bkvC_		Alignment	not modelled	15.4	31	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**t3-785; **PDBTitle:** collagen
35	c6b2wB_		Alignment	not modelled	14.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative peptidyl-arginine deiminase family protein; **PDBTitle:** c. jejuni c315s agmatine deiminase with substrate bound
36	c2ke4A_		Alignment	not modelled	13.8	63	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
37	d1paqa_		Alignment	not modelled	13.4	20	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
38	c1paqA_		Alignment	not modelled	13.4	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor eif-2b epsilon **PDBTitle:** crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
39	c2l5aA_		Alignment	not modelled	12.9	22	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein cse4, protein scm3, **PDBTitle:** structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
40	c4el8A_		Alignment	not modelled	12.4	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 48; **PDBTitle:** the unliganded structure of c.bescii cela gh48 module
41	c3h6pB_		Alignment	not modelled	11.5	36	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**esat-6 like protein esxs; **PDBTitle:** crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
42	c5lc5a_		Alignment	not modelled	10.5	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-ubiquinone oxidoreductase chain 3; **PDBTitle:** structure of mammalian respiratory complex i, class2
43	c3juiA_		Alignment	not modelled	10.2	23	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
44	c2hzkB_		Alignment	not modelled	10.2	14	**PDB header:**ligand binding, transport protein **Chain:** B: **PDB Molecule:**trap-t family sorbitol/mannitol transporter, periplasmic **PDBTitle:** crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
45	c4kkkA_		Alignment	not modelled	9.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoglucanase s; **PDBTitle:** complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
46	c3ttlB_		Alignment	not modelled	9.2	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**polyamine transport protein; **PDBTitle:** crystal structure of apo-spue
47	d1zbra1		Alignment	not modelled	9.1	17	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
48	c5lzkB_		Alignment	not modelled	9.0	9	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**protein fam83b; **PDBTitle:** structure of the domain of unknown function duf1669 from human fam83b
49	c1l2aD_		Alignment	not modelled	8.9	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
50	d1l1ya_		Alignment	not modelled	8.9	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
51	c4fusA_		Alignment	not modelled	8.8	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rtx toxins and related ca2+-binding protein; **PDBTitle:** the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
52	c3zfsA_		Alignment	not modelled	8.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**f420-reducing hydrogenase, subunit alpha; **PDBTitle:** cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
53	c4xfeA_		Alignment	not modelled	8.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**trap dicarboxylate transporter subunit dctp; **PDBTitle:** crystal structure of a trap periplasmic solute binding

						protein from2 pseudomonas putida f1 (pput_1203), target efi-500184, with bound d-3 glucuronate
54	c2ahmG_	Alignment	not modelled	8.2	26	**PDB header:**viral protein, replication **Chain:** G: **PDB Molecule:**replicase polyprotein 1ab, heavy chain; **PDBTitle:** crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
55	c5i4rA_	Alignment	not modelled	8.0	57	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**contact-dependent inhibitor a; **PDBTitle:** contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
56	d1jyaa_	Alignment	not modelled	7.9	23	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
57	c2dbfA_	Alignment	not modelled	7.8	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p105 subunit; **PDBTitle:** solution structure of the death domain in human nuclear2 factor nf-kappa-b p105 subunit
58	c3qthA_	Alignment	not modelled	7.8	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a dinb-like protein (cps_3021) from colwellia2 psychrerythraea 34h at 2.20 a resolution
59	c4jjjA_	Alignment	not modelled	7.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulose 1,4-beta-cellobiosidase; **PDBTitle:** the structure of t. fusca gh48 d224n mutant
60	c1gk9A_	Alignment	not modelled	7.7	18	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**penicillin g acylase alpha subunit; **PDBTitle:** crystal structures of penicillin acylase enzyme-substrate2 complexes: structural insights into the catalytic mechanism
61	d2cmua1	Alignment	not modelled	7.5	14	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
62	c2kwuA_	Alignment	not modelled	7.3	38	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
63	c3j21Y_	Alignment	not modelled	7.2	31	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**50s ribosomal protein l30p; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
64	c5hl8B_	Alignment	not modelled	7.2	18	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**type ii secretion system protein l; **PDBTitle:** 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspl3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
65	d1g9ga_	Alignment	not modelled	7.2	21	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
66	c4nn3A_	Alignment	not modelled	7.1	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens (desal_2161), target efi-510109, with bound3 orotic acid
67	c3ub0D_	Alignment	not modelled	7.1	17	**PDB header:**replication **Chain:** D: **PDB Molecule:**non-structural protein 6, nsp6,; **PDBTitle:** crystal structure of the nonstructural protein 7 and 8 complex of2 feline coronavirus
68	c3j3bF_	Alignment	not modelled	7.1	38	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**60s ribosomal protein l7; **PDBTitle:** structure of the human 60s ribosomal proteins
69	c2kp7A_	Alignment	not modelled	7.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81; **PDBTitle:** solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
70	c5ec0A_	Alignment	not modelled	6.9	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**alp7a; **PDBTitle:** crystal structure of actin-like protein alp7a
71	c3r5zB_	Alignment	not modelled	6.7	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
72	c2wybA_	Alignment	not modelled	6.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-homoserine lactone acylase pvdq subunit **PDBTitle:** the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
73	c6o9l6_	Alignment	not modelled	6.7	40	**PDB header:**transcription/dna **Chain:** 6: **PDB Molecule:**general transcription factor iih subunit 2; **PDBTitle:** human holo-pic in the closed state
74	c4n91A_	Alignment	not modelled	6.4	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate
75	c3j39F_	Alignment	not modelled	6.4	38	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**60s ribosomal protein l7; **PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins
76	c2zdjA_	Alignment	not modelled	6.2	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttma177; **PDBTitle:** crystal structure of ttma177, a hypothetical protein from2 thermus thermophilus phage tma
77	c3fy6A_	Alignment	not modelled	6.2	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v. cholerae.

						integron cassette2 protein vch_cass3
78	c2np3A_	Alignment	not modelled	6.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family regulator; **PDBTitle:** crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
79	c2nvjA_	Alignment	not modelled	6.1	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**25mer peptide from vacuolar atp synthase subunit **PDBTitle:** nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
80	c4yk1A_	Alignment	not modelled	6.1	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bartonella effector protein (bep) substrate of virb t4ss; **PDBTitle:** crystal structure of the bid domain of bep6 from bartonella rochalimae
81	c4i6jB_	Alignment	not modelled	6.0	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**f-box/lrr-repeat protein 3; **PDBTitle:** a ubiquitin ligase-substrate complex
82	c1d1dA_	Alignment	not modelled	6.0	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (capsid protein); **PDBTitle:** nmr solution structure of the capsid protein from rous2 sarcoma virus
83	c4c5eG_	Alignment	not modelled	5.9	39	**PDB header:**transcription **Chain:** G: **PDB Molecule:**polycomb protein pho; **PDBTitle:** crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
84	c4c5eH_	Alignment	not modelled	5.9	39	**PDB header:**transcription **Chain:** H: **PDB Molecule:**polycomb protein pho; **PDBTitle:** crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
85	d1fcda3	Alignment	not modelled	5.9	23	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
86	d1luaa2	Alignment	not modelled	5.9	24	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Methylene-tetrahydromethanopterin dehydrogenase
87	c2jtwA_	Alignment	not modelled	5.8	38	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**transmembrane helix 7 of yeast vatpase; **PDBTitle:** solution structure of tm7 bound to dpc micelles
88	c2rpwX_	Alignment	not modelled	5.8	38	**PDB header:**transport protein **Chain:** X: **PDB Molecule:**25 meric peptide from v-type proton atpase **PDBTitle:** structure of a peptide derived from h+-v-atpase subunit a
89	d2apla1	Alignment	not modelled	5.8	12	**Fold:**PG0816-like **Superfamily:**PG0816-like **Family:**PG0816-like
90	c4gl0A_	Alignment	not modelled	5.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lmo0810 protein; **PDBTitle:** putative spermidine/putrescine abc transporter from listeria2 monocytogenes
91	c3p8cF_	Alignment	not modelled	5.7	22	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**abl interactor 2; **PDBTitle:** structure and control of the actin regulatory wave complex
92	d1r76a_	Alignment	not modelled	5.6	22	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
93	c4y9iA_	Alignment	not modelled	5.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mycobacterium tuberculosis paralogous family 11; **PDBTitle:** structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
94	c4wpyA_	Alignment	not modelled	5.5	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein dl-rv1738; **PDBTitle:** racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
95	c3n6xA_	Alignment	not modelled	5.5	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative glutathionylspermidine synthase; **PDBTitle:** crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methylobacillus flagellatus kt at 2.35 a resolution
96	d1saza2	Alignment	not modelled	5.5	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
97	c3izce_	Alignment	not modelled	5.5	19	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**60s ribosomal protein rpl11 (l5p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
98	c3mopC_	Alignment	not modelled	5.4	38	**PDB header:**signaling protein, immune system **Chain:** C: **PDB Molecule:**myeloid differentiation primary response protein myd88; **PDBTitle:** the ternary death domain complex of myd88, irak4, and irak2
99	c1d0rA_	Alignment	not modelled	5.3	40	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water