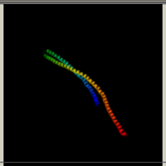
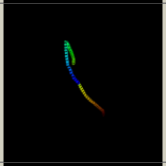
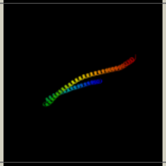
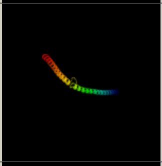
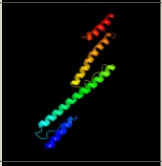
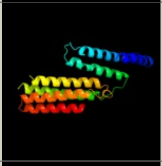
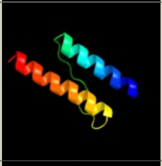
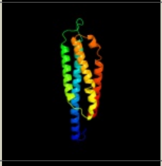
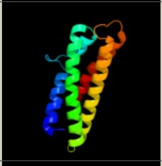
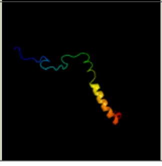
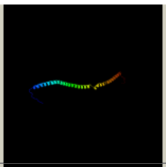
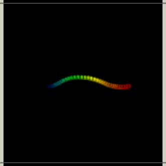
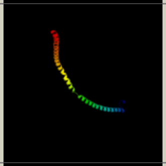
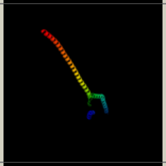
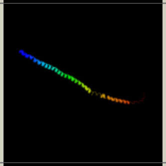
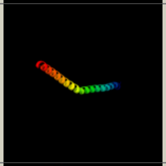
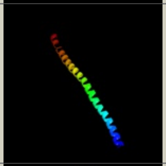
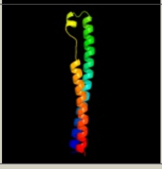
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P05704
Date	Thu Jan 5 10:58:48 GMT 2012
Unique Job ID	c7abcd33ff569cea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qu7A_	 Alignment		99.7	69	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i; **PDBTitle:** four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
2	c2ch7A_	 Alignment		99.3	29	**PDB header:**chemotaxis **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
3	c3g67A_	 Alignment		98.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima
4	c2wpqA_	 Alignment		95.5	6	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**trimeric autotransporter adhesin fragment; **PDBTitle:** salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
5	c2d4uA_	 Alignment		95.2	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i; **PDBTitle:** crystal structure of the ligand binding domain of the bacterial serine2 chemoreceptor tsr
6	c3lnrA_	 Alignment		92.6	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**aerotaxis transducer aer2; **PDBTitle:** crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
7	c1sj8A_	 Alignment		90.1	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin 1; **PDBTitle:** crystal structure of talin residues 482-789
8	d2asxa1	 Alignment		86.0	25	**Fold:**HAMP domain-like **Superfamily:**HAMP domain-like **Family:**HAMP domain
9	d2liga_	 Alignment		84.0	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Aspartate receptor, ligand-binding domain **Family:**Aspartate receptor, ligand-binding domain
10	c2kbbA_	 Alignment		80.1	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the talin rod domain, 1655-1822
11	c2rm8A_	 Alignment		79.9	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensory rhodopsin ii transducer; **PDBTitle:** the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis

12	c1ei3E_	Alignment		77.2	6	**PDB header:** **PDB COMPND:**
13	c2qihA_	Alignment		70.5	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein uspa1; **PDBTitle:** crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
14	c1ei3C_	Alignment		70.0	6	**PDB header:** **PDB COMPND:**
15	c3ojaB_	Alignment		66.1	9	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
16	c1deqO_	Alignment		59.2	11	**PDB header:** **PDB COMPND:**
17	c3b5nF_	Alignment		53.9	14	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**protein sso1; **PDBTitle:** structure of the yeast plasma membrane snare complex
18	c1urqA_	Alignment		52.5	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m-tomosyn isoform; **PDBTitle:** crystal structure of neuronal q-snares in complex with2 r-snare motif of tomosyn
19	c3ipdB_	Alignment		51.3	9	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
20	c2ieqC_	Alignment		49.5	11	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
21	c1deqF_	Alignment	not modelled	47.8	7	**PDB header:** **PDB COMPND:**
22	c3hd7A_	Alignment	not modelled	43.1	20	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
23	c1sfcJ_	Alignment	not modelled	42.9	10	**PDB header:**transport protein **Chain:** J: **PDB Molecule:**protein (syntaxin 1a); **PDBTitle:** neuronal synaptic fusion complex
24	c2kseA_	Alignment	not modelled	39.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein qsec; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor qsec, center for structures of3 membrane proteins (csmp) target 4311c
25	c1n7sB_	Alignment	not modelled	39.7	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**syntaxin 1a; **PDBTitle:** high resolution structure of a truncated neuronal snare2 complex
26	c1n7sA_	Alignment	not modelled	34.7	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** high resolution structure of a truncated neuronal snare2 complex
27	c1sfcI_	Alignment	not modelled	34.3	20	**PDB header:**transport protein **Chain:** I: **PDB Molecule:**protein (synaptobrevin 2); **PDBTitle:** neuronal synaptic fusion complex
28	c1gl2A_	Alignment	not modelled	34.2	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**endobrevin; **PDBTitle:** crystal structure of an endosomal snare core complex

29	c2vs0B_	Alignment	not modelled	33.8	13	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
30	c2npsB_	Alignment	not modelled	33.6	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**syntaxin 13; **PDBTitle:** crystal structure of the early endosomal snare complex
31	c2npsA_	Alignment	not modelled	31.6	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 4; **PDBTitle:** crystal structure of the early endosomal snare complex
32	c3b5nE_	Alignment	not modelled	28.2	20	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**synaptobrevin homolog 1; **PDBTitle:** structure of the yeast plasma membrane snare complex
33	c3gvmA_	Alignment	not modelled	27.9	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
34	c1nafA_	Alignment	not modelled	27.6	15	**PDB header:**signaling protein, membrane protein **Chain:** A: **PDB Molecule:**adp-ribosylation factor binding protein gga1; **PDBTitle:** crystal structure of the human gga1 gat domain
35	c3ok8A_	Alignment	not modelled	21.4	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein **PDBTitle:** i-bar of pinkbar
36	d1eq1a_	Alignment	not modelled	17.6	12	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
37	c1zvaA_	Alignment	not modelled	16.7	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
38	d1oxza_	Alignment	not modelled	15.9	14	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
39	c1oxzA_	Alignment	not modelled	15.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adp-ribosylation factor binding protein gga1; **PDBTitle:** crystal structure of the human gga1 gat domain
40	c2bezC_	Alignment	not modelled	15.2	9	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** structure of a proteolitically resistant core from the2 severe acute respiratory syndrome coronavirus s2 fusion3 protein
41	d2qamn1	Alignment	not modelled	15.0	20	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
42	d2zjrk1	Alignment	not modelled	14.9	20	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
43	d2b0ha1	Alignment	not modelled	14.8	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**VBS domain
44	c2efrB_	Alignment	not modelled	14.7	8	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 alpha chain; **PDBTitle:** crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
45	c1sfcD_	Alignment	not modelled	14.3	8	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**protein (snap-25b); **PDBTitle:** neuronal synaptic fusion complex
46	c1l4aD_	Alignment	not modelled	13.6	7	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**s-snap25 fusion protein; **PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
47	c3bboP_	Alignment	not modelled	13.4	33	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**ribosomal protein l17; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
48	c1kmiZ_	Alignment	not modelled	13.4	9	**PDB header:**signaling protein **Chain:** Z: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of an e.coli chemotaxis protein, chez
49	c2d3eD_	Alignment	not modelled	13.3	11	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
50	d1ez3a_	Alignment	not modelled	13.2	11	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
51	d1wr6a1	Alignment	not modelled	13.1	8	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
52	c3ghgK_	Alignment	not modelled	12.7	6	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
53	c1m1jA_	Alignment	not modelled	12.3	11	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
54	d2asra_	Alignment	not modelled	12.2	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**Aspartate receptor, ligand-binding domain **Family:**Aspartate receptor, ligand-binding domain

55	c2jp3A_		Alignment	not modelled	12.1	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
56	c2npsD_		Alignment	not modelled	11.6	11	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**syntaxin-6; **PDBTitle:** crystal structure of the early endosomal snare complex
57	c1wyyB_		Alignment	not modelled	11.4	9	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
58	d1rkea1		Alignment	not modelled	11.4	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
59	c2d4yA_		Alignment	not modelled	11.1	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 1; **PDBTitle:** crystal structure of a 49k fragment of hap1 (flgk)
60	c2jo1A_		Alignment	not modelled	10.7	16	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
61	c2kvpA_		Alignment	not modelled	10.6	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the talin vbs3 domain, 1815-1973
62	c2l10A_		Alignment	not modelled	10.6	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** structure of the talin rod residues, domain c
63	c3zrwB_		Alignment	not modelled	10.5	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**af1503 protein, osmolarity sensor protein envz; **PDBTitle:** the structure of the dimeric hamp-dhp fusion a291v mutant
64	c2l7nA_		Alignment	not modelled	10.4	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the b domain of talin
65	c1bf5A_		Alignment	not modelled	10.4	7	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
66	c2fxmB_		Alignment	not modelled	10.4	6	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
67	c3c98B_		Alignment	not modelled	9.9	10	**PDB header:**endocytosis/exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** revised structure of the munc18a-syntaxin1 complex
68	c3arcl_		Alignment	not modelled	9.7	30	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
69	c2l9uA_		Alignment	not modelled	9.7	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
70	c1zv8l_		Alignment	not modelled	9.7	7	**PDB header:**viral protein **Chain:** l: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
71	c3bz2L_		Alignment	not modelled	9.6	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
72	c2axtl_		Alignment	not modelled	9.6	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
73	c1s5lL_		Alignment	not modelled	9.6	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
74	d2axtl1		Alignment	not modelled	9.6	30	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
75	c3bz1L_		Alignment	not modelled	9.6	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
76	c3a0bL_		Alignment	not modelled	9.6	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
77	c3a0bl_		Alignment	not modelled	9.6	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
78	c3kziL_		Alignment	not modelled	9.6	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
79	c3prrL_		Alignment	not modelled	9.6	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
80	c3prqL_		Alignment	not modelled	9.6	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in

						complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
81	c1s5ll_	Alignment	not modelled	9.6	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
82	c3arcL_	Alignment	not modelled	9.6	30	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
83	c2axtL_	Alignment	not modelled	9.6	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
84	c1wdfA_	Alignment	not modelled	9.3	9	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** crystal structure of mhv spike protein fusion core
85	c3gxvD_	Alignment	not modelled	9.3	6	**PDB header:**hydrolase/replication **Chain:** D: **PDB Molecule:**replicative dna helicase; **PDBTitle:** three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
86	d1s94a_	Alignment	not modelled	9.3	14	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
87	c1s94A_	Alignment	not modelled	9.3	14	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**s-syntaxin; **PDBTitle:** crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
88	c2zxeG_	Alignment	not modelled	9.2	15	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
89	d1o3xa_	Alignment	not modelled	9.1	16	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
90	d1x79a_	Alignment	not modelled	9.0	14	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
91	d1g40a1	Alignment	not modelled	9.0	25	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
92	c3s90A_	Alignment	not modelled	9.0	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**vinculin; **PDBTitle:** human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
93	c2kpeB_	Alignment	not modelled	8.9	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
94	c2kpeA_	Alignment	not modelled	8.9	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
95	c2xzrA_	Alignment	not modelled	8.8	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
96	c3gxvC_	Alignment	not modelled	8.8	6	**PDB header:**hydrolase/replication **Chain:** C: **PDB Molecule:**replicative dna helicase; **PDBTitle:** three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
97	c3m9bK_	Alignment	not modelled	8.6	14	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
98	c2l16A_	Alignment	not modelled	8.5	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatad; **PDBTitle:** solution structure of bacillus subtilits tatad protein in dpc micelles
99	c1i49A_	Alignment	not modelled	8.5	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**arfaptin 2; **PDBTitle:** crystal structure analysis of arfaptin