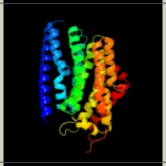
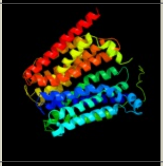
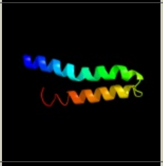
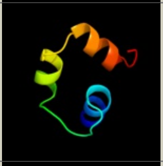
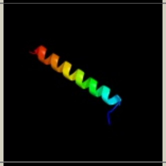
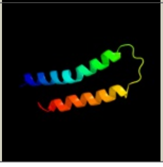
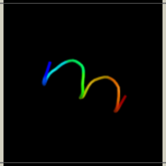
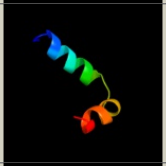
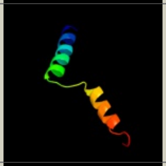
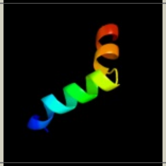
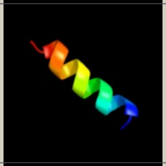
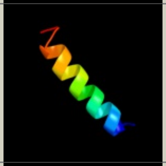
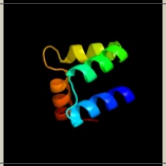
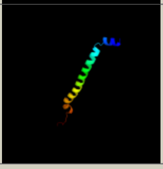
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77377
Date	Thu Jan 5 12:28:20 GMT 2012
Unique Job ID	db7bf36f4d393ca3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mkuA_	Alignment		99.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
2	d1pv7a_	Alignment		65.5	10	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
3	c3rkoN_	Alignment		16.9	14	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**nadh-quinone oxidoreductase subunit n; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
4	d1pw4a_	Alignment		12.4	7	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
5	d2iuba2	Alignment		12.2	20	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
6	d1irxa1	Alignment		11.8	21	**Fold:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Superfamily:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Family:**C-terminal domain of class I lysyl-tRNA synthetase
7	c2jwaA_	Alignment		11.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
8	c2pcoA_	Alignment		10.9	6	**PDB header:**toxin **Chain:** A: **PDB Molecule:**latarcin-1; **PDBTitle:** spatial structure and membrane permeabilization for2 latarcin-1, a spider antimicrobial peptide
9	c3iz5q_	Alignment		10.8	20	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
10	c3izrq_	Alignment		10.8	20	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
11	c2bbjB_	Alignment		10.5	14	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter

12	c2okrC_	Alignment		10.0	30	**PDB header:**transferase **Chain:** C: **PDB Molecule:**map kinase-activated protein kinase 2; **PDBTitle:** crystal structure of the p38a-mapkap kinase 2 heterodimer
13	c2okrF_	Alignment		10.0	30	**PDB header:**transferase **Chain:** F: **PDB Molecule:**map kinase-activated protein kinase 2; **PDBTitle:** crystal structure of the p38a-mapkap kinase 2 heterodimer
14	c2yukA_	Alignment		9.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
15	c3nd0A_	Alignment		9.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
16	d1udxa3	Alignment		9.3	16	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
17	c2jo8B_	Alignment		9.2	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase 4; **PDBTitle:** solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
18	c1b9uA_	Alignment		9.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
19	d1o82a_	Alignment		9.0	12	**Fold:**Saposin-like **Superfamily:**Bacteriocin AS-48 **Family:**Bacteriocin AS-48
20	c1p84D_	Alignment		8.9	9	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
21	c1r6rA_	Alignment	not modelled	8.7	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** solution structure of dengue virus capsid protein reveals a2 new fold
22	d1r6ra_	Alignment	not modelled	8.7	15	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
23	c1qvrB_	Alignment	not modelled	8.7	23	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
24	c3lmbA_	Alignment	not modelled	8.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum tls
25	d2hkja2	Alignment	not modelled	8.3	11	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
26	d1wwra1	Alignment	not modelled	8.2	12	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
27	c2qdqA_	Alignment	not modelled	8.2	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** crystal structure of the talin dimerisation domain
28	d2q7ra1	Alignment	not modelled	8.1	19	**Fold:**MAPEG domain-like **Superfamily:**MAPEG domain-like **Family:**MAPEG domain
						Fold: Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1

29	d2fyuk1	Alignment	not modelled	8.1	16	complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
30	c2l16A_	Alignment	not modelled	8.1	21	**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
31	d1sfka_	Alignment	not modelled	8.0	17	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
32	c3trrA_	Alignment	not modelled	8.0	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
33	d3ehbb2	Alignment	not modelled	8.0	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
34	c3cwbQ_	Alignment	not modelled	8.0	6	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
35	c3u5en_	Alignment	not modelled	8.0	11	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l15-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 resolution
36	c3izcq_	Alignment	not modelled	8.0	11	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein rpl5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
37	c3izsq_	Alignment	not modelled	8.0	11	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein rpl5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
38	c3u5in_	Alignment	not modelled	8.0	11	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l15-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
39	d1j2jb_	Alignment	not modelled	7.7	12	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
40	d2p7tc1	Alignment	not modelled	7.7	17	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
41	c2ww9B_	Alignment	not modelled	7.7	8	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
42	c1m2zB_	Alignment	not modelled	7.6	44	**PDB header:**hormone/hormone activator **Chain:** B: **PDB Molecule:**nuclear receptor coactivator 2; **PDBTitle:** crystal structure of a dimer complex of the human2 glucocorticoid receptor ligand-binding domain bound to3 dexamethasone and a tif2 coactivator motif
43	c3qnqD_	Alignment	not modelled	7.6	16	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
44	d1l0nk_	Alignment	not modelled	7.6	15	**Fold:**Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
45	c3h81A_	Alignment	not modelled	7.6	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase echa8; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
46	c3pxiB_	Alignment	not modelled	7.5	23	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
47	d1z3aa1	Alignment	not modelled	7.5	11	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
48	d1e7la1	Alignment	not modelled	7.4	24	**Fold:**LEM/SAP HeH motif **Superfamily:**Recombination endonuclease VII, C-terminal and dimerization domains **Family:**Recombination endonuclease VII, C-terminal and dimerization domains
49	c1m2zE_	Alignment	not modelled	7.4	44	**PDB header:**hormone/hormone activator **Chain:** E: **PDB Molecule:**nuclear receptor coactivator 2; **PDBTitle:** crystal structure of a dimer complex of the human2 glucocorticoid receptor ligand-binding domain bound to3 dexamethasone and a tif2 coactivator motif
50	c3dh4A_	Alignment	not modelled	7.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
51	d1x6fa1	Alignment	not modelled	7.3	32	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
52	d1xqoa_	Alignment	not modelled	7.2	6	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like

53	c2xq2A_	Alignment	not modelled	7.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
54	c1q2iA_	Alignment	not modelled	7.1	10	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**pnc27; **PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
55	c2z99A_	Alignment	not modelled	7.1	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of scpb from mycobacterium tuberculosis
56	c3fshC_	Alignment	not modelled	7.1	12	**PDB header:**ligase **Chain:** C: **PDB Molecule:**autocrine motility factor receptor, isoform 2; **PDBTitle:** crystal structure of the ubiquitin conjugating enzyme2 ube2g2 bound to the g2br domain of ubiquitin ligase gp78
57	c3hinA_	Alignment	not modelled	7.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative 3-hydroxybutyryl-coa dehydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from2 rhodopseudomonas palustris cga009
58	c1qcrD_	Alignment	not modelled	7.0	6	**PDB header:** **PDB COMPND:**
59	c2ap7A_	Alignment	not modelled	6.9	47	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bombinin h2; **PDBTitle:** solution structure of bombinin h2 in dpc micelles
60	c3qooA_	Alignment	not modelled	6.9	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
61	d1cjya2	Alignment	not modelled	6.9	0	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase
62	c2hn8A_	Alignment	not modelled	6.9	17	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein pb1-f2; **PDBTitle:** structural characterization and oligomerization of pb1-f2,2 a pro-apoptotic influenza a virus protein
63	c3jteA_	Alignment	not modelled	6.8	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
64	c2hw5F_	Alignment	not modelled	6.8	12	**PDB header:**lyase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1
65	c3g64A_	Alignment	not modelled	6.8	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
66	c1yhnB_	Alignment	not modelled	6.8	25	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**rab interacting lysosomal protein; **PDBTitle:** structure basis of rilp recruitment by rab7
67	d1jo5a_	Alignment	not modelled	6.7	14	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
68	c2qziA_	Alignment	not modelled	6.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a conserved protein of unknown function from2 streptococcus thermophilus lmg 18311.
69	c3emlA_	Alignment	not modelled	6.7	11	**PDB header:**membrane protein, receptor **Chain:** A: **PDB Molecule:**human adenosine a2a receptor/t4 lysozyme chimera; **PDBTitle:** the 2.6 a crystal structure of a human a2a adenosine2 receptor bound to zm241385.
70	d1krra_	Alignment	not modelled	6.7	30	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
71	c2i88A_	Alignment	not modelled	6.7	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**colicin-e1; **PDBTitle:** crystal structure of the channel-forming domain of colicin2 e1
72	c3a4cA_	Alignment	not modelled	6.7	5	**PDB header:**cell cycle, replication **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** crystal structure of cdt1 c terminal domain
73	c1sneA_	Alignment	not modelled	6.6	100	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**tetrameric beta-beta-alpha mini-protein; **PDBTitle:** an oligomeric domain-swapped beta-beta-alpha mini-protein
74	c1sneB_	Alignment	not modelled	6.6	100	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**tetrameric beta-beta-alpha mini-protein; **PDBTitle:** an oligomeric domain-swapped beta-beta-alpha mini-protein
75	d2diia1	Alignment	not modelled	6.5	19	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain
76	c2qnaB_	Alignment	not modelled	6.5	28	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of human importin-beta (127-876) in complex with the2 ibb-domain of snurportin1 (1-65)
77	c2g9pA_	Alignment	not modelled	6.5	19	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
						Fold:DNA/RNA-binding 3-helical bundle

78	d2a5yb1	Alignment	not modelled	6.5	33	**Superfamily:**"Winged helix" DNA-binding domain **Family:**CED-4 C-terminal domain-like
79	c1irxA_	Alignment	not modelled	6.4	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of class i lysyl-trna synthetase
80	c1vdfB_	Alignment	not modelled	6.4	14	**PDB header:**extracellular matrix protein **Chain:** B: **PDB Molecule:**cartilage oligomeric matrix protein; **PDBTitle:** assembly domain of cartilage oligomeric matrix protein
81	c2diiA_	Alignment	not modelled	6.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
82	c1t6sB_	Alignment	not modelled	6.4	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
83	c2ap8A_	Alignment	not modelled	6.4	43	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bombinin h4; **PDBTitle:** solution structure of bombinin h4 in dpc micelles
84	d2o5ha1	Alignment	not modelled	6.3	10	**Fold:**NMB0513-like **Superfamily:**NMB0513-like **Family:**NMB0513-like
85	c3hrxD_	Alignment	not modelled	6.3	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of phenylacetic acid degradation protein paag
86	c3kikF_	Alignment	not modelled	6.3	10	**PDB header:**transcription **Chain:** F: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
87	c3kikE_	Alignment	not modelled	6.3	10	**PDB header:**transcription **Chain:** E: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
88	c2kncA_	Alignment	not modelled	6.3	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
89	c1jdmA_	Alignment	not modelled	6.3	3	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sarcolipin; **PDBTitle:** nmr structure of sarcolipin
90	c3kikH_	Alignment	not modelled	6.2	10	**PDB header:**transcription **Chain:** H: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
91	d1unda_	Alignment	not modelled	6.2	14	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
92	c2nx8A_	Alignment	not modelled	6.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna-specific adenosine deaminase; **PDBTitle:** the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
93	d1wgma_	Alignment	not modelled	6.2	13	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
94	c3kikG_	Alignment	not modelled	6.2	10	**PDB header:**transcription **Chain:** G: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
95	c1zxaB_	Alignment	not modelled	6.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cgmp-dependent protein kinase 1, alpha isozyme; **PDBTitle:** solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
96	c2kesA_	Alignment	not modelled	6.2	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**synphilin-1; **PDBTitle:** solution structure of the coiled-coil domain of synphilin-1
97	c2ww9O_	Alignment	not modelled	6.1	14	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l39; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
98	c3kjlF_	Alignment	not modelled	6.1	10	**PDB header:**transcription **Chain:** F: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
99	c3zs9D_	Alignment	not modelled	6.1	29	**PDB header:**hydrolase/transport protein **Chain:** D: **PDB Molecule:**golgi to er traffic protein 2; **PDBTitle:** s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment