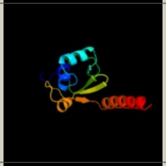
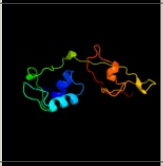
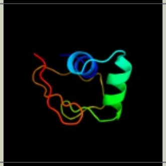
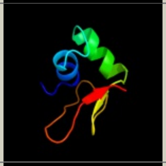
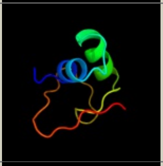
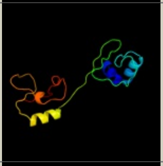
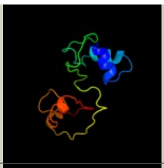
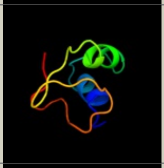
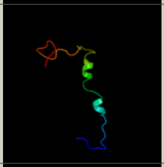
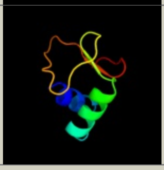
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0ACG8
Date	Thu Jan 5 11:18:09 GMT 2012
Unique Job ID	b3d446910b7f3cf1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1dm9A_	Alignment		100.0	100	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
2	d1dm9a_	Alignment		100.0	100	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
3	c2k6pA_	Alignment		99.7	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
4	c3dh3C_	Alignment		99.5	24	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
5	d2uubd1	Alignment		99.5	29	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
6	d1vioa2	Alignment		99.4	21	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
7	d1c06a_	Alignment		99.4	31	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
8	d2gy9d1	Alignment		99.4	31	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
9	c1kskA_	Alignment		99.4	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
10	c3bbnD_	Alignment		99.3	27	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
11	d1p9ka_	Alignment		99.3	15	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like

12	c1vioA_	Alignment		99.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridylate synthase
13	c2cqjA_	Alignment		99.2	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u3 small nucleolar ribonucleoprotein protein **PDBTitle:** solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
14	c3hp7A_	Alignment		99.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
15	c2xzmD_	Alignment		98.7	16	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
16	c1s1hD_	Alignment		98.7	24	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s9-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
17	d1h3fa2	Alignment		97.9	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
18	c1h3eA_	Alignment		97.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from thermus thermophilus complexed2 with wild-type trnatyr(gua) and with atp and tyrosinol
19	c3iz6C_	Alignment		97.6	23	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**40s ribosomal protein s9 (s4p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
20	d1kska3	Alignment		97.3	21	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
21	c2janD_	Alignment	not modelled	97.2	23	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
22	d1jh3a_	Alignment	not modelled	97.2	25	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
23	c3kbgA_	Alignment	not modelled	93.8	13	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s4e; **PDBTitle:** crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
24	c2xzmW_	Alignment	not modelled	93.4	9	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**40s ribosomal protein s4; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
25	c3iz6D_	Alignment	not modelled	90.5	7	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
26	c1yj5C_	Alignment	not modelled	85.2	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
27	d2g1la1	Alignment	not modelled	83.4	12	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
						PDB header:ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein rps4 (s4e);

28	c3izbD_	Alignment	not modelled	80.0	10	**PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
29	c3kt9A_	Alignment	not modelled	79.3	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
30	c3fm8A_	Alignment	not modelled	78.1	8	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
31	c3hvzB_	Alignment	not modelled	77.8	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
32	c2eh0A_	Alignment	not modelled	76.5	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**kinesin-like protein kif1b; **PDBTitle:** solution structure of the fha domain from human kinesin-2 like protein kif1b
33	c2kmmA_	Alignment	not modelled	74.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
34	d1yjma1	Alignment	not modelled	73.3	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
35	d2ff4a3	Alignment	not modelled	73.3	17	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
36	c3po0A_	Alignment	not modelled	72.3	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
37	c3elsA_	Alignment	not modelled	72.2	10	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** crystal structure of yeast pml1p, residues 51-204
38	d1wlna1	Alignment	not modelled	70.1	16	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
39	c3poaA_	Alignment	not modelled	70.0	14	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
40	d1fm0d_	Alignment	not modelled	69.7	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
41	d1g6ga_	Alignment	not modelled	69.7	13	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
42	d2affa1	Alignment	not modelled	68.7	9	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
43	d1wxqa2	Alignment	not modelled	67.5	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
44	d1vjka_	Alignment	not modelled	67.3	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
45	c2ktlA_	Alignment	not modelled	66.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of c-terminal domain from mttyrrs of a. nidulans
46	d1tkea1	Alignment	not modelled	66.8	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
47	c2qieB_	Alignment	not modelled	66.2	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
48	c2jkdB_	Alignment	not modelled	65.9	10	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** structure of the yeast pml1 splicing factor and its2 integration into the res complex
49	c3dwmA_	Alignment	not modelled	63.3	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
50	d1g3ga_	Alignment	not modelled	60.7	11	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
51	c2ff4B_	Alignment	not modelled	60.4	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable regulatory protein embr; **PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
52	c1r21A_	Alignment	not modelled	60.0	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
53	c3hx1B_	Alignment	not modelled	58.7	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
						PDB header:cell cycle

54	c2jqlA_	Alignment	not modelled	57.9	23	**Chain:** A: **PDB Molecule:**dna damage response protein kinase dun1; **PDBTitle:** nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
55	d1zud21	Alignment	not modelled	57.6	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
56	c3cwiA_	Alignment	not modelled	56.6	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
57	c3gqsB_	Alignment	not modelled	56.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
58	d1xo3a_	Alignment	not modelled	54.7	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
59	d1xnea_	Alignment	not modelled	53.8	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
60	d2piea1	Alignment	not modelled	51.6	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
61	d1nyra2	Alignment	not modelled	50.0	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
62	d1ujxa_	Alignment	not modelled	49.8	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
63	d2cu3a1	Alignment	not modelled	48.3	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
64	c1v8cA_	Alignment	not modelled	47.2	32	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
65	c2qjlA_	Alignment	not modelled	46.7	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
66	c1gxcA_	Alignment	not modelled	45.1	20	**PDB header:**phosphoprotein-binding domain **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase chk2; **PDBTitle:** fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
67	d1gxca_	Alignment	not modelled	45.1	20	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
68	c2g1eA_	Alignment	not modelled	44.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
69	d1v8ca1	Alignment	not modelled	43.4	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
70	d1s04a_	Alignment	not modelled	43.3	22	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
71	d1wgka_	Alignment	not modelled	42.6	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
72	c2kl0A_	Alignment	not modelled	42.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
73	c2k9xA_	Alignment	not modelled	42.0	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
74	d1tygb_	Alignment	not modelled	41.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
75	c2jpeA_	Alignment	not modelled	40.2	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear inhibitor of protein phosphatase 1; **PDBTitle:** fha domain of nipp1
76	c3mmlE_	Alignment	not modelled	40.2	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**allophanate hydrolase subunit 2; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
77	c3gmgB_	Alignment	not modelled	39.0	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
78	c2kklA_	Alignment	not modelled	38.4	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
79	c3rpfC_	Alignment	not modelled	37.5	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdopterin converting factor, subunit 1 (moad); **PDBTitle:** protein-protein complex of subunit 1 and 2 of

						molybdopterin-converting2 factor from helicobacter pylori 26695
80	c2l52A_	Alignment	not modelled	36.3	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**methanosarcina acetivorans samp1 homolog; **PDBTitle:** solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
81	d1rwsa_	Alignment	not modelled	36.2	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
82	c2jv2A_	Alignment	not modelled	34.8	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500; **PDBTitle:** solution structure of the n-terminal domain of ph1500
83	d2brfa1	Alignment	not modelled	33.6	28	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
84	c2ekiA_	Alignment	not modelled	33.1	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**developmentally-regulated gtp-binding protein 1; **PDBTitle:** solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
85	c1tygG_	Alignment	not modelled	32.2	14	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
86	d2exda1	Alignment	not modelled	30.9	12	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
87	c1mhsA_	Alignment	not modelled	30.5	17	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
88	c3j09A_	Alignment	not modelled	30.5	19	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
89	c1wwtA_	Alignment	not modelled	30.3	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
90	c2zxeA_	Alignment	not modelled	29.8	14	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
91	d1lgpa_	Alignment	not modelled	29.6	10	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
92	d1ryja_	Alignment	not modelled	29.3	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
93	c2hj1A_	Alignment	not modelled	28.9	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
94	d2hj1a1	Alignment	not modelled	28.9	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
95	c3b8eC_	Alignment	not modelled	28.8	14	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
96	c2zagB_	Alignment	not modelled	28.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oligosaccharyl transferase stt3 subunit related protein; **PDBTitle:** crystal structure of the semet-substituted soluble domain of stt3 from2 p. furiosus
97	c2k5hA_	Alignment	not modelled	28.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
98	d1uhta_	Alignment	not modelled	27.8	14	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
99	c3ixzA_	Alignment	not modelled	27.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
100	d1k25a2	Alignment	not modelled	27.2	10	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
101	c2hc8A_	Alignment	not modelled	27.1	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
102	c3cp0A_	Alignment	not modelled	26.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
103	c3j08A_	Alignment	not modelled	25.6	20	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
104	d1dmza_	Alignment	not modelled	22.7	9	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain

105	c3oepA_	Alignment	not modelled	22.2	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988; **PDBTitle:** crystal structure of ttha0988 in space group p43212
106	d1aoza1	Alignment	not modelled	21.9	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
107	d2hd9a1	Alignment	not modelled	21.5	8	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like