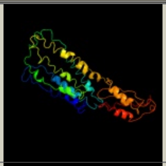
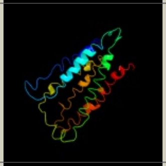
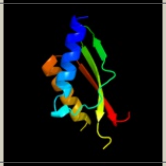
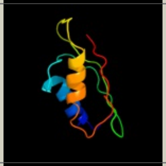
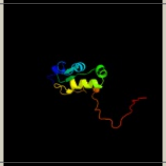
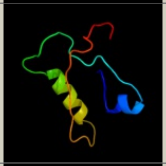
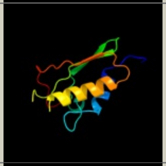
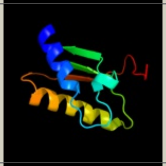
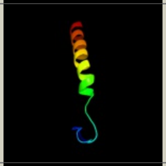
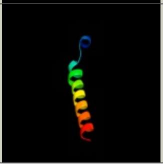
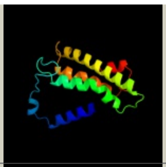
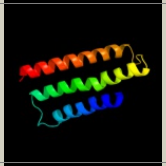
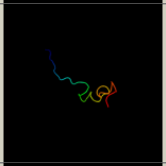
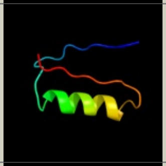
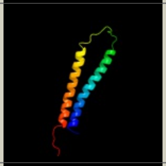
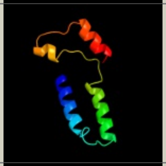
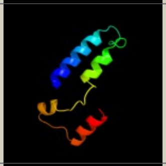
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P75757
Date	Thu Jan 5 12:13:49 GMT 2012
Unique Job ID	bbb6409794b166b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qfiB_	Alignment		100.0	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**ferrous-iron efflux pump fief; **PDBTitle:** structure of the zinc transporter yiip
2	d2qfia2	Alignment		100.0	25	**Fold:**Cation efflux protein transmembrane domain-like **Superfamily:**Cation efflux protein transmembrane domain-like **Family:**Cation efflux protein transmembrane domain-like
3	c2zztA_	Alignment		99.3	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
4	d3bypa1	Alignment		99.3	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
5	d2qfia1	Alignment		99.2	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
6	c2jsxA_	Alignment		83.9	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
7	d2cu6a1	Alignment		80.7	12	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
8	d1uwda_	Alignment		68.4	8	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
9	c3lnoA_	Alignment		49.3	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis
10	c2jp3A_	Alignment		38.7	14	**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
11	c2zxeG_	Alignment		30.1	29	**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

12	c3b9yA_	Alignment		27.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
13	c3pdsA_	Alignment		25.0	9	**PDB header:**membrane protein/hydrolase **Chain:** A: **PDB Molecule:**fusion protein beta-2 adrenergic receptor/lysozyme; **PDBTitle:** irreversible agonist-beta2 adrenoceptor complex
14	c2kpsA_	Alignment		22.6	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of domain iv from the ybbr family protein of2 desulfitobacterium hafniense
15	c2k2pA_	Alignment		21.2	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
16	c1v55B_	Alignment		20.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** bovine heart cytochrome c oxidase at the fully reduced state
17	d1dlca3	Alignment		20.4	12	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
18	d1u19a_	Alignment		19.8	15	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Rhodopsin-like
19	d1ji6a3	Alignment		19.8	17	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
20	c1oy8A_	Alignment		18.8	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
21	c2ksaA_	Alignment	not modelled	16.0	4	**PDB header:**neuropeptide receptor/neuropeptide **Chain:** A: **PDB Molecule:**substance-p receptor; **PDBTitle:** substance p in dmpc/chaps isotropic q=0.25 bicelles as a ligand for2 nk1r
22	d1i1ga2	Alignment	not modelled	16.0	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
23	d1ddfa_	Alignment	not modelled	15.7	24	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
24	c2jo1A_	Alignment	not modelled	15.4	35	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
25	c3rkoK_	Alignment	not modelled	15.1	14	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
26	c1ji6A_	Alignment	not modelled	14.1	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidial crystal protein cry3bb; **PDBTitle:** crystal structure of the insecticidal bacterial del2 endotoxin cry3bb1 bacillus thuringiensis
27	d1x38a2	Alignment	not modelled	13.9	8	**Fold:**Flavodoxin-like **Superfamily:**Beta-D-glucan exohydrolase, C-terminal domain **Family:**Beta-D-glucan exohydrolase, C-terminal domain
28	c2vt4D_	Alignment	not modelled	13.8	11	**PDB header:**receptor **Chain:** D: **PDB Molecule:**beta1 adrenergic receptor; **PDBTitle:** turkey beta1 adrenergic receptor with stabilising mutations2 and bound cyanopindolol
						PDB header:transcription

29	c1u8sB_	Alignment	not modelled	13.6	6	**Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
30	c3mc8A_	Alignment	not modelled	12.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**alr2269 protein; **PDBTitle:** potra1-3 of the periplasmic domain of omp85 from anabaena
31	c2ziyA_	Alignment	not modelled	12.0	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhodopsin; **PDBTitle:** crystal structure of squid rhodopsin
32	d1fftb2	Alignment	not modelled	11.9	10	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
33	c3eb7B_	Alignment	not modelled	11.6	17	**PDB header:**toxin **Chain:** B: **PDB Molecule:**insecticidal delta-endotoxin cry8ea1; **PDBTitle:** crystal structure of insecticidal delta-endotoxin cry8ea1 from2 bacillus thuringiensis at 2.2 angstroms resolution
34	c2djwF_	Alignment	not modelled	11.6	21	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
35	c2kj5A_	Alignment	not modelled	11.4	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage2 integrase protein nmul_a0064 from nitrosospira multiformis,3 northeast structural genomics consortium target nmr46c
36	c3ibwA_	Alignment	not modelled	10.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
37	c2crlA_	Alignment	not modelled	10.6	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase
38	c2zbcH_	Alignment	not modelled	10.3	21	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
39	c2rh1A_	Alignment	not modelled	10.3	9	**PDB header:**membrane protein / hydrolase **Chain:** A: **PDB Molecule:**beta-2-adrenergic receptor/t4-lysozyme chimera; **PDBTitle:** high resolution crystal structure of human b2-adrenergic g protein-2 coupled receptor.
40	d2cg4a2	Alignment	not modelled	10.3	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
41	d1iwga1	Alignment	not modelled	9.1	13	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
42	c3rzeA_	Alignment	not modelled	9.0	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histamine h1 receptor, lysozyme chimera; **PDBTitle:** structure of the human histamine h1 receptor in complex with doxepin
43	c1ex1A_	Alignment	not modelled	8.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (beta-d-glucan exohydrolase isoenzyme exo1); **PDBTitle:** beta-d-glucan exohydrolase from barley
44	c2kt9A_	Alignment	not modelled	8.7	35	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**probable 30s ribosomal protein psrp-3; **PDBTitle:** solution nmr structure of probable 30s ribosomal protein2 psrp-3 (ycf65-like protein) from synechocystis sp. (strain3 pcc 6803), northeast structural genomics consortium target4 target sgr46
45	c3emlA_	Alignment	not modelled	8.5	23	**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.
46	c2e1aD_	Alignment	not modelled	8.5	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
47	c1dlcA_	Alignment	not modelled	8.5	12	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cryiiia; **PDBTitle:** crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
48	d1s6ua_	Alignment	not modelled	8.4	3	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
49	c2aj1A_	Alignment	not modelled	7.7	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
50	d1rl2a2	Alignment	not modelled	7.7	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	d1ysja2	Alignment	not modelled	7.7	9	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain

52	c2l3mA_	Alignment	not modelled	7.6	7	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
53	c2kppA_	Alignment	not modelled	7.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0431 protein; **PDBTitle:** solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
54	c2k5eA_	Alignment	not modelled	7.4	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
55	c2yvxD_	Alignment	not modelled	7.4	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
56	c3aynA_	Alignment	not modelled	7.3	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhodopsin; **PDBTitle:** crystal structure of squid isorhodopsin
57	c2z73A_	Alignment	not modelled	7.3	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**rhodopsin; **PDBTitle:** crystal structure of squid rhodopsin
58	c3aymA_	Alignment	not modelled	7.3	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhodopsin; **PDBTitle:** crystal structure of the batho intermediate of squid rhodopsin
59	c2rogA_	Alignment	not modelled	7.3	7	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
60	c2jxpA_	Alignment	not modelled	7.1	38	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein b; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
61	d3ehbb2	Alignment	not modelled	6.8	14	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
62	c2kt2A_	Alignment	not modelled	6.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
63	c3ac0B_	Alignment	not modelled	6.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
64	c3dxsX_	Alignment	not modelled	6.7	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
65	c1i1gA_	Alignment	not modelled	6.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
66	c3pblB_	Alignment	not modelled	6.6	17	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**d(3) dopamine receptor, lysozyme chimera; **PDBTitle:** structure of the human dopamine d3 receptor in complex with2 eticlopride
67	d1ln6a_	Alignment	not modelled	6.6	15	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Rhodopsin-like
68	d2qamc2	Alignment	not modelled	6.4	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
69	c2ropA_	Alignment	not modelled	6.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
70	c2b2hA_	Alignment	not modelled	6.3	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
71	c3n23E_	Alignment	not modelled	6.3	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
72	c1yg0A_	Alignment	not modelled	6.3	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
73	c2z73B_	Alignment	not modelled	6.2	8	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**rhodopsin; **PDBTitle:** crystal structure of squid rhodopsin
74	c3aynB_	Alignment	not modelled	6.2	8	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**rhodopsin; **PDBTitle:** crystal structure of squid isorhodopsin
75	d2qifa1	Alignment	not modelled	6.1	3	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
76	c2l3bA_	Alignment	not modelled	5.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics

						consortium target3 btr376
77	c3oe6A_	Alignment	not modelled	5.9	10	**PDB header:**signaling protein,hydrolase **Chain:** A: **PDB Molecule:**c-x-c chemokine receptor type 4, lysozyme chimera; **PDBTitle:** crystal structure of the cxcr4 chemokine receptor in complex with a2 small molecule antagonist it1t in i222 spacegroup
78	d1cpza_	Alignment	not modelled	5.9	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
79	c2jmrA_	Alignment	not modelled	5.9	63	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimf; **PDBTitle:** nmr structure of the e. coli type 1 pilus subunit fimf
80	c3ftjA_	Alignment	not modelled	5.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrolide export atp-binding/permease protein **PDBTitle:** crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
81	c2e7xA_	Alignment	not modelled	5.8	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
82	c2ofhX_	Alignment	not modelled	5.8	14	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
83	c2kcqA_	Alignment	not modelled	5.7	55	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mov34/mpn/pad-1 family; **PDBTitle:** solution structure of protein sru_2040 from salinibacter2 ruber (strain dsm 13855) . northeast structural genomics3 consortium target srr106
84	d2hiya1	Alignment	not modelled	5.7	11	**Fold:**SP0830-like **Superfamily:**SP0830-like **Family:**SP0830-like
85	c2lc4A_	Alignment	not modelled	5.6	50	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**pilp protein; **PDBTitle:** solution structure of pilp from pseudomonas aeruginosa
86	c3sn6R_	Alignment	not modelled	5.6	10	**PDB header:**signaling protein/hydrolase **Chain:** R: **PDB Molecule:**lysozyme, beta-2 adrenergic receptor; **PDBTitle:** crystal structure of the beta2 adrenergic receptor-gs protein complex
87	d1v54b2	Alignment	not modelled	5.5	17	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
88	c2ga7A_	Alignment	not modelled	5.4	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
89	c2iqcA_	Alignment	not modelled	5.4	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fanconi anemia group f protein; **PDBTitle:** crystal structure of human fancf protein that functions in2 the assembly of a dna damage signaling complex
90	c2zw2B_	Alignment	not modelled	5.3	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
91	c2cg4B_	Alignment	not modelled	5.3	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
92	c2js4A_	Alignment	not modelled	5.3	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
93	c2k49A_	Alignment	not modelled	5.2	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein so_3888; **PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
94	d1u8sa2	Alignment	not modelled	5.2	4	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
95	d2cyya2	Alignment	not modelled	5.2	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
96	c3lq9B_	Alignment	not modelled	5.2	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**dna-damage-inducible transcript 4 protein; **PDBTitle:** crystal strucure of human redd1, a hypoxia-induced regulator2 of mtor
97	c3g79A_	Alignment	not modelled	5.1	70	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; **PDBTitle:** crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1