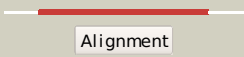

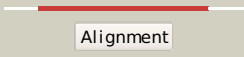

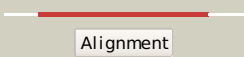

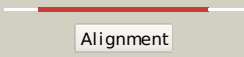



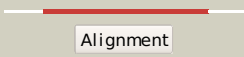
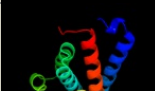
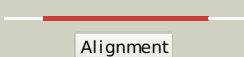
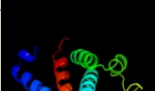
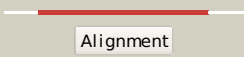

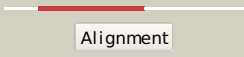

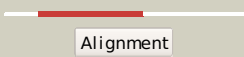

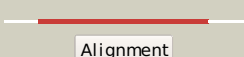

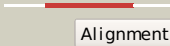

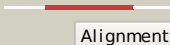

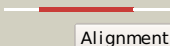

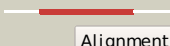





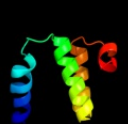
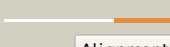

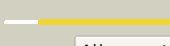

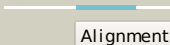


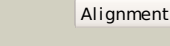


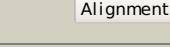
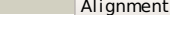


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2prra1</a>	 Alignment		100.0	19	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
2	<a href="#">d2pfxa1</a>	 Alignment		100.0	15	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
3	<a href="#">d2oyoa1</a>	 Alignment		100.0	23	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
4	<a href="#">c3c1lB_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative antioxidant defense protein mlr4105; <b>PDBTitle:</b> crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
5	<a href="#">c3lvyB_</a>	 Alignment		100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxymuconolactone decarboxylase family; <b>PDBTitle:</b> crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
6	<a href="#">d2o4da1</a>	 Alignment		100.0	23	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
7	<a href="#">d2gmya1</a>	 Alignment		100.0	23	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
8	<a href="#">d2ouwa1</a>	 Alignment		99.9	22	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> TTHA0727-like
9	<a href="#">c2qeuA_</a>	 Alignment		99.6	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxymuconolactone decarboxylase; <b>PDBTitle:</b> crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
10	<a href="#">d2cwqa1</a>	 Alignment		99.4	18	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> TTHA0727-like
11	<a href="#">d2q0ta1</a>	 Alignment		99.3	18	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> AhpD

12	<a href="#">c1p8cD_</a>	 Alignment		99.3	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of tm1620 (apc4843) from thermotoga2 maritima
13	<a href="#">c3beyC_</a>	 Alignment		99.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> conserved protein o27018; <b>PDBTitle:</b> crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
14	<a href="#">d1vkea_</a>	 Alignment		99.2	10	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
15	<a href="#">c3d7iB_</a>	 Alignment		99.1	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxymuconolactone decarboxylase family protein; <b>PDBTitle:</b> crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
16	<a href="#">d1vkeb_</a>	 Alignment		98.9	10	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
17	<a href="#">d1knca_</a>	 Alignment		98.8	9	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> AhpD
18	<a href="#">d2af7a1</a>	 Alignment		97.6	17	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
19	<a href="#">d1a9xa1</a>	 Alignment		80.3	12	<b>Fold:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Superfamily:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Family:</b> Carbamoyl phosphate synthetase, large subunit connection domain
20	<a href="#">c3bjxB_</a>	 Alignment		75.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> halocarboxylic acid dehalogenase dehi; <b>PDBTitle:</b> structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
21	<a href="#">d2p7vb1</a>	 Alignment	not modelled	33.9	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
22	<a href="#">c3gk0H_</a>	 Alignment	not modelled	26.9	19	<b>PDB header:</b> transferrase <b>Chain:</b> H: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
23	<a href="#">d1m5wa_</a>	 Alignment	not modelled	24.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Pyridoxine 5'-phosphate synthase <b>Family:</b> Pyridoxine 5'-phosphate synthase
24	<a href="#">c2k8sA_</a>	 Alignment	not modelled	21.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution nmr structure of dimeric thioredoxin-like protein2 ne0084 from nitrosomonas europaea: northeast structural3 genomics target net6
25	<a href="#">d1khda1</a>	 Alignment	not modelled	18.8	12	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
26	<a href="#">c2k9lA_</a>	 Alignment	not modelled	18.6	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> structure of the core binding domain of sigma54
27	<a href="#">d1wgla_</a>	 Alignment	not modelled	17.2	14	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> CUE domain
28	<a href="#">c3l9vE_</a>	 Alignment	not modelled	15.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> putative thiol-disulfide isomerase or thioredoxin;

					<b>PDBTitle:</b> crystal structure of salmonella enterica serovar typhimurium srga
29	<a href="#">c1t3bA_</a>	Alignment	not modelled	13.4	22 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> x-ray structure of dsbc from haemophilus influenzae
30	<a href="#">c3dvwA_</a>	Alignment	not modelled	12.7	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of reduced dsba1 from neisseria2 meningitidis
31	<a href="#">c2k9mA_</a>	Alignment	not modelled	11.9	13 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> structure of the core binding domain of sigma54
32	<a href="#">d1v8ga1</a>	Alignment	not modelled	11.8	11 <b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
33	<a href="#">d2fug21</a>	Alignment	not modelled	11.4	17 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> NQO2-like
34	<a href="#">d1t3ba1</a>	Alignment	not modelled	11.4	22 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
35	<a href="#">c3f4tA_</a>	Alignment	not modelled	11.3	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
36	<a href="#">c1jmtB_</a>	Alignment	not modelled	11.2	29 <b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> splicing factor u2af 65 kda subunit; <b>PDBTitle:</b> x-ray structure of a core u2af65/u2af35 heterodimer
37	<a href="#">d1beda_</a>	Alignment	not modelled	10.9	17 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
38	<a href="#">c2jvlA_</a>	Alignment	not modelled	10.5	20 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> trmbf1; <b>PDBTitle:</b> nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
39	<a href="#">c2dhyA_</a>	Alignment	not modelled	10.4	7 <b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cue domain-containing protein 1; <b>PDBTitle:</b> solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
40	<a href="#">c3gmFA_</a>	Alignment	not modelled	10.3	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-disulfide isomerase; <b>PDBTitle:</b> crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
41	<a href="#">d1ddfa_</a>	Alignment	not modelled	10.2	7 <b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH domain, DD
42	<a href="#">c1v57A_</a>	Alignment	not modelled	9.7	17 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbg; <b>PDBTitle:</b> crystal structure of the disulfide bond isomerase dsbg
43	<a href="#">d1uoua1</a>	Alignment	not modelled	9.6	9 <b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
44	<a href="#">c2p0oA_</a>	Alignment	not modelled	9.5	19 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf871; <b>PDBTitle:</b> crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
45	<a href="#">c1jzdA_</a>	Alignment	not modelled	9.4	11 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> dsbc-dsbdalpha complex
46	<a href="#">d1eeja1</a>	Alignment	not modelled	9.3	22 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
47	<a href="#">c3bciA_</a>	Alignment	not modelled	9.2	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide bond protein a; <b>PDBTitle:</b> crystal structure of staphylococcus aureus dsba
48	<a href="#">c1hyuA_</a>	Alignment	not modelled	9.1	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf
49	<a href="#">d1u6pa_</a>	Alignment	not modelled	8.9	33 <b>Fold:</b> Retrovirus zinc finger-like domains <b>Superfamily:</b> Retrovirus zinc finger-like domains <b>Family:</b> Retrovirus zinc finger-like domains
50	<a href="#">c2yqfA_</a>	Alignment	not modelled	8.8	9 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin-1; <b>PDBTitle:</b> solution structure of the death domain of ankyrin-1
51	<a href="#">c1m6vE_</a>	Alignment	not modelled	8.7	12 <b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain; <b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
52	<a href="#">d1luxda_</a>	Alignment	not modelled	8.6	4 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
53	<a href="#">d1dpua_</a>	Alignment	not modelled	8.6	11 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of RPA32
54	<a href="#">c1dpuA_</a>	Alignment	not modelled	8.6	11 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a (rpa32) c-terminal domain;

						<b>PDBTitle:</b> solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
55	<a href="#">c3hd5A_</a>	Alignment	not modelled	8.4	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
56	<a href="#">c3c7mB_</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba-like; <b>PDBTitle:</b> crystal structure of reduced dsbl
57	<a href="#">c3gv1A_</a>	Alignment	not modelled	8.4	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide interchange protein; <b>PDBTitle:</b> crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
58	<a href="#">d1ngra_</a>	Alignment	not modelled	7.6	9	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH domain, DD
59	<a href="#">c3t72o_</a>	Alignment	not modelled	7.4	5	<b>PDB header:</b> transcription/dna <b>Chain:</b> O: <b>PDB Molecule:</b> pho box dna (strand 1); <b>PDBTitle:</b> phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
60	<a href="#">c2kw0A_</a>	Alignment	not modelled	7.4	0	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ccmh protein; <b>PDBTitle:</b> solution structure of n-terminal domain of ccmh from escherichia.coli
61	<a href="#">c2jblC_</a>	Alignment	not modelled	7.4	17	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> photosynthetic reaction center cytochrome c <b>PDBTitle:</b> photosynthetic reaction center from blastochloris viridis
62	<a href="#">c3feuA_</a>	Alignment	not modelled	7.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
63	<a href="#">c3h93A_</a>	Alignment	not modelled	7.3	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa dsba
64	<a href="#">c2hl7A_</a>	Alignment	not modelled	7.2	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccmh; <b>PDBTitle:</b> crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
65	<a href="#">c3o6cA_</a>	Alignment	not modelled	7.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
66	<a href="#">c3msuA_</a>	Alignment	not modelled	7.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> crystal structure of citrate synthase from francisella tularensis
67	<a href="#">c2remB_</a>	Alignment	not modelled	6.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase dsba from xylella2 fastidiosa
68	<a href="#">d1go3e2</a>	Alignment	not modelled	6.7	15	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> N-terminal, heterodimerisation domain of RBP7 (RpoE) <b>Family:</b> N-terminal, heterodimerisation domain of RBP7 (RpoE)
69	<a href="#">d1fvka_</a>	Alignment	not modelled	6.5	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Dsba-like
70	<a href="#">d1t33a2</a>	Alignment	not modelled	6.5	6	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
71	<a href="#">d1abaa_</a>	Alignment	not modelled	6.5	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
72	<a href="#">c1eysC_</a>	Alignment	not modelled	6.4	19	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> photosynthetic reaction center; <b>PDBTitle:</b> crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
73	<a href="#">d1eysc_</a>	Alignment	not modelled	6.4	19	<b>Fold:</b> Multiheme cytochromes <b>Superfamily:</b> Multiheme cytochromes <b>Family:</b> Photosynthetic reaction centre (cytochrome subunit)
74	<a href="#">d2c35b2</a>	Alignment	not modelled	6.4	19	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> N-terminal, heterodimerisation domain of RBP7 (RpoE) <b>Family:</b> N-terminal, heterodimerisation domain of RBP7 (RpoE)
75	<a href="#">d1brwa1</a>	Alignment	not modelled	6.4	9	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
76	<a href="#">c3gykC_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 27kda outer membrane protein; <b>PDBTitle:</b> the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
77	<a href="#">c2w36B_</a>	Alignment	not modelled	6.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
78	<a href="#">c3thgA_</a>	Alignment	not modelled	6.3	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> crystal structure of the creosote rubisco activase c-domain
79	<a href="#">c3oq9C_</a>	Alignment	not modelled	6.2	9	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> structure of the fas/fadd death domain assembly

80	<a href="#">d2i5nc1</a>	Alignment	not modelled	6.2	17	<b>Fold:</b> Multiheme cytochromes <b>Superfamily:</b> Multiheme cytochromes <b>Family:</b> Photosynthetic reaction centre (cytochrome subunit)
81	<a href="#">d1pbwa_</a>	Alignment	not modelled	6.0	17	<b>Fold:</b> GTPase activation domain, GAP <b>Superfamily:</b> GTPase activation domain, GAP <b>Family:</b> BCR-homology GTPase activation domain (BH-domain)
82	<a href="#">d1eaka1</a>	Alignment	not modelled	6.0	12	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
83	<a href="#">d1x4pa1</a>	Alignment	not modelled	5.9	17	<b>Fold:</b> Surp module (SWAP domain) <b>Superfamily:</b> Surp module (SWAP domain) <b>Family:</b> Surp module (SWAP domain)
84	<a href="#">d1o17a1</a>	Alignment	not modelled	5.9	14	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
85	<a href="#">d2hsqa1</a>	Alignment	not modelled	5.9	8	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
86	<a href="#">c3odnA_</a>	Alignment	not modelled	5.8	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dally-like protein; <b>PDBTitle:</b> the crystal structure of drosophila dally-like protein core domain
87	<a href="#">d1ttya_</a>	Alignment	not modelled	5.8	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
88	<a href="#">c2qgpA_</a>	Alignment	not modelled	5.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease; <b>PDBTitle:</b> x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.
89	<a href="#">c1klsA_</a>	Alignment	not modelled	5.8	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger y-chromosomal protein; <b>PDBTitle:</b> nmr structure of the zfy-6[tty10l] zinc finger
90	<a href="#">d1qpza1</a>	Alignment	not modelled	5.8	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
91	<a href="#">d1klra_</a>	Alignment	not modelled	5.7	40	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
92	<a href="#">c1klrA_</a>	Alignment	not modelled	5.7	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger y-chromosomal protein; <b>PDBTitle:</b> nmr structure of the zfy-6[tty10f] zinc finger
93	<a href="#">d2cbia2</a>	Alignment	not modelled	5.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
94	<a href="#">c1xrza_</a>	Alignment	not modelled	5.6	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger y-chromosomal protein; <b>PDBTitle:</b> nmr structure of a zinc finger with cyclohexanylalanine2 substituted for the central aromatic residue
95	<a href="#">d2g7la2</a>	Alignment	not modelled	5.6	10	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
96	<a href="#">c2yx0A_</a>	Alignment	not modelled	5.6	43	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> radical sam enzyme; <b>PDBTitle:</b> crystal structure of p. horikoshii tyw1
97	<a href="#">c2lcva_</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
98	<a href="#">c3ghaA_</a>	Alignment	not modelled	5.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide bond formation protein d; <b>PDBTitle:</b> crystal structure of etda-treated bdbd (reduced)
99	<a href="#">d2w6ka1</a>	Alignment	not modelled	5.2	15	<b>Fold:</b> CobE/GbiG C-terminal domain-like <b>Superfamily:</b> CobE/GbiG C-terminal domain-like <b>Family:</b> CobE/GbiG C-terminal domain-like