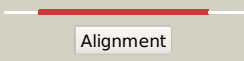

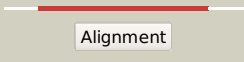

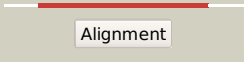

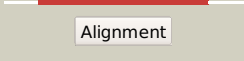

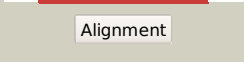

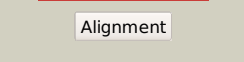

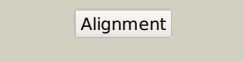

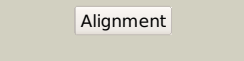

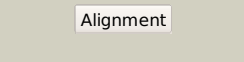

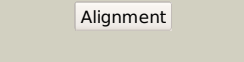

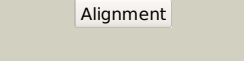

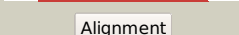





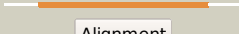

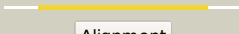

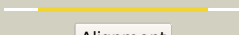



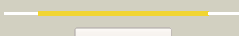



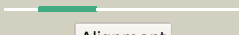


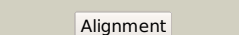

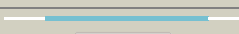

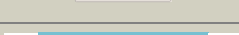
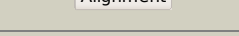


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3364c (- )_3774653_3775045
Date	Fri Aug 9 18:20:02 BST 2019
Unique Job ID	367c1b2334d8d70d

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3kyeC_</a>	 Alignment		100.0	41	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> roadblock/lc7 domain, rob1_lc7; <b>PDBTitle:</b> crystal structure of roadblock/lc7 domain from streptomyces2 avermitilis
2	<a href="#">dlj3wa_</a>	 Alignment		99.9	18	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
3	<a href="#">clj3wB_</a>	 Alignment		99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> gliding protein-mglb; <b>PDBTitle:</b> structure of gliding protein-mglb from thermus thermophilus hb8
4	<a href="#">c3leqA_</a>	 Alignment		99.9	39	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein cvnb5; <b>PDBTitle:</b> the crystal structure of the roadblock/lc7 domain from streptomyces2 avermitilis to 1.85a
5	<a href="#">d1vetb_</a>	 Alignment		99.9	20	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
6	<a href="#">d3cptal</a>	 Alignment		99.2	12	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
7	<a href="#">c1skoA_</a>	 Alignment		99.2	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase 1 <b>PDBTitle:</b> mp1-p14 complex
8	<a href="#">d1y4oa1</a>	 Alignment		98.4	11	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
9	<a href="#">d2hz5a1</a>	 Alignment		98.1	12	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
10	<a href="#">c6ehrD_</a>	 Alignment		96.7	23	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> ragulator complex protein lamtor4; <b>PDBTitle:</b> the crystal structure of the human lamtor-raga ctd-ragc ctd complex
11	<a href="#">c3ms6A_</a>	 Alignment		96.7	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> hepatitis b virus x-interacting protein; <b>PDBTitle:</b> crystal structure of hepatitis b x-interacting protein (hbxiip)

12	<a href="#">d1acfa_</a>	 Alignment		90.9	17	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein) <b>Family:</b> Profilin (actin-binding protein)
13	<a href="#">d1ypra_</a>	 Alignment		87.1	15	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein) <b>Family:</b> Profilin (actin-binding protein)
14	<a href="#">d1g5ua_</a>	 Alignment		85.6	18	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein) <b>Family:</b> Profilin (actin-binding protein)
15	<a href="#">d1f2ka_</a>	 Alignment		84.3	14	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein) <b>Family:</b> Profilin (actin-binding protein)
16	<a href="#">d3nula_</a>	 Alignment		79.3	14	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein) <b>Family:</b> Profilin (actin-binding protein)
17	<a href="#">c3davA_</a>	 Alignment		77.2	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> profilin; <b>PDBTitle:</b> schizosaccharomyces pombe profilin crystallized from sodium formate
18	<a href="#">c5o7jA_</a>	 Alignment		76.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase; <b>PDBTitle:</b> structural insights into the periplasmic sensor domain of the gacs2 histidine kinase controlling biofilm formation in pseudomonas3 aeruginosa
19	<a href="#">d1cqaa_</a>	 Alignment		74.4	17	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein) <b>Family:</b> Profilin (actin-binding protein)
20	<a href="#">c4xtbA_</a>	 Alignment		60.4	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium uniporter protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the human mitochondrial2 calcium uniporter
21	<a href="#">c6o58C_</a>	 Alignment	not modelled	45.9	25	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> calcium uniporter protein, mitochondrial; <b>PDBTitle:</b> human mcu-emre complex, dimer of channel
22	<a href="#">d1p0za_</a>	 Alignment	not modelled	44.8	9	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Sensory domain-like <b>Family:</b> Sensory domain of two-component sensor kinase
23	<a href="#">c5nzvN_</a>	 Alignment	not modelled	44.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> N: <b>PDB Molecule:</b> coatamer subunit delta; <b>PDBTitle:</b> the structure of the cop1 coat linkage iv
24	<a href="#">c3lgoA_</a>	 Alignment	not modelled	42.2	8	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein slm4; <b>PDBTitle:</b> structure of gse1p, member of the gse/ego complex
25	<a href="#">c5ereA_</a>	 Alignment	not modelled	39.8	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular ligand-binding receptor; <b>PDBTitle:</b> extracellular ligand binding receptor from desulfohalobium retbaense2 dsm5692
26	<a href="#">c5mu7B_</a>	 Alignment	not modelled	38.1	14	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> coatamer subunit delta-like protein; <b>PDBTitle:</b> crystal structure of the beta/delta-cop1 core complex
27	<a href="#">d3by8a1</a>	 Alignment	not modelled	31.4	10	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Sensory domain-like <b>Family:</b> Sensory domain of two-component sensor kinase
28	<a href="#">c6cesA_</a>	 Alignment	not modelled	30.9	7	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ras-related gtp-binding protein a; <b>PDBTitle:</b> cryo-em structure of gator1-rag
29	<a href="#">d1d1ja_</a>	 Alignment	not modelled	26.9	11	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein)

						<b>Family:</b> Profilin (actin-binding protein)
30	<a href="#">c5a1vP_</a>	Alignment	not modelled	25.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> P: <b>PDB Molecule:</b> coatomer subunit delta; <b>PDBTitle:</b> the structure of the copI coat linkage i
31	<a href="#">c5iddA_</a>	Alignment	not modelled	22.1	10	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> mon1; <b>PDBTitle:</b> crystal structure of the heterodimeric gef mon1-ccz1 in complex with2 ypt7
32	<a href="#">c4ywwA_</a>	Alignment	not modelled	21.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein kinase walk; <b>PDBTitle:</b> crystal structure of the extracellular receptor domain of the2 essential sensor kinase walk from staphylococcus aureus
33	<a href="#">c3fosA_</a>	Alignment	not modelled	19.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
34	<a href="#">c1eb0A_</a>	Alignment	not modelled	19.0	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> urease accessory protein uree; <b>PDBTitle:</b> crystal structure of bacillus pasteurii uree at 1.85 a, phased by2 siras. type i crystal form.
35	<a href="#">d1p5dx4</a>	Alignment	not modelled	18.5	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> Phosphoglucomutase, C-terminal domain <b>Family:</b> Phosphoglucomutase, C-terminal domain
36	<a href="#">c5ey2A_</a>	Alignment	not modelled	17.4	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from bacillus cereus
37	<a href="#">c3ny0D_</a>	Alignment	not modelled	17.3	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> urease accessory protein uree; <b>PDBTitle:</b> crystal structure of uree from helicobacter pylori (ni2+ bound form)
38	<a href="#">c4pdeA_</a>	Alignment	not modelled	17.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein fdhd; <b>PDBTitle:</b> crystal structure of fdhd in complex with gdp
39	<a href="#">c2nupC_</a>	Alignment	not modelled	17.0	17	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> vesicle-trafficking protein sec22b; <b>PDBTitle:</b> crystal structure of the human sec23a/24a heterodimer, complexed with2 the snare protein sec22b
40	<a href="#">c3egdC_</a>	Alignment	not modelled	17.0	17	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> vesicle-trafficking protein sec22b; <b>PDBTitle:</b> crystal structure of the mammalian copii-coat protein sec23a/24a2 complexed with the snare protein sec22 and bound to the transport3 signal sequence of vesicular stomatitis virus glycoprotein
41	<a href="#">c6dt0D_</a>	Alignment	not modelled	16.4	17	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> mitochondrial calcium uniporter; <b>PDBTitle:</b> cryo-em structure of a mitochondrial calcium uniporter
42	<a href="#">d1gw5s_</a>	Alignment	not modelled	15.0	11	<b>Fold:</b> Profilin-like <b>Superfamily:</b> SNARE-like <b>Family:</b> Clathrin coat assembly domain
43	<a href="#">c3oi8B_</a>	Alignment	not modelled	13.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of functionally unknown conserved protein domain2 from neisseria meningitidis mc58
44	<a href="#">d1jfua_</a>	Alignment	not modelled	13.5	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
45	<a href="#">c4onxB_</a>	Alignment	not modelled	12.5	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor histidine kinase; <b>PDBTitle:</b> 2.8 angstrom crystal structure of sensor domain of histidine kinase2 from clostridium perfringens.
46	<a href="#">d1i1ga2</a>	Alignment	not modelled	11.9	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
47	<a href="#">c5ltvA_</a>	Alignment	not modelled	11.8	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotactic transducer pctc; <b>PDBTitle:</b> ligand binding regions of pseudomonas aeruginosa pao1 amino acid2 chemoreceptors pctc in complex with gaba
48	<a href="#">d2cyya2</a>	Alignment	not modelled	11.2	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
49	<a href="#">c4qwoA_</a>	Alignment	not modelled	10.8	10	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> profilin; <b>PDBTitle:</b> 1.52 angstrom crystal structure of a42r profilin-like protein from2 monkeypox virus zaire-96-t-16
50	<a href="#">c5tfqA_</a>	Alignment	not modelled	10.8	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of a representative of class a beta-lactamase from2 bacteroides cellulosilyticus dsm 14838
51	<a href="#">d1pvma4</a>	Alignment	not modelled	10.6	16	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
52	<a href="#">c2djwF_</a>	Alignment	not modelled	10.2	26	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> probable transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of ttha0845 from thermus thermophilus hb8
53	<a href="#">d1gw5m2</a>	Alignment	not modelled	10.1	9	<b>Fold:</b> Profilin-like <b>Superfamily:</b> SNARE-like <b>Family:</b> Clathrin coat assembly domain
54	<a href="#">c6dtmA_</a>	Alignment	not modelled	10.0	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein ttpa; <b>PDBTitle:</b> crystal structure of helicobacter pylori ttpa chemoreceptor ligand2 binding domain
						<b>PDB header:</b> transferase

55	<a href="#">c5fq1A_</a>	Alignment	not modelled	10.0	6	<b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase; <b>PDBTitle:</b> structure of the cytoplasmic pas domain of the geobacillus2 thermodenitrificans histidine kinase cita
56	<a href="#">c1w63T_</a>	Alignment	not modelled	9.6	11	<b>PDB header:</b> endocytosis <b>Chain:</b> T: <b>PDB Molecule:</b> adapter-related protein complex 1 sigma 1a subunit; <b>PDBTitle:</b> ap1 clathrin adaptor core
57	<a href="#">c2z0fA_</a>	Alignment	not modelled	9.6	9	<b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphoglucomutase; <b>PDBTitle:</b> crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
58	<a href="#">c5a1yH_</a>	Alignment	not modelled	9.3	6	<b>PDB header:</b> transport protein <b>Chain:</b> H: <b>PDB Molecule:</b> coatomer subunit delta; <b>PDBTitle:</b> the structure of the copi coat linkage iv
59	<a href="#">c3w66A_</a>	Alignment	not modelled	9.2	22	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> magnetosome protein mamm; <b>PDBTitle:</b> mamm-ctd d249a and h285a
60	<a href="#">c2gj3A_</a>	Alignment	not modelled	8.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen fixation regulatory protein; <b>PDBTitle:</b> crystal structure of the fad-containing pas domain of the protein nifl2 from azotobacter vinelandii.
61	<a href="#">c3gbyA_</a>	Alignment	not modelled	8.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ct1051; <b>PDBTitle:</b> crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
62	<a href="#">c2gx5B_</a>	Alignment	not modelled	8.9	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> n-terminal gaf domain of transcriptional pleiotropic repressor cody
63	<a href="#">c3lifA_</a>	Alignment	not modelled	8.9	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative diguanylate cyclase (ggdef) with pas/pac domain; <b>PDBTitle:</b> crystal structure of the extracellular domain of the putative2 histidine kinase rphk1s-z16
64	<a href="#">c5ey0A_</a>	Alignment	not modelled	8.9	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from staphylococcus aureus with gtp and ile
65	<a href="#">c1gmuB_</a>	Alignment	not modelled	8.8	11	<b>PDB header:</b> metallochaperone <b>Chain:</b> B: <b>PDB Molecule:</b> uree; <b>PDBTitle:</b> structure of uree
66	<a href="#">c2zalD_</a>	Alignment	not modelled	8.7	7	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
67	<a href="#">c4xsjA_</a>	Alignment	not modelled	8.5	25	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme,calcium uniporter protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the human mitochondrial2 calcium uniporter fused with t4 lysozyme
68	<a href="#">d2fr5a1</a>	Alignment	not modelled	8.3	10	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
69	<a href="#">c3hf7A_</a>	Alignment	not modelled	8.2	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized cbs-domain protein; <b>PDBTitle:</b> the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
70	<a href="#">d1mvfd_</a>	Alignment	not modelled	7.8	14	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Kis/PemI addiction antidote
71	<a href="#">c2e1cA_</a>	Alignment	not modelled	7.7	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
72	<a href="#">c3lhhA_</a>	Alignment	not modelled	7.6	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cbs domain protein; <b>PDBTitle:</b> the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
73	<a href="#">c4nocA_</a>	Alignment	not modelled	7.5	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal transduction protein with cbs domains; <b>PDBTitle:</b> the crystal structure of a cbs domain-containing protein of unknown2 function from kribbella flavida dsm 17836.
74	<a href="#">c3ocmA_</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
75	<a href="#">c2mrnB_</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin maze; <b>PDBTitle:</b> structure of truncated ecmaze
76	<a href="#">c2lxtC_</a>	Alignment	not modelled	7.4	24	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> cyclic amp-responsive element-binding protein 1; <b>PDBTitle:</b> allosteric communication in the kix domain proceeds through dynamic2 re-packing of the hydrophobic core
77	<a href="#">c2zbcH_</a>	Alignment	not modelled	7.4	11	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 83aa long hypothetical transcriptional regulator asnc; <b>PDBTitle:</b> crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
78	<a href="#">d1ndba2</a>	Alignment	not modelled	7.4	10	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
						<b>Fold:</b> CBS-domain pair

79	<a href="#">d2yzqa1</a>	Alignment	not modelled	7.3	13	<b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
80	<a href="#">d1nwza</a>	Alignment	not modelled	7.3	13	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> PYP-like
81	<a href="#">d2riha1</a>	Alignment	not modelled	7.3	23	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
82	<a href="#">c3kpbA</a>	Alignment	not modelled	7.1	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0100; <b>PDBTitle:</b> crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
83	<a href="#">c2cfxD</a>	Alignment	not modelled	7.0	7	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
84	<a href="#">d1o50a3</a>	Alignment	not modelled	6.9	22	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
85	<a href="#">c3kxrA</a>	Alignment	not modelled	6.9	6	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> magnesium transporter, putative; <b>PDBTitle:</b> structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
86	<a href="#">c3hleA</a>	Alignment	not modelled	6.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transesterase; <b>PDBTitle:</b> simvastatin synthase (lovd), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
87	<a href="#">d1wjwa</a>	Alignment	not modelled	6.5	14	<b>Fold:</b> TBP-like <b>Superfamily:</b> Phosphoglucomutase, C-terminal domain <b>Family:</b> Phosphoglucomutase, C-terminal domain
88	<a href="#">c2r37A</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 3; <b>PDBTitle:</b> crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
89	<a href="#">c3me8B</a>	Alignment	not modelled	6.4	7	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative electron transfer protein aq_2194 from2 aquifex aeolicus vf5
90	<a href="#">c2yzqA</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph1780; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
91	<a href="#">d1gp1a</a>	Alignment	not modelled	6.3	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
92	<a href="#">c2zalB</a>	Alignment	not modelled	6.3	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
93	<a href="#">c3kcmC</a>	Alignment	not modelled	6.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> the crystal structure of thioredoxin protein from geobacter2 metallireducens
94	<a href="#">c3mq0A</a>	Alignment	not modelled	6.2	15	<b>PDB header:</b> transcription repressor <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor of the blcabc operon; <b>PDBTitle:</b> crystal structure of agobacterium tumefaciens repressor blcr
95	<a href="#">c5ks7A</a>	Alignment	not modelled	6.0	23	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine transport atp-binding protein opuca; <b>PDBTitle:</b> crystal structure of listeria monocytogenes opuca cbs domain dimer in2 complex with cyclic-di-amp
96	<a href="#">c6gc1A</a>	Alignment	not modelled	5.9	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nhl repeat-containing protein 2; <b>PDBTitle:</b> crystal structure of trx-like and nhl repeat containing domains of2 human nhlc2
97	<a href="#">d2cg4a2</a>	Alignment	not modelled	5.8	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
98	<a href="#">c2m72A</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized thioredoxin-like protein; <b>PDBTitle:</b> solution structure of uncharacterized thioredoxin-like protein pg_21752 from porphyromonas gingivalis
99	<a href="#">c1t3mD</a>	Alignment	not modelled	5.7	7	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli