



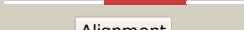

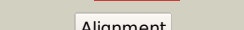

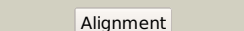
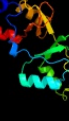






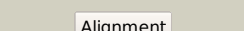
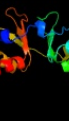
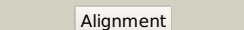





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2366c_(-)_2647070_2648377
Date	Mon Aug 5 13:25:52 BST 2019
Unique Job ID	c292c7c34853052b

Detailed template information


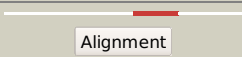
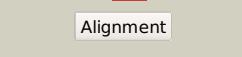
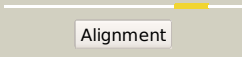
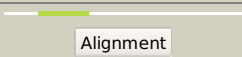
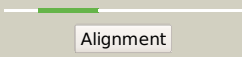
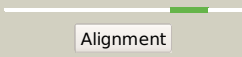
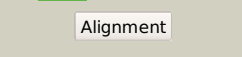
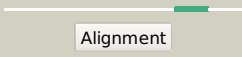
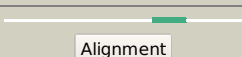
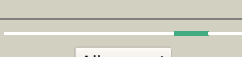
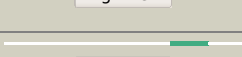
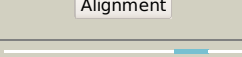
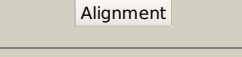
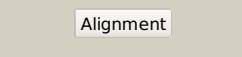
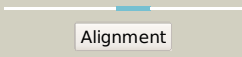

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hg0A_	 Alignment		100.0	36	PDB header: transport protein Chain: A: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: crystal structure of magnesium and cobalt efflux protein corc,2 northeast structural genomics consortium (nesg) target er40
2	c3ocmA_	 Alignment		100.0	31	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
3	c3ocmB_	 Alignment		100.0	32	PDB header: membrane protein Chain: B: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
4	c3oi8B_	 Alignment		99.9	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of functionally unknown conserved protein domain2 from neisseria meningitidis mc58
5	c3ocoB_	 Alignment		99.9	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hemolysin-like protein containing cbs domains; PDBTitle: the crystal structure of a hemolysin-like protein containing cbs2 domain of oenococcus oeni psu
6	c3lhhA_	 Alignment		99.9	29	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
7	c4iy3B_	 Alignment		99.9	32	PDB header: metal transport Chain: B: PDB Molecule: metal transporter cnm4; PDBTitle: structural and ligand binding properties of the bateman domain of2 human magnesium transporters cnm2 and cnm4
8	c6h1wA_	 Alignment		99.9	14	PDB header: unknown function Chain: A: PDB Molecule: mj1004; PDBTitle: crystal structure of protein mj1004 from mathanocaldococcus jannaschii
9	c3iv9A_	 Alignment		99.9	34	PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
10	c3hf7A_	 Alignment		99.9	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized cbs-domain protein; PDBTitle: the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
11	c3jtfB_	 Alignment		99.9	38	PDB header: transport protein Chain: B: PDB Molecule: magnesium and cobalt efflux protein; PDBTitle: the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp

12	c3i8nB_	Alignment		99.9	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp2912; PDBTitle: a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633.
13	c3lfrB_	Alignment		99.9	45	PDB header: transport protein Chain: B: PDB Molecule: putative metal ion transporter; PDBTitle: the crystal structure of a cbs domain from a putative metal ion2 transporter bound to amp from pseudomonas syringae to 1.55a
14	c3nqrD_	Alignment		99.9	37	PDB header: transport protein Chain: D: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: a putative cbs domain-containing protein from salmonella typhimurium2 lt2
15	c3kxrA_	Alignment		99.8	15	PDB header: transport protein Chain: A: PDB Molecule: magnesium transporter, putative; PDBTitle: structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
16	c2yvxD_	Alignment		99.8	22	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
17	c6qvcB_	Alignment		99.8	15	PDB header: membrane protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: cryoem structure of the human clc-1 chloride channel, cbs state 1
18	c1yavB_	Alignment		99.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein yukl2 from bacillus subtilis
19	d2ooxe1	Alignment		99.8	12	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
20	c3ctuB_	Alignment		99.8	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
21	c2yvxA_	Alignment	not modelled	99.8	18	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
22	c3orgB_	Alignment	not modelled	99.8	19	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
23	c3lqnA_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
24	d2plia1	Alignment	not modelled	99.8	30	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
25	d2p13a1	Alignment	not modelled	99.8	23	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
26	c3dedB_	Alignment	not modelled	99.8	17	PDB header: membrane protein Chain: B: PDB Molecule: probable hemolysin; PDBTitle: c-terminal domain of probable hemolysin from chromobacterium violaceum
27	d3deda1	Alignment	not modelled	99.8	17	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
28	c3llbA_	Alignment	not modelled	99.8	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
						Fold: FAD-binding/transporter-associated domain-like

29	d2nqwa1	Alignment	not modelled	99.8	24	Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
30	c2emqA	Alignment	not modelled	99.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
31	c2ouxB	Alignment	not modelled	99.8	18	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
32	d2r2za1	Alignment	not modelled	99.8	24	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
33	d2nyca1	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
34	c2qh1B	Alignment	not modelled	99.8	16	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ta0289; PDBTitle: structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
35	d2plsA1	Alignment	not modelled	99.7	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
36	c6cozB	Alignment	not modelled	99.7	14	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic domain
37	c1zfaA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
38	c4o9kB	Alignment	not modelled	99.7	18	PDB header: isomerase Chain: B: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: crystal structure of the cbs pair of a putative d-arabinose 5-2 phosphate isomerase from methylococcus capsulatus in complex with3 cmp-kdo
39	d2o1ra1	Alignment	not modelled	99.7	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
40	d1yava3	Alignment	not modelled	99.7	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
41	c5tr1A	Alignment	not modelled	99.7	14	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein; PDBTitle: cryo-electron microscopy structure of a bovine clc-k chloride channel,2 alternate (class 2) conformation
42	c5nmuC	Alignment	not modelled	99.7	19	PDB header: photosynthesis Chain: C: PDB Molecule: cbs-cp12; PDBTitle: structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
43	d2d4za3	Alignment	not modelled	99.7	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
44	c3sl7B	Alignment	not modelled	99.7	20	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain-containing protein cbsx2; PDBTitle: crystal structure of cbs-pair protein, cbsx2 from arabidopsis thaliana
45	c4gqvA	Alignment	not modelled	99.7	19	PDB header: protein binding Chain: A: PDB Molecule: cbs domain-containing protein cbsx1, chloroplastic; PDBTitle: crystal structure of cbs-pair protein, cbsx1 from arabidopsis thaliana
46	c5x8oA	Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
47	c4l3vB	Alignment	not modelled	99.7	17	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
48	d2j9la1	Alignment	not modelled	99.7	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
49	c3pc3A	Alignment	not modelled	99.7	19	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
50	d2o3ga1	Alignment	not modelled	99.7	24	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
51	c2d4zB	Alignment	not modelled	99.7	15	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
52	c4z87B	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
53	d2v8qe2	Alignment	not modelled	99.7	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
54	c3fnaA	Alignment	not modelled	99.7	14	PDB header: isomerase Chain: A: PDB Molecule: possible arabinose 5-phosphate isomerase;

						PDBTitle: crystal structure of the cbs pair of possible d-arabinose 5-phosphate2 isomerase yrbh from escherichia coli cft073
55	d2rc3a1	Alignment	not modelled	99.7	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
56	c3fwrB_	Alignment	not modelled	99.7	11	PDB header: transcription Chain: B: PDB Molecule: yqzcb protein; PDBTitle: crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
57	d2rk5a1	Alignment	not modelled	99.7	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
58	d2oux2	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
59	d3ddja1	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
60	d2yzia1	Alignment	not modelled	99.7	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
61	c3tsdA_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
62	d2v8qe1	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
63	c2p9mD_	Alignment	not modelled	99.7	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0922; PDBTitle: crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
64	d2p3ha1	Alignment	not modelled	99.7	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
65	d1pvma4	Alignment	not modelled	99.7	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
66	d1y5ha3	Alignment	not modelled	99.7	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
67	d1vr9a3	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
68	d1pbja3	Alignment	not modelled	99.7	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
69	d2oaia1	Alignment	not modelled	99.7	27	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
70	d2ooxe2	Alignment	not modelled	99.7	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
71	c5ks7A_	Alignment	not modelled	99.6	15	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: carntine transport atp-binding protein opuca; PDBTitle: crystal structure of listeria monocytogenes opuca cbs domain dimer in2 complex with cyclic-di-amp
72	c1vr9B_	Alignment	not modelled	99.6	19	PDB header: unknown function Chain: B: PDB Molecule: cbs domain protein/act domain protein; PDBTitle: crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
73	c4fryA_	Alignment	not modelled	99.6	20	PDB header: signaling protein Chain: A: PDB Molecule: putative signal-transduction protein with cbs domains; PDBTitle: the structure of a putative signal-transduction protein with cbs2 domains from burkholderia ambifaria mc40-6
74	d2ef7a1	Alignment	not modelled	99.6	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
75	d1o50a3	Alignment	not modelled	99.6	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
76	d2riha1	Alignment	not modelled	99.6	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
77	d2yzqa1	Alignment	not modelled	99.6	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
78	c3gbyA_	Alignment	not modelled	99.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ct1051; PDBTitle: crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
79	d1zfja4	Alignment	not modelled	99.6	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
80	c2nr1E_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: E: PDB Molecule: protein c1556.08c;

80	c2qlE_	Alignment	not modelled	99.8	13	PDBTitle: crystal structure of the adenylate sensor from amp-activated protein2 kinase in complex with adp
81	d2o16a3	Alignment	not modelled	99.6	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
82	c2pfiA_	Alignment	not modelled	99.6	8	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein clc-ka; PDBTitle: crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
83	c2qlvF_	Alignment	not modelled	99.6	11	PDB header: transferase/protein binding Chain: F: PDB Molecule: nuclear protein snf4; PDBTitle: crystal structure of the heterotrimer core of the s. cerevisiae ampk2 homolog snf1
84	c4esyB_	Alignment	not modelled	99.6	17	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain containing membrane protein; PDBTitle: crystal structure of the cbs domain of cbs domain containing membrane2 protein from sphaerobacter thermophilus
85	d2yvxa2	Alignment	not modelled	99.6	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
86	c5ohxB_	Alignment	not modelled	99.6	17	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
87	c4nocA_	Alignment	not modelled	99.6	18	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein with cbs domains; PDBTitle: the crystal structure of a cbs domain-containing protein of unknown2 function from kribbella flavida dsm 17836.
88	c5aweA_	Alignment	not modelled	99.6	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acetoin utilization protein, acetoin PDBTitle: crystal structure of a hypothetical protein, ttha0829 from thermus2 thermophilus hb8, composed of cystathionine-beta-synthase (cbs) and3 aspartate-kinase chorismate-mutase tyra (act) domains
89	c2v8qE_	Alignment	not modelled	99.6	18	PDB header: transferase Chain: E: PDB Molecule: 5'-amp-activated protein kinase subunit gamma-1; PDBTitle: crystal structure of the regulatory fragment of mammalian2 ampk in complexes with amp
90	c4dqwB_	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
91	c3fhmD_	Alignment	not modelled	99.5	20	PDB header: structural genomics, unknown function, n Chain: D: PDB Molecule: uncharacterized protein atu1752; PDBTitle: crystal structure of the cbs-domain containing protein atu1752 from2 agrobacterium tumefaciens
92	c3kpbA_	Alignment	not modelled	99.5	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mj0100; PDBTitle: crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
93	d2p4pa1	Alignment	not modelled	99.5	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
94	c4qfsC_	Alignment	not modelled	99.5	13	PDB header: signaling protein/inhibitor/activator Chain: C: PDB Molecule: 5'-amp-activated protein kinase subunit gamma-1; PDBTitle: structure of ampk in complex with br2-a769662core activator and2 staurosporine inhibitor
95	c3ddjA_	Alignment	not modelled	99.5	21	PDB header: amp-binding protein Chain: A: PDB Molecule: cbs domain-containing protein; PDBTitle: crystal structure of a cbs domain-containing protein in complex with2 amp (sso3205) from sulfolobus solfataricus at 1.80 a resolution
96	d3ddja2	Alignment	not modelled	99.5	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
97	c3kh5A_	Alignment	not modelled	99.4	27	PDB header: unknown function Chain: A: PDB Molecule: protein mj1225; PDBTitle: crystal structure of protein mj1225 from methanocaldococcus2 jannaschii, a putative archaeal homolog of g-ampk.
98	c5iipA_	Alignment	not modelled	99.4	17	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
99	c5g5rA_	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: A: PDB Molecule: site-2 protease; PDBTitle: cbs domain tandem of site-2 protease from archaeoglobus fulgidus in2 complex with llama nanobody - apo form
100	c3l31B_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: B: PDB Molecule: probable manganase-dependent inorganic PDBTitle: crystal structure of the cbs and drtg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
101	d2yzqa2	Alignment	not modelled	99.2	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
102	c2yzqA_	Alignment	not modelled	99.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1780; PDBTitle: crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
103	c4fxsA_	Alignment	not modelled	99.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid

104	c3fioB_	 Alignment	not modelled	98.0	18	PDB header: nucleotide binding protein, metal bindin Chain: B: PDB Molecule: a cystathionine beta-synthase domain protein PDBTitle: crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
105	d1jcna4	 Alignment	not modelled	97.1	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
106	d1jr1a4	 Alignment	not modelled	97.0	29	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
107	d1udxa3	 Alignment	not modelled	78.8	17	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
108	c5azdA_	 Alignment	not modelled	60.0	14	PDB header: transport protein Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of thermophilic rhodopsin.
109	c5nikK_	 Alignment	not modelled	57.8	14	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
110	d1nq4a_	 Alignment	not modelled	56.4	21	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
111	c3ug9A_	 Alignment	not modelled	53.3	11	PDB header: membrane protein Chain: A: PDB Molecule: archaeal-type opsin 1, archaeal-type opsin 2; PDBTitle: crystal structure of the closed state of channelrhodopsin
112	d2pp6a1	 Alignment	not modelled	45.5	15	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
113	c3ia1A_	 Alignment	not modelled	41.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thio-disulfide isomerase/thioredoxin; PDBTitle: crystal structure of thio-disulfide isomerase from thermus2 thermophilus
114	c3ce7A_	 Alignment	not modelled	40.7	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: specific mitochondrial acyl carrier protein; PDBTitle: crystal structure of toxoplasma specific mitochondrial acyl carrier2 protein, 59.m03510
115	d1or5a_	 Alignment	not modelled	40.0	19	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
116	d1t3ta1	 Alignment	not modelled	39.3	26	Fold: RuvA C-terminal domain-like Superfamily: FGAM synthase PurL, linker domain Family: FGAM synthase PurL, linker domain
117	c3nwuB_	 Alignment	not modelled	37.8	27	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
118	d2a29a1	 Alignment	not modelled	37.6	29	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
119	c5ws4A_	 Alignment	not modelled	37.1	12	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
120	c4xtnJ_	 Alignment	not modelled	37.1	19	PDB header: membrane protein Chain: J: PDB Molecule: sodium pumping rhodopsin; PDBTitle: crystal structure of the light-driven sodium pump kr2 in the2 pentameric red form, ph 4.9