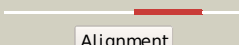
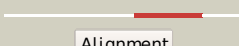
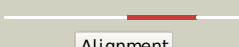
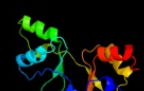
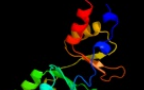
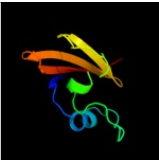


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ocmA_	 Alignment		100.0	52	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
2	c3ocmB_	 Alignment		100.0	52	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
3	c3oi8B_	 Alignment		100.0	26	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
4	c3ocoB_	 Alignment		100.0	20	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
5	c3lhhA_	 Alignment		100.0	34	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
6	c3lv9A_	 Alignment		100.0	25	PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
7	c3lfrB_	 Alignment		99.9	32	PDB header: transport protein Chain: B: PDB Molecule: putative metal ion transporter; PDBTitle: the crystal structure of a cbs domain from a putative metal2 ion transporter bound to amp from pseudomonas syringae to3 1.55a
8	c3i8nB_	 Alignment		99.9	25	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.
9	c3jtfB_	 Alignment		99.9	34	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
10	c3hf7A_	 Alignment		99.9	33	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	c3nqrD_	 Alignment		99.9	34	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

12	c1yavB_	Alignment		99.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein ykuL2 from bacillus subtilis
13	c3kxrA_	Alignment		99.9	10	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.
14	c3ctuB_	Alignment		99.8	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
15	d2plsa1	Alignment		99.8	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
16	c3dedB_	Alignment		99.8	22	PDB header: membrane protein Chain: B: PDB Molecule: probable hemolysin; PDBTitle: c-terminal domain of probable hemolysin from chromobacterium violaceum
17	d3deda1	Alignment		99.8	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
18	d2p13a1	Alignment		99.8	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
19	c2yvzA_	Alignment		99.8	19	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
20	c2yvxD_	Alignment		99.8	18	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
21	c3lqnA_	Alignment	not modelled	99.8	14	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
22	c3orgB_	Alignment	not modelled	99.8	23	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
23	d2ooxe1	Alignment	not modelled	99.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
24	d2nqwa1	Alignment		99.8	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
25	d2nyca1	Alignment	not modelled	99.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
26	c2emqA_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus

27	d2o3ga1	Alignment		99.8	29	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
28	d2plia1	Alignment	not modelled	99.8	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
29	d2o1ra1	Alignment	not modelled	99.8	27	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
30	c1zfjA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
31	c3llbA_	Alignment	not modelled	99.8	28	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
32	d1yava3	Alignment	not modelled	99.8	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
33	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
34	c2ouxB_	Alignment	not modelled	99.8	22	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
35	c3fnaA_	Alignment	not modelled	99.8	15	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
36	d2d4za3	Alignment	not modelled	99.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
37	d2oai1	Alignment	not modelled	99.8	25	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
38	c2qh1B_	Alignment	not modelled	99.8	15	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
39	c2d4zB_	Alignment	not modelled	99.8	14	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
40	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
41	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
42	d3ddja1	Alignment	not modelled	99.7	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
43	d2j9la1	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
44	d2v8qe2	Alignment	not modelled	99.7	12	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
45	d1vr9a3	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
46	c1vr9B_	Alignment	not modelled	99.7	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
47	d2p3ha1	Alignment	not modelled	99.7	23	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
48	c3fwrB_	Alignment	not modelled	99.7	12	PDB header: transcription Chain: B: PDB Molecule: yqzb protein; PDBTitle: crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
49	d2ef7a1	Alignment	not modelled	99.7	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
50	d2oux2	Alignment	not modelled	99.7	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
51	d2v8qe1	Alignment	not modelled	99.7	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
52	d2rc3a1	Alignment	not modelled	99.7	10	Fold: CBS-domain pair Superfamily: CBS-domain pair

					Family: CBS-domain pair
53	d1zfja4	Alignment	not modelled	99.7	15 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
54	d2p4pa1	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
55	d2yzqa1	Alignment	not modelled	99.7	18 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
56	d2yzia1	Alignment	not modelled	99.7	14 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
57	c2p9mD_	Alignment	not modelled	99.7	19 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
58	d1y5ha3	Alignment	not modelled	99.7	16 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
59	d1pvma4	Alignment	not modelled	99.7	15 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
60	d1o50a3	Alignment	not modelled	99.7	15 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
61	c3gbyA_	Alignment	not modelled	99.7	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
62	d1pbja3	Alignment	not modelled	99.7	15 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
63	d2o16a3	Alignment	not modelled	99.7	14 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
64	d2riha1	Alignment	not modelled	99.7	18 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
65	d2ooxe2	Alignment	not modelled	99.6	14 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
66	c2pfiA_	Alignment	not modelled	99.6	13 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
67	c2qr1E_	Alignment	not modelled	99.6	13 PDB header: transferase Chain: E: PDB Molecule: protein c1556.08c; PDBTitle: crystal structure of the adenylate sensor from amp-activated protein2 kinase in complex with adp
68	c2qlvF_	Alignment	not modelled	99.6	12 PDB header: transferase/protein binding Chain: F: PDB Molecule: nuclear protein snf4; PDBTitle: crystal structure of the heterotrimer core of the s.2 cerevisiae ampk homolog snf1
69	d2yvxa2	Alignment	not modelled	99.6	20 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
70	c3kpbA_	Alignment	not modelled	99.6	16 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.
71	c2v8qE_	Alignment	not modelled	99.6	17 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
72	c3fhmD_	Alignment	not modelled	99.6	18 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
73	d3ddja2	Alignment	not modelled	99.6	12 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
74	c3kh5A_	Alignment	not modelled	99.5	22 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.
75	d2yzqa2	Alignment	not modelled	99.4	19 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
76	c3l3lB_	Alignment	not modelled	99.3	21 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
77	c2yzqA_	Alignment	not modelled	99.3	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1780; PDBTitle: crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii PDB header: amp-binding protein

78	c3ddjA_	Alignment	not modelled	99.3	13	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
79	c3fioB_	Alignment	not modelled	97.8	20	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
80	d1jcna4	Alignment	not modelled	97.4	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
81	d1jr1a4	Alignment	not modelled	97.2	27	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
82	d2pp6a1	Alignment	not modelled	48.8	24	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
83	d2af8a_	Alignment	not modelled	43.5	22	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
84	d2a29a1	Alignment	not modelled	38.4	17	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
85	c3ce7A_	Alignment	not modelled	38.1	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: specific mitochondrial acyl carrier protein; PDBTitle: crystal structure of toxoplasma specific mitochondrial acyl2 carrier protein, 59.m03510
86	d1nq4a_	Alignment	not modelled	33.4	19	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
87	d1or5a_	Alignment	not modelled	31.3	19	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
88	c3hcza_	Alignment	not modelled	28.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: possible thiol-disulfide isomerase; PDBTitle: the crystal structure of a domain of possible thiol-disulfide2 isomerase from cytophaga hutchinsonii atcc 33406.
89	c2l4ba_	Alignment	not modelled	25.3	14	PDB header: transferase Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
90	d1y0na_	Alignment	not modelled	24.8	20	Fold: YehU-like Superfamily: YehU-like Family: YehU-like
91	d1yj5a1	Alignment	not modelled	22.6	21	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
92	d2vv5a1	Alignment	not modelled	22.6	19	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
93	d1g8fa1	Alignment	not modelled	22.6	14	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
94	d1x6va1	Alignment	not modelled	22.3	14	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
95	d1dv5a_	Alignment	not modelled	21.4	16	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: apo-D-alanyl carrier protein
96	c3nwb_	Alignment	not modelled	21.3	33	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
97	d1lcya2	Alignment	not modelled	20.3	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
98	d1pbwa_	Alignment	not modelled	19.7	17	Fold: GTPase activation domain, GAP Superfamily: GTPase activation domain, GAP Family: BCR-homology GTPase activation domain (BH-domain)
99	c2koyA_	Alignment	not modelled	19.7	8	PDB header: metal transport Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: structure of the e1064a mutant of the n-domain of wilson disease2 associated protein