

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ocmA_	 Alignment		100.0	30	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	31	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	c3ocoB_	 Alignment		100.0	23	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
4	c3oi8B_	 Alignment		100.0	28	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	c3lhhA_	 Alignment		99.9	33	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		99.9	31	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	c3i8nB_	 Alignment		99.9	24	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.
8	c3ltfB_	 Alignment		99.9	33	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
9	c3lfrB_	 Alignment		99.9	31	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
10	c3hf7A_	 Alignment		99.9	27	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	29	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	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
13	d3deda1	Alignment		99.8	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
14	d2p13a1	Alignment		99.8	25	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
15	d2pls1a1	Alignment		99.8	28	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
16	d2plia1	Alignment		99.8	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
17	c1yavB_	Alignment		99.8	17	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
18	d2nqwa1	Alignment		99.8	26	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
19	c3kxrA_	Alignment		99.8	21	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.
20	c3l1ba_	Alignment		99.8	23	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
21	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
22	c3ctuB_	Alignment	not modelled	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
23	c2yvzA_	Alignment	not modelled	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
24	c2yvxD_	Alignment	not modelled	99.8	19	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
25	d2r2za1	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	d2nyca1	Alignment	not modelled	99.8	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
27	d2o3ga1	Alignment	not modelled	99.8	31	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
28	c3lqnA_	Alignment	not modelled	99.8	21	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
29	c2emvA_	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein;

29	c2emqA	Alignment	not modelled	99.8	18	PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
30	d2ooxe1	Alignment	not modelled	99.8	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
31	c3orgB	Alignment	not modelled	99.8	18	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
32	c1zfjA	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
33	d2oaia1	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	d2rk5a1	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
35	d1yava3	Alignment	not modelled	99.8	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
36	d2p3ha1	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
37	d2d4za3	Alignment	not modelled	99.7	23	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
38	c2ouxB	Alignment	not modelled	99.7	19	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
39	c2d4zB	Alignment	not modelled	99.7	24	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	c3fnaA	Alignment	not modelled	99.7	17	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
41	d2j9la1	Alignment	not modelled	99.7	23	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
42	c2qh1B	Alignment	not modelled	99.7	18	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
43	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
44	d3ddja1	Alignment	not modelled	99.7	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
45	d1vr9a3	Alignment	not modelled	99.7	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
46	d2v8qe2	Alignment	not modelled	99.7	12	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
47	d1zfja4	Alignment	not modelled	99.7	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
48	d2ef7a1	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
49	c3fwrB	Alignment	not modelled	99.7	19	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
50	c1vr9B	Alignment	not modelled	99.7	25	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
51	d2ouxa2	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
52	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
53	d2rc3a1	Alignment	not modelled	99.7	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
54	d2yzqa1	Alignment	not modelled	99.7	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
55	d2riha1	Alignment	not modelled	99.7	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
						Fold: CBS-domain pair

56	d2v8qe1	Alignment	not modelled	99.6	20	Superfamily: CBS-domain pair Family: CBS-domain pair
57	d2yzia1	Alignment	not modelled	99.6	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
58	d1pvma4	Alignment	not modelled	99.6	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
59	d1y5ha3	Alignment	not modelled	99.6	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
60	d1pbja3	Alignment	not modelled	99.6	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
61	d2o16a3	Alignment	not modelled	99.6	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
62	c3gbyA_	Alignment	not modelled	99.6	20	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
63	c2p9mD_	Alignment	not modelled	99.6	20	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	d1o50a3	Alignment	not modelled	99.6	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
65	d2ooxe2	Alignment	not modelled	99.6	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
66	d2yvxa2	Alignment	not modelled	99.6	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
67	c2pfiA_	Alignment	not modelled	99.6	20	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
68	c2qr1E_	Alignment	not modelled	99.6	19	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
69	c3kpbA_	Alignment	not modelled	99.6	19	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.
70	c2qlvF_	Alignment	not modelled	99.5	14	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
71	c2v8qE_	Alignment	not modelled	99.5	21	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	c3ddjA_	Alignment	not modelled	99.5	19	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
73	d3ddja2	Alignment	not modelled	99.5	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
74	c3fhmD_	Alignment	not modelled	99.5	19	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
75	c3kh5A_	Alignment	not modelled	99.4	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.
76	c3l31B_	Alignment	not modelled	99.3	16	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	c2yzqaA_	Alignment	not modelled	99.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1780; PDBTitle: crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
78	d2yzqa2	Alignment	not modelled	99.2	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
79	c3fioB_	Alignment	not modelled	97.7	23	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	97.2	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
						Fold: CBS-domain pair

81	dljr1a4	Alignment	not modelled	96.7	22	Superfamily: CBS-domain pair Family: CBS-domain pair
82	dludxa3	Alignment	not modelled	84.4	16	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
83	dlor5a_	Alignment	not modelled	56.0	15	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
84	dlnq4a_	Alignment	not modelled	52.6	9	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
85	c3ce7A_	Alignment	not modelled	42.8	11	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	c3hcza_	Alignment	not modelled	36.5	11	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.
87	d2pp6a1	Alignment	not modelled	35.9	17	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
88	c2l4ba_	Alignment	not modelled	30.1	9	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
89	dlyj5a1	Alignment	not modelled	27.8	8	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
90	d1pbwa_	Alignment	not modelled	24.8	24	Fold: GTPase activation domain, GAP Superfamily: GTPase activation domain, GAP Family: BCR-homology GTPase activation domain (BH-domain)
91	c3nwbU_	Alignment	not modelled	23.5	40	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
92	d1lcya2	Alignment	not modelled	20.8	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
93	d1t3ta1	Alignment	not modelled	20.5	26	Fold: RuvA C-terminal domain-like Superfamily: FGAM synthase PurL, linker domain Family: FGAM synthase PurL, linker domain
94	c2rcel_	Alignment	not modelled	19.6	33	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz
95	d2af8a_	Alignment	not modelled	18.7	11	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
96	c3nziA_	Alignment	not modelled	18.5	40	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
97	d1ky9a2	Alignment	not modelled	18.1	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
98	c2ke4A_	Alignment	not modelled	18.1	31	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
99	d1l1ja_	Alignment	not modelled	17.9	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases