Phyre2

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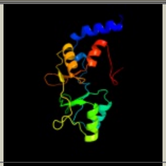
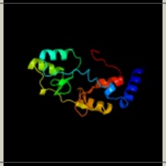
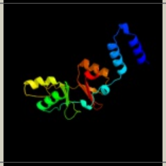
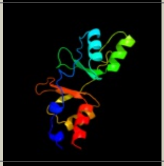
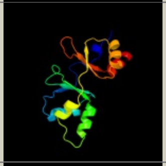
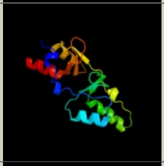
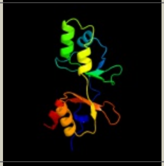
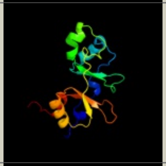
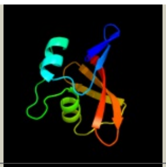
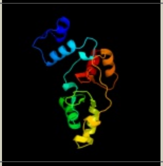
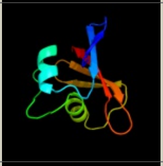
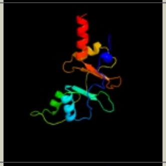
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ocmA_	Alignment		100.0	24	**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	25	**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		99.9	25	**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		99.9	18	**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		99.9	28	**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	28	**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	c3hf7A_	Alignment		99.9	91	**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
8	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
9	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.
10	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
11	c3nqrD_	Alignment		99.9	28	**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	d2plia1	Alignment		99.8	20	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
13	c3kxrA_	Alignment		99.8	13	**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	c3llbA_	Alignment		99.8	20	**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
15	c1yavB_	Alignment		99.8	14	**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
16	c3dedB_	Alignment		99.8	23	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable hemolysin; **PDBTitle:** c-terminal domain of probable hemolysin from chromobacterium violaceum
17	c2yvzA_	Alignment		99.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
18	d2o1ra1	Alignment		99.8	58	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
19	d3deda1	Alignment		99.8	23	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
20	c2yvxD_	Alignment		99.8	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
21	d2nqwa1	Alignment	not modelled	99.8	20	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
22	d2r2za1	Alignment	not modelled	99.8	22	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
23	d2plsa1	Alignment	not modelled	99.8	20	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
24	c3ctuB_	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
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	d2ooxe1	Alignment	not modelled	99.8	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
27	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
28	d2nyca1	Alignment	not modelled	99.8	15	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
29	c2emqA	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein;

29	c2emqA_	Alignment	not modelled	99.8	14	**PDBTitle:** hypothetical conserved protein (gk1048) from geobacillus kaustophilus
30	c2ouxB_	Alignment	not modelled	99.8	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium transporter; **PDBTitle:** crystal structure of the soluble part of a magnesium transporter
31	d2o3ga1	Alignment	not modelled	99.8	26	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
32	d2rk5a1	Alignment	not modelled	99.8	22	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
33	d1yava3	Alignment	not modelled	99.8	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
34	c1zfjA_	Alignment	not modelled	99.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
35	d2p3ha1	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
36	c3orgB_	Alignment	not modelled	99.7	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
37	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
38	d2v8qe2	Alignment	not modelled	99.7	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
39	c3pc3A_	Alignment	not modelled	99.7	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
40	d2oaia1	Alignment	not modelled	99.7	22	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
41	c3fwrB_	Alignment	not modelled	99.7	14	**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
42	c3fnaA_	Alignment	not modelled	99.7	16	**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
43	d2d4za3	Alignment	not modelled	99.7	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
44	d2j9la1	Alignment	not modelled	99.7	15	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
45	c2d4zB_	Alignment	not modelled	99.7	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride channel protein; **PDBTitle:** crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
46	d2ouxa2	Alignment	not modelled	99.7	15	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
47	d3ddja1	Alignment	not modelled	99.7	11	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
48	d2yzia1	Alignment	not modelled	99.7	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
49	d1vr9a3	Alignment	not modelled	99.7	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
50	d2v8qe1	Alignment	not modelled	99.7	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
51	c2p9mD_	Alignment	not modelled	99.7	12	**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
52	c1vr9B_	Alignment	not modelled	99.7	16	**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
53	d2rc3a1	Alignment	not modelled	99.7	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
54	d2ef7a1	Alignment	not modelled	99.7	14	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
55	d1pbja3	Alignment	not modelled	99.7	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
						PDB header:structural genomics, unknown function

56	c3gbyA_	Alignment	not modelled	99.7	12	**Chain:** A: **PDB Molecule:**uncharacterized protein ct1051; **PDBTitle:** crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
57	d1o50a3	Alignment	not modelled	99.7	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
58	d1y5ha3	Alignment	not modelled	99.7	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
59	d2o16a3	Alignment	not modelled	99.7	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
60	d1pvma4	Alignment	not modelled	99.7	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
61	d1zfja4	Alignment	not modelled	99.6	11	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
62	c2qlvF_	Alignment	not modelled	99.6	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
63	d2yzqa1	Alignment	not modelled	99.6	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
64	d2riha1	Alignment	not modelled	99.6	15	**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	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
67	c2pfiA_	Alignment	not modelled	99.6	11	**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	d2yvxa2	Alignment	not modelled	99.6	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
69	d2p4pa1	Alignment	not modelled	99.6	26	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
70	c2v8qE_	Alignment	not modelled	99.6	13	**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
71	c3kpbA_	Alignment	not modelled	99.6	17	**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.
72	c3kh5A_	Alignment	not modelled	99.5	29	**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.
73	c3ddjA_	Alignment	not modelled	99.5	18	**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
74	c3fhmD_	Alignment	not modelled	99.5	9	**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	d3ddja2	Alignment	not modelled	99.5	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
76	c3l31B_	Alignment	not modelled	99.4	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable manganase-dependent inorganic **PDBTitle:** crystal structure of the cbs and drtgg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
77	d2yzqa2	Alignment	not modelled	99.3	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
78	c2yzqA_	Alignment	not modelled	99.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1780; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
79	c3fioB_	Alignment	not modelled	98.2	13	**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	97.3	22	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
						Fold:CBS-domain pair

81	d1jr1a4	Alignment	not modelled	97.3	12	**Superfamily:**CBS-domain pair **Family:**CBS-domain pair
82	d1udxa3	Alignment	not modelled	71.5	22	**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	d1t3ta1	Alignment	not modelled	62.6	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**FGAM synthase PurL, linker domain **Family:**FGAM synthase PurL, linker domain
84	d1nq4a_	Alignment	not modelled	58.2	16	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
85	c3ce7A_	Alignment	not modelled	49.5	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**specific mitochodrial acyl carrier protein; **PDBTitle:** crystal structure of toxoplasma specific mitochodrial acyl2 carrier protein, 59.m03510
86	d1or5a_	Alignment	not modelled	44.3	14	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
87	d1pbwa_	Alignment	not modelled	42.2	13	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
88	d1g8fa1	Alignment	not modelled	41.1	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
89	c3nwuB_	Alignment	not modelled	40.1	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
90	d1lcya2	Alignment	not modelled	39.6	40	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
91	d2pp6a1	Alignment	not modelled	39.6	21	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
92	c2l4bA_	Alignment	not modelled	38.5	15	**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
93	c3nziA_	Alignment	not modelled	34.7	40	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
94	d1yj5a1	Alignment	not modelled	34.6	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
95	d1x6va1	Alignment	not modelled	33.8	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
96	d2qf3a1	Alignment	not modelled	33.5	40	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
97	d1jmxa1	Alignment	not modelled	32.5	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
98	c2rceI_	Alignment	not modelled	31.9	36	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**protease degs; **PDBTitle:** dfp modified degs delta pdz
99	c3k6zA_	Alignment	not modelled	31.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible membrane-associated serine protease; **PDBTitle:** crystal structure of rv3671c protease, inactive form
100	d1ky9a2	Alignment	not modelled	31.7	40	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
101	c1t3tA_	Alignment	not modelled	30.6	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
102	d1l1ja_	Alignment	not modelled	29.9	29	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
103	c1xa6A_	Alignment	not modelled	29.9	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**beta2-chimaerin; **PDBTitle:** crystal structure of the human beta2-chimaerin
104	d1pbya1	Alignment	not modelled	29.6	5	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
105	c3stiC_	Alignment	not modelled	29.4	33	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease domain of degq from escherichia coli
106	c1pbwB_	Alignment	not modelled	28.5	13	**PDB header:**phosphotransferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase; **PDBTitle:** structure of bcr-homology (bh) domain
107	c1r6xA_	Alignment	not modelled	28.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:sulfate adenylyltransferase; **PDBTitle:** the crystal structure of a truncated form of yeast atp2

						sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
108	c3am6C_	Alignment	not modelled	27.4	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**rhodopsin-2; **PDBTitle:** crystal structure of the proton pumping rhodopsin ar2 from marine alga2 acetabularia acetabulum
109	c3lwaA_	Alignment	not modelled	27.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**secreted thiol-disulfide isomerase; **PDBTitle:** the crystal structure of a secreted thiol-disulfide2 isomerase from corynebacterium glutamicum to 1.75a
110	c2fq2A_	Alignment	not modelled	26.6	18	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
111	c3hczA_	Alignment	not modelled	25.9	21	**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.
112	d1p0za_	Alignment	not modelled	25.9	20	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
113	c1g8gB_	Alignment	not modelled	25.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
114	c3ixzB_	Alignment	not modelled	24.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
115	c1x3oA_	Alignment	not modelled	23.8	10	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
116	c3fk2B_	Alignment	not modelled	22.9	27	**PDB header:**signaling protein, hydrolase activator **Chain:** B: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** crystal structure of the rhogap domain of human2 glucocorticoid receptor dna-binding factor 1
117	d1h2sa_	Alignment	not modelled	22.5	21	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like