Phyre2

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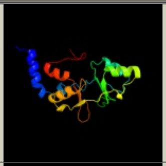
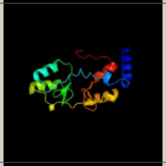
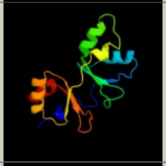
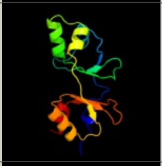
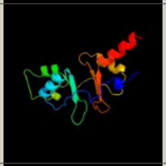
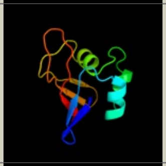
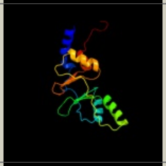
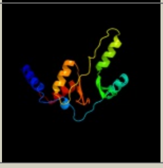
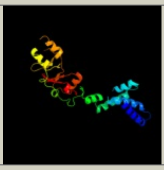
Description	P0AE45
Date	Thu Jan 5 11:22:30 GMT 2012
Unique Job ID	c1130e0b8683870b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ocmA_	Alignment		100.0	21	**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	22	**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	20	**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	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
5	c3lhhA_	Alignment		99.9	30	**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	22	**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	18	**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	30	**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	26	**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	25	**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	24	**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	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.
13	c3dedB_	Alignment		99.8	40	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable hemolysin; **PDBTitle:** c-terminal domain of probable hemolysin from chromobacterium violaceum
14	d3deda1	Alignment		99.8	39	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
15	c1yavB_	Alignment		99.8	12	**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	d2plsa1	Alignment		99.8	33	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
17	d2plia1	Alignment		99.8	30	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
18	c3ctuB_	Alignment		99.8	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
19	c2yvxD_	Alignment		99.8	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
20	d2ooxe1	Alignment		99.8	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
21	d2nqwa1	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
22	d2p13a1	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
23	c3llbA_	Alignment	not modelled	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
24	d2o3ga1	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
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	d2o1ra1	Alignment	not modelled	99.8	18	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
27	c3lqnA_	Alignment	not modelled	99.8	16	**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	c2yvzA_	Alignment	not modelled	99.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
29	c2emqA_	Alignment	not modelled	99.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** hypothetical conserved protein (gk1048) from

						geobacillus kaustophilus
30	c3orgB_	Alignment		99.8	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
31	d2nyca1	Alignment	not modelled	99.8	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
32	c1zfjA_	Alignment	not modelled	99.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
33	c2ouxB_	Alignment	not modelled	99.8	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium transporter; **PDBTitle:** crystal structure of the soluble part of a magnesium transporter
34	d2d4za3	Alignment	not modelled	99.8	15	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
35	d1yava3	Alignment	not modelled	99.8	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
36	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
37	c2d4zB_	Alignment	not modelled	99.8	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride channel protein; **PDBTitle:** crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
38	d2oaia1	Alignment		99.8	36	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
39	d2p3ha1	Alignment	not modelled	99.8	29	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
40	d2v8qe2	Alignment	not modelled	99.7	11	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
41	d3ddja1	Alignment	not modelled	99.7	15	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
42	d2rk5a1	Alignment	not modelled	99.7	20	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
43	c3fnaA_	Alignment	not modelled	99.7	12	**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
44	d2j9la1	Alignment	not modelled	99.7	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
45	c3fwrB_	Alignment	not modelled	99.7	13	**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
46	c3pc3A_	Alignment	not modelled	99.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
47	d1vr9a3	Alignment	not modelled	99.7	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
48	d2ouxa2	Alignment	not modelled	99.7	14	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
49	d2yzqa1	Alignment	not modelled	99.7	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
50	d2ef7a1	Alignment	not modelled	99.7	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
51	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
52	d2riha1	Alignment	not modelled	99.7	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
53	d2rc3a1	Alignment	not modelled	99.7	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
						Fold:CBS-domain pair

54	d2yzia1	Alignment	not modelled	99.7	19	**Superfamily:**CBS-domain pair **Family:**CBS-domain pair
55	d2v8qe1	Alignment	not modelled	99.7	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
56	d1zfja4	Alignment	not modelled	99.7	7	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
57	c2p9mD_	Alignment	not modelled	99.7	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
58	d1y5ha3	Alignment	not modelled	99.7	20	**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	c3gbyA_	Alignment	not modelled	99.7	14	**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
61	d2p4pa1	Alignment		99.7	52	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
62	d1o50a3	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	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
64	d1pbja3	Alignment	not modelled	99.7	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
65	c2qlvF_	Alignment	not modelled	99.7	17	**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
66	d2ooxe2	Alignment	not modelled	99.6	14	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
67	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
68	c2qr1E_	Alignment	not modelled	99.6	15	**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	d2yvxa2	Alignment	not modelled	99.6	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
70	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
71	c3kpbA_	Alignment	not modelled	99.6	14	**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	c3fhmD_	Alignment	not modelled	99.6	15	**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	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
74	c3ddjA_	Alignment	not modelled	99.5	23	**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
75	c3kh5A_	Alignment	not modelled	99.5	18	**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	99.4	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	c2yzqA_	Alignment	not modelled	99.4	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
						Fold:CBS-domain pair

78	d2yzqa2	Alignment	not modelled	99.3	22	**Superfamily:**CBS-domain pair **Family:**CBS-domain pair
79	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
80	d1jcna4	Alignment	not modelled	97.4	24	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
81	d1jr1a4	Alignment	not modelled	97.3	22	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
82	d1udxa3	Alignment	not modelled	74.8	18	**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	d2pp6a1	Alignment	not modelled	52.1	36	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
84	c2ejbA_	Alignment	not modelled	40.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
85	d1pbwa_	Alignment	not modelled	37.0	11	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
86	c3hczA_	Alignment	not modelled	36.3	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	c3nwuB_	Alignment	not modelled	33.9	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
88	d1t3ta1	Alignment	not modelled	33.4	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**FGAM synthase PurL, linker domain **Family:**FGAM synthase PurL, linker domain
89	c3nziA_	Alignment	not modelled	33.3	33	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
90	d1g8fa1	Alignment	not modelled	33.2	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
91	d1lcya2	Alignment	not modelled	32.7	29	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
92	c3ia1A_	Alignment	not modelled	31.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
93	d2qf3a1	Alignment	not modelled	31.0	27	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
94	d2a29a1	Alignment	not modelled	30.3	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
95	c3k6zA_	Alignment	not modelled	30.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible membrane-associated serine protease; **PDBTitle:** crystal structure of rv3671c protease, inactive form
96	c2rceI_	Alignment	not modelled	30.2	29	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**protease degs; **PDBTitle:** dfp modified degs delta pdz
97	c3lwaA_	Alignment	not modelled	29.9	11	**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
98	d1nq4a_	Alignment	not modelled	28.8	16	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
99	d1l1ja_	Alignment	not modelled	28.5	36	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
100	d1y0na_	Alignment	not modelled	27.2	13	**Fold:**YehU-like **Superfamily:**YehU-like **Family:**YehU-like
101	c3ce7A_	Alignment	not modelled	25.9	22	**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
102	d1or5a_	Alignment	not modelled	25.3	13	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
103	c1pbwB_	Alignment	not modelled	24.6	6	**PDB header:**phosphotransferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase; **PDBTitle:** structure of bcr-homology (bh) domain
104	c3stiC_	Alignment	not modelled	24.5	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease domain of degq from

						escherichia coli
105	d1yj5a1	Alignment	not modelled	24.4	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
106	d1ky9a2	Alignment	not modelled	24.2	29	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
107	d1x6va1	Alignment	not modelled	23.8	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
108	d1h2sa_	Alignment	not modelled	23.2	7	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
109	d1p0za_	Alignment	not modelled	23.0	27	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
110	d1uaza_	Alignment	not modelled	22.9	11	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
111	c1r6xA_	Alignment	not modelled	21.9	16	**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