






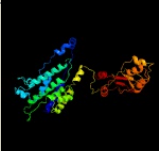








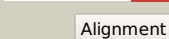
















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2625c (-) _2951332_2952513
Date	Wed Aug 7 12:50:27 BST 2019
Unique Job ID	13978dad82b59f90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3b4rA_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc metalloprotease mj0392; <b>PDBTitle:</b> site-2 protease from methanocaldococcus jannaschii
2	<a href="#">c3b4rB_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative zinc metalloprotease mj0392; <b>PDBTitle:</b> site-2 protease from methanocaldococcus jannaschii
3	<a href="#">c5tr1A_</a>	 Alignment		99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chloride channel protein; <b>PDBTitle:</b> cryo-electron microscopy structure of a bovine clc-k chloride channel,2 alternate (class 2) conformation
4	<a href="#">c6qvcB_</a>	 Alignment		99.9	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride channel protein 1; <b>PDBTitle:</b> cryoem structure of the human clc-1 chloride channel, cbs state 1
5	<a href="#">c3orgB_</a>	 Alignment		99.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cmclc; <b>PDBTitle:</b> crystal structure of a eukaryotic clc transporter
6	<a href="#">c4l3vB_</a>	 Alignment		99.9	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> crystal structure of delta516-525 human cystathionine beta-synthase
7	<a href="#">c2qh1B_</a>	 Alignment		99.8	20	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ta0289; <b>PDBTitle:</b> structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
8	<a href="#">c6h1wA_</a>	 Alignment		99.8	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mj1004; <b>PDBTitle:</b> crystal structure of protein mj1004 from methanocaldococcus jannaschii
9	<a href="#">c3fwrB_</a>	 Alignment		99.8	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> yqzb protein; <b>PDBTitle:</b> crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
10	<a href="#">c2yvxD_</a>	 Alignment		99.8	19	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
11	<a href="#">c2p9mD_</a>	 Alignment		99.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein mj0922; <b>PDBTitle:</b> crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661

12	<a href="#">d2d4za3</a>	Alignment		99.8	12	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
13	<a href="#">d3ddja1</a>	Alignment		99.8	13	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
14	<a href="#">d2yza1</a>	Alignment		99.8	16	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
15	<a href="#">d2yzqa1</a>	Alignment		99.8	17	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
16	<a href="#">c3pc3A_</a>	Alignment		99.8	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cg1753, isoform a; <b>PDBTitle:</b> full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
17	<a href="#">d1pvma4</a>	Alignment		99.8	20	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
18	<a href="#">c2ouxB_</a>	Alignment		99.8	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> magnesium transporter; <b>PDBTitle:</b> crystal structure of the soluble part of a magnesium transporter
19	<a href="#">c4o9kB_</a>	Alignment		99.8	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> arabinose 5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of the cbs pair of a putative d-arabinose 5-2 phosphate isomerase from methylococcus capsulatus in complex with3 cmp-kdo
20	<a href="#">c3gbyA_</a>	Alignment		99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ct1051; <b>PDBTitle:</b> crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
21	<a href="#">c1zfa_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
22	<a href="#">c2d4zB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride channel protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
23	<a href="#">c3ocmA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
24	<a href="#">d1vr9a3</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
25	<a href="#">c6cozB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride channel protein 1; <b>PDBTitle:</b> human clc-1 chloride ion channel, c-terminal cytosolic domain
26	<a href="#">c5ohxB_</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> structure of active cystathionine b-synthase from apis mellifera
27	<a href="#">c3hf7A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized cbs-domain protein; <b>PDBTitle:</b> the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
28	<a href="#">c3i8nB_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein vp2912; <b>PDBTitle:</b> a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633. <b>PDB header:</b> transport protein

29	<a href="#">c3kxrA_</a>	Alignment	not modelled	99.8	11	<b>Chain:</b> A: <b>PDB Molecule:</b> magnesium transporter, putative; <b>PDBTitle:</b> structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
30	<a href="#">c4hg0A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> magnesium and cobalt efflux protein corc; <b>PDBTitle:</b> crystal structure of magnesium and cobalt efflux protein corc,2 northeast structural genomics consortium (nesg) target er40
31	<a href="#">c5nmuC_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> photosynthesis <b>Chain:</b> C: <b>PDB Molecule:</b> cbs-cp12; <b>PDBTitle:</b> structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
32	<a href="#">c1vr9B_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cbs domain protein/act domain protein; <b>PDBTitle:</b> crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
33	<a href="#">c3lv9A_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transporter; <b>PDBTitle:</b> crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
34	<a href="#">c3lhhA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cbs domain protein; <b>PDBTitle:</b> the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
35	<a href="#">c3lfrB_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative metal ion transporter; <b>PDBTitle:</b> the crystal structure of a cbs domain from a putative metal ion2 transporter bound to amp from pseudomonas syringae to 1.55a
36	<a href="#">d2ef7a1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
37	<a href="#">d2ouxax2</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
38	<a href="#">d2j9la1</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
39	<a href="#">c2yvzA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
40	<a href="#">c5ks7A_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine transport atp-binding protein opuca; <b>PDBTitle:</b> crystal structure of listeria monocytogenes opuca cbs domain dimer in2 complex with cyclic-di-amp
41	<a href="#">c3sl7B_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> cbs domain-containing protein cbsx2; <b>PDBTitle:</b> crystal structure of cbs-pair protein, cbsx2 from arabidopsis thaliana
42	<a href="#">d2ooxe1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
43	<a href="#">c3jtfB_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> magnesium and cobalt efflux protein; <b>PDBTitle:</b> the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp
44	<a href="#">d1o50a3</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
45	<a href="#">c3ocmB_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
46	<a href="#">d1y5ha3</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
47	<a href="#">c2emqA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein; <b>PDBTitle:</b> hypothetical conserved protein (gk1048) from geobacillus kaustophilus
48	<a href="#">c4nocA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal transduction protein with cbs domains; <b>PDBTitle:</b> the crystal structure of a cbs domain-containing protein of unknown2 function from kribbella flavida dsm 17836.
49	<a href="#">c4esyB_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> cbs domain containing membrane protein; <b>PDBTitle:</b> crystal structure of the cbs domain of cbs domain containing membrane2 protein from sphaerobacter thermophilus
50	<a href="#">d2ooxe2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
51	<a href="#">c3lqnA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cbs domain protein; <b>PDBTitle:</b> crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
52	<a href="#">d2v8qe2</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
53	<a href="#">c3kpbA_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0100; <b>PDBTitle:</b> crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
						<b>Fold:</b> CBS-domain pair

54	<a href="#">d1pbja3</a>	Alignment	not modelled	99.7	15	<b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
55	<a href="#">d1yava3</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
56	<a href="#">c3ocoB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hemolysin-like protein containing cbs domains; <b>PDBTitle:</b> the crystal structure of a hemolysin-like protein containing cbs2 domain of oenococcus oeni psu
57	<a href="#">c3nqrD_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> magnesium and cobalt efflux protein corc; <b>PDBTitle:</b> a putative cbs domain-containing protein from salmonella typhimurium2 lt2
58	<a href="#">c4fryA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal-transduction protein with cbs domains; <b>PDBTitle:</b> the structure of a putative signal-transduction protein with cbs2 domains from burkholderia ambifaria mc40-6
59	<a href="#">c2qlvF_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> nuclear protein snf4; <b>PDBTitle:</b> crystal structure of the heterotrimer core of the s. cerevisiae ampk2 homolog snf1
60	<a href="#">c1yavB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein bsu14130; <b>PDBTitle:</b> crystal structure of cbs domain-containing protein yku12 from bacillus subtilis
61	<a href="#">d2o16a3</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
62	<a href="#">c2pfiA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chloride channel protein clc-ka; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
63	<a href="#">d2nyca1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
64	<a href="#">c4iy3B_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> metal transporter cnm4; <b>PDBTitle:</b> structural and ligand binding properties of the bateman domain of2 human magnesium transporters cnm2 and cnm4
65	<a href="#">c4z87B_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> structure of the imp dehydrogenase from ashbya gossypii bound to gdp
66	<a href="#">c2qr1E_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> protein c1556.08c; <b>PDBTitle:</b> crystal structure of the adenylate sensor from amp-activated protein2 kinase in complex with adp
67	<a href="#">c2v8qE_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> 5'-amp-activated protein kinase subunit gamma-1; <b>PDBTitle:</b> crystal structure of the regulatory fragment of mammalian2 ampk in complexes with amp
68	<a href="#">d2v8qe1</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
69	<a href="#">c3tsdA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
70	<a href="#">d2rc3a1</a>	Alignment	not modelled	99.7	9	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
71	<a href="#">c4gqvA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> cbs domain-containing protein cbsx1, chloroplastic; <b>PDBTitle:</b> crystal structure of cbs-pair protein, cbsx1 from arabidopsis thaliana
72	<a href="#">d2riha1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
73	<a href="#">c3fnaA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> possible arabinose 5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of the cbs pair of possible d-arabinose 5-phosphate2 isomerase yrbh from escherichia coli cft073
74	<a href="#">c5aweA_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetoin utilization protein, acetoin <b>PDBTitle:</b> 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
75	<a href="#">c3oi8B_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of functionally unknown conserved protein domain2 from neisseria meningitidis mc58
76	<a href="#">c3ctuB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cbs domain protein; <b>PDBTitle:</b> crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
77	<a href="#">c5x8oA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of gmp reductase from trypanosoma

						brucei with2 guanosine 5'-triphosphate
78	<a href="#">d2yvxa2</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
79	<a href="#">d1zfja4</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
80	<a href="#">c3l31B_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable manganase-dependent inorganic <b>PDBTitle:</b> crystal structure of the cbs and drtgg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
81	<a href="#">c3fhmD_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> structural genomics, unknown function, n <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein atu1752; <b>PDBTitle:</b> crystal structure of the cbs-domain containing protein atu1752 from2 agrobacterium tumefaciens
82	<a href="#">c4dqwb_</a>	Alignment	not modelled	99.6	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure analysis of pa3770
83	<a href="#">c5iipA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline abc transporter%2c atp- <b>PDBTitle:</b> staphylococcus aureus opuca
84	<a href="#">c5g5rA_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> site-2 protease; <b>PDBTitle:</b> cbs domain tandem of site-2 protease from archaeoglobus fulgidus in2 complex with llama nanobody - apo form
85	<a href="#">d3ddja2</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
86	<a href="#">c3kh5A_</a>	Alignment	not modelled	99.6	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein mj1225; <b>PDBTitle:</b> crystal structure of protein mj1225 from methanocaldococcus2 jannaschii, a putative archaeal homolog of g-ampk.
87	<a href="#">d2yzqa2</a>	Alignment	not modelled	99.6	26	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
88	<a href="#">c4qfsC_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> signaling protein/inhibitor/activator <b>Chain:</b> C: <b>PDB Molecule:</b> 5'-amp-activated protein kinase subunit gamma-1; <b>PDBTitle:</b> structure of ampk in complex with br2-a769662core activator and2 staurosporine inhibitor
89	<a href="#">c2yzqA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph1780; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
90	<a href="#">c3ddjA_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> amp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cbs domain-containing protein; <b>PDBTitle:</b> crystal structure of a cbs domain-containing protein in complex with2 amp (sso3205) from sulfolobus solfataricus at 1.80 a resolution
91	<a href="#">c4fxsA_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
92	<a href="#">d1jcna4</a>	Alignment	not modelled	98.5	17	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
93	<a href="#">c3fioB_</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> nucleotide binding protein, metal bindin <b>Chain:</b> B: <b>PDB Molecule:</b> a cystathionine beta-synthase domain protein <b>PDBTitle:</b> crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
94	<a href="#">d1jr1a4</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
95	<a href="#">d2di4a1</a>	Alignment	not modelled	83.1	15	<b>Fold:</b> FtsH protease domain-like <b>Superfamily:</b> FtsH protease domain-like <b>Family:</b> FtsH protease domain-like
96	<a href="#">c2di4B_</a>	Alignment	not modelled	79.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh homolog; <b>PDBTitle:</b> crystal structure of the ftsh protease domain
97	<a href="#">d1cxva_</a>	Alignment	not modelled	68.1	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
98	<a href="#">d2ce7a1</a>	Alignment	not modelled	67.5	19	<b>Fold:</b> FtsH protease domain-like <b>Superfamily:</b> FtsH protease domain-like <b>Family:</b> FtsH protease domain-like
99	<a href="#">d1mmqa_</a>	Alignment	not modelled	67.3	31	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
100	<a href="#">c2xs4A_</a>	Alignment	not modelled	67.2	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> karilysin protease; <b>PDBTitle:</b> structure of karilysin catalytic mmp domain in complex with magnesium
101	<a href="#">d1cgla_</a>	Alignment	not modelled	67.1	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
102	<a href="#">dli76a_</a>	Alignment	not modelled	66.9	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain



103	<a href="#">d1qjba_</a>	Alignment	not modelled	66.8	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
104	<a href="#">d1rm8a_</a>	Alignment	not modelled	66.5	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
105	<a href="#">c6o6dA_</a>	Alignment	not modelled	66.2	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-3; <b>PDBTitle:</b> n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori
106	<a href="#">d1q3aa_</a>	Alignment	not modelled	66.2	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
107	<a href="#">d1hy7a_</a>	Alignment	not modelled	66.0	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
108	<a href="#">d1xuca1</a>	Alignment	not modelled	65.7	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
109	<a href="#">d1hfca_</a>	Alignment	not modelled	65.7	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
110	<a href="#">d1lotsa_</a>	Alignment	not modelled	64.1	10	<b>Fold:</b> Clc chloride channel <b>Superfamily:</b> Clc chloride channel <b>Family:</b> Clc chloride channel
111	<a href="#">d1y93a1</a>	Alignment	not modelled	63.7	31	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
112	<a href="#">d2ovxa1</a>	Alignment	not modelled	62.8	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
113	<a href="#">d1tifa_</a>	Alignment	not modelled	62.6	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Translation initiation factor IF3, N-terminal domain <b>Family:</b> Translation initiation factor IF3, N-terminal domain
114	<a href="#">d1eaka2</a>	Alignment	not modelled	62.5	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
115	<a href="#">c2jsdA_</a>	Alignment	not modelled	62.3	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-20; <b>PDBTitle:</b> solution structure of mmp20 complexed with nngH
116	<a href="#">c5th6D_</a>	Alignment	not modelled	62.2	46	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> matrix metalloproteinase-9,matrix metalloproteinase-9; <b>PDBTitle:</b> structure determination of a potent, selective antibody inhibitor of2 human mmp9 (apo mmp9)
117	<a href="#">d1fbla2</a>	Alignment	not modelled	61.9	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
118	<a href="#">d1hova_</a>	Alignment	not modelled	60.1	46	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
119	<a href="#">c1slmA_</a>	Alignment	not modelled	59.9	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> stromelysin-1; <b>PDBTitle:</b> crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
120	<a href="#">d1hv5a_</a>	Alignment	not modelled	59.8	38	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain