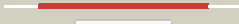



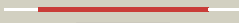



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2406c (-)_2704019_2704447
Date	Wed Aug 7 12:50:02 BST 2019
Unique Job ID	5db97e0879845b55

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2rc3a1	 Alignment		99.9	41	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
2	c4fryA_	 Alignment		99.9	37	PDB header: signaling protein Chain: A: PDB Molecule: putative signal-transduction protein with cbs domains; PDBTitle: the structure of a putative signal-transduction protein with cbs2 domains from burkholderia ambifaria mc40-6
3	c4o9kB_	 Alignment		99.9	18	PDB header: isomerase Chain: B: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: crystal structure of the cbs pair of a putative d-arabinose 5-2 phosphate isomerase from methylococcus capsulatus in complex with3 cmp-kdo
4	c2qh1B_	 Alignment		99.9	19	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
5	d2d4za3	 Alignment		99.9	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
6	c6h1wA_	 Alignment		99.9	18	PDB header: unknown function Chain: A: PDB Molecule: mj1004; PDBTitle: crystal structure of protein mj1004 from mathanocaldococcus jannaschii
7	d2o16a3	 Alignment		99.9	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
8	c5aweA_	 Alignment		99.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acetoin utilization protein, acetoin PDBTitle: 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
9	c5nmuC_	 Alignment		99.9	27	PDB header: photosynthesis Chain: C: PDB Molecule: cbs-cp12; PDBTitle: structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
10	d3ddja1	 Alignment		99.9	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
11	d1y5ha3	 Alignment		99.9	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair

12	c3lhhA_	Alignment		99.9	17	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
13	c6cozB_	Alignment		99.9	16	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic domain
14	c3lfrB_	Alignment		99.9	20	PDB header: transport protein Chain: B: PDB Molecule: putative metal ion transporter; PDBTitle: the crystal structure of a cbs domain from a putative metal ion2 transporter bound to amp from pseudomonas syringae to 1.55a
15	c3jtfB_	Alignment		99.9	17	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
16	d1pvma4	Alignment		99.9	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
17	c4hg0A_	Alignment		99.9	19	PDB header: transport protein Chain: A: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: crystal structure of magnesium and cobalt efflux protein corc,2 northeast structural genomics consortium (nesg) target er40
18	d2ef7a1	Alignment		99.9	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
19	c2d4zB_	Alignment		99.9	20	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
20	d1pbja3	Alignment		99.9	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
21	c2pfiA_	Alignment	not modelled	99.9	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
22	c3hf7A_	Alignment	not modelled	99.9	13	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
23	d2yzia1	Alignment	not modelled	99.9	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
24	d2j9la1	Alignment	not modelled	99.9	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
25	c3i8nB_	Alignment	not modelled	99.9	13	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.
26	c4esyB_	Alignment	not modelled	99.9	29	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain containing membrane protein; PDBTitle: crystal structure of the cbs domain of cbs domain containing membrane2 protein from sphaerobacter thermophilus
27	c4l3vB_	Alignment	not modelled	99.9	19	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
28	c3nqrD_	Alignment	not modelled	99.9	19	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 PDB header: isomerase

29	c3fnaA_	Alignment	not modelled	99.9	16	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
30	d2yzqa1	Alignment	not modelled	99.9	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
31	c5tr1A_	Alignment	not modelled	99.9	13	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein; PDBTitle: cryo-electron microscopy structure of a bovine clc-k chloride channel,2 alternate (class 2) conformation
32	c3gbyA_	Alignment	not modelled	99.9	11	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
33	c3lv9A_	Alignment	not modelled	99.9	20	PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
34	c3ocmA_	Alignment	not modelled	99.9	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
35	c3lqnA_	Alignment	not modelled	99.9	11	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
36	c5ks7A_	Alignment	not modelled	99.9	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: carnitine transport atp-binding protein opuca; PDBTitle: crystal structure of listeria monocytogenes opuca cbs domain dimer in2 complex with cyclic-di-amp
37	d2riha1	Alignment	not modelled	99.9	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
38	d1vr9a3	Alignment	not modelled	99.9	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
39	c3fhmD_	Alignment	not modelled	99.9	43	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
40	c3pc3A_	Alignment	not modelled	99.9	20	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
41	d1yava3	Alignment	not modelled	99.9	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
42	c4gqvA_	Alignment	not modelled	99.9	21	PDB header: protein binding Chain: A: PDB Molecule: cbs domain-containing protein cbsx1, chloroplastic; PDBTitle: crystal structure of cbs-pair protein, cbsx1 from arabidopsis thaliana
43	c6qvcB_	Alignment	not modelled	99.9	17	PDB header: membrane protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: cryoem structure of the human clc-1 chloride channel, cbs state 1
44	c3ocoB_	Alignment	not modelled	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
45	c1vr9B_	Alignment	not modelled	99.9	21	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
46	c3sl7B_	Alignment	not modelled	99.9	20	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain-containing protein cbsx2; PDBTitle: crystal structure of cbs-pair protein, cbsx2 from arabidopsis thaliana
47	c2emqA_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
48	c3ocmB_	Alignment	not modelled	99.8	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
49	c3fwrB_	Alignment	not modelled	99.8	22	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	c4iy3B_	Alignment	not modelled	99.8	15	PDB header: metal transport Chain: B: PDB Molecule: metal transporter cnm4; PDBTitle: structural and ligand binding properties of the bateman domain of2 human magnesium transporters cnm2 and cnm4
51	c1yavB_	Alignment	not modelled	99.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein yku12 from bacillus subtilis
52	c4nocA_	Alignment	not modelled	99.8	16	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein with cbs domains; PDBTitle: the crystal structure of a cbs domain-containing protein of unknown2 function from kribbella flavida dsm 17836.
53	d2ooxe1	Alignment	not modelled	99.8	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair

54	c5g5rA	Alignment	not modelled	99.8	27	PDB header: hydrolase Chain: A: PDB Molecule: site-2 protease; PDBTitle: cbs domain tandem of site-2 protease from archaeoglobus fulgidus in2 complex with llama nanobody - apo form
55	c3kpbA	Alignment	not modelled	99.8	22	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.
56	d2nyca1	Alignment	not modelled	99.8	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
57	d2v8qe2	Alignment	not modelled	99.8	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
58	c2ouxB	Alignment	not modelled	99.8	24	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
59	d2v8qe1	Alignment	not modelled	99.8	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
60	d2ouxa2	Alignment	not modelled	99.8	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
61	c2qr1E	Alignment	not modelled	99.8	24	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
62	c5ohxB	Alignment	not modelled	99.8	16	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
63	c2yvxD	Alignment	not modelled	99.8	23	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
64	c1zfaA	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
65	c2p9mD	Alignment	not modelled	99.8	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
66	c2v8qE	Alignment	not modelled	99.8	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
67	d2oaxe2	Alignment	not modelled	99.8	27	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
68	c3orgB	Alignment	not modelled	99.8	17	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
69	c2qlvF	Alignment	not modelled	99.8	19	PDB header: transferase/protein binding Chain: F: PDB Molecule: nuclear protein snf4; PDBTitle: crystal structure of the heterotrimer core of the s. cerevisiae ampk2 homolog snf1
70	c3kxrA	Alignment	not modelled	99.8	19	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.
71	c4z87B	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
72	d3ddja2	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
73	c3ctuB	Alignment	not modelled	99.8	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
74	d1o50a3	Alignment	not modelled	99.8	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
75	d2yvxa2	Alignment	not modelled	99.8	23	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
76	c3kh5A	Alignment	not modelled	99.8	44	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.
77	c3tsdA	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
78	c3oi8B	Alignment	not modelled	99.8	13	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
79	d1zfja4	Alignment	not modelled	99.8	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
80	c2yvzA	Alignment	not modelled	99.8	23	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
81	c3l31B	Alignment	not modelled	99.7	24	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
82	c5x8oA	Alignment	not modelled	99.7	25	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
83	c2yzqA	Alignment	not modelled	99.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1780; PDBTitle: crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
84	c4dqwb	Alignment	not modelled	99.7	28	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
85	c5iipA	Alignment	not modelled	99.7	16	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
86	c4qfsC	Alignment	not modelled	99.7	17	PDB header: signaling protein/inhibitor/activator Chain: C: PDB Molecule: 5'-amp-activated protein kinase subunit gamma-1; PDBTitle: structure of ampk in complex with br2-a769662core activator and2 staurosporine inhibitor
87	c3ddjA	Alignment	not modelled	99.7	13	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
88	d2yzqa2	Alignment	not modelled	99.7	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
89	c4fxsA	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
90	c3fioB	Alignment	not modelled	99.2	21	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
91	d1jcna4	Alignment	not modelled	98.9	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
92	d1jr1a4	Alignment	not modelled	98.0	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
93	c2d7cD	Alignment	not modelled	60.7	29	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of human rab11 in complex with fip3 rab-2 binding domain
94	c2m46A	Alignment	not modelled	39.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase, putative; PDBTitle: solution nmr structure of sac010876 from staphylococcus aureus col,2 nesg target zr353 and csgid target idp00841
95	c2arfA	Alignment	not modelled	38.1	21	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp
96	c2hv8D	Alignment	not modelled	28.8	26	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
97	c3gkxB	Alignment	not modelled	23.4	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative arsc family related protein; PDBTitle: crystal structure of putative arsc family related protein from2 bacteroides fragilis
98	c2koyA	Alignment	not modelled	22.8	21	PDB header: metal transport Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: structure of the e1064a mutant of the n-domain of wilson disease2 associated protein
99	c4onxB	Alignment	not modelled	16.9	27	PDB header: transferase Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: 2.8 angstrom crystal structure of sensor domain of histidine kinase2 from clostridium perfringens.