















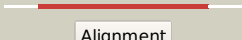

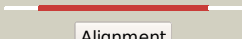

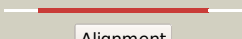




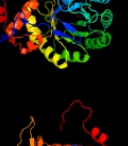
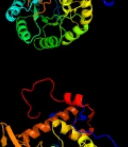



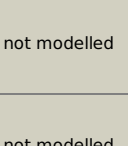


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3411c_guaB2)_3830110_3831699
Date	Fri Aug 9 18:20:08 BST 2019
Unique Job ID	ec277968372b8d5b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zfa_	 Alignment		100.0	51	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
2	c4z87B_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
3	c4fxsA_	 Alignment		100.0	52	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
4	c3tsdA_	 Alignment		100.0	55	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
5	c5x8oA_	 Alignment		100.0	48	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
6	c5upxA_	 Alignment		100.0	57	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from listeria monocytogenes in the presence of3 xanthosine monophosphate
7	d1zfa1	 Alignment		100.0	55	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
8	c4zqrD_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from mycobacterium tuberculosis
9	c4dqwb_	 Alignment		100.0	55	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
10	c4af0B_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
11	c4q33F_	 Alignment		100.0	59	PDB header: oxidoreductase Chain: F: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5'-monophosphate dehydrogenase from2 clostridium perfringens complexed with imp and a110

12	d1pvna1	Alignment		100.0	40	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
13	c4xtiA	Alignment		100.0	44	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: structure of imp dehydrogenase of ashbya gossypii with imp bound to2 the active site
14	c4mz1A	Alignment		100.0	62	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a internal deletion of cbs domain from campylobacter jejuni complexed3 with inhibitor compound p12
15	d2cu0a1	Alignment		100.0	59	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
16	d1jr1a1	Alignment		100.0	45	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
17	c4ff0B	Alignment		100.0	59	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
18	c2cu0B	Alignment		100.0	58	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
19	c1jcnA	Alignment		100.0	44	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
20	c6gk9C	Alignment		100.0	53	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
21	c1me9A	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
22	c3r2gA	Alignment	not modelled	100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
23	c2a7rD	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
24	d1lepa	Alignment	not modelled	100.0	50	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
25	c1vrdA	Alignment	not modelled	100.0	60	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
26	c4avfD	Alignment	not modelled	100.0	62	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase
27	d1jcna1	Alignment	not modelled	100.0	47	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)

28	d1vrda1	Alignment	not modelled	100.0	62	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
29	c2qr6A	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase; PDBTitle: crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
30	c4mjmD	Alignment	not modelled	100.0	58	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a short internal deletion of cbs domain from bacillus anthracis str.3 ames
31	c3khjE	Alignment	not modelled	100.0	55	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
32	c3ffsC	Alignment	not modelled	100.0	50	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
33	c1ypfB	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
34	c6bkaA	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus
35	c2z6jB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acyl reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
36	c3bo9B	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkane dioxygenase; PDBTitle: crystal structure of putative nitroalkane dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
37	c2qjlA	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
38	c3bw2A	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces anschromogenes
39	c5ismF	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
40	c4iqjB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acyl reductase ii2 (fabk) with cofactors nadph and fmn
41	c4z38B	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: mlna; PDBTitle: crystal structure of enoyl reductase domain of mlna from the2 macrolactin biosynthesis cluster from bacillus amyloliquefaciens
42	c3sr7C	Alignment	not modelled	99.9	24	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase
43	c4z9rA	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: omega-3 polyunsaturated fatty acid synthase subunit pfad; PDBTitle: crystal structure of pfad from shewanella oneidensis in complex with2 nad+ determined by in-situ diffraction.
44	c2zrvC	Alignment	not modelled	99.9	26	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfolobus shibatae isopentenyl diphosphate2 isomerase in complex with reduced fmn.
45	d1p0ka	Alignment	not modelled	99.9	28	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
46	c6a0gA	Alignment	not modelled	99.9	25	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
47	c4n02A	Alignment	not modelled	99.9	18	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae
48	c2rdtA	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
49	d1goxa	Alignment	not modelled	99.9	26	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
50	c2e77B	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
51	d1vcfa1	Alignment	not modelled	99.9	28	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
52	d1tb3a1	Alignment	not modelled	99.9	23	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
						PDB header: oxidoreductase

53	c2a7nA	Alignment	not modelled	99.9	20	Chain: A: PDB Molecule: !(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
54	c4cw5B	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens
55	d1p4ca	Alignment	not modelled	99.9	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
56	c1kbiB	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
57	c2cdh1	Alignment	not modelled	99.8	28	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
58	d1kbia1	Alignment	not modelled	99.8	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
59	c2rduA	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
60	d1zfja4	Alignment	not modelled	99.8	43	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
61	c2qh1B	Alignment	not modelled	99.8	25	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
62	c6dvhF	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant
63	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
64	c6h1wA	Alignment	not modelled	99.8	20	PDB header: unknown function Chain: A: PDB Molecule: mj1004; PDBTitle: crystal structure of protein mj1004 from mathanocaldococcus jannaschii
65	c4l3vB	Alignment	not modelled	99.8	22	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
66	c1fcbA	Alignment	not modelled	99.8	20	PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
67	c3jtfB	Alignment	not modelled	99.8	20	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
68	d3ddja1	Alignment	not modelled	99.8	26	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
69	c5tr1A	Alignment	not modelled	99.8	15	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
70	c3ocmA	Alignment	not modelled	99.8	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
71	c2qr1E	Alignment	not modelled	99.8	17	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
72	c5ks7A	Alignment	not modelled	99.8	22	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
73	d1vr9a3	Alignment	not modelled	99.8	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
74	c5nmuC	Alignment	not modelled	99.8	25	PDB header: photosynthesis Chain: C: PDB Molecule: cbs-cp12; PDBTitle: structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
75	d1o50a3	Alignment	not modelled	99.8	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
76	c3lhhA	Alignment	not modelled	99.8	22	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
77	c2qlvF	Alignment	not modelled	99.8	22	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
78	d2ouxax2	Alignment	not modelled	99.8	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair

79	c3ocmB	Alignment	not modelled	99.8	21	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
80	c4hg0A	Alignment	not modelled	99.8	18	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
81	c1vr9B	Alignment	not modelled	99.8	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
82	c6qvcB	Alignment	not modelled	99.8	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
83	c3orgB	Alignment	not modelled	99.8	15	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
84	c3lfrB	Alignment	not modelled	99.8	16	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
85	d1pvma4	Alignment	not modelled	99.8	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
86	c3kxrA	Alignment	not modelled	99.8	16	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.
87	d2d4za3	Alignment	not modelled	99.8	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
88	c2yvxD	Alignment	not modelled	99.8	29	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
89	c3fnaA	Alignment	not modelled	99.8	24	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
90	c2yvzA	Alignment	not modelled	99.8	27	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
91	d2yzqa1	Alignment	not modelled	99.8	31	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
92	c2v8qE	Alignment	not modelled	99.8	20	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
93	c3sl7B	Alignment	not modelled	99.8	26	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain-containing protein cbsx2; PDBTitle: crystal structure of cbs-pair protein, cbsx2 from arabidopsis thaliana
94	c2d4zB	Alignment	not modelled	99.8	18	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
95	c6cozB	Alignment	not modelled	99.8	23	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic domain
96	c3fwrB	Alignment	not modelled	99.8	18	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
97	c4nocA	Alignment	not modelled	99.7	18	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.
98	c4o9kB	Alignment	not modelled	99.7	23	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
99	c3lv9A	Alignment	not modelled	99.7	21	PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
100	c3pc3A	Alignment	not modelled	99.7	25	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
101	d1juba	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
102	c3nqrD	Alignment	not modelled	99.7	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
103	d1y5ha3	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair

						Family: CBS-domain pair
104	c3kpbA	Alignment	not modelled	99.7	27	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.
105	c3oi8B	Alignment	not modelled	99.7	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
106	c3i8nB	Alignment	not modelled	99.7	11	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.
107	d2yzia1	Alignment	not modelled	99.7	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
108	c5aweA	Alignment	not modelled	99.7	32	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
109	c3hf7A	Alignment	not modelled	99.7	19	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
110	c2emqA	Alignment	not modelled	99.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
111	c3ocoB	Alignment	not modelled	99.7	19	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
112	d2nyca1	Alignment	not modelled	99.7	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
113	d2ooxe2	Alignment	not modelled	99.7	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
114	d2ef7a1	Alignment	not modelled	99.7	32	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
115	c3gbyA	Alignment	not modelled	99.7	17	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
116	c4fryA	Alignment	not modelled	99.7	29	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
117	c5ohxB	Alignment	not modelled	99.7	10	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
118	d2j9la1	Alignment	not modelled	99.7	27	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
119	c3l31B	Alignment	not modelled	99.7	21	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
120	d2v8qe1	Alignment	not modelled	99.7	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair