

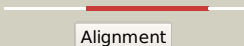

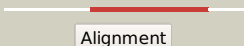







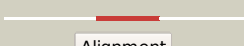











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1232c_(-)_1374867_1376174
Date	Wed Jul 31 22:05:32 BST 2019
Unique Job ID	9ca698ec52b07da2

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ouxB_	 Alignment		100.0	23	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
2	c2yvxD_	 Alignment		100.0	29	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
3	c2yvzA_	 Alignment		100.0	29	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
4	c3kxrA_	 Alignment		100.0	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.
5	d2oux2	 Alignment		99.9	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
6	d2yvxa2	 Alignment		99.9	30	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
7	d2oux1	 Alignment		99.9	23	Fold: alpha-alpha superhelix Superfamily: MgtE N-terminal domain-like Family: MgtE N-terminal domain-like
8	c3ocmB_	 Alignment		99.9	13	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
9	c5x8oA_	 Alignment		99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
10	d2yvxa1	 Alignment		99.8	28	Fold: alpha-alpha superhelix Superfamily: MgtE N-terminal domain-like Family: MgtE N-terminal domain-like
11	c3ocmA_	 Alignment		99.8	13	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

12	c4hg0A_	Alignment		99.8	14	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
13	d1vr9a3	Alignment		99.8	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
14	c3oi8B_	Alignment		99.8	19	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
15	c1vr9B_	Alignment		99.8	25	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
16	c2qh1B_	Alignment		99.8	20	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
17	d2d4za3	Alignment		99.8	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
18	c4l3vB_	Alignment		99.8	22	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
19	d1pvma4	Alignment		99.8	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
20	d3ddja1	Alignment		99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
21	c3jtfB_	Alignment	not modelled	99.8	19	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
22	c3lhhA_	Alignment	not modelled	99.8	19	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
23	c4z87B_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
24	c3lv9A_	Alignment	not modelled	99.8	17	PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
25	c1zfjA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
26	c4esyB_	Alignment	not modelled	99.8	24	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	c3ocoB_	Alignment	not modelled	99.8	15	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
28	d2ef7a1	Alignment	not modelled	99.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair

						Family: CBS-domain pair
29	c3i8nB_	Alignment	not modelled	99.8	22	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.
30	c5nmuC_	Alignment	not modelled	99.8	22	PDB header: photosynthesis Chain: C: PDB Molecule: cbs-cp12; PDBTitle: structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
31	c3hf7A_	Alignment	not modelled	99.7	14	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
32	c3tsdA_	Alignment	not modelled	99.7	19	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
33	c3lfrB_	Alignment	not modelled	99.7	18	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
34	d2yzqa1	Alignment	not modelled	99.7	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
35	c5ks7A_	Alignment	not modelled	99.7	21	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
36	d1y5ha3	Alignment	not modelled	99.7	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
37	c3sl7B_	Alignment	not modelled	99.7	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
38	c3gbyA_	Alignment	not modelled	99.7	29	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
39	c2d4zB_	Alignment	not modelled	99.7	22	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
40	c3nqrD_	Alignment	not modelled	99.7	15	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
41	c4iy3B_	Alignment	not modelled	99.7	17	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
42	c6cozB_	Alignment	not modelled	99.7	18	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic domain
43	d2j9la1	Alignment	not modelled	99.7	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
44	c4gqvA_	Alignment	not modelled	99.7	28	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
45	d1zfja4	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
46	c4nocA_	Alignment	not modelled	99.7	20	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.
47	d2yzia1	Alignment	not modelled	99.7	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
48	c5aweA_	Alignment	not modelled	99.7	26	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
49	c3pc3A_	Alignment	not modelled	99.7	19	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
50	c3kpbA_	Alignment	not modelled	99.7	18	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.
51	d1o50a3	Alignment	not modelled	99.7	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
52	d2nyca1	Alignment	not modelled	99.7	15	Fold: CBS-domain pair Superfamily: CBS-domain pair

						Family: CBS-domain pair
53	c3fnaA_	Alignment	not modelled	99.7	17	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
54	d2o16a3	Alignment	not modelled	99.7	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
55	c5ohxB_	Alignment	not modelled	99.7	12	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
56	c3fwrB_	Alignment	not modelled	99.7	16	PDB header: transcription Chain: B: PDB Molecule: yyqzb protein; PDBTitle: crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
57	c4fryA_	Alignment	not modelled	99.7	18	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
58	c2emqA_	Alignment	not modelled	99.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
59	c5g5rA_	Alignment	not modelled	99.7	18	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
60	d1pbja3	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
61	c5tr1A_	Alignment	not modelled	99.7	21	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
62	c1yavB_	Alignment	not modelled	99.7	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein yukl2 from bacillus subtilis
63	c6qvcB_	Alignment	not modelled	99.7	15	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
64	c4o9kB_	Alignment	not modelled	99.7	22	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
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. cerevisiae ampk2 homolog snf1
66	d2riha1	Alignment	not modelled	99.6	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
67	d2rc3a1	Alignment	not modelled	99.6	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
68	c2p9mD_	Alignment	not modelled	99.6	18	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
69	c2v8qE_	Alignment	not modelled	99.6	16	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
70	d2ooxe2	Alignment	not modelled	99.6	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
71	d1yava3	Alignment	not modelled	99.6	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
72	d1lkvx_	Alignment	not modelled	99.6	16	Fold: alpha-alpha superhelix Superfamily: FliG Family: FliG
73	c2qr1E_	Alignment	not modelled	99.6	14	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
74	d2ooxe1	Alignment	not modelled	99.6	12	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
75	c3pkrA_	Alignment	not modelled	99.6	14	PDB header: motor protein Chain: A: PDB Molecule: flagellar motor switch protein; PDBTitle: crystal structure of flig (residue 86-343) from h. pylori
76	d2v8qe2	Alignment	not modelled	99.6	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
77	d2v8qe1	Alignment	not modelled	99.6	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
						Fold: CBS-domain pair

78	d3ddja2	Alignment	not modelled	99.6	17	Superfamily: CBS-domain pair Family: CBS-domain pair
79	c5iipA_	Alignment	not modelled	99.6	20	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
80	c3ctuB_	Alignment	not modelled	99.6	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
81	c4dqwb_	Alignment	not modelled	99.6	26	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
82	c3orgB_	Alignment	not modelled	99.6	17	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
83	c2pfiA_	Alignment	not modelled	99.6	23	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
84	c3lqnA_	Alignment	not modelled	99.6	17	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
85	c3ddjA_	Alignment	not modelled	99.5	16	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
86	c2yzqA_	Alignment	not modelled	99.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1780; PDBTitle: crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
87	d2yzqa2	Alignment	not modelled	99.5	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
88	c3fhmD_	Alignment	not modelled	99.5	20	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
89	c3l3lB_	Alignment	not modelled	99.5	31	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
90	c4qfsC_	Alignment	not modelled	99.4	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
91	c4fxsA_	Alignment	not modelled	99.4	17	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
92	c3pl4A_	Alignment	not modelled	99.3	17	PDB header: motor protein Chain: A: PDB Molecule: flagellar motor switch protein; PDBTitle: crystal structure of flig (residue 116-343) from h. pylori
93	c3kh5A_	Alignment	not modelled	99.3	19	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.
94	c3hjlA_	Alignment	not modelled	98.9	20	PDB header: proton transport Chain: A: PDB Molecule: flagellar motor switch protein flig; PDBTitle: the structure of full-length flig from aquifex aeolicus
95	c3fioB_	Alignment	not modelled	98.4	19	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
96	d1jcna4	Alignment	not modelled	98.2	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
97	d1jr1a4	Alignment	not modelled	97.7	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
98	c1k6nH_	Alignment	not modelled	97.7	21	PDB header: photosynthesis Chain: H: PDB Molecule: photosynthetic reaction center h subunit; PDBTitle: e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
99	d1rzhh1	Alignment	not modelled	97.7	20	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
100	c3htrB_	Alignment	not modelled	97.6	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized prc-barrel domain protein; PDBTitle: crystal structure of prc-barrel domain protein from2 rhodopseudomonas palustris
101	c1eysH_	Alignment	not modelled	97.4	29	PDB header: electron transport Chain: H: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
102	d1eysh1	Alignment	not modelled	97.3	29	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain

103	d2i5nh1	Alignment	not modelled	97.3	20	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
104	c2i5nH	Alignment	not modelled	97.0	20	PDB header: photosynthesis Chain: H: PDB Molecule: reaction center protein h chain; PDBTitle: 1.96 a x-ray structure of photosynthetic reaction center from 2 rhodospseudomonas viridis:crystals grown by microfluidic technique
105	c5wujB	Alignment	not modelled	96.9	20	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: crystal structure of flif-flig complex from h. pylori
106	d1pm3a	Alignment	not modelled	96.7	21	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: MTH1895
107	d2f1la1	Alignment	not modelled	96.0	20	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: RimM C-terminal domain-like
108	c3sohB	Alignment	not modelled	95.6	28	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
109	c3h9nA	Alignment	not modelled	95.2	25	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome maturation factor rimm; PDBTitle: crystal structure of a putative 16s ribosomal maturation factor rimm2 (hi0203) from h.influenzae. northeast structural genomics3 consortium target ir66.
110	c2dyiA	Alignment	not modelled	94.8	19	PDB header: ribosome Chain: A: PDB Molecule: probable 16s rrna-processing protein rimm; PDBTitle: crystal structure of 16s ribosomal rna processing protein rimm from 2 thermus thermophilus hb8
111	c2f1IA	Alignment	not modelled	94.7	20	PDB header: unknown function Chain: A: PDB Molecule: 16s rrna processing protein; PDBTitle: crystal structure of a putative 16s ribosomal rna processing protein2 rimm (pa3744) from pseudomonas aeruginosa at 2.46 a resolution
112	c2qggA	Alignment	not modelled	94.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 16s rrna-processing protein rimm; PDBTitle: x-ray structure of the protein q6f7i0 from acinetobacter calcoaceticus2 amms 248. northeast structural genomics consortium target asr73.
113	d1qc7a	Alignment	not modelled	89.6	17	Fold: alpha-alpha superhelix Superfamily: FliG Family: FliG
114	d1qc7b	Alignment	not modelled	89.3	17	Fold: alpha-alpha superhelix Superfamily: FliG Family: FliG
115	c5tdyD	Alignment	not modelled	87.4	16	PDB header: motor protein Chain: D: PDB Molecule: flagellar motor switch protein flig; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
116	c6fo1G	Alignment	not modelled	86.2	15	PDB header: chaperone Chain: G: PDB Molecule: rna polymerase ii-associated protein 3; PDBTitle: human r2tp subcomplex containing 1 ruvbl1-ruvbl2 hexamer bound to 12 rbd domain from rpap3.
117	c2n5xA	Alignment	not modelled	78.0	31	PDB header: chaperone Chain: A: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: c-terminal domain of cdc37 cochaperone
118	d1lcyA2	Alignment	not modelled	66.2	29	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
119	c3nwuB	Alignment	not modelled	64.8	29	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
120	c3k6zA	Alignment	not modelled	64.3	36	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form