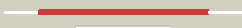














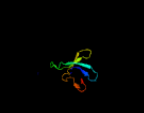

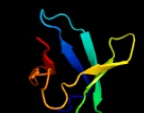

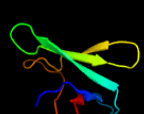




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2907c_rimM_3216371_3216901
Date	Thu Aug 8 16:20:06 BST 2019
Unique Job ID	42cbd06df44b33e0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3h9nA_</a>	 Alignment		100.0	31	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> ribosome maturation factor rimm; <b>PDBTitle:</b> crystal structure of the ribosome maturation factor rimm2 (hi0203) from h.influenzae. northeast structural genomics3 consortium target ir66.
2	<a href="#">c2f1A_</a>	 Alignment		100.0	31	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> 16s rrna processing protein; <b>PDBTitle:</b> crystal structure of a putative 16s ribosomal rna processing protein2 rimm (pa3744) from pseudomonas aeruginosa at 2.46 a resolution
3	<a href="#">c2qggA_</a>	 Alignment		100.0	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> 16s rrna-processing protein rimm; <b>PDBTitle:</b> x-ray structure of the protein q6f7i0 from acinetobacter calcoaceticus2 amms 248. northeast structural genomics consortium target asr73.
4	<a href="#">c2dyiA_</a>	 Alignment		100.0	33	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> probable 16s rrna-processing protein rimm; <b>PDBTitle:</b> crystal structure of 16s ribosomal rna processing protein rimm from2 thermus thermophilus hb8
5	<a href="#">d2f1la2</a>	 Alignment		99.9	28	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> RimM N-terminal domain-like
6	<a href="#">c2dogA_</a>	 Alignment		99.9	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> probable 16s rrna-processing protein rimm; <b>PDBTitle:</b> solution structure of the n-terminal domain of rimm from thermus2 thermophilus hb8
7	<a href="#">d2f1la1</a>	 Alignment		99.9	33	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> RimM C-terminal domain-like
8	<a href="#">d1eysh1</a>	 Alignment		97.5	25	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
9	<a href="#">c1eysH_</a>	 Alignment		97.4	25	<b>PDB header:</b> electron transport <b>Chain:</b> H; <b>PDB Molecule:</b> photosynthetic reaction center; <b>PDBTitle:</b> crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
10	<a href="#">c1k6nH_</a>	 Alignment		97.1	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> H; <b>PDB Molecule:</b> photosynthetic reaction center h subunit; <b>PDBTitle:</b> e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
11	<a href="#">d1rzhh1</a>	 Alignment		97.1	25	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain

12	<a href="#">c2i5nH_</a>	Alignment		97.0	27	<b>PDB header:</b> photosynthesis <b>Chain:</b> H; <b>PDB Molecule:</b> reaction center protein h chain; <b>PDBTitle:</b> 1.96 a x-ray structure of photosynthetic reaction center from2 rhodospseudomonas viridis:crystals grown by microfluidic technique
13	<a href="#">d2i5nh1</a>	Alignment		96.9	27	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
14	<a href="#">c3htrB_</a>	Alignment		96.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized prc-barrel domain protein; <b>PDBTitle:</b> crystal structure of prc-barrel domain protein from2 rhodospseudomonas palustris
15	<a href="#">d1pm3a_</a>	Alignment		94.1	30	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> MTH1895
16	<a href="#">c4a1dH_</a>	Alignment		92.4	22	<b>PDB header:</b> ribosome <b>Chain:</b> H; <b>PDB Molecule:</b> rpl35a; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
17	<a href="#">c3j3bf_</a>	Alignment		91.1	23	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 60s ribosomal protein l7; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
18	<a href="#">c3zf7l_</a>	Alignment		90.0	23	<b>PDB header:</b> ribosome <b>Chain:</b> L; <b>PDB Molecule:</b> 60s ribosomal protein l11, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
19	<a href="#">d1sqra_</a>	Alignment		88.7	27	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Ribosomal protein L35ae
20	<a href="#">c3izcj_</a>	Alignment		86.7	19	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> 60s ribosomal protein rpl12 (l11p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
21	<a href="#">c3j39f_</a>	Alignment	not modelled	86.6	17	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 60s ribosomal protein l7; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
22	<a href="#">c3iz5j_</a>	Alignment	not modelled	85.0	15	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> 60s ribosomal protein l12 (l11p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
23	<a href="#">c2hvyB_</a>	Alignment	not modelled	74.8	19	<b>PDB header:</b> isomerase/biosynthetic protein/rna <b>Chain:</b> B; <b>PDB Molecule:</b> small nucleolar rnp similar to gar1; <b>PDBTitle:</b> crystal structure of an h/aca box rnp from pyrococcus furiosus
24	<a href="#">d2ey4c1</a>	Alignment	not modelled	71.3	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Gar1-like SnoRNP
25	<a href="#">c3uaiC_</a>	Alignment	not modelled	65.5	14	<b>PDB header:</b> isomerase/chaperone <b>Chain:</b> C; <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 1; <b>PDBTitle:</b> structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
26	<a href="#">c2eqnA_</a>	Alignment	not modelled	35.3	11	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein loc92345; <b>PDBTitle:</b> solution structure of the naf1 domain of hypothetical2 protein bc008207 [homo sapiens]
27	<a href="#">c3zey1_</a>	Alignment	not modelled	23.5	11	<b>PDB header:</b> ribosome <b>Chain:</b> 1; <b>PDB Molecule:</b> 40s ribosomal protein s4, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
28	<a href="#">d2b78a1</a>	Alignment	not modelled	22.4	14	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Hypothetical RNA methyltransferase domain (HRMD)
						<b>PDB header:</b> ribosomal protein

29	<a href="#">c2mf1A_</a>	Alignment	not modelled	21.2	19	<b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> domain 2 of e. coli ribosomal protein s1
30	<a href="#">d1ts9a_</a>	Alignment	not modelled	17.9	14	<b>Fold:</b> Rof/RNase P subunit-like <b>Superfamily:</b> Rof/RNase P subunit-like <b>Family:</b> RNase P subunit p29-like
31	<a href="#">d1qhka_</a>	Alignment	not modelled	17.2	12	<b>Fold:</b> MbtH/L9 domain-like <b>Superfamily:</b> L9 N-domain-like <b>Family:</b> N-terminal domain of RNase HI
32	<a href="#">c1zxaA_</a>	Alignment	not modelled	14.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> at5g01750 protein; <b>PDBTitle:</b> x-ray structure of protein from arabidopsis thaliana at5g01750
33	<a href="#">d2q4ma1</a>	Alignment	not modelled	14.8	14	<b>Fold:</b> Tubby C-terminal domain-like <b>Superfamily:</b> Tubby C-terminal domain-like <b>Family:</b> At5g01750-like
34	<a href="#">d1kl9a2</a>	Alignment	not modelled	13.5	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
35	<a href="#">d1qtra1</a>	Alignment	not modelled	12.6	11	<b>Fold:</b> Ribosomal protein L25-like <b>Superfamily:</b> Ribosomal protein L25-like <b>Family:</b> Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain
36	<a href="#">c2hz7A_</a>	Alignment	not modelled	12.5	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-tRNA synthetase; <b>PDBTitle:</b> crystal structure of the glutamyl-tRNA synthetase from deinococcus2 radiodurans
37	<a href="#">c4p2bA_</a>	Alignment	not modelled	12.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine aminoacyl-tRNA synthetase; <b>PDBTitle:</b> crystal structure of the apo form of the glutamyl-tRNA synthetase2 catalytic domain from toxoplasma gondii.
38	<a href="#">d1wgsa_</a>	Alignment	not modelled	11.5	19	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Chromo domain-like <b>Family:</b> Chromo barrel domain
39	<a href="#">d1oqka_</a>	Alignment	not modelled	11.3	30	<b>Fold:</b> Rof/RNase P subunit-like <b>Superfamily:</b> Rof/RNase P subunit-like <b>Family:</b> RNase P subunit p29-like
40	<a href="#">d1wb1a2</a>	Alignment	not modelled	11.0	29	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
41	<a href="#">c2my3B_</a>	Alignment	not modelled	10.7	75	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna leakage protein 1; <b>PDBTitle:</b> snu17p-pml1p structure intermediate during res complex assembly
42	<a href="#">c2v3mF_</a>	Alignment	not modelled	10.3	19	<b>PDB header:</b> ribosomal protein <b>Chain:</b> F: <b>PDB Molecule:</b> naf1; <b>PDBTitle:</b> structure of the gar1 domain of naf1
43	<a href="#">d2rdea1</a>	Alignment	not modelled	9.1	10	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> PilZ domain-like <b>Family:</b> PilZ domain
44	<a href="#">c3k6zA_</a>	Alignment	not modelled	8.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible membrane-associated serine protease; <b>PDBTitle:</b> crystal structure of rv3671c protease, inactive form
45	<a href="#">d1go3e1</a>	Alignment	not modelled	8.6	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
46	<a href="#">c2qf4A_</a>	Alignment	not modelled	8.5	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell shape determining protein mreC; <b>PDBTitle:</b> high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mreC (orthorhombic form)
47	<a href="#">d1fnoa3</a>	Alignment	not modelled	8.3	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
48	<a href="#">c3mlqE_</a>	Alignment	not modelled	8.2	19	<b>PDB header:</b> transferase/transcription <b>Chain:</b> E: <b>PDB Molecule:</b> transcription-repair coupling factor; <b>PDBTitle:</b> crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
49	<a href="#">c2w7aA_</a>	Alignment	not modelled	8.2	29	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> line-1 orf1p; <b>PDBTitle:</b> structure of the human line-1 orf1p central domain
50	<a href="#">c5ag8A_</a>	Alignment	not modelled	8.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gingipain r2; <b>PDBTitle:</b> crystal structure of a mutant (665i6h) of the c-terminal2 domain of rgpb
51	<a href="#">d1xxaa_</a>	Alignment	not modelled	8.1	23	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
52	<a href="#">c3l31B_</a>	Alignment	not modelled	8.0	15	<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 drtg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
53	<a href="#">c2ymaB_</a>	Alignment	not modelled	8.0	11	<b>PDB header:</b> carbohydrate binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein os-9 homolog; <b>PDBTitle:</b> x-ray structure of the yos9 dimerization domain
54	<a href="#">c2kk4A_</a>	Alignment	not modelled	8.0	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein af_2094; <b>PDBTitle:</b> solution nmr structure of protein af2094 from archaeoglobus2 fulgidus. northeast structural genomics consotium (nesg)3 target gt2 <b>PDB header:</b> ribosome

55	<a href="#">c4v19T_</a>	Alignment	not modelled	7.9	7	<b>Chain:</b> T; <b>PDB Molecule:</b> mitoribosomal protein bl19m, mrpl19; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
56	<a href="#">c3l4qA_</a>	Alignment	not modelled	7.8	21	<b>PDB header:</b> viral protein/protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> non-structural protein 1; <b>PDBTitle:</b> structural insights into phosphoinositide 3-kinase activation by the2 influenza a virus ns1 protein
57	<a href="#">d1ub4c_</a>	Alignment	not modelled	7.7	27	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Kis/Peml addiction antidote
58	<a href="#">d2ooka1_</a>	Alignment	not modelled	7.6	13	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Sfri0576-like
59	<a href="#">c4gqvA_</a>	Alignment	not modelled	7.6	40	<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
60	<a href="#">c2mkcB_</a>	Alignment	not modelled	7.4	75	<b>PDB header:</b> splicing <b>Chain:</b> B; <b>PDB Molecule:</b> pre-mrna leakage protein 1; <b>PDBTitle:</b> cooperative structure of the heterotrimeric pre-mrna retention and2 splicing complex
61	<a href="#">d2gx9a1_</a>	Alignment	not modelled	7.2	21	<b>Fold:</b> Ns1 effector domain-like <b>Superfamily:</b> Ns1 effector domain-like <b>Family:</b> Ns1 effector domain-like
62	<a href="#">c3gbyA_</a>	Alignment	not modelled	7.2	27	<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
63	<a href="#">c3kpbA_</a>	Alignment	not modelled	7.0	33	<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.
64	<a href="#">d2riha1_</a>	Alignment	not modelled	7.0	40	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
65	<a href="#">c4ye6A_</a>	Alignment	not modelled	7.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamine--trna ligase; <b>PDBTitle:</b> the crystal structure of the intact human glhrs
66	<a href="#">c4wznB_</a>	Alignment	not modelled	6.9	55	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of the 2b protein soluble domain from hepatitis a2 virus
67	<a href="#">c5zwzA_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> agenet domain-containing protein; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana agdp1 agd34
68	<a href="#">c3jtfB_</a>	Alignment	not modelled	6.6	33	<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
69	<a href="#">c3kxrA_</a>	Alignment	not modelled	6.5	47	<b>PDB header:</b> transport protein <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.
70	<a href="#">c2yvzA_</a>	Alignment	not modelled	6.5	47	<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
71	<a href="#">d1b4ba_</a>	Alignment	not modelled	6.4	4	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
72	<a href="#">d2yzqa2_</a>	Alignment	not modelled	6.4	25	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
73	<a href="#">c3lv9A_</a>	Alignment	not modelled	6.1	40	<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
74	<a href="#">c3ereD_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D; <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
75	<a href="#">c3d6rA_</a>	Alignment	not modelled	6.0	21	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> non-structural protein 1; <b>PDBTitle:</b> structure of an avian influenza a virus ns1 protein2 effector domain
76	<a href="#">c5iipA_</a>	Alignment	not modelled	5.9	20	<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
77	<a href="#">c5jvoA_</a>	Alignment	not modelled	5.8	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor from the pathogenic2 bacterium corynebacterium pseudotuberculosis
78	<a href="#">c3bsuF_</a>	Alignment	not modelled	5.8	33	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> F; <b>PDB Molecule:</b> ribonuclease h1; <b>PDBTitle:</b> hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna
79	<a href="#">d1ydlA1_</a>	Alignment	not modelled	5.7	10	<b>Fold:</b> TFB5-like <b>Superfamily:</b> TFB5-like <b>Family:</b> TFB5-like
80	<a href="#">c5zwoZ_</a>	Alignment	not modelled	5.7	75	<b>PDB header:</b> splicing <b>Chain:</b> Z; <b>PDB Molecule:</b> pre-mrna leakage protein 1; <b>PDBTitle:</b> cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom

81	<a href="#">d2p5ma1</a>	Alignment	not modelled	5.7	4	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
82	<a href="#">c2pdtD</a>	Alignment	not modelled	5.6	19	<b>PDB header:</b> circadian clock protein <b>Chain:</b> D: <b>PDB Molecule:</b> vidvid pas protein vvd; <b>PDBTitle:</b> 2.3 angstrom structure of phosphodiesterase treated vidvid
83	<a href="#">d2j01t1</a>	Alignment	not modelled	5.6	13	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal protein L19
84	<a href="#">d2yzqa1</a>	Alignment	not modelled	5.6	27	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
85	<a href="#">c3nqrD</a>	Alignment	not modelled	5.5	33	<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
86	<a href="#">c3oi8B</a>	Alignment	not modelled	5.5	33	<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
87	<a href="#">c3cagF</a>	Alignment	not modelled	5.5	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
88	<a href="#">c1kl9A</a>	Alignment	not modelled	5.4	15	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 2 subunit 1; <b>PDBTitle:</b> crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha
89	<a href="#">d1vr9a3</a>	Alignment	not modelled	5.4	27	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
90	<a href="#">c1vr9B</a>	Alignment	not modelled	5.4	27	<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
91	<a href="#">c3i8nB</a>	Alignment	not modelled	5.4	33	<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.
92	<a href="#">d1fr3a</a>	Alignment	not modelled	5.2	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> Molybdate/tungstate binding protein MOP
93	<a href="#">c6ceqC</a>	Alignment	not modelled	5.2	19	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> the aer2 receptor from vibrio cholerae is a dual pas-heme oxygen2 sensor
94	<a href="#">d1bywa</a>	Alignment	not modelled	5.1	7	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> Flavin-binding PAS domain
95	<a href="#">c2gj3A</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen fixation regulatory protein; <b>PDBTitle:</b> crystal structure of the fad-containing pas domain of the protein nif2 from azotobacter vinelandii.
96	<a href="#">c2o0i1</a>	Alignment	not modelled	5.1	8	<b>PDB header:</b> surface active protein <b>Chain:</b> 1: <b>PDB Molecule:</b> c protein alpha-antigen; <b>PDBTitle:</b> crystal structure of the r185a mutant of the n-terminal domain of the2 group b streptococcus alpha c protein
97	<a href="#">c2ouxB</a>	Alignment	not modelled	5.1	20	<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
98	<a href="#">c2p9mD</a>	Alignment	not modelled	5.1	27	<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