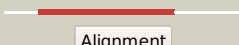
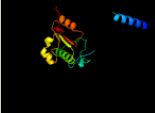


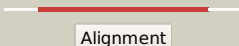

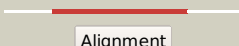

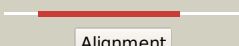
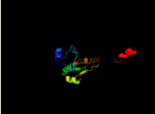
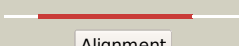

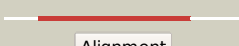








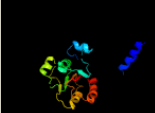


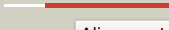










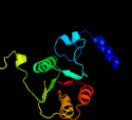








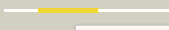
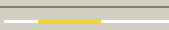
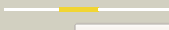
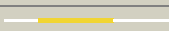


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3395c_(-)_3811202_3811816
Date	Fri Aug 9 18:20:06 BST 2019
Unique Job ID	62f2a54baf637f91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cmwA_</a>	 Alignment		99.6	20	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the recassdna/dsdna2 structures
2	<a href="#">c3cmuA_</a>	 Alignment		99.3	23	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the recassdna/dsdna2 structures
3	<a href="#">c2recB_</a>	 Alignment		99.0	24	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
4	<a href="#">c1xp8A_</a>	 Alignment		99.0	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> reca protein; <b>PDBTitle:</b> deinococcus radiodurans reca in complex with atp-gamma-s
5	<a href="#">c3cmvG_</a>	 Alignment		98.9	25	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the recassdna/dsdna2 structures
6	<a href="#">c2zroA_</a>	 Alignment		98.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
7	<a href="#">c3hr8A_</a>	 Alignment		98.8	24	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
8	<a href="#">d1mo6a1</a>	 Alignment		98.7	31	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
9	<a href="#">d1xp8a1</a>	 Alignment		98.6	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
10	<a href="#">d1u94a1</a>	 Alignment		98.6	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
11	<a href="#">d1ubea1</a>	 Alignment		98.6	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)

12	<a href="#">c3io5B_</a>	 Alignment		98.5	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination and repair protein; <b>PDBTitle:</b> crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
13	<a href="#">c1oftC_</a>	 Alignment		97.6	16	<b>PDB header:</b> bacterial cell division inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein pa3008; <b>PDBTitle:</b> crystal structure of sula from pseudomonas aeruginosa
14	<a href="#">d1ofux_</a>	 Alignment		97.4	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Bacterial cell division inhibitor Sula
15	<a href="#">d2i1qa2</a>	 Alignment		90.4	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
16	<a href="#">d1v5wa_</a>	 Alignment		88.9	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
17	<a href="#">c2w0mA_</a>	 Alignment		87.5	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfolobus solfataricus p2
18	<a href="#">c3bh0A_</a>	 Alignment		85.9	14	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p
19	<a href="#">d1tf7a2</a>	 Alignment		84.7	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
20	<a href="#">c2dr3A_</a>	 Alignment		84.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0273 protein ph0284; <b>PDBTitle:</b> crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
21	<a href="#">c4wiaA_</a>	 Alignment	not modelled	84.1	18	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flagella-related protein h; <b>PDBTitle:</b> crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
22	<a href="#">c2zjbB_</a>	 Alignment	not modelled	83.0	15	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> meiotic recombination protein dmc1/lim15 homolog; <b>PDBTitle:</b> crystal structure of the human dmc1-m200v polymorphic2 variant
23	<a href="#">d1pzna2</a>	 Alignment	not modelled	82.4	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
24	<a href="#">c1pznG_</a>	 Alignment	not modelled	78.1	13	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
25	<a href="#">d1szpa2</a>	 Alignment	not modelled	76.2	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
26	<a href="#">c1t4gA_</a>	 Alignment	not modelled	74.7	16	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rada; <b>PDBTitle:</b> atpase in complex with amp-pnp
27	<a href="#">c4ydsA_</a>	 Alignment	not modelled	73.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagella-related protein h; <b>PDBTitle:</b> flah from sulfolobus acidocaldarius with atp and mg-ion
28	<a href="#">c4a1fB_</a>	 Alignment	not modelled	72.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase

29	<a href="#">c3bgwD</a>	Alignment	not modelled	71.2	11	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> the structure of a dnab-like replicative helicase and its interactions2 with primase
30	<a href="#">c3bs4A</a>	Alignment	not modelled	70.8	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0321; <b>PDBTitle:</b> crystal structure of uncharacterized protein ph0321 from pyrococcus2 horikoshii in complex with an unknown peptide
31	<a href="#">d1n0wa</a>	Alignment	not modelled	68.9	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
32	<a href="#">c2dfIA</a>	Alignment	not modelled	68.7	19	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rada; <b>PDBTitle:</b> crystal structure of left-handed rada filament
33	<a href="#">c3ldaA</a>	Alignment	not modelled	68.5	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> yeast rad51 h352y filament interface mutant
34	<a href="#">c1pznA</a>	Alignment	not modelled	66.0	13	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
35	<a href="#">c2v3cC</a>	Alignment	not modelled	62.5	21	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
36	<a href="#">c2cvhB</a>	Alignment	not modelled	54.3	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair and recombination protein radb; <b>PDBTitle:</b> crystal structure of the radb recombinase
37	<a href="#">c1szpC</a>	Alignment	not modelled	51.5	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> a crystal structure of the rad51 filament
38	<a href="#">d1tf7a1</a>	Alignment	not modelled	50.1	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
39	<a href="#">d1nlfa</a>	Alignment	not modelled	48.0	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
40	<a href="#">c5jzcG</a>	Alignment	not modelled	47.8	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair protein rad51 homolog 1; <b>PDBTitle:</b> helical filament
41	<a href="#">c4nmnA</a>	Alignment	not modelled	47.0	21	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
42	<a href="#">c5gafi</a>	Alignment	not modelled	44.0	19	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein I10; <b>PDBTitle:</b> rnc in complex with srp
43	<a href="#">c2ztsB</a>	Alignment	not modelled	42.6	17	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ph0186; <b>PDBTitle:</b> crystal structure of kaic-like protein ph0186 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
44	<a href="#">c1u9IA</a>	Alignment	not modelled	39.5	19	<b>PDB header:</b> circadian clock protein <b>Chain:</b> A: <b>PDB Molecule:</b> kaic; <b>PDBTitle:</b> crystal structure of circadian clock protein kaic with phosphorylation2 sites
45	<a href="#">c1qzwC</a>	Alignment	not modelled	38.1	16	<b>PDB header:</b> signaling protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
46	<a href="#">c1e1cA</a>	Alignment	not modelled	37.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant
47	<a href="#">d1xi8a3</a>	Alignment	not modelled	36.7	15	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
48	<a href="#">c6qeIB</a>	Alignment	not modelled	36.7	15	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> e. coli dnabc apo complex
49	<a href="#">d2jfga1</a>	Alignment	not modelled	34.2	25	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
50	<a href="#">c5fmsA</a>	Alignment	not modelled	33.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> intraflagellar transport protein 52 homolog; <b>PDBTitle:</b> mmift52 n-terminal domain
51	<a href="#">c3b9qA</a>	Alignment	not modelled	32.8	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpftsyl from arabidopsis thaliana
52	<a href="#">d1wu2a3</a>	Alignment	not modelled	30.2	15	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
53	<a href="#">c3rhtB</a>	Alignment	not modelled	30.2	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> (gatase1)-like protein; <b>PDBTitle:</b> crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
54	<a href="#">c3kbqA</a>	Alignment	not modelled	29.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein ta0487; <b>PDBTitle:</b> the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
55	<a href="#">d1okkd2</a>	Alianment	not modelled	27.6	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases

						<b>Family:</b> Nitrogenase iron protein-like
56	<a href="#">c5fmrC</a>	Alignment	not modelled	27.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> intraflagellar transport protein component ift52; <b>PDBTitle:</b> crift52 n-terminal domain
57	<a href="#">d1cr2a</a>	Alignment	not modelled	26.9	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
58	<a href="#">c5jwqA</a>	Alignment	not modelled	25.6	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> circadian clock protein kinase kaic; <b>PDBTitle:</b> crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
59	<a href="#">c5l3rC</a>	Alignment	not modelled	23.8	13	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
60	<a href="#">d2ftsA3</a>	Alignment	not modelled	23.3	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
61	<a href="#">d2h1qa1</a>	Alignment	not modelled	22.5	24	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> Dhaf3308-like <b>Family:</b> Dhaf3308-like
62	<a href="#">c1zu4A</a>	Alignment	not modelled	22.3	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsY; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
63	<a href="#">d1oi7a1</a>	Alignment	not modelled	21.6	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
64	<a href="#">c4tskA</a>	Alignment	not modelled	20.9	13	<b>PDB header:</b> oxidoreductase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
65	<a href="#">c1m7IA</a>	Alignment	not modelled	20.6	29	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pulmonary surfactant-associated protein d; <b>PDBTitle:</b> solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d
66	<a href="#">d1np3a2</a>	Alignment	not modelled	19.9	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
67	<a href="#">c3bicA</a>	Alignment	not modelled	19.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase, mitochondrial precursor; <b>PDBTitle:</b> crystal structure of human methylmalonyl-coa mutase
68	<a href="#">d2nu7a1</a>	Alignment	not modelled	18.6	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
69	<a href="#">c2iy3A</a>	Alignment	not modelled	18.6	16	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein, signal recognition <b>PDBTitle:</b> structure of the e. coli signal recognition particle
70	<a href="#">d1euca1</a>	Alignment	not modelled	18.5	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
71	<a href="#">c5yegB</a>	Alignment	not modelled	18.5	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase (nadp(+)); <b>PDBTitle:</b> the structure of sac-kari protein
72	<a href="#">c2qy9A</a>	Alignment	not modelled	16.8	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
73	<a href="#">d2nqra3</a>	Alignment	not modelled	16.6	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
74	<a href="#">c2q5cA</a>	Alignment	not modelled	16.3	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc family transcriptional regulator; <b>PDBTitle:</b> crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
75	<a href="#">d1pjqa1</a>	Alignment	not modelled	16.0	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
76	<a href="#">c4lhbC</a>	Alignment	not modelled	15.9	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> molybdopterin adenyltransferase; <b>PDBTitle:</b> crystal structure of tungsten cofactor synthesizing protein moab from2 pyrococcus furiosus
77	<a href="#">c2vyeA</a>	Alignment	not modelled	15.3	15	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnaC-ssdna complex
78	<a href="#">c3iynR</a>	Alignment	not modelled	14.9	30	<b>PDB header:</b> virus <b>Chain:</b> R: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
79	<a href="#">c3w01A</a>	Alignment	not modelled	14.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> heptaprenylglyceryl phosphate synthase; <b>PDBTitle:</b> crystal structure of pcrb complexed with peg from staphylococcus2 aureus subsp. aureus mu3
80	<a href="#">d1kola2</a>	Alignment	not modelled	14.7	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
81	<a href="#">c2q9cA</a>	Alignment	not modelled	13.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of ftsy:gmppnp with mgcl complex

82	<a href="#">d1uz5a3</a>	Alignment	not modelled	13.4	21	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
83	<a href="#">c2j289</a>	Alignment	not modelled	13.3	19	<b>PDB header:</b> ribosome <b>Chain:</b> 9; <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
84	<a href="#">c1vmaA</a>	Alignment	not modelled	13.2	20	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
85	<a href="#">c2f1rA</a>	Alignment	not modelled	12.9	26	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis <b>PDBTitle:</b> crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
86	<a href="#">c4cgbE</a>	Alignment	not modelled	12.2	10	<b>PDB header:</b> cell cycle <b>Chain:</b> E; <b>PDB Molecule:</b> echinoderm microtubule-associated protein-like 2; <b>PDBTitle:</b> crystal structure of the trimerization domain of eml2
87	<a href="#">c4xdzB</a>	Alignment	not modelled	12.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
88	<a href="#">c2g4rB</a>	Alignment	not modelled	11.7	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> molybdopterin biosynthesis mog protein; <b>PDBTitle:</b> anomalous substructure of moga
89	<a href="#">c2pjuD</a>	Alignment	not modelled	11.6	12	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon regulatory protein2 prpr
90	<a href="#">c5mc9B</a>	Alignment	not modelled	11.3	26	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> laminin subunit beta-1; <b>PDBTitle:</b> crystal structure of the heterotrimeric integrin-binding region of2 laminin-111
91	<a href="#">c2og2A</a>	Alignment	not modelled	11.2	17	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
92	<a href="#">c3fk4A</a>	Alignment	not modelled	10.9	14	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> rubisco-like protein; <b>PDBTitle:</b> crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
93	<a href="#">d1y5ea1</a>	Alignment	not modelled	10.9	13	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
94	<a href="#">c3dm5A</a>	Alignment	not modelled	10.8	19	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
95	<a href="#">c4cgbA</a>	Alignment	not modelled	10.7	10	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> echinoderm microtubule-associated protein-like 2; <b>PDBTitle:</b> crystal structure of the trimerization domain of eml2
96	<a href="#">c2yfqA</a>	Alignment	not modelled	10.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nad-specific glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
97	<a href="#">c3rfqC</a>	Alignment	not modelled	10.7	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C; <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
98	<a href="#">c4bucA</a>	Alignment	not modelled	9.8	11	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> crystal structure of murd ligase from thermotoga maritima in apo form
99	<a href="#">d1mkza</a>	Alignment	not modelled	9.7	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like