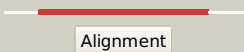

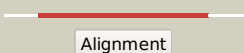
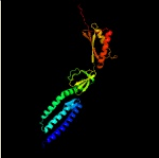
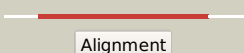
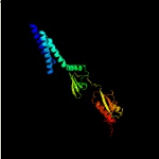
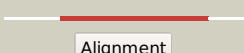
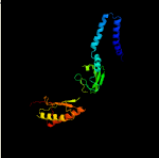

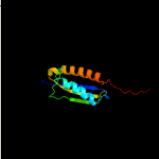


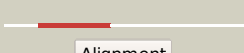

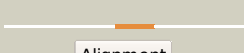
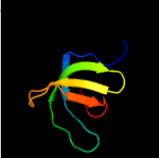

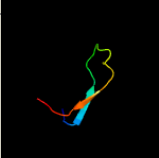

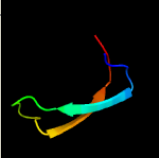

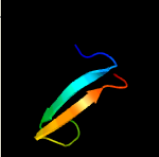


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3104c (-)_3471849_3472775
Date	Thu Aug 8 16:20:28 BST 2019
Unique Job ID	84d28aa988236eaa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3t9nG_</a>	 Alignment		100.0	27	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> small-conductance mechanosensitive channel; <b>PDBTitle:</b> crystal structure of a membrane protein
2	<a href="#">c2vv5D_</a>	 Alignment		100.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> small-conductance mechanosensitive channel; <b>PDBTitle:</b> the open structure of mscs
3	<a href="#">c4hw9E_</a>	 Alignment		100.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> mechanosensitive channel mscs; <b>PDBTitle:</b> crystal structure of helicobacter pylori mscs (closed state)
4	<a href="#">c5y4oA_</a>	 Alignment		100.0	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> low conductance mechanosensitive channel ynai; <b>PDBTitle:</b> cryo-em structure of mscs channel, ynai
5	<a href="#">d2vv5a2</a>	 Alignment		99.7	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain <b>Family:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain
6	<a href="#">d2vv5a1</a>	 Alignment		99.6	31	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Mechanosensitive channel protein MscS (YggB), middle domain
7	<a href="#">d2vv5a3</a>	 Alignment		98.7	19	<b>Fold:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region <b>Family:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region
8	<a href="#">c2e6zA_</a>	 Alignment		85.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> solution structure of the second kow motif of human2 transcription elongation factor spt5
9	<a href="#">d1nz9a_</a>	 Alignment		83.8	27	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain
10	<a href="#">d1nppa2</a>	 Alignment		83.8	38	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain
11	<a href="#">c2kvqG_</a>	 Alignment		81.7	27	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> solution structure of nuse:nusg-ctd complex

12	<a href="#">c2jvvA_</a>	Alignment		81.7	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> solution structure of e. coli nusg carboxyterminal domain
13	<a href="#">c5xonW_</a>	Alignment		81.1	10	<b>PDB header:</b> transcription/rna <b>Chain:</b> W: <b>PDB Molecule:</b> protein that forms a complex with spt4p; <b>PDBTitle:</b> rna polymerase ii elongation complex bound with spt4/5 and tfiis
14	<a href="#">c2mi6A_</a>	Alignment		79.2	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination/antitermination protein nusg; <b>PDBTitle:</b> solution structure of the carboxy terminal domain of nusg from2 mycobacterium tuberculosis
15	<a href="#">c2zkrt_</a>	Alignment		79.1	19	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> T: <b>PDB Molecule:</b> rna expansion segment es39 part iii; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
16	<a href="#">c4ytiB_</a>	Alignment		77.2	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
17	<a href="#">c3p8bB_</a>	Alignment		72.0	27	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
18	<a href="#">d2hqha1</a>	Alignment		70.9	35	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
19	<a href="#">c4zn3A_</a>	Alignment		61.7	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> crystal structure of mjspt4:spt5 complex conformation b
20	<a href="#">c2lcIA_</a>	Alignment		57.3	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional activator rfah; <b>PDBTitle:</b> solution structure of rfah carboxyterminal domain
21	<a href="#">c1m1gB_</a>	Alignment	not modelled	56.6	38	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
22	<a href="#">d1t9ha1</a>	Alignment	not modelled	50.7	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
23	<a href="#">d2do3a1</a>	Alignment	not modelled	48.0	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> SPT5 KOW domain-like
24	<a href="#">c2lq8A_</a>	Alignment	not modelled	47.4	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> domain interaction in thermotoga maritima nusg
25	<a href="#">d1jcb4</a>	Alignment	not modelled	44.8	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Anticodon-binding domain of PheRS <b>Family:</b> Anticodon-binding domain of PheRS
26	<a href="#">d2cp6a1</a>	Alignment	not modelled	43.2	33	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
27	<a href="#">c6fc6A_</a>	Alignment	not modelled	42.8	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear fusion protein bik1; <b>PDBTitle:</b> bik1 cap-gly domain with etf peptide from bim1
28	<a href="#">d1yeza1</a>	Alignment	not modelled	42.8	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TRAM domain
29	<a href="#">d1yvca1</a>	Alignment	not modelled	41.7	30	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins

						<b>Family:</b> TRAM domain
30	<a href="#">d1whka_</a>	Alignment	not modelled	40.8	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
31	<a href="#">d1u0la1</a>	Alignment	not modelled	40.8	39	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
32	<a href="#">d2cqaa1</a>	Alignment	not modelled	40.7	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TIP49 domain
33	<a href="#">c1vw4Q_</a>	Alignment	not modelled	40.6	16	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 54s ribosomal protein l40, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
34	<a href="#">c2vfyA_</a>	Alignment	not modelled	38.2	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> akap18 delta; <b>PDBTitle:</b> akap18 delta central domain
35	<a href="#">c4a1cS_</a>	Alignment	not modelled	38.1	23	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> rpl26; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
36	<a href="#">c4mzqG_</a>	Alignment	not modelled	37.9	18	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> beta-alanyl-coa:ammonia lyase; <b>PDBTitle:</b> beta-alanyl-coa:ammonia lyase from clostridium propionicum in complex2 with propionyl-coa
37	<a href="#">c3j21R_</a>	Alignment	not modelled	36.8	21	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 50s ribosomal protein l21e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
38	<a href="#">d1vqot1</a>	Alignment	not modelled	36.7	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
39	<a href="#">c3cmqA_</a>	Alignment	not modelled	36.6	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial phenylalanine trna synthetase
40	<a href="#">d2coya1</a>	Alignment	not modelled	36.4	32	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
41	<a href="#">c1t9hA_</a>	Alignment	not modelled	35.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> the crystal structure of yloq, a circularly permuted gtpase.
42	<a href="#">c2gvhC_</a>	Alignment	not modelled	35.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> agr_1_2016p; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
43	<a href="#">d1whma_</a>	Alignment	not modelled	33.6	23	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
44	<a href="#">c5tbzK_</a>	Alignment	not modelled	33.4	15	<b>PDB header:</b> transcription/rna <b>Chain:</b> K: <b>PDB Molecule:</b> transcription termination/antitermination protein nusg; <b>PDBTitle:</b> e. coli rna polymerase complexed with nusg
45	<a href="#">c3zf7Z_</a>	Alignment	not modelled	31.9	19	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein l26, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
46	<a href="#">d2e3ia1</a>	Alignment	not modelled	31.8	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
47	<a href="#">c3b7kA_</a>	Alignment	not modelled	31.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 12; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 12
48	<a href="#">c3j4rA_</a>	Alignment	not modelled	31.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> a-kinase anchor protein 18; <b>PDBTitle:</b> pseudo-atomic model of the akap18-pka complex in a linear conformation2 derived from electron microscopy
49	<a href="#">c3iz5Y_</a>	Alignment	not modelled	30.8	27	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 60s ribosomal protein l26 (l24p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
50	<a href="#">d1ylia1</a>	Alignment	not modelled	30.4	23	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
51	<a href="#">c2e4hA_</a>	Alignment	not modelled	30.3	30	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> restin; <b>PDBTitle:</b> solution structure of cytoskeletal protein in complex with2 tubulin tail
52	<a href="#">c5o60Q_</a>	Alignment	not modelled	30.2	19	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 50s ribosomal protein l19; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
53	<a href="#">c2yv5A_</a>	Alignment	not modelled	29.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yjeq protein; <b>PDBTitle:</b> crystal structure of yjeq from aquifex aeolicus
54	<a href="#">c5ounA_</a>	Alignment	not modelled	29.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like protein 2; <b>PDBTitle:</b> nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae
55	<a href="#">c4npkA_</a>	Alignment	not modelled	29.7	23	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s1;

55	<a href="#">c4m1kA_</a>	Alignment	not modelled	29.7	43	<b>PDBTitle:</b> structural basis for targeting the ribosomal protein s1 of2 mycobacterium tuberculosis by pyrazinamide
56	<a href="#">c4l5gA_</a>	Alignment	not modelled	29.6	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> card; <b>PDBTitle:</b> crystal structure of thermus thermophilus card
57	<a href="#">c2mf1A_</a>	Alignment	not modelled	29.6	18	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s1; <b>PDBTitle:</b> domain 2 of e. coli ribosomal protein s1
58	<a href="#">c4ienB_</a>	Alignment	not modelled	29.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative acyl-coa hydrolase; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
59	<a href="#">d2cp0a1</a>	Alignment	not modelled	29.3	26	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
60	<a href="#">d2coza1</a>	Alignment	not modelled	29.1	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
61	<a href="#">d1vqoq1</a>	Alignment	not modelled	29.0	23	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
62	<a href="#">c2xhcA_</a>	Alignment	not modelled	29.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
63	<a href="#">c3j21U_</a>	Alignment	not modelled	28.2	31	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l24p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
64	<a href="#">c5oikZ_</a>	Alignment	not modelled	27.8	22	<b>PDB header:</b> transcription <b>Chain:</b> Z: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> structure of an rna polymerase ii-disf transcription elongation2 complex
65	<a href="#">c1u0lB_</a>	Alignment	not modelled	27.7	37	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> crystal structure of yjeq from thermotoga maritima
66	<a href="#">c2p9rA_</a>	Alignment	not modelled	27.7	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-2-macroglobulin; <b>PDBTitle:</b> human alpha2-macroglobulin is composed of multiple domains,2 as predicted by homology with complement component c3
67	<a href="#">c2e70A_</a>	Alignment	not modelled	27.4	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> solution structure of the fifth kow motif of human2 transcription elongation factor spt5
68	<a href="#">d2cowa1</a>	Alignment	not modelled	27.2	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
69	<a href="#">c2dxcG_</a>	Alignment	not modelled	27.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> thiocyanate hydrolase subunit alpha; <b>PDBTitle:</b> recombinant thiocyanate hydrolase, fully-matured form
70	<a href="#">c2z0wA_</a>	Alignment	not modelled	27.0	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> cap-gly domain-containing linker protein 4; <b>PDBTitle:</b> crystal structure of the 2nd cap-gly domain in human restin-2 like protein 2 reveals a swapped-dimer
71	<a href="#">d2gvha1</a>	Alignment	not modelled	26.9	16	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
72	<a href="#">c2v1oF_</a>	Alignment	not modelled	26.6	7	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of n-terminal domain of acyl-coa2 thioesterase 7
73	<a href="#">d2cp2a1</a>	Alignment	not modelled	26.0	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
74	<a href="#">d2cp5a1</a>	Alignment	not modelled	25.9	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
75	<a href="#">c5zy8A_</a>	Alignment	not modelled	25.4	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0336 protein rv0637; <b>PDBTitle:</b> crystal structure of c terminal truncated hadbc (3r-hydroxyacyl-acp2 dehydratase) complex from mycobacterium tuberculosis
76	<a href="#">d1whla_</a>	Alignment	not modelled	24.7	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
77	<a href="#">c2qq2C_</a>	Alignment	not modelled	24.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
78	<a href="#">c2eisA_</a>	Alignment	not modelled	24.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tthb207; <b>PDBTitle:</b> x-ray structure of acyl-coa hydrolase-like protein, tt1379, from2 thermus thermophilus hb8
79	<a href="#">c3qz9D_</a>	Alignment	not modelled	24.5	23	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> co-type nitrile hydratase beta subunit; <b>PDBTitle:</b> crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
80	<a href="#">d1whja_</a>	Alignment	not modelled	24.5	27	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain

81	<a href="#">c3cnrA</a>	Alignment	not modelled	23.8	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> type iv fimbriae assembly protein; <b>PDBTitle:</b> crystal structure of pilz (xac1133) from xanthomonas axonopodis pv2 citri
82	<a href="#">d2e3ha1</a>	Alignment	not modelled	23.6	33	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
83	<a href="#">d1v29b</a>	Alignment	not modelled	22.8	12	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Nitrile hydratase beta chain
84	<a href="#">c4zv3B</a>	Alignment	not modelled	22.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of the n- and c-terminal domains of mouse acyl-coa2 thioesterase 7
85	<a href="#">d2gvha2</a>	Alignment	not modelled	22.1	27	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
86	<a href="#">c4kbmB</a>	Alignment	not modelled	22.1	26	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase-binding transcription factor card; <b>PDBTitle:</b> structure of the mtb card/rnap beta subunit b1-b2 domains complex
87	<a href="#">c4fm4D</a>	Alignment	not modelled	21.8	25	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrile hydratase beta subunit; <b>PDBTitle:</b> wild type fe-type nitrile hydratase from comamonas testosteroni ni1
88	<a href="#">c2m9uA</a>	Alignment	not modelled	21.5	27	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase p46; <b>PDBTitle:</b> solution nmr structure of the c-terminal domain (ctd) of moloney2 murine leukemia virus integrase, northeast structural genomics target3 or41a
89	<a href="#">c1q8kA</a>	Alignment	not modelled	21.3	14	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 2 <b>PDBTitle:</b> solution structure of alpha subunit of human eif2
90	<a href="#">d2cp3a1</a>	Alignment	not modelled	20.4	33	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
91	<a href="#">c1q46A</a>	Alignment	not modelled	20.0	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 alpha subunit; <b>PDBTitle:</b> crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
92	<a href="#">c2lwjA</a>	Alignment	not modelled	19.5	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, card family; <b>PDBTitle:</b> nmr solution structure myxococcus xanthus cdnl
93	<a href="#">c2zkrq</a>	Alignment	not modelled	19.5	24	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> Q: <b>PDB Molecule:</b> rna expansion segment es31 part ii; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
94	<a href="#">d1vpma</a>	Alignment	not modelled	19.3	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
95	<a href="#">c5uz4Z</a>	Alignment	not modelled	19.2	31	<b>PDB header:</b> ribosome/hydrolase <b>Chain:</b> Z: <b>PDB Molecule:</b> small ribosomal subunit biogenesis gtpase rsga; <b>PDBTitle:</b> the cryo-em structure of yjeq bound to the 30s subunit suggests a2 fidelity checkpoint function for this protein in ribosome assembly
96	<a href="#">d1v6ga2</a>	Alignment	not modelled	18.7	23	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
97	<a href="#">c4rtdA</a>	Alignment	not modelled	18.7	26	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized lipoprotein yfhm; <b>PDBTitle:</b> escherichia coli alpha-2-macroglobulin activated by porcine elastase
98	<a href="#">c3pifD</a>	Alignment	not modelled	18.5	28	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 5'->3' exoribonuclease (xrn1); <b>PDBTitle:</b> crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
99	<a href="#">c4b6mA</a>	Alignment	not modelled	18.4	26	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> tubulin-specific chaperone, putative; <b>PDBTitle:</b> trypanosoma brucei tubulin binding cofactor b cap-gly domain