


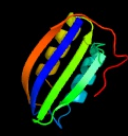


















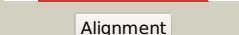
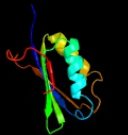




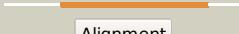



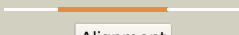








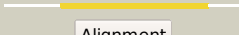


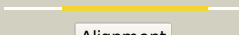

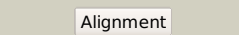



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2922A_acyP_3237828_3238109
Date	Thu Aug 8 16:20:08 BST 2019
Unique Job ID	63b9856eb5141ab4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3br8A_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable acylphosphatase; <b>PDBTitle:</b> crystal structure of acylphosphatase from bacillus subtilis
2	<a href="#">c2bjeA_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acylphosphatase; <b>PDBTitle:</b> acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
3	<a href="#">c2gv1A_</a>	 Alignment		100.0	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable acylphosphatase; <b>PDBTitle:</b> nmr solution structure of the acylphosphatase from2 eschaerichia coli
4	<a href="#">c2lxfA_</a>	 Alignment		100.0	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of a potential acylphosphatase from giardia2 lamblia, seattle structural genomics center for infectious disease3 target gilaa.01396.a
5	<a href="#">c4hi2B_</a>	 Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acylphosphatase; <b>PDBTitle:</b> crystal structure of an acylphosphatase protein cage
6	<a href="#">d1w2ia_</a>	 Alignment		100.0	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like
7	<a href="#">d1ulra_</a>	 Alignment		100.0	46	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like
8	<a href="#">d2acya_</a>	 Alignment		100.0	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like
9	<a href="#">d1urra_</a>	 Alignment		100.0	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like
10	<a href="#">d1lapsa_</a>	 Alignment		100.0	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like
11	<a href="#">d1gxua_</a>	 Alignment		100.0	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like

12	<a href="#">c3vthA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
13	<a href="#">c4g9iA_</a>	 Alignment		99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation protein hypf; <b>PDBTitle:</b> crystal structure of t.kodakarensis hypf
14	<a href="#">c4f67A_</a>	 Alignment		94.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0176 protein lpg2838; <b>PDBTitle:</b> three dimensional structure of the double mutant of upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nesg) target lgr82
15	<a href="#">c2kb2A_</a>	 Alignment		87.3	24	<b>PDB header:</b> signaling protein, hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> blrp1; <b>PDBTitle:</b> blrp1 bluf
16	<a href="#">d2buna1</a>	 Alignment		85.7	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> BLUF domain
17	<a href="#">c3jcrK_</a>	 Alignment		85.0	33	<b>PDB header:</b> splicing <b>Chain:</b> K: <b>PDB Molecule:</b> hprp3; <b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
18	<a href="#">d1yrxa1</a>	 Alignment		84.5	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> BLUF domain
19	<a href="#">c2hfnJ_</a>	 Alignment		81.1	12	<b>PDB header:</b> electron transport <b>Chain:</b> J: <b>PDB Molecule:</b> synechocystis photoreceptor (slr1694); <b>PDBTitle:</b> crystal structures of the synechocystis photoreceptor slr1694 reveal2 distinct structural states related to signaling
20	<a href="#">d2byca1</a>	 Alignment		80.0	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> BLUF domain
21	<a href="#">d2qswa1</a>	 Alignment	not modelled	77.7	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
22	<a href="#">d1x0pa1</a>	 Alignment	not modelled	77.4	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> BLUF domain
23	<a href="#">d2f1fa2</a>	 Alignment	not modelled	77.4	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
24	<a href="#">d2fgca1</a>	 Alignment	not modelled	75.0	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
25	<a href="#">c4hh0B_</a>	 Alignment	not modelled	73.6	17	<b>PDB header:</b> flavoprotein,signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> appa protein; <b>PDBTitle:</b> dark-state structure of appa c20s without the cys-rich region from rb.2 sphaeroides
26	<a href="#">d2pc6a1</a>	 Alignment	not modelled	72.8	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
27	<a href="#">d2if1a_</a>	 Alignment	not modelled	71.1	15	<b>Fold:</b> eIF1-like <b>Superfamily:</b> eIF1-like <b>Family:</b> eIF1-like
28	<a href="#">c4yhwa_</a>	 Alignment	not modelled	70.9	26	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> yeast prp3 (296-469) in complex with fragment of u4/u6 di-srna <b>PDB header:</b> translation

29	<a href="#">c2oghA</a>	Alignment	not modelled	69.1	14	<b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor eif1; <b>PDBTitle:</b> solution structure of yeast eif1
30	<a href="#">c2xznF</a>	Alignment	not modelled	68.3	13	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> eif1; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
31	<a href="#">c5gapG</a>	Alignment	not modelled	66.9	26	<b>PDB header:</b> transcription <b>Chain:</b> G; <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> body region of the u4/u6.u5 tri-snrnp
32	<a href="#">c2fgcA</a>	Alignment	not modelled	58.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetolactate synthase, small subunit; <b>PDBTitle:</b> crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
33	<a href="#">c3c5tB</a>	Alignment	not modelled	57.3	11	<b>PDB header:</b> signaling protein/signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> exendin-4; <b>PDBTitle:</b> crystal structure of the ligand-bound glucagon-like peptide-1 receptor2 extracellular domain
34	<a href="#">c2f1fA</a>	Alignment	not modelled	54.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetolactate synthase isozyme iii small subunit; <b>PDBTitle:</b> crystal structure of the regulatory subunit of acetoxyacid2 synthase isozyme iii from e. coli
35	<a href="#">c3jcmK</a>	Alignment	not modelled	52.5	26	<b>PDB header:</b> transcription <b>Chain:</b> K; <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> cryo-em structure of the spliceosomal u4/u6.u5 tri-snrnp
36	<a href="#">c2pc6C</a>	Alignment	not modelled	49.9	17	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> probable acetolactate synthase isozyme iii (small subunit); <b>PDBTitle:</b> crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
37	<a href="#">c5o9zE</a>	Alignment	not modelled	49.6	33	<b>PDB header:</b> splicing <b>Chain:</b> E; <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
38	<a href="#">c6mrrA</a>	Alignment	not modelled	46.8	20	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> foldit1; <b>PDBTitle:</b> de novo designed protein foldit1
39	<a href="#">d3dhxa1</a>	Alignment	not modelled	46.7	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
40	<a href="#">c5nbyA</a>	Alignment	not modelled	46.4	10	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> beta subunit of photoactivated adenyl cyclase; <b>PDBTitle:</b> structure of a bacterial light-regulated adenyl cyclase
41	<a href="#">c2rjzA</a>	Alignment	not modelled	43.1	2	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> pilo protein; <b>PDBTitle:</b> crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
42	<a href="#">c6b3jP</a>	Alignment	not modelled	41.6	12	<b>PDB header:</b> signaling protein <b>Chain:</b> P; <b>PDB Molecule:</b> exendin-p5; <b>PDBTitle:</b> 3.3 angstrom phase-plate cryo-em structure of a biased agonist-bound2 human glp-1 receptor-gs complex
43	<a href="#">d2qrra1</a>	Alignment	not modelled	34.7	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
44	<a href="#">c3zf7y</a>	Alignment	not modelled	29.3	15	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> 60s ribosomal protein l24, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
45	<a href="#">c3fhaD</a>	Alignment	not modelled	27.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase; <b>PDBTitle:</b> structure of endo-beta-n-acetylglucosaminidase a
46	<a href="#">d1fx0a2</a>	Alignment	not modelled	27.0	32	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
47	<a href="#">d2jdia2</a>	Alignment	not modelled	24.1	32	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
48	<a href="#">c4mo0A</a>	Alignment	not modelled	23.0	11	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> protein translation factor sui1 homolog; <b>PDBTitle:</b> crystal structure of aif1 from methanocaldococcus jannaschii
49	<a href="#">c3j39H</a>	Alignment	not modelled	22.6	17	<b>PDB header:</b> ribosome <b>Chain:</b> H; <b>PDB Molecule:</b> 60s ribosomal protein l9; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
50	<a href="#">d3ceda1</a>	Alignment	not modelled	21.8	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
51	<a href="#">c2dclB</a>	Alignment	not modelled	21.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical upf0166 protein ph1503; <b>PDBTitle:</b> structure of ph1503 protein from pyrococcus horikoshii ot3
52	<a href="#">c2mvzA</a>	Alignment	not modelled	21.1	12	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> solution structure for cyclophilin a from geobacillus kaustophilus
53	<a href="#">c3iz5F</a>	Alignment	not modelled	20.6	13	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 60s ribosomal protein l9 (l6p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

54	<a href="#">c4yusA</a>	Alignment	not modelled	20.4	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> family 3 adenylate cyclase; <b>PDBTitle:</b> crystal structure of photoactivated adenylyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
55	<a href="#">d1skyb2</a>	Alignment	not modelled	15.6	28	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
56	<a href="#">c6ge2A</a>	Alignment	not modelled	15.5	12	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> exendin-4; <b>PDBTitle:</b> exendin-4 based dual glp-1/glucagon receptor agonist
57	<a href="#">c2zkrE</a>	Alignment	not modelled	14.9	13	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> E: <b>PDB Molecule:</b> rna expansion segment es7 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
58	<a href="#">c3qm2A</a>	Alignment	not modelled	14.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
59	<a href="#">c2jz2A</a>	Alignment	not modelled	13.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ssl0352 protein; <b>PDBTitle:</b> solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
60	<a href="#">d1maba2</a>	Alignment	not modelled	13.1	32	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
61	<a href="#">c3gwpA</a>	Alignment	not modelled	12.8	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon-sulfur lyase involved in aluminum resistance; <b>PDBTitle:</b> crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution
62	<a href="#">c1qp6B</a>	Alignment	not modelled	12.7	17	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein (alpha2d); <b>PDBTitle:</b> solution structure of alpha2d
63	<a href="#">c1yzxB</a>	Alignment	not modelled	12.3	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase kappa 1; <b>PDBTitle:</b> crystal structure of human kappa class glutathione transferase
64	<a href="#">d2fgca2</a>	Alignment	not modelled	12.2	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> llvH-like
65	<a href="#">d2pc6a2</a>	Alignment	not modelled	11.1	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> llvH-like
66	<a href="#">c1lrjA</a>	Alignment	not modelled	10.9	11	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> exendin-4; <b>PDBTitle:</b> solution structure of exendin-4 in 30-vol% trifluoroethanol
67	<a href="#">c3ucoB</a>	Alignment	not modelled	10.9	13	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> coccomyxa beta-carbonic anhydrase in complex with iodide
68	<a href="#">d1a0ia1</a>	Alignment	not modelled	10.7	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
69	<a href="#">d1ydua1</a>	Alignment	not modelled	10.4	14	<b>Fold:</b> At5g01610-like <b>Superfamily:</b> At5g01610-like <b>Family:</b> At5g01610-like
70	<a href="#">c3c9gB</a>	Alignment	not modelled	10.3	8	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> upf0200/upf0201 protein af_1395; <b>PDBTitle:</b> crystal structure of uncharacterized upf0201 protein af_135
71	<a href="#">d1i6pa</a>	Alignment	not modelled	10.1	14	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
72	<a href="#">c5zcyA</a>	Alignment	not modelled	9.8	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> protein translation factor sui1 homolog; <b>PDBTitle:</b> crystal structure of archaeal translation initiation factor 1 at 1.52 angstroms resolution
73	<a href="#">c3hfkB</a>	Alignment	not modelled	9.5	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-methylmuconolactone methylisomerase; <b>PDBTitle:</b> crystal structure of 4-methylmuconolactone methylisomerase (h52a) in2 complex with 4-methylmuconolactone
74	<a href="#">d2hh8a1</a>	Alignment	not modelled	9.4	19	<b>Fold:</b> YdfO-like <b>Superfamily:</b> YdfO-like <b>Family:</b> YdfO-like
75	<a href="#">c2a5vB</a>	Alignment	not modelled	9.1	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase (carbonate dehydratase) (carbonic <b>PDBTitle:</b> crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
76	<a href="#">c1d0rA</a>	Alignment	not modelled	9.1	13	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> glucagon-like peptide-1-(7-36)-amide; <b>PDBTitle:</b> solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water
77	<a href="#">d1d1ra</a>	Alignment	not modelled	8.9	18	<b>Fold:</b> eIF1-like <b>Superfamily:</b> eIF1-like <b>Family:</b> eIF1-like
						<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 11.4 kd protein ycih in pyrf-

78	<a href="#">c1d1rA_</a>	Alignment	not modelled	8.9	18	osmb <b>PDBTitle:</b> nmr solution structure of the e. coli ycih2 gene.
79	<a href="#">d2fyxa1</a>	Alignment	not modelled	8.7	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Transposase IS200-like <b>Family:</b> Transposase IS200-like
80	<a href="#">c5swcE_</a>	Alignment	not modelled	8.6	26	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> the structure of the beta-carbonic anhydrase ccaa
81	<a href="#">c5yiiA_</a>	Alignment	not modelled	8.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of 45 amino acid deleted from n-terminal of 2 phosphoserine aminotransferase (psat) of entamoeba histolytica
82	<a href="#">c2wuhD_</a>	Alignment	not modelled	8.4	100	<b>PDB header:</b> receptor/peptide <b>Chain:</b> D: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
83	<a href="#">c2vicA_</a>	Alignment	not modelled	8.3	11	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transposase orfa; <b>PDBTitle:</b> crystal structure of the ishp608 transposase in complex2 with left end 26-mer dna and manganese
84	<a href="#">c2wuhC_</a>	Alignment	not modelled	8.1	100	<b>PDB header:</b> receptor/peptide <b>Chain:</b> C: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
85	<a href="#">c2wuhB_</a>	Alignment	not modelled	8.1	100	<b>PDB header:</b> receptor/peptide <b>Chain:</b> B: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
86	<a href="#">c3j21N_</a>	Alignment	not modelled	8.0	12	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 50s ribosomal protein l10e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by 2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
87	<a href="#">d2ckca1</a>	Alignment	not modelled	7.8	19	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
88	<a href="#">c2ckcA_</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding protein 7; <b>PDBTitle:</b> solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
89	<a href="#">d1nvma1</a>	Alignment	not modelled	7.8	19	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> post-HMGL domain-like <b>Family:</b> DmpG/LeuA communication domain-like
90	<a href="#">c3eyxB_</a>	Alignment	not modelled	7.7	29	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of carbonic anhydrase nce103 from 2 saccharomyces cerevisiae
91	<a href="#">c3nrbd_</a>	Alignment	not modelled	7.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
92	<a href="#">c2yy3B_</a>	Alignment	not modelled	7.3	19	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 1-beta; <b>PDBTitle:</b> crystal structure of translation elongation factor ef-1 beta from 2 pyrococcus horikoshii
93	<a href="#">d1vqoh1</a>	Alignment	not modelled	7.0	20	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Ribosomal protein L16p/L10e <b>Family:</b> Ribosomal protein L10e
94	<a href="#">d2cz4a1</a>	Alignment	not modelled	6.9	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
95	<a href="#">d2v0ea1</a>	Alignment	not modelled	6.9	19	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
96	<a href="#">d2f1fa1</a>	Alignment	not modelled	6.8	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
97	<a href="#">d3bida1</a>	Alignment	not modelled	6.8	23	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
98	<a href="#">c3tenD_</a>	Alignment	not modelled	6.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cs2 hydrolase; <b>PDBTitle:</b> holo form of carbon disulfide hydrolase
99	<a href="#">c6f45D_</a>	Alignment	not modelled	6.6	19	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> receptor recognition protein; <b>PDBTitle:</b> crystal structure of the gp37-gp38 adhesin tip complex of the 2 bacteriophage s16 long tail fiber