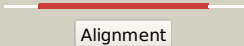

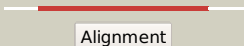

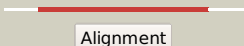


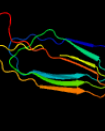
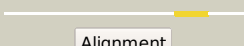

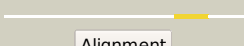

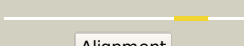






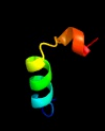



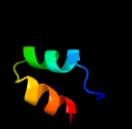



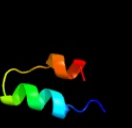





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1462_(-) _1649532_1650725
Date	Fri Aug 2 13:30:04 BST 2019
Unique Job ID	38d11490c9ebb821

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1vh4a_</a>	 Alignment		100.0	23	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Stabilizer of iron transporter SufD <b>Family:</b> Stabilizer of iron transporter SufD
2	<a href="#">c5awfA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transport protein/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fes cluster assembly protein sufB; <b>PDBTitle:</b> crystal structure of sufB-sufC-sufD complex from escherichia coli
3	<a href="#">c4dn7B_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of putative abc transporter, atp-binding protein2 from methanosarcina mazei go1
4	<a href="#">c3sf5D_</a>	 Alignment		90.6	14	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> urease accessory protein ureh; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
5	<a href="#">c2dagA_</a>	 Alignment		78.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 5; <b>PDBTitle:</b> solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
6	<a href="#">d1whca_</a>	 Alignment		71.7	20	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
7	<a href="#">c2daiA_</a>	 Alignment		70.6	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin associated domain containing 1; <b>PDBTitle:</b> solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadc1)
8	<a href="#">d1veka_</a>	 Alignment		66.4	15	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
9	<a href="#">c5w34A_</a>	 Alignment		63.5	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna primase; <b>PDBTitle:</b> crystal structure of the rna polymerase domain (rpd) of mycobacterium2 tuberculosis primase dnag in complex with double-stranded dna3 gaccggaagtgg
10	<a href="#">c1dd9A_</a>	 Alignment		62.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna primase; <b>PDBTitle:</b> structure of the dnag catalytic core
11	<a href="#">d1dd9a_</a>	 Alignment		62.4	22	<b>Fold:</b> DNA primase core <b>Superfamily:</b> DNA primase core <b>Family:</b> DNA primase DnaG catalytic core

12	<a href="#">c2crnA_</a>	Alignment		62.2	20	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> ubash3a protein; <b>PDBTitle:</b> solution structure of the uba domain of human ubash3a2 protein
13	<a href="#">d1wiva_</a>	Alignment		60.0	26	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
14	<a href="#">c2mroB_</a>	Alignment		59.2	15	<b>PDB header:</b> transport protein/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna damage-inducible protein 1; <b>PDBTitle:</b> structure of the complex of ubiquitin and the uba domain from dna-2 damage-inducible 1 protein (ddi1)
15	<a href="#">c5gujA_</a>	Alignment		57.6	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna primase; <b>PDBTitle:</b> crystal structure of the bacillus subtilis dnag rna polymerase domain,2 natural degradation of full length dnag
16	<a href="#">c4edvA_</a>	Alignment		56.7	25	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dna primase; <b>PDBTitle:</b> the structure of the s. aureus dnag rna polymerase domain bound to2 pppgpp and manganese
17	<a href="#">c2lbcA_</a>	Alignment		54.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 13; <b>PDBTitle:</b> solution structure of tandem uba of usp13
18	<a href="#">c5svdA_</a>	Alignment		54.3	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleolar protein 9; <b>PDBTitle:</b> nop9, a new puf-like protein, prevents premature pre-rna cleavage to2 correctly process mature 18s rna
19	<a href="#">c5vazB_</a>	Alignment		54.3	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna primase; <b>PDBTitle:</b> crystal structure of a dna primase domain from pseudomonas aeruginosa
20	<a href="#">c4jrbA_</a>	Alignment		53.6	15	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion
21	<a href="#">d1nuia1</a>	Alignment	not modelled	50.0	27	<b>Fold:</b> DNA primase core <b>Superfamily:</b> DNA primase core <b>Family:</b> Primase fragment of primase-helicase protein
22	<a href="#">d2csba4</a>	Alignment	not modelled	49.6	32	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
23	<a href="#">d1p32a_</a>	Alignment	not modelled	49.1	30	<b>Fold:</b> Mitochondrial glycoprotein MAM33-like <b>Superfamily:</b> Mitochondrial glycoprotein MAM33-like <b>Family:</b> Mitochondrial glycoprotein MAM33-like
24	<a href="#">c2dakA_</a>	Alignment	not modelled	48.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 5; <b>PDBTitle:</b> solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
25	<a href="#">d2cpwa1</a>	Alignment	not modelled	47.6	29	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
26	<a href="#">c6gcsc_</a>	Alignment	not modelled	47.4	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 49-kda protein (nucm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
27	<a href="#">d2crna1</a>	Alignment	not modelled	46.9	21	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
28	<a href="#">c2cpwA_</a>	Alignment	not modelled	45.3	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cbl-interacting protein sts-1 variant; <b>PDBTitle:</b> solution structure of rsgi ruh-031, a uba domain from human2 cdna
29	<a href="#">c2p2kA_</a>	Alignment	not modelled	43.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase;

29	<a href="#">c0v26A</a>	Alignment	not modelled	43.7	44	<b>PDBTitle:</b> crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n <b>PDB header:</b> oxidoreductase
30	<a href="#">c3ic3C</a>	Alignment	not modelled	43.3	29	<b>Chain:</b> C; <b>PDB Molecule:</b> putative pyruvate dehydrogenase; <b>PDBTitle:</b> structure of a putative pyruvate dehydrogenase from the photosynthetic2 bacterium rhodospseudomonas palustris cga009
31	<a href="#">d1yqfa1</a>	Alignment	not modelled	43.1	35	<b>Fold:</b> Mitochondrial glycoprotein MAM33-like <b>Superfamily:</b> Mitochondrial glycoprotein MAM33-like <b>Family:</b> Mitochondrial glycoprotein MAM33-like
32	<a href="#">c2f46A</a>	Alignment	not modelled	41.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
33	<a href="#">c3qv0A</a>	Alignment	not modelled	40.1	39	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> mitochondrial acidic protein mam33; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mam33
34	<a href="#">c1q57G</a>	Alignment	not modelled	38.5	27	<b>PDB header:</b> transferase <b>Chain:</b> G; <b>PDB Molecule:</b> dna primase/helicase; <b>PDBTitle:</b> the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
35	<a href="#">d1vega</a>	Alignment	not modelled	37.8	16	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
36	<a href="#">c3fp5A</a>	Alignment	not modelled	37.6	20	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-coa binding protein; <b>PDBTitle:</b> crystal structure of acbp from monilophthora perniciosa
37	<a href="#">c3jv1A</a>	Alignment	not modelled	37.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> p22 protein; <b>PDBTitle:</b> crystal structure of the trypanosoma brucei p22 protein
38	<a href="#">d1mska</a>	Alignment	not modelled	37.1	22	<b>Fold:</b> Methionine synthase activation domain-like <b>Superfamily:</b> Methionine synthase activation domain-like <b>Family:</b> Methionine synthase SAM-binding domain
39	<a href="#">d1rfza</a>	Alignment	not modelled	35.7	15	<b>Fold:</b> YutG-like <b>Superfamily:</b> YutG-like <b>Family:</b> YutG-like
40	<a href="#">c2wknE</a>	Alignment	not modelled	34.6	35	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> formamidase; <b>PDBTitle:</b> gamma lactamase from delftia acidovorans
41	<a href="#">d1ifya</a>	Alignment	not modelled	34.6	19	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
42	<a href="#">d1wfdA</a>	Alignment	not modelled	32.8	17	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> MIT domain <b>Family:</b> MIT domain
43	<a href="#">d1n9pa</a>	Alignment	not modelled	32.3	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Cytoplasmic domain of inward rectifier potassium channel
44	<a href="#">c2zc1A</a>	Alignment	not modelled	29.7	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> organophosphorus hydrolase from deinococcus radiodurans
45	<a href="#">c2au3A</a>	Alignment	not modelled	29.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dna primase; <b>PDBTitle:</b> crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
46	<a href="#">d1oqya1</a>	Alignment	not modelled	28.1	15	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
47	<a href="#">d2e1za2</a>	Alignment	not modelled	28.1	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
48	<a href="#">c3e3vA</a>	Alignment	not modelled	27.7	13	<b>PDB header:</b> recombination <b>Chain:</b> A; <b>PDB Molecule:</b> regulatory protein recx; <b>PDBTitle:</b> crystal structure of recx from lactobacillus salivarius
49	<a href="#">c5lnkn</a>	Alignment	not modelled	27.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N; <b>PDB Molecule:</b> mitochondrial complex i, nd2 subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
50	<a href="#">d1g99a2</a>	Alignment	not modelled	25.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
51	<a href="#">d2g3qa1</a>	Alignment	not modelled	24.6	17	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
52	<a href="#">c3tn6A</a>	Alignment	not modelled	24.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> crystal structure of gkap mutant r230h from geobacillus kaustophilus2 hta426
53	<a href="#">c5cqvb</a>	Alignment	not modelled	23.2	11	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae
54	<a href="#">d1yqga1</a>	Alignment	not modelled	23.1	17	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> ProC C-terminal domain-like
55	<a href="#">c3slcA</a>	Alignment	not modelled	23.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of apo form of acetate kinase (acka) from salmonella2 typhimurium
56	<a href="#">d1v3aa</a>	Alignment	not modelled	22.2	18	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II

						<b>Family:</b> Dual specificity phosphatase-like
57	<a href="#">c6ioyD_</a>	Alignment	not modelled	22.2	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis acetate kinase
58	<a href="#">d2ddha2</a>	Alignment	not modelled	21.5	27	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> acyl-CoA oxidase C-terminal domains
59	<a href="#">c4zv4C_</a>	Alignment	not modelled	20.9	25	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> tse6; <b>PDBTitle:</b> structure of tse6 in complex with ef-tu
60	<a href="#">c4rg6S_</a>	Alignment	not modelled	20.7	40	<b>PDB header:</b> protein binding <b>Chain:</b> S: <b>PDB Molecule:</b> anaphase-promoting complex subunit 16; <b>PDBTitle:</b> crystal structure of apc3-apc16 complex
61	<a href="#">c4rg9S_</a>	Alignment	not modelled	20.5	40	<b>PDB header:</b> protein binding <b>Chain:</b> S: <b>PDB Molecule:</b> anaphase-promoting complex subunit 16; <b>PDBTitle:</b> crystal structure of apc3-apc16 complex (selenomethionine derivative)
62	<a href="#">c1tuuA_</a>	Alignment	not modelled	20.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase crystallized with atpgs
63	<a href="#">c3ff5B_</a>	Alignment	not modelled	20.1	8	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal biogenesis factor 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
64	<a href="#">d1kx5d_</a>	Alignment	not modelled	18.8	21	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
65	<a href="#">c1nuvA_</a>	Alignment	not modelled	18.4	27	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna primase/helicase; <b>PDBTitle:</b> crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
66	<a href="#">c3khyA_</a>	Alignment	not modelled	18.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> propionate kinase; <b>PDBTitle:</b> crystal structure of a propionate kinase from francisella tularensis2 subsp. tularensis schu s4
67	<a href="#">d1auaa1</a>	Alignment	not modelled	18.2	23	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> CRAL/TRIO N-terminal domain <b>Family:</b> CRAL/TRIO N-terminal domain
68	<a href="#">c5l87A_</a>	Alignment	not modelled	18.2	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiases.
69	<a href="#">c4ijnB_</a>	Alignment	not modelled	17.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of an acetate kinase from mycobacterium smegmatis2 bound to amp and sulfate
70	<a href="#">c3rhgA_</a>	Alignment	not modelled	17.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphotriesterase; <b>PDBTitle:</b> crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
71	<a href="#">c5cofA_</a>	Alignment	not modelled	17.6	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
72	<a href="#">d1oiza1</a>	Alignment	not modelled	17.5	31	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> CRAL/TRIO N-terminal domain <b>Family:</b> CRAL/TRIO N-terminal domain
73	<a href="#">c2kerA_</a>	Alignment	not modelled	17.5	43	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase inhibitor z-2685; <b>PDBTitle:</b> alpha-amylase inhibitor parvulostat (z-2685) from2 streptomyces parvulus
74	<a href="#">d1ok0a_</a>	Alignment	not modelled	17.5	29	<b>Fold:</b> alpha-Amylase inhibitor tendamistat <b>Superfamily:</b> alpha-Amylase inhibitor tendamistat <b>Family:</b> alpha-Amylase inhibitor tendamistat
75	<a href="#">c2d9sA_</a>	Alignment	not modelled	17.1	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cbl e3 ubiquitin protein ligase; <b>PDBTitle:</b> solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
76	<a href="#">c1sazA_</a>	Alignment	not modelled	16.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable butyrate kinase 2; <b>PDBTitle:</b> membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
77	<a href="#">c4if2A_</a>	Alignment	not modelled	16.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase homology protein; <b>PDBTitle:</b> structure of the phosphotriesterase from mycobacterium tuberculosis
78	<a href="#">c4n6cB_</a>	Alignment	not modelled	16.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36.
79	<a href="#">c1x3nA_</a>	Alignment	not modelled	16.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> propionate kinase; <b>PDBTitle:</b> crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
80	<a href="#">c4h0pB_</a>	Alignment	not modelled	16.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of acetate kinase from cryptococcus neoformans
81	<a href="#">c4wzxA_</a>	Alignment	not modelled	16.5	17	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase ulk3; <b>PDBTitle:</b> ulk3 regulates cytokinetic abscission by phosphorylating escrt-iii2 proteins
						<b>PDB header:</b> transport protein

82	<a href="#">c3hy5A_</a>	Alignment	not modelled	16.4	21	<b>Chain:</b> A; <b>PDB Molecule:</b> retinaldehyde-binding protein 1; <b>PDBTitle:</b> crystal structure of cralbp
83	<a href="#">d1eqzb_</a>	Alignment	not modelled	16.2	26	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
84	<a href="#">c3my3A_</a>	Alignment	not modelled	15.9	10	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> mterf domain-containing protein 1, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial transcription termination2 factor 3
85	<a href="#">c2w85A_</a>	Alignment	not modelled	15.7	8	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> peroxisomal membrane anchor protein pex14; <b>PDBTitle:</b> structure of pex14 in complex with pex19
86	<a href="#">c3okzB_</a>	Alignment	not modelled	15.6	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein gbs0355; <b>PDBTitle:</b> crystal structure of protein gbs0355 from streptococcus agalactiae,2 northeast structural genomics consortium target sar127
87	<a href="#">d1wjia_</a>	Alignment	not modelled	15.6	17	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
88	<a href="#">c5aonB_</a>	Alignment	not modelled	15.5	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
89	<a href="#">d1s32d_</a>	Alignment	not modelled	15.2	21	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
90	<a href="#">d2ahra1</a>	Alignment	not modelled	15.1	14	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> ProC C-terminal domain-like
91	<a href="#">d1saza2</a>	Alignment	not modelled	15.0	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
92	<a href="#">c5v8cA_</a>	Alignment	not modelled	14.6	28	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> lytr-csp2a-psr enzyme from actinomyces oris
93	<a href="#">d2gcla1</a>	Alignment	not modelled	14.5	17	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> SSRP1-like
94	<a href="#">c3m66A_</a>	Alignment	not modelled	14.3	10	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> mterf domain-containing protein 1, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial transcription termination2 factor 3
95	<a href="#">c4ui9E_</a>	Alignment	not modelled	14.2	40	<b>PDB header:</b> cell cycle <b>Chain:</b> E; <b>PDB Molecule:</b> anaphase-promoting complex subunit 16; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
96	<a href="#">c2v6xA_</a>	Alignment	not modelled	13.5	15	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4; <b>PDBTitle:</b> structural insight into the interaction between escrt-iii and vps4
97	<a href="#">d1aopa3</a>	Alignment	not modelled	13.5	12	<b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like <b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like
98	<a href="#">c2iirj_</a>	Alignment	not modelled	13.3	16	<b>PDB header:</b> transferase <b>Chain:</b> J; <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase from a hypothermophile thermotoga maritima
99	<a href="#">d2gu3a1</a>	Alignment	not modelled	13.1	36	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Cystatin/monellin <b>Family:</b> PepSY-like