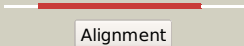

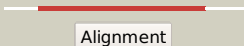

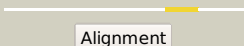

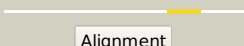

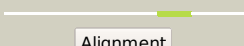

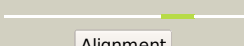

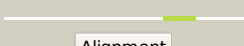


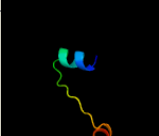

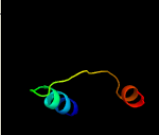






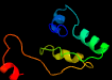

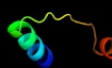






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3229c_(-)_3605748_3607031
Date	Thu Aug 8 16:20:43 BST 2019
Unique Job ID	880ed187f1984e36

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4zyoA_</a>	 Alignment		99.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase; <b>PDBTitle:</b> crystal structure of human integral membrane stearyl-coa desaturase2 with substrate
2	<a href="#">c4ymkA_</a>	 Alignment		99.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase 1; <b>PDBTitle:</b> crystal structure of stearyl-coenzyme a desaturase 1
3	<a href="#">c3frrA_</a>	 Alignment		79.6	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein kiaa0174; <b>PDBTitle:</b> structure of human ist1(ntd) - (residues 1-189)(p21)
4	<a href="#">c5xyiM_</a>	 Alignment		75.3	10	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein l7ae, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
5	<a href="#">d1pa7a_</a>	 Alignment		64.5	16	<b>Fold:</b> CH domain-like <b>Superfamily:</b> Calponin-homology domain, CH-domain <b>Family:</b> Calponin-homology domain, CH-domain
6	<a href="#">c2bh7A_</a>	 Alignment		64.1	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase; <b>PDBTitle:</b> crystal structure of a semet derivative of amid at 2.22 angstroms
7	<a href="#">c5xxuM_</a>	 Alignment		63.9	14	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein es12; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
8	<a href="#">c3cg6A_</a>	 Alignment		62.6	8	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> growth arrest and dna-damage-inducible 45 gamma; <b>PDBTitle:</b> crystal structure of gadd45 gamma
9	<a href="#">c3j3aM_</a>	 Alignment		62.2	7	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 40s ribosomal protein s12; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
10	<a href="#">c2r8uA_</a>	 Alignment		61.7	21	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> microtubule-associated protein rp/eb family member 1; <b>PDBTitle:</b> structure of fragment of human end-binding protein 1 (eb1) containing2 the n-terminal domain at 1.35 a resolution
11	<a href="#">d2bgxa2</a>	 Alignment		59.7	9	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like

12	<a href="#">c4ivvA_</a>	Alignment		56.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> autolysin; <b>PDBTitle:</b> catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumoniae
13	<a href="#">c2lbwA_</a>	Alignment		55.4	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 2; <b>PDBTitle:</b> solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
14	<a href="#">d2i5ia1</a>	Alignment		54.6	17	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> YdjC-like
15	<a href="#">c2e67D_</a>	Alignment		54.1	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein tthb029; <b>PDBTitle:</b> crystal structure of the hypothetical protein tthb029 from thermus2 thermophilus hb8
16	<a href="#">c3v7qB_</a>	Alignment		53.6	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable ribosomal protein ylxq; <b>PDBTitle:</b> crystal structure of b. subtilis ylxq at 1.55 a resolution
17	<a href="#">c2xznU_</a>	Alignment		53.0	13	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> ribosomal protein l7ae containing protein; <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
18	<a href="#">c4olsA_</a>	Alignment		52.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> the amidase-2 domain of lysgh15
19	<a href="#">c5ghaC_</a>	Alignment		49.9	17	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sulfur transferase ttua; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
20	<a href="#">c3on1A_</a>	Alignment		48.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2414 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from bacillus2 halodurans c
21	<a href="#">c4bolA_</a>	Alignment	not modelled	47.7	4	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ampdh2; <b>PDBTitle:</b> crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
22	<a href="#">c1kh2D_</a>	Alignment	not modelled	47.3	13	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> argininosuccinate synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
23	<a href="#">c3zeyF_</a>	Alignment	not modelled	46.7	7	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 40s ribosomal protein s12; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
24	<a href="#">c3varA_</a>	Alignment	not modelled	46.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl aminopeptidase; <b>PDBTitle:</b> crystal structure of dnpep, znzn form
25	<a href="#">c3latB_</a>	Alignment	not modelled	46.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional autolysin; <b>PDBTitle:</b> crystal structure of staphylococcus peptidoglycan hydrolase2 amie
26	<a href="#">d2gtsa1</a>	Alignment	not modelled	45.8	8	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> HP0062-like <b>Family:</b> HP0062-like
27	<a href="#">c5e4vA_</a>	Alignment	not modelled	45.5	21	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein,phosphoprotein; <b>PDBTitle:</b> crystal structure of measles n0-p complex
28	<a href="#">c5ewrA_</a>	Alignment	not modelled	44.5	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> box c/d snornc and u4 snrnc component snu13p; <b>PDBTitle:</b> c merolae u4 snrnc protein snu13
						<b>Fold:</b> Phosphorylase/hydrolase-like

29	<a href="#">d1y0ya2</a>	Alignment	not modelled	44.4	22	<b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
30	<a href="#">d1j3ga</a>	Alignment	not modelled	44.1	8	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
31	<a href="#">d1xpja</a>	Alignment	not modelled	43.4	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein VC0232
32	<a href="#">c3j38M</a>	Alignment	not modelled	43.3	14	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 40s ribosomal protein s12; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
33	<a href="#">c3ggzC</a>	Alignment	not modelled	43.2	24	<b>PDB header:</b> protein transport, endocytosis <b>Chain:</b> C: <b>PDB Molecule:</b> increased sodium tolerance protein 1; <b>PDBTitle:</b> crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
34	<a href="#">d2czwa1</a>	Alignment	not modelled	42.7	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
35	<a href="#">c2zkrf</a>	Alignment	not modelled	42.0	16	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> rna expansion segment es7 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
36	<a href="#">c3u5cM</a>	Alignment	not modelled	41.7	20	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 40s ribosomal protein s12; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
37	<a href="#">c3o85A</a>	Alignment	not modelled	41.7	17	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein l7ae; <b>PDBTitle:</b> giardia lamblia 15.5kd rna binding protein
38	<a href="#">d1t0kb</a>	Alignment	not modelled	41.4	8	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
39	<a href="#">c1l5jB</a>	Alignment	not modelled	41.3	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aconitate hydratase 2; <b>PDBTitle:</b> crystal structure of e. coli aconitase b.
40	<a href="#">c3t7yB</a>	Alignment	not modelled	41.3	15	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> yop proteins translocation protein u; <b>PDBTitle:</b> structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
41	<a href="#">c2kmaA</a>	Alignment	not modelled	40.9	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> talín 1; <b>PDBTitle:</b> nmr structure of the f0f1 double domain (residues 1-202) of2 the talin ferm domain
42	<a href="#">c4bxdB</a>	Alignment	not modelled	40.5	19	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> B: <b>PDB Molecule:</b> ampdh3; <b>PDBTitle:</b> crystal structure of ampdh3 from pseudomonas aeruginosa in2 complex with tetrasaccharide pentapeptide
43	<a href="#">d2aifa1</a>	Alignment	not modelled	40.2	28	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
44	<a href="#">d2ozba1</a>	Alignment	not modelled	40.2	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
45	<a href="#">d1yb0a1</a>	Alignment	not modelled	40.0	21	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
46	<a href="#">c1y7eA</a>	Alignment	not modelled	39.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable m18-family aminopeptidase 1; <b>PDBTitle:</b> the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
47	<a href="#">d1w6ta1</a>	Alignment	not modelled	39.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
48	<a href="#">d2fc3a1</a>	Alignment	not modelled	39.7	21	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
49	<a href="#">c3nquA</a>	Alignment	not modelled	39.6	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone h3-like centromeric protein a; <b>PDBTitle:</b> crystal structure of partially trypsinized (cenp-a/h4)2 heterotetramer
50	<a href="#">c5tw9D</a>	Alignment	not modelled	39.3	30	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> iron uptake system component efo; <b>PDBTitle:</b> 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efo from yersinia pestis.
51	<a href="#">d2obba1</a>	Alignment	not modelled	39.3	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
52	<a href="#">c3cpqB</a>	Alignment	not modelled	39.1	8	<b>PDB header:</b> ribosomal protein <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l30e; <b>PDBTitle:</b> crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
53	<a href="#">d2gl5a1</a>	Alignment	not modelled	39.0	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
54	<a href="#">d1rlga</a>	Alignment	not modelled	38.3	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
						<b>Fold:</b> Adenine nucleotide alpha hydrolase-like

55	<a href="#">d1k92a1</a>	Alignment	not modelled	38.2	13	<b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
56	<a href="#">c3vrhA</a>	Alignment	not modelled	38.0	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0300; <b>PDBTitle:</b> crystal structure of ph0300
57	<a href="#">d2fyma1</a>	Alignment	not modelled	38.0	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
58	<a href="#">c2daeA</a>	Alignment	not modelled	37.7	41	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa0733 protein; <b>PDBTitle:</b> solution structure of the n-terminal cue domain in the2 human mitogen-activated protein kinase kinase kinase 73 interacting protein 2 (map3k7ip2)
59	<a href="#">c2y8pA</a>	Alignment	not modelled	37.6	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-type membrane-bound lytic murein transglycosylase a; <b>PDBTitle:</b> crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
60	<a href="#">c4a1dG</a>	Alignment	not modelled	37.1	7	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> rpl30; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
61	<a href="#">d1uw0a</a>	Alignment	not modelled	36.1	16	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> PARP-type zinc finger
62	<a href="#">d1vqof1</a>	Alignment	not modelled	35.5	17	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
63	<a href="#">c3l6sA</a>	Alignment	not modelled	35.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl aminopeptidase; <b>PDBTitle:</b> crystal structure of human aspartyl aminopeptidase (dnpep), in complex2 with aspartic acid hydroxamate
64	<a href="#">d1h3oa</a>	Alignment	not modelled	35.5	11	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
65	<a href="#">c1h3oA</a>	Alignment	not modelled	35.5	11	<b>PDB header:</b> transcription/tdp-associated factors <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor tfiid 135 kda subunit; <b>PDBTitle:</b> crystal structure of the human taf4-taf12 (tafi135-tafii20) complex
66	<a href="#">d1sura</a>	Alignment	not modelled	35.4	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
67	<a href="#">c3hmaA</a>	Alignment	not modelled	35.3	0	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase xlya; <b>PDBTitle:</b> amidase from bacillus subtilis
68	<a href="#">c3b0zB</a>	Alignment	not modelled	35.2	19	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar biosynthetic protein flhb; <b>PDBTitle:</b> crystal structure of cytoplasmic domain of flhb from salmonella2 typhimurium
69	<a href="#">d1w41a1</a>	Alignment	not modelled	35.2	11	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
70	<a href="#">c3c00B</a>	Alignment	not modelled	34.7	14	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structural of the mutated g247t escu/spas c-terminal domain
71	<a href="#">c5ipmF</a>	Alignment	not modelled	34.6	11	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpos; <b>PDBTitle:</b> sigmas-transcription initiation complex with 4-nt nascent rna
72	<a href="#">c2ltuA</a>	Alignment	not modelled	34.5	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-amp-activated protein kinase catalytic subunit alpha-2; <b>PDBTitle:</b> solution structure of autoinhibitory domain of human amp-activated2 protein kinase catalytic subunit
73	<a href="#">c2greC</a>	Alignment	not modelled	34.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deblocking aminopeptidase; <b>PDBTitle:</b> crystal structure of deblocking aminopeptidase from bacillus cereus
74	<a href="#">c1vl2C</a>	Alignment	not modelled	34.2	10	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
75	<a href="#">d1e8ga1</a>	Alignment	not modelled	34.1	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
76	<a href="#">d1io1a</a>	Alignment	not modelled	34.0	14	<b>Fold:</b> Phase 1 flagellin <b>Superfamily:</b> Phase 1 flagellin <b>Family:</b> Phase 1 flagellin
77	<a href="#">c3v7eB</a>	Alignment	not modelled	33.9	13	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> ribosome-associated protein l7ae-like; <b>PDBTitle:</b> crystal structure of ybxf bound to the sam-i riboswitch aptamer
78	<a href="#">d1y7ea2</a>	Alignment	not modelled	33.4	11	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
79	<a href="#">c3k8wA</a>	Alignment	not modelled	33.4	21	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellin homolog; <b>PDBTitle:</b> crysatl structure of a bacterial cell-surface flagellin n20c45
						<b>PDB header:</b> structural protein

80	<a href="#">c4cfiA_</a>	Alignment	not modelled	33.4	22	<b>Chain:</b> A: <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> 3d structure of flic from burkholderia pseudomallei
81	<a href="#">c4mcjC_</a>	Alignment	not modelled	33.2	50	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative nucleoside deoxyribosyltransferase2 (bdi_0649) from parabacteroides distasonis atcc 8503 at 2.40 a3 resolution
82	<a href="#">d1iyxa1</a>	Alignment	not modelled	33.1	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
83	<a href="#">c2kc2A_</a>	Alignment	not modelled	32.6	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> taln-1; <b>PDBTitle:</b> nmr structure of the f1 domain (residues 86-202) of the2 talin
84	<a href="#">c3qi7A_</a>	Alignment	not modelled	32.4	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
85	<a href="#">c2nz2A_</a>	Alignment	not modelled	32.2	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
86	<a href="#">d1ni5a1</a>	Alignment	not modelled	32.2	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
87	<a href="#">c6hlwB_</a>	Alignment	not modelled	32.2	33	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
88	<a href="#">c2zbiB_</a>	Alignment	not modelled	32.2	21	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellin homolog; <b>PDBTitle:</b> crystal structure of a bacterial cell-surface flagellin
89	<a href="#">c1iyxA_</a>	Alignment	not modelled	32.0	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of enolase from enterococcus hirae
90	<a href="#">d1xbia1</a>	Alignment	not modelled	31.9	21	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
91	<a href="#">c4r8fB_</a>	Alignment	not modelled	31.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar aminopeptidase 1; <b>PDBTitle:</b> crystal structure of yeast aminopeptidase 1 (ape1)
92	<a href="#">c3zf7g_</a>	Alignment	not modelled	31.5	10	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
93	<a href="#">c2v9yA_</a>	Alignment	not modelled	31.4	7	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> human aminoimidazole ribonucleotide synthetase
94	<a href="#">c3b1sB_</a>	Alignment	not modelled	31.3	15	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar biosynthetic protein flhb; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus
95	<a href="#">c2vt1B_</a>	Alignment	not modelled	31.2	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> surface presentation of antigens protein spa5; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of spa40, the specificity2 switch for the shigella flexneri type iii secretion system
96	<a href="#">d1w85i_</a>	Alignment	not modelled	31.1	10	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
97	<a href="#">d1ujpa_</a>	Alignment	not modelled	31.1	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
98	<a href="#">d2e1fa1</a>	Alignment	not modelled	30.6	13	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> HRDC domain from helicases
99	<a href="#">c5lnkc_</a>	Alignment	not modelled	30.2	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
100	<a href="#">c2lxmB_</a>	Alignment	not modelled	30.0	29	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> charged multivesicular body protein 5; <b>PDBTitle:</b> lip5-chmp5
101	<a href="#">c6hmvB_</a>	Alignment	not modelled	29.9	25	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, lvvy mutant)
102	<a href="#">c3pg8B_</a>	Alignment	not modelled	29.8	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phospho-2-dehydro-3-deoxyheptonate aldolase; <b>PDBTitle:</b> truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
103	<a href="#">c2ijzF_</a>	Alignment	not modelled	29.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> probable m18-family aminopeptidase 2; <b>PDBTitle:</b> crystal structure of aminopeptidase
104	<a href="#">c2goyC_</a>	Alignment	not modelled	29.4	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
105	<a href="#">d1ijzf_</a>	Alignment	not modelled	29.4	17	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like

						<b>Family:</b> L30e/L7ae ribosomal proteins
106	<a href="#">c2eq7C_</a>	Alignment	not modelled	29.3	0	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e2 component; <b>PDBTitle:</b> crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
107	<a href="#">c2e21A_</a>	Alignment	not modelled	29.2	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
108	<a href="#">c3bzaA_</a>	Alignment	not modelled	29.1	12	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
109	<a href="#">d3bzra1</a>	Alignment	not modelled	29.1	12	<b>Fold:</b> EscU C-terminal domain-like <b>Superfamily:</b> EscU C-terminal domain-like <b>Family:</b> EscU C-terminal domain-like
110	<a href="#">c2zycA_</a>	Alignment	not modelled	29.0	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan hydrolase flgj; <b>PDBTitle:</b> crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
111	<a href="#">c6hltD_</a>	Alignment	not modelled	28.9	33	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)
112	<a href="#">d1myla_</a>	Alignment	not modelled	28.8	21	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
113	<a href="#">c1w4kA_</a>	Alignment	not modelled	28.8	5	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase e2; <b>PDBTitle:</b> peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
114	<a href="#">d1llpa_</a>	Alignment	not modelled	28.7	10	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
115	<a href="#">c3dv0L_</a>	Alignment	not modelled	28.5	10	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> I: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
116	<a href="#">d1l5ja3</a>	Alignment	not modelled	28.4	13	<b>Fold:</b> Aconitase iron-sulfur domain <b>Superfamily:</b> Aconitase iron-sulfur domain <b>Family:</b> Aconitase iron-sulfur domain
117	<a href="#">c3iz5H_</a>	Alignment	not modelled	28.4	21	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 60s ribosomal protein l7a (l7ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
118	<a href="#">c2kj9A_</a>	Alignment	not modelled	28.2	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
119	<a href="#">c3c01H_</a>	Alignment	not modelled	28.2	17	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> surface presentation of antigens protein spas; <b>PDBTitle:</b> crystal structural of native spas c-terminal domain
120	<a href="#">c3t4cD_</a>	Alignment	not modelled	28.2	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 1; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria