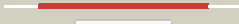


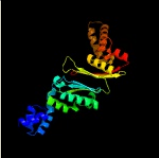
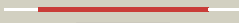


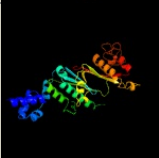














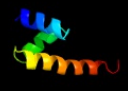

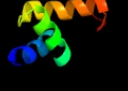
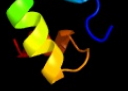



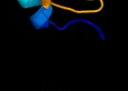
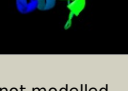


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2889c\_(tsf)\_3198302\_3199117  
 Date Thu Aug 8 16:20:04 BST 2019  
 Unique Job ID 89a9399bdde394b7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1efuB_</a>	 Alignment		100.0	41	<b>PDB header:</b> complex (two elongation factors) <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor ts; <b>PDBTitle:</b> elongation factor complex ef-tu/ef-ts from escherichia coli
2	<a href="#">c3mmpC_</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor tu 2, elongation factor ts; <b>PDBTitle:</b> structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
3	<a href="#">c3agqA_</a>	 Alignment		100.0	42	<b>PDB header:</b> translation,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor ts, elongation factor tu 1, linker, q <b>PDBTitle:</b> structure of viral polymerase form ii
4	<a href="#">c1xb2B_</a>	 Alignment		100.0	28	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor ts, mitochondrial; <b>PDBTitle:</b> crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
5	<a href="#">c1aipG_</a>	 Alignment		100.0	56	<b>PDB header:</b> complex of two elongation factors <b>Chain:</b> G: <b>PDB Molecule:</b> elongation factor ts; <b>PDBTitle:</b> ef-tu ef-ts complex from thermus thermophilus
6	<a href="#">d1efub2</a>	 Alignment		100.0	34	<b>Fold:</b> EF-Ts domain-like <b>Superfamily:</b> Elongation factor Ts (EF-Ts), dimerisation domain <b>Family:</b> Elongation factor Ts (EF-Ts), dimerisation domain
7	<a href="#">d1tfea_</a>	 Alignment		100.0	41	<b>Fold:</b> EF-Ts domain-like <b>Superfamily:</b> Elongation factor Ts (EF-Ts), dimerisation domain <b>Family:</b> Elongation factor Ts (EF-Ts), dimerisation domain
8	<a href="#">d1xb2b2</a>	 Alignment		99.9	31	<b>Fold:</b> EF-Ts domain-like <b>Superfamily:</b> Elongation factor Ts (EF-Ts), dimerisation domain <b>Family:</b> Elongation factor Ts (EF-Ts), dimerisation domain
9	<a href="#">d1efub4</a>	 Alignment		99.9	46	<b>Fold:</b> EF-Ts domain-like <b>Superfamily:</b> Elongation factor Ts (EF-Ts), dimerisation domain <b>Family:</b> Elongation factor Ts (EF-Ts), dimerisation domain
10	<a href="#">d1xb2b3</a>	 Alignment		99.9	26	<b>Fold:</b> EF-Ts domain-like <b>Superfamily:</b> Elongation factor Ts (EF-Ts), dimerisation domain <b>Family:</b> Elongation factor Ts (EF-Ts), dimerisation domain
11	<a href="#">d1efub3</a>	 Alignment		99.8	50	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TS-N domain

12	<a href="#">d1aipc1</a>	Alignment		99.8	45	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TS-N domain
13	<a href="#">d1xb2b1</a>	Alignment		99.8	27	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TS-N domain
14	<a href="#">d2cp9a1</a>	Alignment		99.7	28	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TS-N domain
15	<a href="#">c2mroB_</a>	Alignment		97.0	33	<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)
16	<a href="#">d1ifya_</a>	Alignment		96.8	21	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
17	<a href="#">c1tr8A_</a>	Alignment		96.7	31	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein (mth177); <b>PDBTitle:</b> crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
18	<a href="#">d1wiva_</a>	Alignment		96.5	23	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
19	<a href="#">d1vega_</a>	Alignment		96.4	21	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
20	<a href="#">c2lvaA_</a>	Alignment		96.1	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 28; <b>PDBTitle:</b> nmr solution structure of the n-terminal domain of human usp28,2 northeast structural genomics consortium target ht8470a
21	<a href="#">c2lbcA_</a>	Alignment	not modelled	96.0	16	<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
22	<a href="#">c2daiA_</a>	Alignment	not modelled	96.0	23	<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)
23	<a href="#">c2muxA_</a>	Alignment	not modelled	96.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 25; <b>PDBTitle:</b> sumo2 non-covalently interacts with usp25 and downregulates its2 activity
24	<a href="#">c2dakA_</a>	Alignment	not modelled	95.9	18	<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="#">c2dagA_</a>	Alignment	not modelled	95.2	19	<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)
26	<a href="#">c1wr1B_</a>	Alignment	not modelled	94.9	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein dsk2; <b>PDBTitle:</b> the complex structure of dsk2p uba with ubiquitin
27	<a href="#">d1whca_</a>	Alignment	not modelled	94.7	21	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
28	<a href="#">d1veja1</a>	Alignment	not modelled	94.7	37	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
						<b>PDB header:</b> signaling protein

29	<a href="#">c2jy5A_</a>	Alignment	not modelled	94.7	28	<b>Chain:</b> A: <b>PDB Molecule:</b> ubiquilin-1; <b>PDBTitle:</b> nmr structure of ubiquilin 1 uba domain
30	<a href="#">c2dahA_</a>	Alignment	not modelled	94.6	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquilin-3; <b>PDBTitle:</b> solution structure of the c-terminal uba domain in the2 human ubiquilin 3
31	<a href="#">c2cpwA_</a>	Alignment	not modelled	94.6	32	<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
32	<a href="#">d1oqya1</a>	Alignment	not modelled	94.6	28	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
33	<a href="#">d1wj7a1</a>	Alignment	not modelled	94.6	34	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
34	<a href="#">c2cwbA_</a>	Alignment	not modelled	94.3	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of immunoglobulin g binding protein g <b>PDBTitle:</b> solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
35	<a href="#">d2dnaa1</a>	Alignment	not modelled	94.2	26	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
36	<a href="#">d1veka_</a>	Alignment	not modelled	94.1	22	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
37	<a href="#">c2dnaA_</a>	Alignment	not modelled	94.1	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> unnamed protein product; <b>PDBTitle:</b> solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
38	<a href="#">d2bwba1</a>	Alignment	not modelled	94.0	17	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
39	<a href="#">d2daha1</a>	Alignment	not modelled	93.6	36	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
40	<a href="#">d2cpwa1</a>	Alignment	not modelled	93.5	32	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
41	<a href="#">d2crna1</a>	Alignment	not modelled	93.1	25	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
42	<a href="#">c2crnA_</a>	Alignment	not modelled	92.6	19	<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
43	<a href="#">c2qsfx_</a>	Alignment	not modelled	91.2	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> uv excision repair protein rad23; <b>PDBTitle:</b> crystal structure of the rad4-rad23 complex
44	<a href="#">d1vdla_</a>	Alignment	not modelled	91.1	32	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
45	<a href="#">d1v92a_</a>	Alignment	not modelled	91.0	20	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TAP-C domain-like
46	<a href="#">d2g3qa1</a>	Alignment	not modelled	90.7	28	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
47	<a href="#">d1oaia_</a>	Alignment	not modelled	89.4	9	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TAP-C domain-like
48	<a href="#">c6exzA_</a>	Alignment	not modelled	88.9	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mrna export factor mex67; <b>PDBTitle:</b> crystal structure of mex67 c-term
49	<a href="#">c2damA_</a>	Alignment	not modelled	87.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> etea protein; <b>PDBTitle:</b> solution structure of the novel identified uba-like domain2 in the n-terminal of human etea protein
50	<a href="#">c2jp7A_</a>	Alignment	not modelled	87.4	9	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> mrna export factor mex67; <b>PDBTitle:</b> nmr structure of the mex67 uba domain
51	<a href="#">c2dalA_</a>	Alignment	not modelled	86.6	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein kiaa0794; <b>PDBTitle:</b> solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein
52	<a href="#">c6opfA_</a>	Alignment	not modelled	86.3	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear rna export factor 2, panoramix fusion; <b>PDBTitle:</b> crystal structure of dmnxf2 uba domain fused with panoramix helix
53	<a href="#">d1go5a_</a>	Alignment	not modelled	86.3	11	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> TAP-C domain-like
54	<a href="#">c2do6A_</a>	Alignment	not modelled	86.1	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase cbl-b; <b>PDBTitle:</b> solution structure of rsgi ruh-065, a uba domain from human2 cdna
55	<a href="#">c2d9sA_</a>	Alignment	not modelled	85.6	22	<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
56	<a href="#">c4dbgB_</a>	Alignment	not modelled	84.5	22 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ring finger protein 31; <b>PDBTitle:</b> crystal structure of hoil-1-ubl complexed with a hoip-uba derivative
57	<a href="#">d1oqya2</a>	Alignment	not modelled	84.1	18 <b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
58	<a href="#">c4wp2D_</a>	Alignment	not modelled	84.1	9 <b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative mrna export protein; <b>PDBTitle:</b> chaetomium mex67 uba domain
59	<a href="#">c3bq3A_</a>	Alignment	not modelled	82.3	12 <b>PDB header:</b> cell cycle, ligase <b>Chain:</b> A: <b>PDB Molecule:</b> defective in cullin neddylation protein 1; <b>PDBTitle:</b> crystal structure of s. cerevisiae dcn1
60	<a href="#">c2jnhA_</a>	Alignment	not modelled	79.9	26 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase cbl-b; <b>PDBTitle:</b> solution structure of the uba domain from cbl-b
61	<a href="#">d1dd3a2</a>	Alignment	not modelled	77.1	28 <b>Fold:</b> ClpS-like <b>Superfamily:</b> ClpS-like <b>Family:</b> Ribosomal protein L7/12, C-terminal domain
62	<a href="#">d1ctfa_</a>	Alignment	not modelled	68.8	28 <b>Fold:</b> ClpS-like <b>Superfamily:</b> ClpS-like <b>Family:</b> Ribosomal protein L7/12, C-terminal domain
63	<a href="#">c4ae4B_</a>	Alignment	not modelled	65.9	26 <b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-associated protein 1; <b>PDBTitle:</b> the ubap1 subunit of escrt-i interacts with ubiquitin via a novel2 souba domain
64	<a href="#">d2zjq51</a>	Alignment	not modelled	64.1	26 <b>Fold:</b> ClpS-like <b>Superfamily:</b> ClpS-like <b>Family:</b> Ribosomal protein L7/12, C-terminal domain
65	<a href="#">c2zjq5_</a>	Alignment	not modelled	64.1	26 <b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> interaction of l7 with l11 induced by micrococin binding to the2 deinococcus radiodurans 50s subunit
66	<a href="#">c1giyl_</a>	Alignment	not modelled	62.0	28 <b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> crystal structure of the ribosome at 5.5 a resolution. this2 file, 1giy, contains the 50s ribosome subunit. the 30s3 ribosome subunit, three trna, and mrna molecules are in the4 file 1gix
67	<a href="#">d1z96a1</a>	Alignment	not modelled	60.5	36 <b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
68	<a href="#">d1dv0a_</a>	Alignment	not modelled	56.1	16 <b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
69	<a href="#">d1wjia_</a>	Alignment	not modelled	52.6	28 <b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
70	<a href="#">c6deeA_</a>	Alignment	not modelled	49.4	22 <b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> nck-interacting protein with sh3 domain; <b>PDBTitle:</b> crystal structure of the c-terminus of homo sapiens spin90 (sh3-2 protein interacting with nck), residues 306-722
71	<a href="#">c3k6gA_</a>	Alignment	not modelled	47.9	14 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> telomeric repeat-binding factor 2-interacting protein 1; <b>PDBTitle:</b> crystal structure of rap1 and trf2 complex
72	<a href="#">c2ftcF_</a>	Alignment	not modelled	37.8	14 <b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 39s ribosomal protein l12, mitochondrial; <b>PDBTitle:</b> structural model for the large subunit of the mammalian mitochondrial2 ribosome
73	<a href="#">d1wglA_</a>	Alignment	not modelled	35.1	19 <b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> CUE domain
74	<a href="#">c5nnpG_</a>	Alignment	not modelled	34.1	32 <b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of naa15/naa10 bound to hypk-thb
75	<a href="#">c5uoiA_</a>	Alignment	not modelled	32.0	18 <b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> hhh_rd1_0142; <b>PDBTitle:</b> solution structure of the de novo mini protein hhh_rd1_0142
76	<a href="#">c2l4fA_</a>	Alignment	not modelled	30.0	12 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> defective in cullin neddylation protein 1; <b>PDBTitle:</b> nmr structure of the uba domain of s. cerevisiae dcn1 bound to2 ubiquitin
77	<a href="#">d2qswa1</a>	Alignment	not modelled	29.0	31 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
78	<a href="#">d1fipa_</a>	Alignment	not modelled	27.1	17 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
79	<a href="#">c2dhyA_</a>	Alignment	not modelled	26.6	11 <b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cue domain-containing protein 1; <b>PDBTitle:</b> solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
80	<a href="#">d3dhxa1</a>	Alignment	not modelled	23.8	23 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
81	<a href="#">c2gya3_</a>	Alignment	not modelled	23.2	24 <b>PDB header:</b> ribosome <b>Chain:</b> 3: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> structure of the 50s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056

82	<a href="#">c2ndpA_</a>	Alignment	not modelled	22.1	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone-like dna-binding superfamily protein; <b>PDBTitle:</b> structure of dna-binding hu protein from micoplasma mycoplasma2 gallisepticum
83	<a href="#">c3cz6A_</a>	Alignment	not modelled	21.2	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein rap1; <b>PDBTitle:</b> crystal structure of the rap1 c-terminus
84	<a href="#">c4xhtD_</a>	Alignment	not modelled	20.8	24	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> protein timeless homolog; <b>PDBTitle:</b> crystal structure of timeless_pab domain native form
85	<a href="#">c2m8gX_</a>	Alignment	not modelled	20.5	28	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> structure, function, and tethering of dna-binding domains in 542 transcriptional activators
86	<a href="#">c3fmyA_</a>	Alignment	not modelled	19.5	4	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
87	<a href="#">c5vnyA_</a>	Alignment	not modelled	18.8	21	<b>PDB header:</b> endocytosis, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lethal (2) giant discs 1, isoform b; <b>PDBTitle:</b> crystal structure of dm14-3 domain of Igd
88	<a href="#">c4kdhe_</a>	Alignment	not modelled	16.8	35	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 50s ribosomal protein l3; <b>PDBTitle:</b> 70s ribosome translocation intermediate fa-4.2a containing elongation2 factor efg/fusidic acid/gdp, mrna, and trna bound in the pe*/e state.3 this entry contains the 50s ribosomal subunit a. the 30s subunit a4 can be found in 4kdg. molecule b in the same asymmetric unit is5 deposited as 4kdj (30s) and 4kdk (50s).
89	<a href="#">c2kjqA_</a>	Alignment	not modelled	16.4	28	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> archaeal protein sso6904; <b>PDBTitle:</b> solution structure of an archaeal protein sso6904 from2 hyperthermophilic sulfolobus solfataricus
90	<a href="#">d2cosa1</a>	Alignment	not modelled	16.2	26	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
91	<a href="#">c4q2iA_</a>	Alignment	not modelled	15.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein satb1; <b>PDBTitle:</b> a novel structure-based mechanism for dna-binding of satb1
92	<a href="#">c3c4mC_</a>	Alignment	not modelled	15.7	71	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> parathyroid hormone; <b>PDBTitle:</b> structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
93	<a href="#">c3c4mD_</a>	Alignment	not modelled	15.7	71	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> parathyroid hormone; <b>PDBTitle:</b> structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
94	<a href="#">d1zhva2</a>	Alignment	not modelled	15.4	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Atu0741-like
95	<a href="#">d1etob_</a>	Alignment	not modelled	15.2	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
96	<a href="#">c3k1sE_</a>	Alignment	not modelled	15.1	26	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> pts system, cellobiose-specific iia component; <b>PDBTitle:</b> crystal structure of the pts cellobiose specific enzyme iia from2 bacillus anthracis
97	<a href="#">d2qrra1</a>	Alignment	not modelled	14.9	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
98	<a href="#">d1hsta_</a>	Alignment	not modelled	14.9	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Linker histone H1/H5
99	<a href="#">c4kbue_</a>	Alignment	not modelled	14.6	35	<b>PDB header:</b> ribosome/antibiotic <b>Chain:</b> E: <b>PDB Molecule:</b> 50s ribosomal protein l3; <b>PDBTitle:</b> 70s ribosome translocation intermediate gdpnp-ii containing elongation2 factor efg/gdpnp, mrna, and trna bound in the pe*/e state. this entry3 contains 50s ribosomal subunit a. the full asymmetric unit also4 contains pdb entries 4kbt (30s subunit a), 4kbv (30s subunit b), and5 4kbw (50s subunit b).