








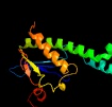



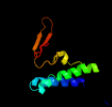









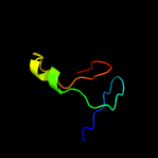
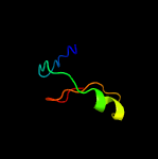
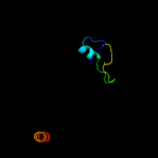
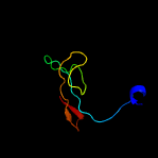
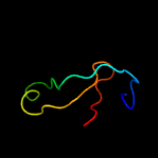





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0922_(-)_1027689_1029341
Date	Fri Jul 26 01:50:51 BST 2019
Unique Job ID	1314fb63c6561750

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6e7aY_</a>	 Alignment		96.5	24	<b>PDB header:</b> dna binding protein/dna/rna <b>Chain:</b> Y; <b>PDB Molecule:</b> casx; <b>PDBTitle:</b> casx-grna-dna(30bp) state ii
2	<a href="#">c5id6A_</a>	 Alignment		95.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cpf1; <b>PDBTitle:</b> structure of cpf1/rna complex
3	<a href="#">c5wtiZ_</a>	 Alignment		94.8	17	<b>PDB header:</b> hydrolase/dna/rna <b>Chain:</b> Z; <b>PDB Molecule:</b> crispr-associated protein; <b>PDBTitle:</b> crystal structure of the crispr-associated protein in complex with2 crrna and dna
4	<a href="#">c5wqeA_</a>	 Alignment		94.5	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> crispr-associated endonuclease c2c1; <b>PDBTitle:</b> crystal structure of alicyclobacillus acidoterrestris c2c1 in complex2 with single-guide rna at 3.1 angstrom resolution
5	<a href="#">c6iv6A_</a>	 Alignment		94.2	23	<b>PDB header:</b> immune system/rna <b>Chain:</b> A; <b>PDB Molecule:</b> nuclease; <b>PDBTitle:</b> cryo-em structure of acrva5-acetylated mbcas12a in complex with crrna
6	<a href="#">c1yuzB_</a>	 Alignment		91.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
7	<a href="#">c6k0bH_</a>	 Alignment		91.4	19	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> H; <b>PDB Molecule:</b> ribonuclease p protein component 4; <b>PDBTitle:</b> cryo-em structure of archaeal ribonuclease p with mature trna
8	<a href="#">c2gb5B_</a>	 Alignment		91.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> nadh pyrophosphatase; <b>PDBTitle:</b> crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
9	<a href="#">c5b43A_</a>	 Alignment		90.1	18	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> A; <b>PDB Molecule:</b> crispr-associated endonuclease cpf1; <b>PDBTitle:</b> crystal structure of acidaminococcus sp. cpf1 in complex with crrna2 and target dna
10	<a href="#">c2zaeB_</a>	 Alignment		86.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ribonuclease p protein component 4; <b>PDBTitle:</b> crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
11	<a href="#">c5ijlA_</a>	 Alignment		84.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dna polymerase ii large subunit; <b>PDBTitle:</b> d-family dna polymerase - dp2 subunit (catalytic subunit)

12	<a href="#">c6f42V_</a>	Alignment		83.9	16	<b>PDB header:</b> transcription <b>Chain:</b> V: <b>PDB Molecule:</b> transcription factor iiib 70 kda subunit; <b>PDBTitle:</b> rna polymerase iii closed complex cc1.
13	<a href="#">c1hk8A_</a>	Alignment		83.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic ribonucleotide-triphosphate reductase; <b>PDBTitle:</b> structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dntp
14	<a href="#">d1hk8a_</a>	Alignment		83.4	23	<b>Fold:</b> PFL-like glycol radical enzymes <b>Superfamily:</b> PFL-like glycol radical enzymes <b>Family:</b> Class III anaerobic ribonucleotide reductase NRDD subunit
15	<a href="#">c5fz5M_</a>	Alignment		82.7	21	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> transcription initiation complex structures elucidate dna opening (cc)
16	<a href="#">c6hmsB_</a>	Alignment		82.1	14	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase ii large subunit,dna polymerase ii large <b>PDBTitle:</b> cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
17	<a href="#">c6cnbR_</a>	Alignment		80.8	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> R: <b>PDB Molecule:</b> transcription factor iiib 70 kda subunit,tata-box-binding <b>PDBTitle:</b> yeast rna polymerase iii initial transcribing complex
18	<a href="#">c4u3eA_</a>	Alignment		79.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside triphosphate reductase; <b>PDBTitle:</b> anaerobic ribonucleotide reductase
19	<a href="#">c3k7aM_</a>	Alignment		79.5	12	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> crystal structure of an rna polymerase ii-tfiib complex
20	<a href="#">c5mgaA_</a>	Alignment		78.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cpf1; <b>PDBTitle:</b> structure of the cpf1 endonuclease r-loop complex after dna cleavage
21	<a href="#">c4qiWp_</a>	Alignment	not modelled	78.3	15	<b>PDB header:</b> transcription <b>Chain:</b> P: <b>PDB Molecule:</b> dna-directed rna polymerase subunit p; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
22	<a href="#">d1pfta_</a>	Alignment	not modelled	78.2	16	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
23	<a href="#">c5iy9M_</a>	Alignment	not modelled	78.1	17	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> human holo-pic in the initial transcribing state (no iis)
24	<a href="#">c3ky9B_</a>	Alignment	not modelled	77.3	11	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> autoinhibited vav1
25	<a href="#">c1nnjA_</a>	Alignment	not modelled	77.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
26	<a href="#">c2vrwB_</a>	Alignment	not modelled	77.2	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> critical structural role for the ph and c1 domains of the2 vav1 exchange factor
27	<a href="#">c2lcqA_</a>	Alignment	not modelled	75.8	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative toxin vapc6; <b>PDBTitle:</b> solution structure of the endonuclease nob1 from p.horikoshii
28	<a href="#">c5iy9Q_</a>	Alignment	not modelled	75.5	18	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> Q: <b>PDB Molecule:</b> general transcription factor iie subunit 1; <b>PDBTitle:</b> human holo-pic in the initial transcribing state (no iis)
						<b>PDB header:</b> membrane protein

29	<a href="#">c1z2qA_</a>	Alignment	not modelled	74.0	22	<b>Chain:</b> A: <b>PDB Molecule:</b> lm5-1; <b>PDBTitle:</b> high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major
30	<a href="#">c3cngC_</a>	Alignment	not modelled	73.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from nitrosomonas europaea
31	<a href="#">c4v1oM_</a>	Alignment	not modelled	73.3	13	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> architecture of the rna polymerase ii-mediator core transcription2 initiation complex
32	<a href="#">c6hv8A_</a>	Alignment	not modelled	71.7	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase epsilon catalytic subunit a; <b>PDBTitle:</b> cryo-em structure of s. cerevisiae polymerase epsilon delcatat mutant
33	<a href="#">c5m45L_</a>	Alignment	not modelled	70.4	31	<b>PDB header:</b> ligase <b>Chain:</b> I: <b>PDB Molecule:</b> acetone carboxylase gamma subunit; <b>PDBTitle:</b> structure of acetone carboxylase purified from xanthobacter2 autotrophicus
34	<a href="#">c2f9iD_</a>	Alignment	not modelled	70.1	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
35	<a href="#">c1k82D_</a>	Alignment	not modelled	69.9	9	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
36	<a href="#">c6gymW_</a>	Alignment	not modelled	69.9	16	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha, <b>PDBTitle:</b> structure of a yeast closed complex with distorted dna (ccd1st)
37	<a href="#">c4bpo9_</a>	Alignment	not modelled	69.6	22	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> 40s ribosomal protein rps31e; <b>PDBTitle:</b> the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 3
38	<a href="#">c3ir9A_</a>	Alignment	not modelled	69.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> peptide chain release factor subunit 1; <b>PDBTitle:</b> c-terminal domain of peptide chain release factor from methanosarcina2 mazei.
39	<a href="#">d2ct1a1</a>	Alignment	not modelled	69.2	27	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
40	<a href="#">d1dl6a_</a>	Alignment	not modelled	69.1	17	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
41	<a href="#">c3t7IA_</a>	Alignment	not modelled	69.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 16; <b>PDBTitle:</b> crystal structure of the fyve domain of endofin (zfyve16) at 1.1a2 resolution
42	<a href="#">c2ba1B_</a>	Alignment	not modelled	68.4	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> archaeal exosome rna binding protein csl4; <b>PDBTitle:</b> archaeal exosome core
43	<a href="#">c3j3v0_</a>	Alignment	not modelled	68.1	13	<b>PDB header:</b> ribosome <b>Chain:</b> 0: <b>PDB Molecule:</b> 50s ribosomal protein l32; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
44	<a href="#">d2j0151</a>	Alignment	not modelled	67.4	17	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
45	<a href="#">c3bjjA_</a>	Alignment	not modelled	67.3	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
46	<a href="#">c5fywW_</a>	Alignment	not modelled	67.3	15	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha; <b>PDBTitle:</b> transcription initiation complex structures elucidate dna opening (oc)
47	<a href="#">c1dvpA_</a>	Alignment	not modelled	67.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine <b>PDBTitle:</b> crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
48	<a href="#">c5vbnB_</a>	Alignment	not modelled	67.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase epsilon catalytic subunit a; <b>PDBTitle:</b> crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit
49	<a href="#">c5oqjW_</a>	Alignment	not modelled	66.5	16	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih
50	<a href="#">c3na7A_</a>	Alignment	not modelled	66.3	18	<b>PDB header:</b> gene regulation, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hp0958; <b>PDBTitle:</b> 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
51	<a href="#">d2f9yb1</a>	Alignment	not modelled	66.0	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
52	<a href="#">c2f9yB_</a>	Alignment	not modelled	66.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> the crystal structure of the carboxyltransferase subunit of

						acc from2 escherichia coli <b>PDB header:</b> hydrolase/transferase <b>Chain:</b> I: <b>PDB Molecule:</b> 3'-5' exoribonuclease csl4 homolog; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
53	<a href="#">c2nn6I_</a>	Alignment	not modelled	65.8	19	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9; <b>PDBTitle:</b> crystal structure of campylobacter jejuni cas9 in complex with sgrna2 and target dna (agaaca pam)
54	<a href="#">c5x2hA_</a>	Alignment	not modelled	65.7	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> churchill protein; <b>PDBTitle:</b> embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-exposed beta-sheet and zinc binuclear cluster
55	<a href="#">c2joxA_</a>	Alignment	not modelled	65.4	19	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> acetophenone carboxylase beta subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
56	<a href="#">c5I9wC_</a>	Alignment	not modelled	65.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical 30.2 kd protein c25g10.02 in <b>PDBTitle:</b> crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
57	<a href="#">c1kcfB_</a>	Alignment	not modelled	64.8	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease viii; <b>PDBTitle:</b> crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
58	<a href="#">c2opfA_</a>	Alignment	not modelled	64.2	12	<b>PDB header:</b> transcription <b>Chain:</b> W: <b>PDB Molecule:</b> transcription factor tfiie subunit; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
59	<a href="#">c5oqmW_</a>	Alignment	not modelled	64.0	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygjt/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygjt/b3021)
60	<a href="#">c3gn5B_</a>	Alignment	not modelled	63.7	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mutm (fpg) protein; <b>PDBTitle:</b> crystal structure of mutm (fpg) protein from thermus thermophilus hb8
61	<a href="#">c1ee8A_</a>	Alignment	not modelled	63.5	12	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> crystal structure of rna polymerase ii in complex with tfiib
62	<a href="#">c3k1fM_</a>	Alignment	not modelled	63.2	13	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9; <b>PDBTitle:</b> crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)
63	<a href="#">c5axwA_</a>	Alignment	not modelled	63.0	18	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
64	<a href="#">d6rxna_</a>	Alignment	not modelled	62.9	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> Q: <b>PDB Molecule:</b> general transcription factor iie subunit 1; <b>PDBTitle:</b> human holo-pic in the closed state
65	<a href="#">c6o9lQ_</a>	Alignment	not modelled	62.9	18	<b>PDB header:</b> transferase/transcription/dna-rna hybrid <b>Chain:</b> S: <b>PDB Molecule:</b> transcription elongation factor s-ii; <b>PDBTitle:</b> rna polymerase ii-tfiis-dna/rna complex
66	<a href="#">c1y1yS_</a>	Alignment	not modelled	62.7	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
67	<a href="#">d1x3za1</a>	Alignment	not modelled	62.5	11	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> rubrerythrin
68	<a href="#">c1dvvA_</a>	Alignment	not modelled	62.1	23	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> FYVE, a phosphatidylinositol-3-phosphate binding domain
69	<a href="#">d1joca1</a>	Alignment	not modelled	61.5	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> pf1283- rubrerythrin from pyrococcus furiosus iron bound form
70	<a href="#">c2hr5B_</a>	Alignment	not modelled	60.8	33	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosidase; <b>PDBTitle:</b> catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
71	<a href="#">c2f5qA_</a>	Alignment	not modelled	60.7	16	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L32p
72	<a href="#">d2zjrz1</a>	Alignment	not modelled	60.7	27	<b>PDB header:</b> transferase/transcription <b>Chain:</b> S: <b>PDB Molecule:</b> transcription elongation factor s-ii; <b>PDBTitle:</b> rna polymerase ii-tfiis complex
73	<a href="#">c1pqvS_</a>	Alignment	not modelled	60.2	14	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> translation initiation factor 2 beta subunit; <b>PDBTitle:</b> crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
74	<a href="#">c2dcuB_</a>	Alignment	not modelled	59.8	33	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state r
75	<a href="#">c6g5iy_</a>	Alignment	not modelled	59.5	35	<b>PDB header:</b> translation <b>Chain:</b> P: <b>PDB Molecule:</b> eukaryotic translation initiation factor 2 subunit beta; <b>PDBTitle:</b> structure of eif2b-eif2 (phosphorylated at ser51) complex (model b)
76	<a href="#">c6qq3P_</a>	Alignment	not modelled	58.8	19	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa12; <b>PDBTitle:</b> structure of rna polymerase i at 2.8 a resolution
77	<a href="#">c4c2mX_</a>	Alignment	not modelled	58.7	11	<b>Fold:</b> Rubredoxin-like

78	<a href="#">d1twfi2</a>	Alignment	not modelled	57.9	14	<b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
79	<a href="#">c2yqmA_</a>	Alignment	not modelled	57.8	11	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> run and fyve domain-containing protein 1; <b>PDBTitle:</b> solution structure of the fyve domain in zinc finger fyve2 domain-containing protein 12
80	<a href="#">d1dvpa2</a>	Alignment	not modelled	57.7	20	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> FYVE, a phosphatidylinositol-3-phosphate binding domain
81	<a href="#">c3a44D_</a>	Alignment	not modelled	57.4	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> hydrogenase nickel incorporation protein hypa; <b>PDBTitle:</b> crystal structure of hypa in the dimeric form
82	<a href="#">c2xzn9_</a>	Alignment	not modelled	56.7	16	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> rps31e; <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
83	<a href="#">d2nn6i1</a>	Alignment	not modelled	56.0	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
84	<a href="#">c5iyuU_</a>	Alignment	not modelled	55.7	14	<b>PDB header:</b> transcription, transferase/dna <b>Chain:</b> U: <b>PDB Molecule:</b> transcription elongation factor a protein 1; <b>PDBTitle:</b> human core-pic in the initial transcribing state
85	<a href="#">c1x4uA_</a>	Alignment	not modelled	55.4	18	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger, fyve domain containing 27 isoform b; <b>PDBTitle:</b> solution structure of the fyve domain from human fyve2 domain containing 27 isoform b protein
86	<a href="#">d2fiya1</a>	Alignment	not modelled	55.4	12	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
87	<a href="#">c3izrm_</a>	Alignment	not modelled	54.8	19	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l23 (l14p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
88	<a href="#">c3cw2M_</a>	Alignment	not modelled	54.6	19	<b>PDB header:</b> translation <b>Chain:</b> M: <b>PDB Molecule:</b> translation initiation factor 2 subunit beta; <b>PDBTitle:</b> crystal structure of the intact archaeal translation initiation factor2 2 from sulfobolus solfataricus .
89	<a href="#">c2qa4Z_</a>	Alignment	not modelled	54.2	11	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae; <b>PDBTitle:</b> a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
90	<a href="#">c2xzm9_</a>	Alignment	not modelled	54.0	16	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> rps31e; <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 1
91	<a href="#">d1kcfaz</a>	Alignment	not modelled	53.9	27	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Mitochondrial resolvase ydc2 catalytic domain
92	<a href="#">c4b6ap_</a>	Alignment	not modelled	53.4	15	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17-a; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
93	<a href="#">d1yuza2</a>	Alignment	not modelled	53.1	43	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
94	<a href="#">c2m4yA_</a>	Alignment	not modelled	52.4	17	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> rubredoxin type protein from mycobacterium ulcerans
95	<a href="#">c3wwnB_</a>	Alignment	not modelled	52.2	17	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orff; <b>PDBTitle:</b> crystal structure of lysz from thermus thermophilus complex with lysw
96	<a href="#">d1k81a_</a>	Alignment	not modelled	52.1	30	<b>Fold:</b> Zinc-binding domain of translation initiation factor 2 beta <b>Superfamily:</b> Zinc-binding domain of translation initiation factor 2 beta <b>Family:</b> Zinc-binding domain of translation initiation factor 2 beta
97	<a href="#">d1ffkw_</a>	Alignment	not modelled	51.8	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
98	<a href="#">c1s1i9_</a>	Alignment	not modelled	51.8	15	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l43; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
99	<a href="#">c2aklA_</a>	Alignment	not modelled	51.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phna-like protein pa0128; <b>PDBTitle:</b> solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
100	<a href="#">d1vqoz1</a>	Alignment	not modelled	50.6	11	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
101	<a href="#">c2qkdA_</a>	Alignment	not modelled	50.5	18	<b>PDB header:</b> signaling protein, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein zpr1; <b>PDBTitle:</b> crystal structure of tandem zpr1 domains
102	<a href="#">c5fmfR_</a>	Alignment	not modelled	50.5	16	<b>PDB header:</b> transcription <b>Chain:</b> R: <b>PDB Molecule:</b> transcription initiation factor iie subunit alpha, tfa1; <b>PDBTitle:</b> the p-lobe of rna polymerase ii pre-initiation complex
103	<a href="#">d1x68a2</a>	Alignment	not modelled	50.3	32	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain)

						<b>Family:</b> LIM domain
104	<a href="#">c5xonU_</a>	Alignment	not modelled	50.0	11	<b>PDB header:</b> transcription/rna <b>Chain:</b> U: <b>PDB Molecule:</b> general transcription elongation factor tfiis; <b>PDBTitle:</b> rna polymerase ii elongation complex bound with spt4/5 and tfiis
105	<a href="#">c1neeA_</a>	Alignment	not modelled	49.9	37	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> probable translation initiation factor 2 beta <b>PDBTitle:</b> structure of archaeal translation factor aif2beta from2 methanobacterium thermoautotrophicum
106	<a href="#">c3zyqA_</a>	Alignment	not modelled	49.7	14	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine kinase <b>PDBTitle:</b> crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
107	<a href="#">c5nfvA_</a>	Alignment	not modelled	49.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cpf1; <b>PDBTitle:</b> crystal structure of catalytically inactive fncas12 mutant bound to an2 r-loop structure containing a pre-crrna mimic and full-length dna3 target
108	<a href="#">c3jyw9_</a>	Alignment	not modelled	49.4	15	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l43; <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
109	<a href="#">c4zlhB_</a>	Alignment	not modelled	49.1	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide assembly protein b; <b>PDBTitle:</b> structure of the lapb cytoplasmic domain at 2 angstroms
110	<a href="#">c3j39p_</a>	Alignment	not modelled	49.0	19	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
111	<a href="#">c3j21i_</a>	Alignment	not modelled	49.0	15	<b>PDB header:</b> ribosome <b>Chain:</b> l: <b>PDB Molecule:</b> 50s ribosomal protein l13p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
112	<a href="#">c2kdxA_</a>	Alignment	not modelled	48.7	14	<b>PDB header:</b> metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein <b>PDBTitle:</b> solution structure of hypa protein
113	<a href="#">d1jj2y_</a>	Alignment	not modelled	48.5	15	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
114	<a href="#">d1lkoa2</a>	Alignment	not modelled	48.2	21	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
115	<a href="#">c3cc4Z_</a>	Alignment	not modelled	48.1	11	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae; <b>PDBTitle:</b> co-crystal structure of anisomycin bound to the 50s ribosomal subunit
116	<a href="#">c3zf7o_</a>	Alignment	not modelled	47.6	11	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l13a, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
117	<a href="#">c2kaeA_</a>	Alignment	not modelled	47.6	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> gata-type transcription factor; <b>PDBTitle:</b> data-driven model of med1:dna complex
118	<a href="#">c2zkrz_</a>	Alignment	not modelled	47.6	22	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> Z: <b>PDB Molecule:</b> e site t-rna; <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
119	<a href="#">d1vfyA_</a>	Alignment	not modelled	46.9	27	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> FYVE, a phosphatidylinositol-3-phosphate binding domain
120	<a href="#">c3twkB_</a>	Alignment	not modelled	46.9	5	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase 1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana fpg