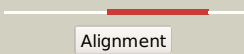

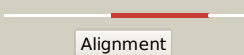

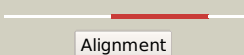

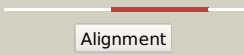
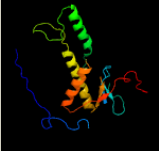
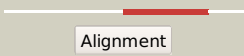
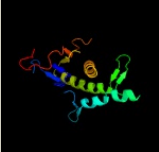
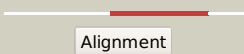

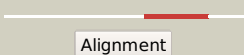

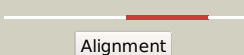

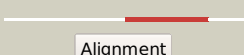


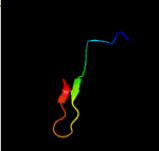

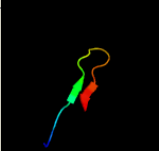


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3827c_(-)_4301741_4302967
Date	Fri Aug 9 18:20:53 BST 2019
Unique Job ID	e49c3979e1c046b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6e7aY_	 Alignment		98.5	21	PDB header: dna binding protein/dna/rna Chain: Y; PDB Molecule: casx; PDBTitle: casx-grna-dna(30bp) state ii
2	c5id6A_	 Alignment		97.9	16	PDB header: hydrolase Chain: A; PDB Molecule: cpf1; PDBTitle: structure of cpf1/rna complex
3	c6iv6A_	 Alignment		97.7	19	PDB header: immune system/rna Chain: A; PDB Molecule: nuclease; PDBTitle: cryo-em structure of acrva5-acetylated mbcas12a in complex with crrna
4	c5b43A_	 Alignment		97.0	20	PDB header: hydrolase/rna/dna Chain: A; PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: crystal structure of acidaminococcus sp. cpf1 in complex with crrna2 and target dna
5	c5nfvA_	 Alignment		96.9	17	PDB header: hydrolase Chain: A; PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: crystal structure of catalytically inactive fncas12 mutant bound to an2 r-loop structure containing a pre-crrna mimic and full-length dna3 target
6	c5mgaA_	 Alignment		96.8	17	PDB header: hydrolase Chain: A; PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: structure of the cpf1 endonuclease r-loop complex after dna cleavage
7	c5wtiZ_	 Alignment		94.6	17	PDB header: hydrolase/dna/rna Chain: Z; PDB Molecule: crispr-associated protein; PDBTitle: crystal structure of the crispr-associated protein in complex with2 crrna and dna
8	d1hjra_	 Alignment		94.1	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
9	d1iv0a_	 Alignment		91.2	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
10	c1kcfB_	 Alignment		89.2	14	PDB header: hydrolase Chain: B; PDB Molecule: hypothetical 30.2 kd protein c25g10.02 in PDBTitle: crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
11	d1kcfA2	 Alignment		86.1	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain

12	c4u3eA_	Alignment		85.5	9	PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
13	d1hk8a_	Alignment		84.4	7	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
14	c1hk8A_	Alignment		84.4	7	PDB header: oxidoreductase Chain: A; PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dgtp
15	c5ijlA_	Alignment		83.7	17	PDB header: transferase Chain: A; PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
16	c4ep5A_	Alignment		83.2	14	PDB header: hydrolase Chain: A; PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure
17	c5wqeA_	Alignment		82.3	15	PDB header: rna binding protein Chain: A; PDB Molecule: crispr-associated endonuclease c2c1; PDBTitle: crystal structure of alicyclobacillus acidoterrestris c2c1 in complex2 with single-guide rna at 3.1 angstrom resolution
18	c5u31A_	Alignment		79.9	16	PDB header: hydrolase/dna Chain: A; PDB Molecule: crispr-associated endonuclease c2c1; PDBTitle: crystal structure of aacc2c1-sgrna-8mer substrate dna ternary complex
19	c2qa4Z_	Alignment		79.6	10	PDB header: ribosome Chain: Z; PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
20	c3j21i_	Alignment		79.5	27	PDB header: ribosome Chain: l; PDB Molecule: 50s ribosomal protein l13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
21	c4b6ap_	Alignment	not modelled	79.2	7	PDB header: ribosome Chain: P; PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
22	c3j39p_	Alignment	not modelled	78.8	13	PDB header: ribosome Chain: P; PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
23	c3izrm_	Alignment	not modelled	78.7	17	PDB header: ribosome Chain: M; PDB Molecule: 60s ribosomal protein l23 (l14p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
24	d1vqoz1	Alignment	not modelled	78.2	10	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
25	c3cc4Z_	Alignment	not modelled	77.8	17	PDB header: ribosome Chain: Z; PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
26	c2zkrz_	Alignment	not modelled	77.3	13	PDB header: ribosomal protein/rna Chain: Z; PDB Molecule: e site t-rna; PDBTitle: 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
27	d1ffkw_	Alignment	not modelled	77.1	20	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
28	c3zf7o_	Alignment	not modelled	76.9	13	PDB header: ribosome Chain: O; PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

29	c1yshD	 Alignment	not modelled	76.8	17	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
30	c1s1i9	 Alignment	not modelled	76.0	7	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: 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.
31	d1jj2y	 Alignment	not modelled	76.0	13	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
32	c6hmsB	 Alignment	not modelled	75.1	14	PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna polymerase ii large PDBTitle: cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
33	c5fmrR	 Alignment	not modelled	71.3	0	PDB header: transcription Chain: R: PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
34	c3jyw9	 Alignment	not modelled	70.9	13	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
35	c4a17Y	 Alignment	not modelled	70.0	23	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
36	d1nu0a	 Alignment	not modelled	69.9	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
37	c5iy9Q	 Alignment	not modelled	69.8	15	PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)
38	c2gb5B	 Alignment	not modelled	69.3	4	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
39	c2aklA	 Alignment	not modelled	69.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
40	c5fywW	 Alignment	not modelled	69.0	0	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
41	c2lqA	 Alignment	not modelled	68.9	12	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
42	d2akla2	 Alignment	not modelled	67.5	20	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
43	c5oqjW	 Alignment	not modelled	66.7	0	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
44	c4zlhB	 Alignment	not modelled	66.6	19	PDB header: metal binding protein Chain: B: PDB Molecule: lipopolysaccharide assembly protein b; PDBTitle: structure of the lapb cytoplasmic domain at 2 angstroms
45	c5oqmW	 Alignment	not modelled	65.9	4	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
46	d1vhxa	 Alignment	not modelled	64.8	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
47	d2j0151	 Alignment	not modelled	64.5	10	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
48	c6gymW	 Alignment	not modelled	64.0	0	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccd1st)
49	c3zyqA	 Alignment	not modelled	62.7	7	PDB header: signaling Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
50	c5axwA	 Alignment	not modelled	60.5	17	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)
51	d1twfi2	 Alignment	not modelled	60.1	4	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
52	c3ky9B	 Alignment	not modelled	59.3	10	PDB header: apoptosis Chain: B: PDB Molecule: proto-oncogene vav; PDBTitle: autoinhibited vav1

53	d1pfta_	Alignment	not modelled	58.5	18	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
54	c3na7A_	Alignment	not modelled	58.3	14	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
55	c2qkdA_	Alignment	not modelled	56.7	9	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
56	c6o9lQ_	Alignment	not modelled	56.2	5	PDB header: transcription/dna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state
57	c1yuzB_	Alignment	not modelled	55.3	7	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
58	c5x2hA_	Alignment	not modelled	55.0	17	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of campylobacter jejuni cas9 in complex with sgna2 and target dna (agaaca pam)
59	c1i3ql_	Alignment	not modelled	54.9	4	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii 14.2kd PDBTitle: rna polymerase ii crystal form i at 3.1 a resolution
60	d3bzka5	Alignment	not modelled	53.5	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
61	c4iloA_	Alignment	not modelled	53.2	9	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
62	d2zjrz1	Alignment	not modelled	53.1	10	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
63	c3j3v0_	Alignment	not modelled	53.1	15	PDB header: ribosome Chain: 0: PDB Molecule: 50s ribosomal protein l32; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
64	c1xawA_	Alignment	not modelled	52.7	18	PDB header: cell adhesion Chain: A: PDB Molecule: occludin; PDBTitle: crystal structure of the cytoplasmic distal c-terminal2 domain of occludin
65	c1wpaA_	Alignment	not modelled	51.8	18	PDB header: cell adhesion Chain: A: PDB Molecule: occludin; PDBTitle: 1.5 angstrom crystal structure of human occludin fragment 413-522
66	d1qypa_	Alignment	not modelled	51.8	15	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
67	d2gnra1	Alignment	not modelled	51.0	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: SSO2064-like
68	c1dvpA_	Alignment	not modelled	49.8	8	PDB header: transferase Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine PDBTitle: crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
69	c3h0gl_	Alignment	not modelled	49.3	13	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
70	c4a18A_	Alignment	not modelled	48.7	30	PDB header: ribosome Chain: A: PDB Molecule: ribosomal protein l37; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
71	c3j3bj_	Alignment	not modelled	48.4	32	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l11; PDBTitle: structure of the human 60s ribosomal proteins
72	c3u5ij_	Alignment	not modelled	47.8	26	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l11-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b
73	c4gopC_	Alignment	not modelled	47.7	8	PDB header: dna binding protein/dna Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
74	d1bupa1	Alignment	not modelled	47.6	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
75	c5xonU_	Alignment	not modelled	47.4	10	PDB header: transcription/rna Chain: U: PDB Molecule: general transcription elongation factor tfiis; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
76	c4c2mX_	Alignment	not modelled	47.2	11	PDB header: transcription Chain: X: PDB Molecule: dna-directed rna polymerase i subunit rpa12; PDBTitle: structure of rna polymerase i at 2.8 a resolution
77	d1h7va_	Alignment	not modelled	47.1	17	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
78	c2hr5B_	Alignment	not modelled	47.0	10	PDB header: metal binding protein Chain: B: PDB Molecule: ruberythrin;

78	c2m3B	Alignment	not modelled	47.0	19	PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
79	d1d6a	Alignment	not modelled	47.0	5	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
80	c5g0fA	Alignment	not modelled	46.5	4	PDB header: cell cycle Chain: A: PDB Molecule: hdac6; PDBTitle: crystal structure of danio rerio hdac6 znf-ubp domain
81	d1dkgd1	Alignment	not modelled	46.0	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
82	c3c5kA	Alignment	not modelled	45.9	5	PDB header: hydrolase Chain: A: PDB Molecule: histone deacetylase 6; PDBTitle: crystal structure of human hdac6 zinc finger domain
83	c1s1Y	Alignment	not modelled	44.9	26	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l37-a; PDBTitle: 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.
84	c3jywY	Alignment	not modelled	44.3	26	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l37(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
85	d1l1oc	Alignment	not modelled	44.1	4	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
86	c6g5iy	Alignment	not modelled	43.8	10	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
87	c5j9wC	Alignment	not modelled	43.7	5	PDB header: ligase Chain: C: PDB Molecule: acetophenone carboxylase beta subunit; PDBTitle: crystal structure of the apc core complex
88	c3c7nB	Alignment	not modelled	43.7	29	PDB header: chaperone/chaperone Chain: B: PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
89	c3j21e	Alignment	not modelled	43.2	15	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein l5p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
90	d1wfpA	Alignment	not modelled	42.9	5	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
91	c1nnjA	Alignment	not modelled	41.5	9	PDB header: hydrolase Chain: A: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
92	d1jcea1	Alignment	not modelled	40.9	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
93	c1u5kA	Alignment	not modelled	40.5	29	PDB header: recombination,replication Chain: A: PDB Molecule: hypothetical protein; PDBTitle: recombinational repair protein reco
94	c5jw9B	Alignment	not modelled	40.4	15	PDB header: protein binding Chain: B: PDB Molecule: rna polymerase ii elongation factor ell2; PDBTitle: the crystal structure of ell2 ocludin domain and aff4 peptide
95	d1vqo11	Alignment	not modelled	40.2	25	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37e
96	c1y5iA	Alignment	not modelled	39.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
97	d1x6ha1	Alignment	not modelled	39.6	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
98	d1wffa	Alignment	not modelled	39.3	11	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
99	c4l9mA	Alignment	not modelled	38.9	4	PDB header: signaling protein Chain: A: PDB Molecule: ras guanyl-releasing protein 1; PDBTitle: autoinhibited state of the ras-specific exchange factor rasgrp1
100	c2k5cA	Alignment	not modelled	38.7	20	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
101	c2ba1B	Alignment	not modelled	38.6	15	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
102	d1y5ia2	Alignment	not modelled	38.5	12	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
103	c1jcgA	Alignment	not modelled	38.1	19	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp Fold: Cysteine-rich domain

104	d1kbea_	Alignment	not modelled	37.6	3	Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
105	d1wfa_	Alignment	not modelled	37.3	15	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
106	c1hpmA_	Alignment	not modelled	36.9	29	PDB header: hydrolase (acting on acid anhydrides) Chain: A: PDB Molecule: 44k atpase fragment (n-terminal) of 7o kd heat- PDBTitle: how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
107	c2zkr2_	Alignment	not modelled	36.7	14	PDB header: ribosomal protein/rna Chain: 2: PDB Molecule: 60s ribosomal protein l37e; PDBTitle: 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
108	c2opfA_	Alignment	not modelled	36.2	5	PDB header: hydrolase/dna Chain: A: PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
109	c2nn6l_	Alignment	not modelled	35.8	15	PDB header: hydrolase/transferase Chain: l: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
110	c4czeA_	Alignment	not modelled	35.7	21	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: c. crescentus mreB, double filament, empty
111	c2ivfA_	Alignment	not modelled	35.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
112	c1dvbA_	Alignment	not modelled	34.3	11	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
113	c1ee8A_	Alignment	not modelled	34.0	21	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
114	d2ey4e1	Alignment	not modelled	33.9	19	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
115	d1vd4a_	Alignment	not modelled	33.8	10	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
116	c2j9uB_	Alignment	not modelled	33.7	20	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 36; PDBTitle: 2 angstrom x-ray structure of the yeast escrt-i vps28 c-terminus in2 complex with the nzf-n domain from escrt-ii
117	d2j9ub1	Alignment	not modelled	33.7	20	Fold: Rubredoxin-like Superfamily: Ran binding protein zinc finger-like Family: Ran binding protein zinc finger-like
118	c6et9H_	Alignment	not modelled	33.2	11	PDB header: transferase Chain: H: PDB Molecule: pfam duf35; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
119	d1qcva_	Alignment	not modelled	32.8	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
120	d2apob1	Alignment	not modelled	32.5	15	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like