

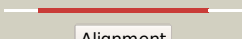










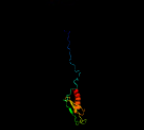


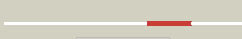
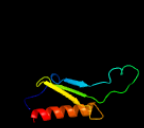




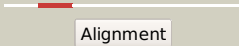


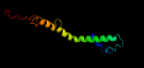


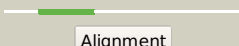

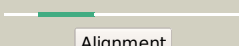

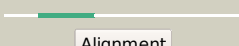
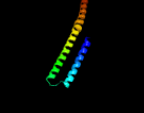
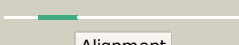
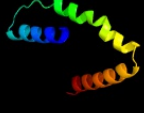

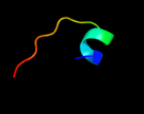

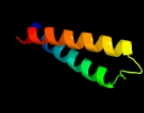



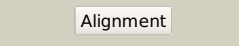



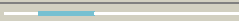


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1299_(prfA)_1455501_1456574
 Date Wed Jul 31 22:05:39 BST 2019
 Unique Job ID b31d3040f5a3e27c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d5cX_	 Alignment		100.0	46	PDB header: ribosome Chain: X: PDB Molecule: peptide chain release factor 1; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
2	d1gqea_	 Alignment		100.0	35	Fold: Release factor Superfamily: Release factor Family: Release factor
3	c2ihr1_	 Alignment		100.0	37	PDB header: translation Chain: 1: PDB Molecule: peptide chain release factor 2; PDBTitle: rf2 of thermus thermophilus
4	d1rq0a_	 Alignment		100.0	46	Fold: Release factor Superfamily: Release factor Family: Release factor
5	c1zbtA_	 Alignment		100.0	40	PDB header: translation Chain: A: PDB Molecule: peptide chain release factor 1; PDBTitle: crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution
6	d2b3tb1	 Alignment		100.0	49	Fold: Release factor Superfamily: Release factor Family: Release factor
7	c2rsmA_	 Alignment		100.0	29	PDB header: translation Chain: A: PDB Molecule: probable peptide chain release factor c12orf65 homolog, PDBTitle: solution structure and sirna-mediated knockdown analysis of the2 mitochondrial disease-related protein c12orf65 (ict2)
8	c2jy9A_	 Alignment		99.9	30	PDB header: hydrolase Chain: A: PDB Molecule: putative trna hydrolase domain; PDBTitle: nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220
9	c2jvaA_	 Alignment		99.8	30	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase domain protein; PDBTitle: nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
10	d1j26a_	 Alignment		99.8	30	Fold: dsRBD-like Superfamily: Peptidyl-tRNA hydrolase domain-like Family: Peptidyl-tRNA hydrolase domain
11	c4v1au_	 Alignment		98.6	28	PDB header: ribosome Chain: U: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2

12	c2lw1A_	 Alignment		96.4	16	PDB header: dna binding protein Chain: A: PDB Molecule: abc transporter atp-binding protein uup; PDBTitle: the c-terminal domain of the uup protein is a dna-binding coiled coil2 motif
13	c3errB_	 Alignment		93.2	12	PDB header: ligase Chain: B: PDB Molecule: fusion protein of microtubule binding domain from mouse PDBTitle: microtubule binding domain from mouse cytoplasmic dynein as a fusion2 with seryl-trna synthetase
14	c3layF_	 Alignment		61.7	17	PDB header: metal binding protein Chain: F: PDB Molecule: zinc resistance-associated protein; PDBTitle: alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
15	d1u5pa2	 Alignment		53.6	14	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
16	d1cuna2	 Alignment		49.0	11	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
17	d2spca_	 Alignment		47.3	12	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
18	d2p90a1	 Alignment		46.2	16	Fold: Phosphorylase/hydrolase-like Superfamily: Cgl1923-like Family: Cgl1923-like
19	c6gcsY_	 Alignment		45.1	27	PDB header: oxidoreductase Chain: Y: PDB Molecule: nuym subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
20	c3sjaG_	 Alignment		44.9	15	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: golgi to er traffic protein 1; PDBTitle: crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
21	c2p90B_	 Alignment	not modelled	43.3	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein cgl1923; PDBTitle: the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
22	c2jyaA_	 Alignment	not modelled	43.3	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1810; PDBTitle: nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
23	d1s35a2	 Alignment	not modelled	39.6	13	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
24	c3s2xB_	 Alignment	not modelled	39.2	27	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa synthase subunit alpha; PDBTitle: structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
25	c4rh7A_	 Alignment	not modelled	38.4	17	PDB header: motor protein Chain: A: PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
26	c4l4iA_	 Alignment	not modelled	38.3	28	PDB header: metal transport Chain: A: PDB Molecule: ryanodine receptor 2; PDBTitle: crystal structure of mouse ryanodine receptor isoform 2 (ryr2) 1-5472 disease mutant r420q
27	c5lnkc_	 Alignment	not modelled	36.1	40	PDB header: oxidoreductase Chain: C: PDB Molecule: PDBTitle: entire ovine respiratory complex i
						Fold: Spectrin repeat-like

28	d1u5pa1	Alignment	not modelled	33.7	14	Superfamily: Spectrin repeat Family: Spectrin repeat
29	c1s1hl_	Alignment	not modelled	33.6	20	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s16; 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, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
30	c2lvwA_	Alignment	not modelled	33.5	12	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetohydroxyacid synthase i (ahas i)
31	c3qo8A_	Alignment	not modelled	31.8	11	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of seryl-trna synthetase from candida albicans
32	c2z9fC_	Alignment	not modelled	31.7	23	PDB header: biosynthetic protein Chain: C: PDB Molecule: cellulose synthase operon protein d; PDBTitle: crystal structure of accesd protein from acetobacter xylinum
33	c2f1fA_	Alignment	not modelled	31.6	12	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli
34	d2ctka1	Alignment	not modelled	31.3	21	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
35	c1i4wA_	Alignment	not modelled	31.2	22	PDB header: transcription Chain: A: PDB Molecule: mitochondrial replication protein mtf1; PDBTitle: the crystal structure of the transcription factor sc-mttfb2 offers intriguing insights into mitochondrial transcription
36	d1i4wa_	Alignment	not modelled	31.2	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
37	c5o5jl_	Alignment	not modelled	30.0	21	PDB header: ribosome Chain: I: PDB Molecule: 30s ribosomal protein s9; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
38	c1wpaA_	Alignment	not modelled	29.5	8	PDB header: cell adhesion Chain: A: PDB Molecule: occludin; PDBTitle: 1.5 angstrom crystal structure of human occludin fragment 413-522
39	c4flaC_	Alignment	not modelled	28.7	12	PDB header: transcription Chain: C: PDB Molecule: regulation of nuclear pre-mrna domain-containing protein PDBTitle: crystal structure of human rprd1b, carboxy-terminal domain
40	c1xawA_	Alignment	not modelled	27.2	8	PDB header: cell adhesion Chain: A: PDB Molecule: occludin; PDBTitle: crystal structure of the cytoplasmic distal c-terminal2 domain of occludin
41	c2vkzH_	Alignment	not modelled	26.8	22	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
42	c3gitA_	Alignment	not modelled	25.8	25	PDB header: transferase Chain: A: PDB Molecule: carbon monoxide dehydrogenase/acetyl-coa synthase subunit PDBTitle: crystal structure of a truncated acetyl-coa synthase
43	c2e1mA_	Alignment	not modelled	25.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
44	d2pc6a2	Alignment	not modelled	25.3	8	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
45	d1s35a1	Alignment	not modelled	24.7	13	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
46	c6h9xA_	Alignment	not modelled	23.8	17	PDB header: ligase Chain: A: PDB Molecule: serine--trna ligase; PDBTitle: klebsiella pneumoniae seryl-trna synthetase in complex with the2 intermediate analog 5'-o-(n-(l-seryl)-sulfamoyl)adenosine
47	c3j20K_	Alignment	not modelled	23.8	31	PDB header: ribosome Chain: K: PDB Molecule: 30s ribosomal protein s9p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
48	c5cesA_	Alignment	not modelled	23.7	22	PDB header: structural protein Chain: A: PDB Molecule: pa0618; PDBTitle: c-terminal domain of the r-type pyocin baseplate protein pa0618
49	d2f1fa1	Alignment	not modelled	23.5	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
50	c5n7kD_	Alignment	not modelled	22.3	12	PDB header: cell adhesion Chain: D: PDB Molecule: marvel domain-containing protein 2; PDBTitle: crystal structure of the coiled-coil domain of human tricellulin
51	d1s05a_	Alignment	not modelled	21.9	15	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
52	d1mqva_	Alignment	not modelled	21.8	18	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like

53	c2xoaA	Alignment	not modelled	21.8	23	PDB header: metal transport Chain: A: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of the n-terminal three domains of the2 skeletal muscle ryanodine receptor (ryr1)
54	c2uval	Alignment	not modelled	21.4	20	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
55	d1gqaa	Alignment	not modelled	20.3	14	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
56	d2vqei1	Alignment	not modelled	19.9	31	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
57	d2gy9i1	Alignment	not modelled	19.3	44	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
58	c6p28A	Alignment	not modelled	19.3	17	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: crystal structure of the mir domain (aa 337-532) of the s. cerevisiae2 mannosyltransferase pmt2
59	d1ru3a	Alignment	not modelled	19.2	38	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
60	c5vnyA	Alignment	not modelled	19.1	18	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: lethal (2) giant discs 1, isoform b; PDBTitle: crystal structure of dm14-3 domain of lgd
61	c2xzml	Alignment	not modelled	17.9	31	PDB header: ribosome Chain: I: PDB Molecule: rps16e; PDBTitle: 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
62	c2r60A	Alignment	not modelled	17.9	17	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
63	c2zkrv	Alignment	not modelled	17.9	21	PDB header: ribosomal protein/rna Chain: V: PDB Molecule: rna expansion segment es9 part2; 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
64	c3zeyK	Alignment	not modelled	17.8	18	PDB header: ribosome Chain: K: PDB Molecule: 40s ribosomal protein s16, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
65	c2gl2B	Alignment	not modelled	17.8	13	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
66	d1ivsa1	Alignment	not modelled	16.9	22	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
67	c5xyiQ	Alignment	not modelled	16.8	29	PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s16, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
68	d2axya1	Alignment	not modelled	16.7	18	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
69	c6a3kA	Alignment	not modelled	16.6	7	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of cytochrome c' from shewanella benthica db6705
70	d1oaoc	Alignment	not modelled	16.5	27	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
71	c6girA	Alignment	not modelled	16.5	15	PDB header: cytosolic protein Chain: A: PDB Molecule: serine--trna ligase, cytoplasmic; PDBTitle: arabidopsis thaliana cytosolic seryl-trna synthetase
72	c3fb2B	Alignment	not modelled	16.4	11	PDB header: structural protein Chain: B: PDB Molecule: spectrin alpha chain, brain spectrin; PDBTitle: crystal structure of the human brain alpha spectrin repeats 15 and 16.2 northeast structural genomics consortium target hr5563a.
73	c6o7xa	Alignment	not modelled	16.3	11	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
74	d1nj1a3	Alignment	not modelled	16.2	12	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
75	d1m0da	Alignment	not modelled	16.1	33	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
76	d1cpqa	Alignment	not modelled	15.9	18	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
77	c2ftcB	Alignment	not modelled	15.8	18	PDB header: ribosome Chain: B: PDB Molecule: mitochondrial ribosomal protein l2; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome

78	c1aq5C	Alignment	not modelled	15.7	18	PDB header: coiled-coil Chain: C: PDB Molecule: cartilage matrix protein; PDBTitle: high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
79	c1aq5B	Alignment	not modelled	15.7	18	PDB header: coiled-coil Chain: B: PDB Molecule: cartilage matrix protein; PDBTitle: high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
80	c5nugB	Alignment	not modelled	15.6	15	PDB header: motor protein Chain: B: PDB Molecule: cytoplasmic dynein 1 heavy chain 1; PDBTitle: motor domains from human cytoplasmic dynein-1 in the phi-particle2 conformation
81	c3hjtB	Alignment	not modelled	15.6	16	PDB header: cell adhesion, transport protein Chain: B: PDB Molecule: lmb; PDBTitle: structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
82	c3bbnI	Alignment	not modelled	15.6	25	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein s9; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
83	c2zkqi	Alignment	not modelled	15.0	29	PDB header: ribosomal protein/rna Chain: I: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
84	c3j6vl	Alignment	not modelled	14.8	30	PDB header: ribosome Chain: I: PDB Molecule: 28s ribosomal protein s9, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
85	d2j8wa1	Alignment	not modelled	14.4	25	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
86	c1wleB	Alignment	not modelled	14.2	24	PDB header: ligase Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
87	c2ps3A	Alignment	not modelled	14.2	14	PDB header: metal transport Chain: A: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
88	c4ulvB	Alignment	not modelled	14.1	18	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c, class ii; PDBTitle: cytochrome c prime from shewanella frigidimarina
89	c3pdgA	Alignment	not modelled	13.6	16	PDB header: unknown function Chain: A: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
90	d1pq4a	Alignment	not modelled	13.6	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
91	c4i58A	Alignment	not modelled	13.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexylamine oxidase; PDBTitle: cyclohexylamine oxidase from brevibacterium oxydans ih-35a
92	d1lp1a	Alignment	not modelled	13.3	15	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
93	d1bbha	Alignment	not modelled	13.3	21	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
94	d2asba3	Alignment	not modelled	13.2	25	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
95	c3ci9B	Alignment	not modelled	13.2	27	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
96	d2foka1	Alignment	not modelled	13.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Restriction endonuclease FokI, N-terminal (recognition) domain
97	d2ba0a3	Alignment	not modelled	13.0	15	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
98	c1h2iG	Alignment	not modelled	13.0	12	PDB header: dna binding protein Chain: G: PDB Molecule: dna repair protein rad52 homolog; PDBTitle: human rad52 protein, n-terminal domain
99	d2fgca2	Alignment	not modelled	12.8	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like