












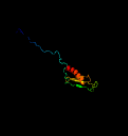





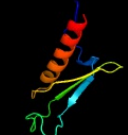

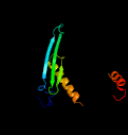


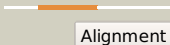
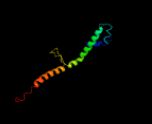
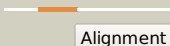

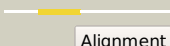
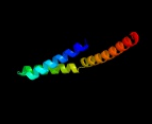
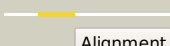
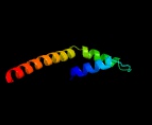
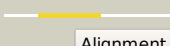
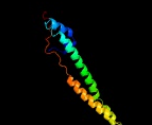
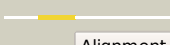
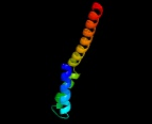



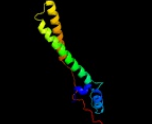
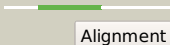
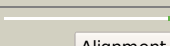
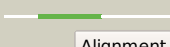
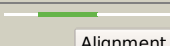


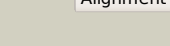
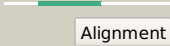


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3105c_(prfB)_3472765_3473901
 Date Thu Aug 8 16:20:28 BST 2019
 Unique Job ID 586b3d7d966c0514

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gqea_	 Alignment		100.0	42	Fold: Release factor Superfamily: Release factor Family: Release factor
2	c2ihr1_	 Alignment		100.0	43	PDB header: translation Chain: 1: PDB Molecule: peptide chain release factor 2; PDBTitle: rf2 of thermus thermophilus
3	c3d5cX_	 Alignment		100.0	36	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.
4	d1rq0a_	 Alignment		100.0	35	Fold: Release factor Superfamily: Release factor Family: Release factor
5	d2b3tb1	 Alignment		100.0	35	Fold: Release factor Superfamily: Release factor Family: Release factor
6	c1zbtA_	 Alignment		100.0	26	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
7	c2rsmA_	 Alignment		99.9	30	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		99.8	27	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		99.7	28	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		99.7	26	Fold: dsRBD-like Superfamily: Peptidyl-tRNA hydrolase domain-like Family: Peptidyl-tRNA hydrolase domain
11	c4v1au_	 Alignment		98.2	18	PDB header: ribosome Chain: U: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2

12	c2lw1A_	 Alignment		96.7	20	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		89.1	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		84.1	12	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	c1wpaA_	 Alignment		79.4	14	PDB header: cell adhesion Chain: A: PDB Molecule: occludin; PDBTitle: 1.5 angstrom crystal structure of human occludin fragment 413-522
16	c5n7kD_	 Alignment		73.1	17	PDB header: cell adhesion Chain: D: PDB Molecule: marvel domain-containing protein 2; PDBTitle: crystal structure of the coiled-coil domain of human tricellulin
17	c2dq0A_	 Alignment		71.7	11	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
18	c1xawA_	 Alignment		70.2	13	PDB header: cell adhesion Chain: A: PDB Molecule: occludin; PDBTitle: crystal structure of the cytoplasmic distal c-terminal2 domain of occludin
19	c5yjeA_	 Alignment		69.6	18	PDB header: gene regulation Chain: A: PDB Molecule: protein hira; PDBTitle: crystal structure of hira(644-1017)
20	d1seta1	 Alignment		61.1	15	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Seryl-tRNA synthetase (SerRS)
21	c6h9xA_	 Alignment	not modelled	59.6	13	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
22	d2ctka1	 Alignment	not modelled	55.6	16	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)
23	c4flaC_	 Alignment	not modelled	55.5	18	PDB header: transcription Chain: C: PDB Molecule: regulation of nuclear pre-mrna domain-containing protein PDBTitle: crystal structure of human rprd1b, carboxy-terminal domain
24	c6o7ua_	 Alignment	not modelled	50.3	14	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
25	c6gcsY_	 Alignment	not modelled	49.2	13	PDB header: oxidoreductase Chain: Y: PDB Molecule: nuym subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
26	c2jyaA_	 Alignment	not modelled	47.3	13	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
27	c3lssA_	 Alignment	not modelled	45.0	13	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: trypanosoma brucei seryl-trna synthetase in complex with atp
28	c3oo8A_	 Alignment	not modelled	43.7	5	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase, cytoplasmic;

28	c3q06A_	Alignment	not modelled	43.7	9	PDBTitle: crystal structure of seryl-trna synthetase from candida albicans
29	c5lnkc_	Alignment	not modelled	41.3	27	PDB header: oxidoreductase Chain: C: PDB Molecule: PDBTitle: entire ovine respiratory complex i
30	d1u5pa2	Alignment	not modelled	40.7	17	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
31	c1s1hl_	Alignment	not modelled	38.6	10	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.
32	c2dq3A_	Alignment	not modelled	36.0	10	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
33	c1u5pA_	Alignment	not modelled	35.1	6	PDB header: structural protein Chain: A: PDB Molecule: spectrin alpha chain, brain; PDBTitle: crystal structure of repeats 15 and 16 of chicken brain2 alpha spectrin
34	c3pdyB_	Alignment	not modelled	34.8	12	PDB header: structural protein Chain: B: PDB Molecule: plectin; PDBTitle: structure of the third and fourth spectrin repeats of the plakin2 domain of plectin
35	d2spca_	Alignment	not modelled	34.0	9	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
36	c3jbrF_	Alignment	not modelled	33.3	30	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
37	c3edvB_	Alignment	not modelled	32.4	14	PDB header: structural protein Chain: B: PDB Molecule: spectrin beta chain, brain 1; PDBTitle: crystal structure of repeats 14-16 of beta2-spectrin
38	d1cuna2	Alignment	not modelled	32.4	6	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
39	d1s35a2	Alignment	not modelled	32.2	8	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
40	d1mqva_	Alignment	not modelled	32.2	12	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
41	c5o5jl_	Alignment	not modelled	31.5	26	PDB header: ribosome Chain: I: PDB Molecule: 30s ribosomal protein s9; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
42	c6o7xa_	Alignment	not modelled	31.2	14	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
43	c5jw9B_	Alignment	not modelled	29.3	9	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
44	c6g7oA_	Alignment	not modelled	29.2	14	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
45	d1u5pa1	Alignment	not modelled	28.6	6	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
46	c5xauB_	Alignment	not modelled	28.6	18	PDB header: cell adhesion Chain: B: PDB Molecule: laminin subunit beta-1; PDBTitle: crystal structure of integrin binding fragment of laminin-511
47	c3pdgA_	Alignment	not modelled	28.4	12	PDB header: unknown function Chain: A: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
48	c1f8sA_	Alignment	not modelled	27.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
49	d1gqaa_	Alignment	not modelled	27.6	14	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
50	c3fpjA_	Alignment	not modelled	27.4	16	PDB header: biosynthetic protein, transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of e81q mutant of mtas in complex with s-2 adenosylmethionine
51	c5xauC_	Alignment	not modelled	26.7	19	PDB header: cell adhesion Chain: C: PDB Molecule: laminin subunit gamma-1; PDBTitle: crystal structure of integrin binding fragment of laminin-511
52	c3s2xB_	Alignment	not modelled	26.6	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
53	d2f66c1	Alignment	not modelled	26.3	41	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS37 C-terminal domain-like

54	c3j20K	Alignment	not modelled	26.2	21	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)
55	d1nj1a3	Alignment	not modelled	25.8	14	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
56	d1s35a1	Alignment	not modelled	25.6	7	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
57	d2vqe1	Alignment	not modelled	24.6	31	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
58	c2lvwA	Alignment	not modelled	24.4	8	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)
59	c5cx2B	Alignment	not modelled	24.2	23	PDB header: structural protein Chain: B; PDB Molecule: coronin; PDBTitle: structure of coiled coil domain of leishmania donovani coronin
60	c5cx2C	Alignment	not modelled	24.2	23	PDB header: structural protein Chain: C; PDB Molecule: coronin; PDBTitle: structure of coiled coil domain of leishmania donovani coronin
61	c5j4oA	Alignment	not modelled	24.1	8	PDB header: structural protein Chain: A; PDB Molecule: spectrin alpha chain, erythrocytic 1; PDBTitle: structure of human erythrocytic spectrin alpha chain repeats 16-17
62	d2gy9i1	Alignment	not modelled	23.9	38	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
63	c2z9fC	Alignment	not modelled	23.8	29	PDB header: biosynthetic protein Chain: C; PDB Molecule: cellulose synthase operon protein d; PDBTitle: crystal structure of axcesd protein from acetobacter xylinum
64	c6p2rB	Alignment	not modelled	23.5	12	PDB header: transferase Chain: B; PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
65	d2pc6a2	Alignment	not modelled	23.2	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
66	d1cpqa	Alignment	not modelled	23.2	7	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
67	c2cazF	Alignment	not modelled	22.9	38	PDB header: protein transport Chain: F; PDB Molecule: protein srn2; PDBTitle: escrt-i core
68	d1m0da	Alignment	not modelled	22.8	25	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
69	c2e1mA	Alignment	not modelled	22.6	22	PDB header: oxidoreductase Chain: A; PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
70	c6oteA	Alignment	not modelled	22.4	11	PDB header: ligase Chain: A; PDB Molecule: seryl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of seryl-trna synthetase (serrs) from2 cryptosporidium parvum complexed with l-serylsulfamoyl adenosine
71	c3hjtB	Alignment	not modelled	21.9	23	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
72	d1ivsa1	Alignment	not modelled	21.9	15	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
73	d2fgca2	Alignment	not modelled	21.7	10	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
74	c3mfqB	Alignment	not modelled	21.6	28	PDB header: metal binding protein Chain: B; PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
75	d1nj8a3	Alignment	not modelled	21.3	14	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
76	c3bbn1	Alignment	not modelled	21.2	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.
77	d2axya1	Alignment	not modelled	21.0	20	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)
78	c5xyiQ	Alignment	not modelled	21.0	21	PDB header: ribosome Chain: Q; PDB Molecule: 40s ribosomal protein s16, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
						PDB header: transferase

79	c2r60A_	Alignment	not modelled	20.6	14	Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
80	c2xzmI_	Alignment	not modelled	20.4	15	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
81	c4r4mB_	Alignment	not modelled	20.3	27	PDB header: dna binding protein Chain: B: PDB Molecule: cgmp-dependent protein kinase 1; PDBTitle: crystal structure of c42l cgmp dependent protein kinase i alpha (pkgi2 alpha) leucine zipper
82	c3zeyK_	Alignment	not modelled	20.2	19	PDB header: ribosome Chain: K: PDB Molecule: 40s ribosomal protein s16, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
83	c2mi2A_	Alignment	not modelled	20.2	11	PDB header: transport protein Chain: A: PDB Molecule: sec-independent protein translocase protein tatb; PDBTitle: solution structure of the e. coli tatb protein in dpc micelles
84	d1pq4a_	Alignment	not modelled	20.2	26	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
85	c3ci9B_	Alignment	not modelled	20.1	16	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
86	d2f1fa1	Alignment	not modelled	19.9	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
87	c2ogwB_	Alignment	not modelled	19.6	19	PDB header: transport protein Chain: B: PDB Molecule: high-affinity zinc uptake system protein znua PDBTitle: structure of abc type zinc transporter from e. coli
88	c6p28A_	Alignment	not modelled	19.4	12	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
89	c1sryB_	Alignment	not modelled	19.3	17	PDB header: ligase(synthetase) Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
90	d1sd4a_	Alignment	not modelled	19.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
91	c4cl2A_	Alignment	not modelled	19.3	16	PDB header: transport protein Chain: A: PDB Molecule: periplasmic solute binding protein; PDBTitle: structure of periplasmic metal binding protein from candidatus2 liberibacter asiaticus
92	c4ll8E_	Alignment	not modelled	19.0	10	PDB header: motor protein/transport protein Chain: E: PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: complex of carboxy terminal domain of myo4p and she3p middle fragment
93	c3neaA_	Alignment	not modelled	18.9	36	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
94	c2zkqi_	Alignment	not modelled	18.7	21	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
95	c3kbtA_	Alignment	not modelled	18.6	13	PDB header: structural protein Chain: A: PDB Molecule: spectrin beta chain, erythrocyte; PDBTitle: crystal structure of the ankyrin binding domain of human erythroid2 beta spectrin (repeats 13-15) in complex with the spectrin binding3 domain of human erythroid ankyrin (zu5-ank)
96	d2gc9a1	Alignment	not modelled	18.6	27	Fold: Lipocalins Superfamily: Lipocalins Family: Phenolic acid decarboxylase (PAD)
97	d2g5ca1	Alignment	not modelled	18.5	21	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
98	c1qpoA_	Alignment	not modelled	18.5	19	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apoenzyme from2 mycobacterium tuberculosis
99	c4ak2A_	Alignment	not modelled	18.2	7	PDB header: heparin-binding protein Chain: A: PDB Molecule: bt_4661; PDBTitle: structure of bt4661, a suse-like surface located polysaccharide2 binding protein from the bacteroides thetaiotaomicron heparin3 utilisation locus