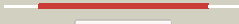



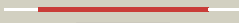

















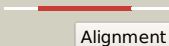

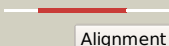

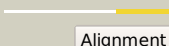
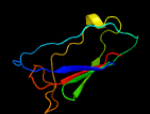
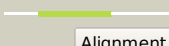

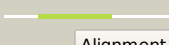

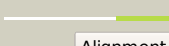

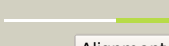

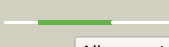


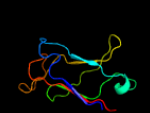
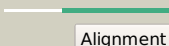
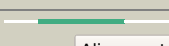
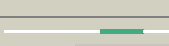
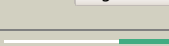
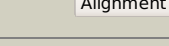
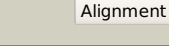
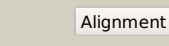
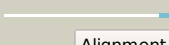


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1412_(ribC)_1588573_1589178
 Date Wed Jul 31 22:05:52 BST 2019
 Unique Job ID a56ed66f96011738

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4e0fB_	 Alignment		100.0	37	PDB header: transferase Chain: B; PDB Molecule: riboflavin synthase subunit alpha; PDBTitle: crystallographic structure of trimeric riboflavin synthase from2 brucella abortus in complex with riboflavin
2	c1kzIA_	 Alignment		100.0	39	PDB header: transferase Chain: A; PDB Molecule: riboflavin synthase; PDBTitle: riboflavin synthase from s.pombe bound to2 carboxyethylumazine
3	cli8dB_	 Alignment		100.0	36	PDB header: transferase Chain: B; PDB Molecule: riboflavin synthase; PDBTitle: crystal structure of riboflavin synthase
4	c3a35B_	 Alignment		100.0	26	PDB header: luminescent protein Chain: B; PDB Molecule: lumazine protein; PDBTitle: crystal structure of lump complexed with riboflavin
5	c3ddyA_	 Alignment		100.0	28	PDB header: luminescent protein Chain: A; PDB Molecule: lumazine protein; PDBTitle: structure of lumazine protein, an optical transponder of luminescent2 bacteria
6	d1kzla2	 Alignment		100.0	36	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Riboflavin synthase
7	d1i8da2	 Alignment		100.0	37	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Riboflavin synthase
8	cli18B_	 Alignment		100.0	36	PDB header: transferase Chain: B; PDB Molecule: riboflavin synthase alpha chain; PDBTitle: solution structure of the n-terminal domain of riboflavin synthase2 from e. coli
9	clhzeB_	 Alignment		100.0	36	PDB header: transferase Chain: B; PDB Molecule: riboflavin synthase alpha chain; PDBTitle: solution structure of the n-terminal domain of riboflavin synthase2 from e. coli
10	d1i8da1	 Alignment		100.0	35	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Riboflavin synthase
11	c1pkvA_	 Alignment		100.0	36	PDB header: transferase Chain: A; PDB Molecule: riboflavin synthase alpha chain; PDBTitle: the n-terminal domain of riboflavin synthase in complex with2 riboflavin

12	d1kzla1	 Alignment		100.0	43	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Riboflavin synthase
13	c1pkvB_	 Alignment		100.0	36	PDB header: transferase Chain: B: PDB Molecule: riboflavin synthase alpha chain; PDBTitle: the n-terminal domain of riboflavin synthase in complex with2 riboflavin
14	c5opjA_	 Alignment		79.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: rhamnogalacturonan lyase; PDBTitle: rhamnogalacturonan lyase
15	d1a3xa1	 Alignment		69.5	25	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
16	d1pkla1	 Alignment		69.1	18	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
17	c5mqoA_	 Alignment		66.4	17	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end beta-l-arabinofuranosidase; PDBTitle: glycoside hydrolase bt_1003
18	c4qk0C_	 Alignment		66.1	18	PDB header: hydrolase Chain: C: PDB Molecule: gh127 beta-l-arabinofuranoside; PDBTitle: crystal structure of ara127n-se, a gh127 beta-l-arabinofuranosidase2 from geobacillus stearothermophilus t6
19	d2g50a1	 Alignment		57.6	29	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
20	c6ex6A_	 Alignment		53.2	12	PDB header: hydrolase Chain: A: PDB Molecule: six-hairpin glycosidase; PDBTitle: the gh127, beta-arabinofuranosidase, bt3674
21	c1vw4N_	 Alignment	not modelled	48.2	16	PDB header: ribosome Chain: N: PDB Molecule: 54s ribosomal protein l49, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
22	d1ep3b1	 Alignment	not modelled	47.2	15	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
23	c3o44G_	 Alignment	not modelled	41.0	35	PDB header: toxin Chain: G: PDB Molecule: hemolysin; PDBTitle: crystal structure of the vibrio cholerae cytolsin (hlya) heptameric2 pore
24	d1krha1	 Alignment	not modelled	40.5	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
25	d1liua1	 Alignment	not modelled	37.7	22	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
26	c1xezA_	 Alignment	not modelled	35.0	35	PDB header: toxin Chain: A: PDB Molecule: hemolysin; PDBTitle: crystal structure of the vibrio cholerae cytolsin (hlya)2 pro-toxin with octylglucoside bound
27	c6cqoH_	 Alignment	not modelled	35.0	16	PDB header: dna binding protein Chain: H: PDB Molecule: single-stranded dna-binding protein rim1, mitochondrial; PDBTitle: crystal structure of mitochondrial single-stranded dna binding2 proteins from s. cerevisiae (semet labeled), rim1 (form2)
28	c3wkxA_	 Alignment	not modelled	33.6	18	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end beta-l-arabinofuranosidase; PDBTitle: crystal structure of gh127 beta-l-arabinofuranosidase

						hypba1 from2 bifidobacterium longum arabinose complex form
29	d1e0ta1	Alignment	not modelled	32.8	24	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
30	d1pkma1	Alignment	not modelled	31.1	22	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
31	c3ca9A_	Alignment	not modelled	30.2	17	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
32	c4pwuC_	Alignment	not modelled	29.7	13	PDB header: signaling protein Chain: C: PDB Molecule: modulator protein mzra; PDBTitle: crystal structure of a modulator protein mzra (kpn_03524) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 2.45 a3 resolution
33	d1f7da_	Alignment	not modelled	29.5	15	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
34	c5xrwA_	Alignment	not modelled	29.3	18	PDB header: motor protein Chain: A: PDB Molecule: flin; PDBTitle: crystal structure of flagellar motor switch complex from h. pylori
35	c3c3iA_	Alignment	not modelled	28.9	18	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
36	d1duna_	Alignment	not modelled	28.0	15	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
37	d1f7ra_	Alignment	not modelled	27.7	20	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
38	c5vjvC_	Alignment	not modelled	27.4	19	PDB header: hydrolase Chain: C: PDB Molecule: dutp pyrophosphatase; PDBTitle: crystal structure of dutp pyrophosphatase protein, from naegleria2 fowleri
39	c2d4nA_	Alignment	not modelled	27.2	11	PDB header: hydrolase Chain: A: PDB Molecule: du; PDBTitle: crystal structure of m-pmv dutpase complexed with dupnpp, substrate2 analogue
40	d1zbfa1	Alignment	not modelled	26.4	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
41	d1tvca1	Alignment	not modelled	24.4	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
42	d1fdra1	Alignment	not modelled	22.4	13	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
43	c2zp2B_	Alignment	not modelled	22.2	18	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
44	c2okdB_	Alignment	not modelled	22.1	20	PDB header: hydrolase Chain: B: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: high resolution crystal structures of vaccinia virus dutpase
45	c1v0eB_	Alignment	not modelled	21.5	20	PDB header: hydrolase Chain: B: PDB Molecule: endo-alpha-sialidase; PDBTitle: endosialidase of bacteriophage k1f
46	c4or1B_	Alignment	not modelled	20.1	50	PDB header: cell adhesion Chain: B: PDB Molecule: invasin homolog aafb, major fimbrial subunit of aggregative PDBTitle: structure and mechanism of fibronectin binding and biofilm formation2 of enteroaggregative escherischia coli aaf fimbriae
47	d1q5uz_	Alignment	not modelled	19.6	17	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
48	c3lqwA_	Alignment	not modelled	18.8	19	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5-triphosphate2 nucleotidohydrolase from entamoeba histolytica
49	c5hbzE_	Alignment	not modelled	18.7	32	PDB header: hydrolase Chain: E: PDB Molecule: non-structural protein 11; PDBTitle: structure of eav nsp11 k170a mutant at 3.10a
50	c1zeqX_	Alignment	not modelled	18.7	26	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
51	c4bwdA_	Alignment	not modelled	18.3	38	PDB header: structural protein Chain: A: PDB Molecule: short coiled-coil protein; PDBTitle: human short coiled coil protein
52	c3ehwA_	Alignment	not modelled	18.3	17	PDB header: hydrolase Chain: A: PDB Molecule: dutp pyrophosphatase; PDBTitle: human dutpase in complex with alpha,beta-imido-dutp and mg2+:2 visualization of the full-length c-termini in all monomers and3 suggestion for an additional metal ion binding site PDB header: transcription,hydrolase Chain: L: PDB Molecule: general control protein gcn4, proteasome-activating PDBTitle: proteasome-activating nucleotidase (pan) n-domain (57-134) from2 archaeoglobus fulgidus fused to gcn4, p61a mutant
53	c2wg6L_	Alignment	not modelled	18.1	16	

54	d1lqsl_	Alignment	not modelled	18.0	25	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
55	c5mmlS_	Alignment	not modelled	17.3	15	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l21, chloroplastic; PDBTitle: structure of the large subunit of the chloroplast ribosome
56	d1vlka_	Alignment	not modelled	17.2	31	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
57	c3nrfA_	Alignment	not modelled	17.1	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: apag protein; PDBTitle: crystal structure of an apag protein (pa1934) from pseudomonas2 aeruginosa pao1 at 1.50 a resolution
58	c3qtgA_	Alignment	not modelled	16.9	15	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from pyrobaculum aerophilum
59	d1lk3a_	Alignment	not modelled	16.9	31	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
60	c3so2A_	Alignment	not modelled	15.7	19	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: chlorella dutpase
61	c3h43F_	Alignment	not modelled	15.5	27	PDB header: hydrolase Chain: F: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
62	c3mmlD_	Alignment	not modelled	14.7	14	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeq0435-2 msmeq0436
63	c5o57A_	Alignment	not modelled	14.7	40	PDB header: signaling protein Chain: A: PDB Molecule: dickkopf-related protein 4; PDBTitle: solution structure of the n-terminal region of dkk4
64	d1vqoq1	Alignment	not modelled	14.6	24	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
65	c3j21R_	Alignment	not modelled	14.4	29	PDB header: ribosome Chain: R: PDB Molecule: 50s ribosomal protein l21e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
66	d1k8kg_	Alignment	not modelled	14.2	29	Fold: alpha-alpha superhelix Superfamily: Arp2/3 complex 16 kDa subunit ARPC5 Family: Arp2/3 complex 16 kDa subunit ARPC5
67	c2izpB_	Alignment	not modelled	13.8	31	PDB header: toxin Chain: B: PDB Molecule: putative membrane antigen; PDBTitle: bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.
68	c3mbqC_	Alignment	not modelled	13.4	19	PDB header: hydrolase Chain: C: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5-triphosphate nucleotidohydrolase2 from brucella melitensis, orthorhombic crystal form
69	c5mlcT_	Alignment	not modelled	13.3	15	PDB header: ribosome Chain: T: PDB Molecule: 50s ribosomal protein l21, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
70	c2lmcB_	Alignment	not modelled	13.1	6	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
71	d2phcb1	Alignment	not modelled	12.8	18	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
72	c3uiyA_	Alignment	not modelled	12.8	19	PDB header: structural protein Chain: A: PDB Molecule: chimera protein of sefd and sefa; PDBTitle: crystal structure of sefd_dsca in h2o
73	d2izpa1	Alignment	not modelled	12.7	31	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
74	c2jz2A_	Alignment	not modelled	12.6	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ssl0352 protein; PDBTitle: solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
75	c2zkrq_	Alignment	not modelled	12.6	18	PDB header: ribosomal protein/rna Chain: Q: PDB Molecule: rna expansion segment es31 part ii; 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
76	c4ce4V_	Alignment	not modelled	12.1	17	PDB header: ribosome Chain: V: PDB Molecule: mrpl21; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
77	c4bq7D_	Alignment	not modelled	12.1	27	PDB header: cell adhesion Chain: D: PDB Molecule: rgm domain family member b; PDBTitle: crystal structure of the rgmb-neo1 complex form 2
78	d3ehwa1	Alignment	not modelled	12.0	17	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
						PDB header: hydrolase Chain: B: PDB Molecule: deoxyuridine 5'-triphosphate

79	c3f4fB_	Alignment	not modelled	11.8	15	nucleotidohydrolase; PDBTitle: crystal structure of dut1p, a dutpase from saccharomyces cerevisiae
80	c3mtvA_	Alignment	not modelled	11.7	33	PDB header: hydrolase Chain: A: PDB Molecule: papain-like cysteine protease; PDBTitle: the crystal structure of the prrsv nonstructural protein nsp1
81	d3bzka4	Alignment	not modelled	11.5	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
82	d1o6aa_	Alignment	not modelled	11.4	18	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
83	c5vgzC_	Alignment	not modelled	11.3	13	PDB header: hydrolase Chain: C: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: conformational landscape of the p28-bound human proteasome regulatory2 particle
84	c1s1iQ_	Alignment	not modelled	11.1	29	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l21-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.
85	d2ilkA_	Alignment	not modelled	10.8	31	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
86	c3zlel_	Alignment	not modelled	10.6	17	PDB header: membrane protein Chain: I: PDB Molecule: apical membrane antigen 1; PDBTitle: crystal structure of toxoplasma gondii sporozoite ama1
87	d1a8pa1	Alignment	not modelled	10.5	12	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
88	c5vgzF_	Alignment	not modelled	10.3	17	PDB header: hydrolase Chain: F: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: conformational landscape of the p28-bound human proteasome regulatory2 particle
89	c5da1B_	Alignment	not modelled	10.3	18	PDB header: hydrolase Chain: B: PDB Molecule: endoribonuclease; PDBTitle: a dimerization-dependent mechanism drives prrsv nsp11 functions as a2 interferon antagonist and endoribonuclease
90	c3kf8D_	Alignment	not modelled	10.3	24	PDB header: structural protein Chain: D: PDB Molecule: protein ten1; PDBTitle: crystal structure of c. tropicalis stn1-ten1 complex
91	c4yxaB_	Alignment	not modelled	10.2	16	PDB header: protein transport Chain: B: PDB Molecule: surface presentation of antigens protein spao; PDBTitle: complex of spao(spao1,2 semet) and orgb(apar)::t4lysozyme fusion2 protein
92	d1vkpa_	Alignment	not modelled	10.1	25	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
93	c2l55A_	Alignment	not modelled	9.9	11	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
94	c2p9oB_	Alignment	not modelled	9.9	15	PDB header: hydrolase Chain: B: PDB Molecule: dutp pyrophosphatase-like protein; PDBTitle: structure of dutpase from arabidopsis thaliana
95	c3e0eA_	Alignment	not modelled	9.8	20	PDB header: replication Chain: A: PDB Molecule: replication protein a; PDBTitle: crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 target mrr110b
96	c3voqA_	Alignment	not modelled	9.4	33	PDB header: membrane protein Chain: A: PDB Molecule: target of rapamycin complex 2 subunit mapkap1; PDBTitle: crystal structure of the pleckstrin homology domain of human sin1, a2 torc2 subunit
97	c3iz5U_	Alignment	not modelled	9.4	35	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein l21 (l21e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
98	c3izcU_	Alignment	not modelled	9.2	29	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein rpl21 (l21e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
99	d1r9fa_	Alignment	not modelled	9.1	55	Fold: Tombusvirus P19 core protein, VP19 Superfamily: Tombusvirus P19 core protein, VP19 Family: Tombusvirus P19 core protein, VP19