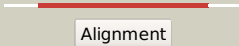
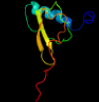
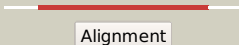

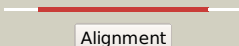

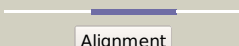
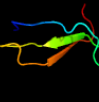
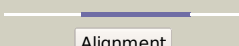

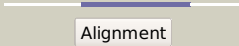
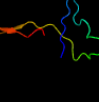
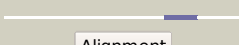
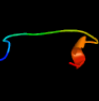




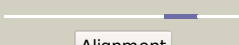
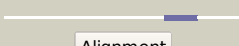
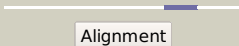

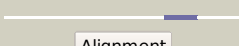

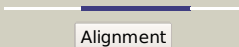


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0705_(rpsS)_803414_803695
 Date Fri Jul 26 01:50:27 BST 2019
 Unique Job ID 9de509b76f3fe166

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bbnS_	Alignment		100.0	62	PDB header: ribosome Chain: S; PDB Molecule: ribosomal protein s19; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
2	c5o5jS_	Alignment		100.0	98	PDB header: ribosome Chain: S; PDB Molecule: 30s ribosomal protein s19; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
3	d2uubs1	Alignment		100.0	69	Fold: Ribosomal protein S19 Superfamily: Ribosomal protein S19 Family: Ribosomal protein S19
4	d2gy9s1	Alignment		100.0	70	Fold: Ribosomal protein S19 Superfamily: Ribosomal protein S19 Family: Ribosomal protein S19
5	c3zeyl_	Alignment		100.0	23	PDB header: ribosome Chain: I; PDB Molecule: 40s ribosomal protein s15, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
6	c5xyiP_	Alignment		100.0	26	PDB header: ribosome Chain: P; PDB Molecule: ribosomal protein s19, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
7	c3j20T_	Alignment		100.0	40	PDB header: ribosome Chain: T; PDB Molecule: 30s ribosomal protein s19p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
8	c2zkqs_	Alignment		100.0	29	PDB header: ribosomal protein/rna Chain: S; 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
9	c2xzmS_	Alignment		100.0	30	PDB header: ribosome Chain: S; PDB Molecule: rps15e; 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
10	c3j38P_	Alignment		100.0	30	PDB header: ribosome Chain: P; PDB Molecule: 40s ribosomal protein s15, isoform a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
11	c3o30I_	Alignment		100.0	26	PDB header: ribosome Chain: I; PDB Molecule: 40s ribosomal protein s15; PDBTitle: yeast 80s ribosome. this entry consists of the 40s subunit of the2 second 80s in the asymmetric unit.

12	c5xxuP_	 Alignment		100.0	27	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein us19; PDBTitle: small subunit of toxoplasma gondii ribosome
13	c3izbR_	 Alignment		100.0	25	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein rps15 (s19p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
14	c1s1hS_	 Alignment		100.0	27	PDB header: ribosome Chain: S: PDB Molecule: 40s ribosomal protein s15; 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.
15	c5aycA_	 Alignment		14.6	18	PDB header: transferase Chain: A: PDB Molecule: 4-o-beta-d-mannosyl-d-glucose phosphorylase; PDBTitle: crystal structure of ruminococcus albus 4-o-beta-d-mannosyl-d-glucose2 phosphorylase (ramp1) in complexes with sulfate and 4-o-beta-d-3 mannosyl-d-glucose
16	d1li1c1	 Alignment		14.0	14	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Noncollagenous (NC1) domain of collagen IV
17	c1t60R_	 Alignment		13.6	14	PDB header: structural protein Chain: R: PDB Molecule: type iv collagen; PDBTitle: crystal structure of type iv collagen nc1 domain from2 bovine lens capsule
18	c5dz7A_	 Alignment		12.9	36	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
19	d1nm2a1	 Alignment		12.5	36	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
20	c5czcA_	 Alignment		11.9	29	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
21	c4rr5A_	 Alignment	not modelled	11.8	36	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase
22	c2cuyA_	 Alignment	not modelled	11.7	36	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-[acyl carrier protein] transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
23	c5dz6A_	 Alignment	not modelled	11.1	43	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
24	c3g87A_	 Alignment	not modelled	10.7	50	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
25	c3ezoA_	 Alignment	not modelled	10.7	43	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein s-malonyltransferase from2 burkholderia pseudomallei 1710b
26	c5u35A_	 Alignment	not modelled	10.3	32	PDB header: de novo protein Chain: A: PDB Molecule: de novo ntf2 with large cavity; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
27	d1t61a1	 Alignment	not modelled	9.8	21	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Noncollagenous (NC1) domain of collagen IV

28	d1roca	Alignment	not modelled	9.8	40	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
29	c3im8A	Alignment	not modelled	9.7	29	PDB header: transferase Chain: A; PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
30	c6fikA	Alignment	not modelled	9.6	57	PDB header: biosynthetic protein Chain: A; PDB Molecule: polyketide synthase; PDBTitle: acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks
31	c3im9A	Alignment	not modelled	9.5	36	PDB header: transferase Chain: A; PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus
32	c2jfkD	Alignment	not modelled	9.4	50	PDB header: transferase Chain: D; PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
33	c3tzzA	Alignment	not modelled	9.3	36	PDB header: transferase Chain: A; PDB Molecule: polyketide synthase pks13; PDBTitle: crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a
34	c5ypvA	Alignment	not modelled	9.1	36	PDB header: transferase Chain: A; PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of fabd from acinetobacter baumannii
35	c4ammA	Alignment	not modelled	8.7	43	PDB header: transferase Chain: A; PDB Molecule: dyne8; PDBTitle: crystal structure of the acyltransferase domain of the2 iterative polyketide synthase in enediyne biosynthesis3 reveals the molecular basis of substrate specificity
36	c3htxA	Alignment	not modelled	8.6	36	PDB header: transferase/rna Chain: A; PDB Molecule: hen1; PDBTitle: crystal structure of small rna methyltransferase hen1
37	c3hhdC	Alignment	not modelled	8.5	50	PDB header: transferase, hydrolase Chain: C; PDB Molecule: fatty acid synthase; PDBTitle: structure of the human fatty acid synthase ks-mat didomain as a2 framework for inhibitor design.
38	d1t3qa2	Alignment	not modelled	8.5	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
39	c3eenA	Alignment	not modelled	8.4	36	PDB header: transferase Chain: A; PDB Molecule: malonyl coa-acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
40	c2cdh9	Alignment	not modelled	8.2	36	PDB header: transferase Chain: 9; PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
41	c6iytA	Alignment	not modelled	7.7	50	PDB header: transferase Chain: A; PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase
42	d2gtlo1	Alignment	not modelled	7.7	20	Fold: Streptavidin-like Superfamily: Extracellular hemoglobin linker subunit, receptor domain Family: Extracellular hemoglobin linker subunit, receptor domain
43	c6iyrA	Alignment	not modelled	7.5	43	PDB header: transferase Chain: A; PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from module 8 of the2 salinomycin polyketide synthase
44	c4qbuA	Alignment	not modelled	7.3	29	PDB header: transferase Chain: A; PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
45	c4m1xB	Alignment	not modelled	7.3	29	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein 201phi2-1p060; PDBTitle: tetrameric ring structure of 201phi2-1p060 from pseudomonas phage2 201phi2-1
46	c2h1yA	Alignment	not modelled	7.2	36	PDB header: transferase Chain: A; PDB Molecule: malonyl coenzyme a-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori
47	c3tqeA	Alignment	not modelled	7.2	43	PDB header: transferase Chain: A; PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: structure of the malonyl coa-acyl carrier protein transacylase (fabd)2 from coxiella burnetii
48	c6iyoA	Alignment	not modelled	7.0	43	PDB header: transferase Chain: A; PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase
49	c4mz0B	Alignment	not modelled	6.9	29	PDB header: transferase Chain: B; PDB Molecule: curl; PDBTitle: structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase
50	d1mlaa1	Alignment	not modelled	6.6	60	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
51	c3rgiA	Alignment	not modelled	6.4	43	PDB header: transferase Chain: A; PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
52	d1t61c1	Alignment	not modelled	6.3	14	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Noncollagenous (NC1) domain of collagen IV

53	d1vlba2	Alignment	not modelled	6.3	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
54	c3ptwA	Alignment	not modelled	6.3	36	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
55	c2idcA	Alignment	not modelled	6.1	40	PDB header: replication/chaperone Chain: A: PDB Molecule: anti-silencing protein 1 and histone h3 chimera; PDBTitle: structure of the histone h3-asf1 chaperone interaction
56	d1td6a	Alignment	not modelled	6.1	31	Fold: Hypothetical protein MPN330 Superfamily: Hypothetical protein MPN330 Family: Hypothetical protein MPN330
57	d1ex4a1	Alignment	not modelled	6.0	63	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
58	c3qatB	Alignment	not modelled	5.8	50	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
59	d1quba5	Alignment	not modelled	5.8	16	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
60	c2qo3A	Alignment	not modelled	5.7	50	PDB header: transferase Chain: A: PDB Molecule: eryaii erythromycin polyketide synthase modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase
61	c1c6vX	Alignment	not modelled	5.7	50	PDB header: dna binding protein Chain: X: PDB Molecule: protein (siu89134); PDBTitle: siv integrase (catalytic domain + dna binding domain comprising2 residues 50-293) mutant with phe 185 replaced by his (f185h)
62	d1c6vx	Alignment	not modelled	5.7	50	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
63	c3pntD	Alignment	not modelled	5.7	50	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: immunity factor for spn; PDBTitle: crystal structure of the streptococcus pyogenes nad+ glycohydrolase2 spn in complex with ifs, the immunity factor for spn
64	d1c1za5	Alignment	not modelled	5.4	16	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
65	c6c9uA	Alignment	not modelled	5.4	50	PDB header: transferase/immune system Chain: A: PDB Molecule: 6-deoxyerythronolide-b synthase erya2, modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase in complex with antibody fragment (fab)
66	c4r1A	Alignment	not modelled	5.3	60	PDB header: transferase Chain: A: PDB Molecule: type i polyketide synthase aves 1; PDBTitle: structural and functional analysis of a loading acyltransferase from2 the avermectin modular polyketide synthase
67	d2i32a1	Alignment	not modelled	5.2	35	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
68	c2i32A	Alignment	not modelled	5.2	35	PDB header: replication chaperone Chain: A: PDB Molecule: anti-silencing factor 1 paralog a; PDBTitle: structure of a human asf1a-hira complex and insights into specificity2 of histone chaperone complex assembly
69	d1s6la2	Alignment	not modelled	5.2	32	Fold: NosL/MerB-like Superfamily: NosL/MerB-like Family: MerB-like
70	c1t60W	Alignment	not modelled	5.2	21	PDB header: structural protein Chain: W: PDB Molecule: type iv collagen; PDBTitle: crystal structure of type iv collagen nc1 domain from2 bovine lens capsule