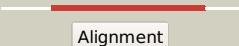



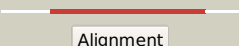



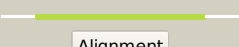

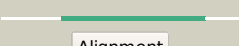

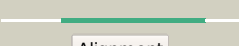






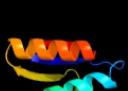



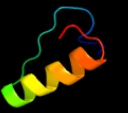

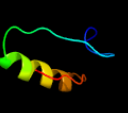


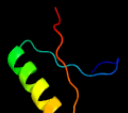

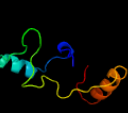


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1331_clpS_1500667_1500972
 Date Wed Jul 31 22:05:43 BST 2019
 Unique Job ID 263b532ec765d1d2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4yxB_	 Alignment		100.0	22	PDB header: protein binding Chain: B; PDB Molecule: atp-dependent clp protease adapter protein clps 2; PDBTitle: the structure of agrobacterium tumefaciens clps2 bound to l-2 phenylalaninamide
2	c3dnjB_	 Alignment		100.0	31	PDB header: peptide binding protein Chain: B; PDB Molecule: atp-dependent clp protease adapter protein clps; PDBTitle: the structure of the caulobacter crescentus clps protease adaptor2 protein in complex with a n-end rule peptide
3	d1r6oc1	 Alignment		100.0	31	Fold: ClpS-like Superfamily: ClpS-like Family: Adaptor protein ClpS (YljA)
4	c4o2xA_	 Alignment		97.5	26	PDB header: transport protein Chain: A; PDB Molecule: maltose-binding periplasmic protein, atp-dependent clp PDBTitle: structure of a malarial protein
5	c2ftcF_	 Alignment		64.7	16	PDB header: ribosome Chain: F; PDB Molecule: 39s ribosomal protein l12, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial l2 ribosome
6	d2zjq51	 Alignment		46.9	17	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
7	c2zjq5_	 Alignment		46.9	17	PDB header: ribosome Chain: 5; PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: interaction of l7 with l11 induced by micrococin binding to the2 deinococcus radiodurans 50s subunit
8	d1dd3a2	 Alignment		44.7	19	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
9	d1nka4	 Alignment		42.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
10	d1ctfa_	 Alignment		40.3	18	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
11	c3mdoB_	 Alignment		33.9	17	PDB header: ligase Chain: B; PDB Molecule: putative phosphoribosylformylglycinamide2 cyclo-ligase; PDBTitle: crystal structure of a putative phosphoribosylformylglycinamide2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution

12	d1a1va2	Alignment		29.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
13	c2f55C	Alignment		24.8	21	PDB header: hydrolase/dna Chain: C: PDB Molecule: polyprotein; PDBTitle: two hepatitis c virus ns3 helicase domains complexed with the same2 strand of dna
14	c2xznM	Alignment		22.3	6	PDB header: ribosome Chain: M: PDB Molecule: rps18e; 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 2
15	d1jr6a	Alignment		22.2	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
16	c3j20O	Alignment		21.8	9	PDB header: ribosome Chain: O: PDB Molecule: 30s ribosomal protein s13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
17	c1giyl	Alignment		20.8	19	PDB header: ribosome Chain: J: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of the ribosome at 5.5 a resolution. this2 file, 1giy, contains the 50s ribosome subunit. the 30s3 ribosome subunit, three trna, and mrna molecules are in the4 file 1gix
18	d1dq3a4	Alignment		18.8	19	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
19	d1r7ma2	Alignment		17.7	19	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
20	d1clia2	Alignment		15.5	19	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
21	c4cdgA	Alignment	not modelled	15.1	16	PDB header: hydrolase Chain: A: PDB Molecule: bloom syndrome protein; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
22	d1uhwa	Alignment	not modelled	14.7	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
23	c3i32A	Alignment	not modelled	14.3	18	PDB header: rna binding protein,hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
24	d2gy9m1	Alignment	not modelled	14.1	5	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
25	c3iz6M	Alignment	not modelled	12.7	10	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18 (s13p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
26	c2zkqm	Alignment	not modelled	12.3	7	PDB header: ribosomal protein/rna Chain: M: 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
27	d1i94m	Alignment	not modelled	11.4	8	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
28	d2phla1	Alignment	not modelled	11.1	7	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein

29	d3bzka1	Alignment	not modelled	11.0	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HHH-containing domain-like
30	c3sk7B_	Alignment	not modelled	10.4	12	PDB header: replication inhibitor Chain: B: PDB Molecule: protein seqa; PDBTitle: crystal structure of v. cholerae seqa
31	d1j3ea_	Alignment	not modelled	10.2	13	Fold: Replication modulator SeqA, C-terminal DNA-binding domain Superfamily: Replication modulator SeqA, C-terminal DNA-binding domain Family: Replication modulator SeqA, C-terminal DNA-binding domain
32	d1utaa_	Alignment	not modelled	10.0	14	Fold: Ferredoxin-like Superfamily: Sporulation related repeat Family: Sporulation related repeat
33	c3a5pD_	Alignment	not modelled	9.9	21	PDB header: sugar binding protein Chain: D: PDB Molecule: haemagglutinin i; PDBTitle: crystal structure of hemagglutinin
34	c2gidP_	Alignment	not modelled	9.7	18	PDB header: translation Chain: P: PDB Molecule: mitochondrial rna-binding protein 2; PDBTitle: crystal structures of trypanosoma brucei mrp1/mrp2
35	c1a1vA_	Alignment	not modelled	9.7	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (ns3 protein); PDBTitle: hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
36	d1v3fa_	Alignment	not modelled	9.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
37	c1wcnA_	Alignment	not modelled	9.3	15	PDB header: rna-binding protein Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: nmr structure of the carboxyterminal domains of escherichia2 coli nusa
38	c5o5jM_	Alignment	not modelled	9.1	4	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
39	d2uubm1	Alignment	not modelled	9.1	7	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
40	c2jgnB_	Alignment	not modelled	9.0	13	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: ddx3 helicase domain
41	d2giaa1	Alignment	not modelled	8.9	18	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Guide RNA binding protein gBP
42	c4zebA_	Alignment	not modelled	8.7	12	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (agrocinopines a PDBTitle: pbp acca from a. tumefaciens c58 in complex with agrocinopine a
43	c6b12B_	Alignment	not modelled	8.5	33	PDB header: antimicrobial protein Chain: B: PDB Molecule: tni2; PDBTitle: structure of tne2 in complex with tni2
44	c2vdcF_	Alignment	not modelled	8.5	19	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadh] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
45	c2z01A_	Alignment	not modelled	8.3	24	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cycloligase; PDBTitle: crystal structure of phosphoribosylaminoimidazole synthetase from2 geobacillus kaustophilus
46	d2g2ja1	Alignment	not modelled	8.2	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
47	c2lcdA_	Alignment	not modelled	8.1	58	PDB header: transcription Chain: A: PDB Molecule: at-rich interactive domain-containing protein 4a; PDBTitle: solution structure of rbbp1 tudor domain
48	d1cmga_	Alignment	not modelled	8.0	10	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
49	d1f1sa3	Alignment	not modelled	8.0	19	Fold: Hyaluronate lyase-like, C-terminal domain Superfamily: Hyaluronate lyase-like, C-terminal domain Family: Hyaluronate lyase-like, C-terminal domain
50	d1kyqa1	Alignment	not modelled	7.8	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
51	c5mmjm_	Alignment	not modelled	7.3	15	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
52	d1n0yb_	Alignment	not modelled	7.2	8	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
53	c3ge5A_	Alignment	not modelled	7.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nad(p)h:fmn oxidoreductase; PDBTitle: crystal structure of a putative nad(p)h:fmn oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution
54	c2z83A_	Alignment	not modelled	7.0	21	PDB header: viral protein Chain: A: PDB Molecule: helicase/nucleoside triphosphatase; PDBTitle: crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a

					resolution 1.8
55	d1n7oa2	Alignment	not modelled	7.0	19 Fold: Hyaluronate lyase-like, C-terminal domain Superfamily: Hyaluronate lyase-like, C-terminal domain Family: Hyaluronate lyase-like, C-terminal domain
56	d2j0sa2	Alignment	not modelled	6.9	9 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
57	d1hv8a2	Alignment	not modelled	6.9	19 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
58	c1x60A	Alignment	not modelled	6.7	23 PDB header: hydrolase Chain: A: PDB Molecule: sporulation-specific n-acetylmuramoyl-l-alanine PDBTitle: solution structure of the peptidoglycan binding domain of 2 b. subtilis cell wall lytic enzyme cwlc
59	d2hkja1	Alignment	not modelled	6.6	12 Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
60	d1t5ia	Alignment	not modelled	6.6	14 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
61	d1w4ma	Alignment	not modelled	6.5	7 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
62	d1di1a	Alignment	not modelled	6.0	12 Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Aristolochene/pentalenene synthase
63	c1ymfA	Alignment	not modelled	5.9	14 PDB header: hydrolase Chain: A: PDB Molecule: genome polyprotein [contains: flavivirin protease ns3 PDBTitle: crystal structure of yellow fever virus ns3 helicase complexed with2 adp
64	c3u5zA	Alignment	not modelled	5.8	11 PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna polymerase accessory protein 62; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
65	c5gi4A	Alignment	not modelled	5.8	13 PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dead; PDBTitle: dead-box rna helicase
66	d1vkwa	Alignment	not modelled	5.7	11 Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: Putative nitroreductase TM1586
67	c1kyqC	Alignment	not modelled	5.7	23 PDB header: oxidoreductase, lyase Chain: C: PDB Molecule: siroheme biosynthesis protein met8; PDBTitle: met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatae involved in siroheme synthesis.
68	c1cliD	Alignment	not modelled	5.7	20 PDB header: ligase Chain: D: PDB Molecule: protein (phosphoribosyl-aminoimidazole synthetase); PDBTitle: x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
69	c2b1uA	Alignment	not modelled	5.3	8 PDB header: metal binding protein Chain: A: PDB Molecule: calmodulin-like protein 5; PDBTitle: solution structure of calmodulin-like skin protein c2 terminal domain
70	c4e8uA	Alignment	not modelled	5.3	38 PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein t8p19.180; PDBTitle: crystal structure of arabidopsis idn2 xs domain along with a small2 segment of adjacent coiled-coil region
71	c1b24A	Alignment	not modelled	5.2	14 PDB header: intron-encoded Chain: A: PDB Molecule: protein (i-dmoi); PDBTitle: i-dmoi, intron-encoded endonuclease
72	d1fsha	Alignment	not modelled	5.2	20 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
73	d2o8ra3	Alignment	not modelled	5.2	15 Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
74	c5xyiS	Alignment	not modelled	5.2	10 PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
75	c2hjbB	Alignment	not modelled	5.2	14 PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase dbpa; PDBTitle: structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein
76	c2jlrA	Alignment	not modelled	5.1	18 PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns3; PDBTitle: dengue virus 4 ns3 helicase in complex with amppnp