
















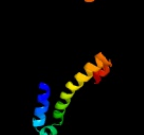



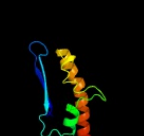

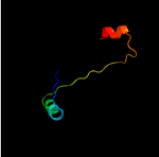

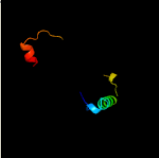

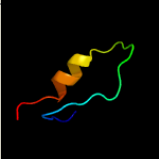
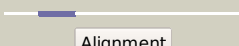
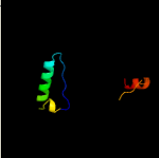
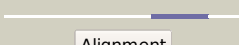
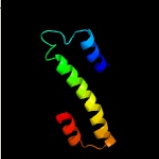
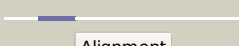
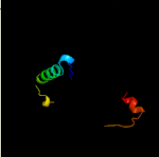

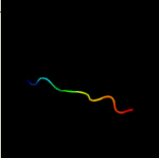

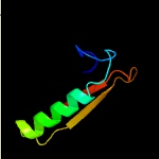

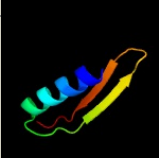



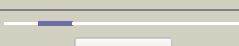
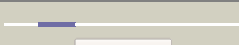




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1366_(-)_1538396_1539217
Date	Wed Jul 31 22:05:47 BST 2019
Unique Job ID	38a6552670157a5c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xnxB_	 Alignment		100.0	20	PDB header: hydrolase, transferase Chain: B: PDB Molecule: bifunctional (p)ppgpp synthase/hydrolase rela; PDBTitle: crystallographic structure of the enzymatically active n-terminal2 domain of the rel protein from mycobacterium tuberculosis
2	c1vj7B_	 Alignment		100.0	18	PDB header: hydrolase, transferase Chain: B: PDB Molecule: bifunctional rela/spot; PDBTitle: crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
3	c5dedA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase yjbm; PDBTitle: crystal structure of the small alarmone synthetase 1 from bacillus2 subtilis bound to its product pppgpp
4	d1vj7a2	 Alignment		100.0	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: RelA/SpoT domain
5	c6fgkA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase ywac; PDBTitle: crystal structure of the small alarmone synthetase 2 from bacillus2 subtilis
6	c3l9dA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: putative gtp pyrophosphokinase; PDBTitle: the crystal structure of smu.1046c from streptococcus mutans ua159
7	d2be3a1	 Alignment		100.0	19	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: RelA/SpoT domain
8	c6ex0B_	 Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of relp (sas2) from staphylococcus aureus bound to2 pppgpp in the post-catalytic state
9	c3u24A_	 Alignment		65.7	17	PDB header: lipid binding protein Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: the structure of a putative lipoprotein of unknown function from2 shewanella oneidensis.
10	d1g71a_	 Alignment		36.0	15	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
11	c4nf9A_	 Alignment		29.4	12	PDB header: cell cycle Chain: A: PDB Molecule: protein casc5; PDBTitle: structure of the knl1/ns1 complex

12	c5suhB_	 Alignment		25.4	27	PDB header: structural protein Chain: B: PDB Molecule: msm0271 protein; PDBTitle: the structure of double ringed trimeric shell protein msm0271 from the2 rmm microcompartment
13	c4ht7G_	 Alignment		23.0	18	PDB header: protein binding Chain: G: PDB Molecule: co2 concentrating mechanism protein p; PDBTitle: co2 concentrating mechanism protein p, ccmp form 2
14	c4ernA_	 Alignment		22.2	27	PDB header: hydrolase Chain: A: PDB Molecule: tfiih basal transcription factor complex helicase xpb PDBTitle: crystal structure of the c-terminal domain of human xpb/ercc-32 excision repair protein at 1.80 a
15	c5v75E_	 Alignment		19.5	11	PDB header: structural protein Chain: E: PDB Molecule: microcompartments protein; PDBTitle: structure of haliangium ochraceum bmc-t ho-5816
16	c3o0yC_	 Alignment		18.1	24	PDB header: lipid binding protein Chain: C: PDB Molecule: lipoprotein; PDBTitle: the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
17	c5v76A_	 Alignment		17.1	16	PDB header: structural protein Chain: A: PDB Molecule: microcompartments protein; PDBTitle: structure of haliangium ochraceum bmc-t ho-3341
18	d2bi7a2	 Alignment		14.3	30	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: UDP-galactopyranose mutase
19	d1v33a_	 Alignment		14.0	17	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
20	d1m55a_	 Alignment		12.4	10	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Replication protein Rep, nuclease domain
21	c3ohmB_	 Alignment	not modelled	12.2	23	PDB header: signaling protein / hydrolase Chain: B: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase PDBTitle: crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3
22	c3f56F_	 Alignment	not modelled	12.2	16	PDB header: structural protein Chain: F: PDB Molecule: csos1d; PDBTitle: the structure of a previously undetected carboxysome shell protein:2 csos1d from prochlorococcus marinus med4
23	c1oegA_	 Alignment	not modelled	11.4	35	PDB header: apolipoprotein Chain: A: PDB Molecule: apolipoprotein e; PDBTitle: peptide of human apoe residues 267-289, nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:sds mole ratio3 of 1:90
24	c3rmsA_	 Alignment	not modelled	11.2	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein svir_20580 from2 saccharomonospora viridis
25	c5j39D_	 Alignment	not modelled	10.9	21	PDB header: structural protein Chain: D: PDB Molecule: rmm microcompartment shell protein msm0275; PDBTitle: the structure of the fused permuted hexameric shell protein msm02752 from the rmm microcompartment
26	d1p5dx4	 Alignment	not modelled	10.3	23	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
27	c6b4aB_	 Alignment	not modelled	9.8	16	PDB header: structural protein Chain: B: PDB Molecule: doublecortin; PDBTitle: crystal structure of the c-terminal domain of doublecortin (tgdcx)2 from toxoplasma gondii me49 PDB header: dna binding protein

28	c4abxB_	Alignment	not modelled	9.7	13	Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
29	c2p6nA_	Alignment	not modelled	9.6	29	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx41; PDBTitle: human dead-box rna helicase ddx41, helicase domain
30	d1bgva2	Alignment	not modelled	9.4	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
31	d1g5ta_	Alignment	not modelled	8.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
32	c1oefA_	Alignment	not modelled	8.6	33	PDB header: apolipoprotein Chain: A: PDB Molecule: apolipoprotein e; PDBTitle: peptide of human apoe residues 263-286, nmr, 5 structures2 at ph 4.8, 37 degrees celsius and peptide:sds mole ratio3 of 1:90
33	c1s1i0_	Alignment	not modelled	8.5	20	PDB header: ribosome Chain: 0: PDB Molecule: 60s ribosomal protein l32; 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.
34	c2l9mA_	Alignment	not modelled	8.4	15	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 2; PDBTitle: structure of ciap1 card
35	d1e52a_	Alignment	not modelled	7.4	21	Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB
36	c3bzjA_	Alignment	not modelled	7.3	18	PDB header: hydrolase Chain: A: PDB Molecule: uv endonuclease; PDBTitle: uvde k229l
37	c6g4ww_	Alignment	not modelled	7.1	22	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s15a; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a
38	c5h29A_	Alignment	not modelled	6.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase/glutathione-related protein; PDBTitle: crystal structure of the ntd_n/c domain of alkylhydroperoxide2 reductase ahpf from enterococcus faecalis (v583)
39	d1tf5a4	Alignment	not modelled	6.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
40	c3earA_	Alignment	not modelled	6.8	23	PDB header: hydrolase Chain: A: PDB Molecule: hera; PDBTitle: novel dimerization motif in the dead box rna helicase hera: form 1,2 partial dimer
41	d1lk6a1	Alignment	not modelled	6.7	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
42	d2z15a1	Alignment	not modelled	6.6	29	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
43	c1r1mA_	Alignment	not modelled	6.5	50	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein class 4; PDBTitle: structure of the ompa-like domain of rmpm from neisseria2 meningitidis
44	d1r1ma_	Alignment	not modelled	6.5	50	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like
45	c4c46B_	Alignment	not modelled	6.5	23	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4, general control protein gcn4; PDBTitle: andrei-n-lvpas fused to gcn4 adaptors
46	c2hvjB_	Alignment	not modelled	6.3	27	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
47	d3e9va1	Alignment	not modelled	6.1	29	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
48	c3iz5h_	Alignment	not modelled	6.0	20	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l7a (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
49	d1t5ia_	Alignment	not modelled	5.9	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
50	c4uj3B_	Alignment	not modelled	5.9	30	PDB header: transport protein Chain: B: PDB Molecule: rab-3a-interacting protein; PDBTitle: crystal structure of human rab11-rabin8-fip3
51	c3j21b_	Alignment	not modelled	5.9	13	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l2p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
52	c2mviA_	Alignment	not modelled	5.8	83	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin plantarican asm1; PDBTitle: structure of the s-glycosylated bacteriocin asm1
						PDB header: dna binding protein/dna Chain: W: PDB Molecule: swi/snf-related matrix-associated actin-

53	c6ne3W_	Alignment	not modelled	5.7	19	dependent regulator PDBTitle: cryo-em structure of singly-bound snf2h-nucleosome complex with snf2h2 bound at shl-2
54	c3j3be_	Alignment	not modelled	5.7	20	PDB header: ribosome Chain: E; PDB Molecule: 60s ribosomal protein l6; PDBTitle: structure of the human 60s ribosomal proteins
55	c4lrVL_	Alignment	not modelled	5.6	40	PDB header: dna binding protein Chain: L; PDB Molecule: dna sulfur modification protein dnde; PDBTitle: crystal structure of dnde from escherichia coli b7a involved in dna2 phosphorothioation modification
56	c6ivuB_	Alignment	not modelled	5.6	17	PDB header: transcription Chain: B; PDB Molecule: rna polymerase sigma factor sigi1; PDBTitle: solution structure of the sigma-anti-sigma factor complex rsgi1n-2 sigi1c from clostridium thermocellum
57	c3zf7i_	Alignment	not modelled	5.5	20	PDB header: ribosome Chain: l; PDB Molecule: 60s ribosomal protein l18; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
58	c2c1iA_	Alignment	not modelled	5.5	18	PDB header: hydrolase Chain: A; PDB Molecule: peptidoglycan glcnac deacetylase; PDBTitle: structure of streptococcus pneumoniae peptidoglycan deacetylase2 (sppgda) d 275 n mutant.
59	d1x93a1	Alignment	not modelled	5.5	7	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
60	c1x93B_	Alignment	not modelled	5.5	7	PDB header: transcription Chain: B; PDB Molecule: hypothetical protein hp0222; PDBTitle: nmr structure of helicobacter pylori hp0222
61	d1vqoy1	Alignment	not modelled	5.4	25	Fold: Barstar-like Superfamily: Ribosomal protein L32e Family: Ribosomal protein L32e
62	c3cceY_	Alignment	not modelled	5.4	25	PDB header: ribosome Chain: Y; PDB Molecule: 50s ribosomal protein l32e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535a
63	c4ct4B_	Alignment	not modelled	5.4	23	PDB header: rna binding protein Chain: B; PDB Molecule: probable atp-dependent rna helicase ddx6; PDBTitle: cnot1 mif4g domain - ddx6 complex
64	d1g64b_	Alignment	not modelled	5.3	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
65	c3vcmP_	Alignment	not modelled	5.1	20	PDB header: hydrolase Chain: P; PDB Molecule: prorenin; PDBTitle: crystal structure of human prorenin