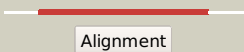

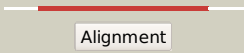



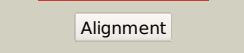


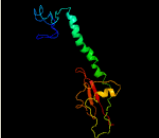
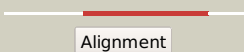

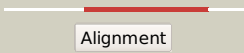

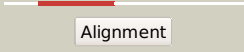

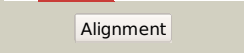



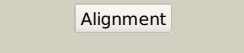
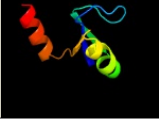
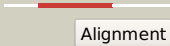

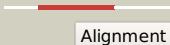

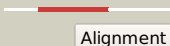


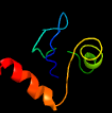




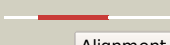

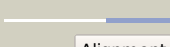

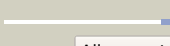
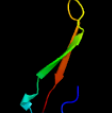
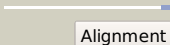

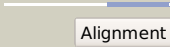
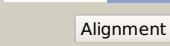
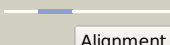
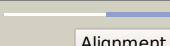
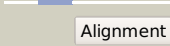
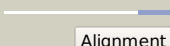


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0056 (rpII)_59406_59864
Date	Tue Jul 23 14:50:08 BST 2019
Unique Job ID	d3482b82df1ca112

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60H_	 Alignment		100.0	73	PDB header: ribosome Chain: H: PDB Molecule: 50s ribosomal protein I9; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	c2qbcH_	 Alignment		100.0	38	PDB header: ribosome Chain: H: PDB Molecule: 50s ribosomal protein I9; PDBTitle: crystal structure of the bacterial ribosome from escherichia coli in2 complex with gentamicin. this file contains the 50s subunit of the3 second 70s ribosome, with gentamicin bound. the entire crystal4 structure contains two 70s ribosomes and is described in remark 400.
3	c2b66I_	 Alignment		100.0	33	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I9; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
4	c2v49I_	 Alignment		100.0	34	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I9; PDBTitle: structure of the ribosome recycling factor bound to the2 thermus thermophilus 70s ribosome with mrna, asl-phe and3 trna-fmet (part 4 of 4). this file contains the 50s4 subunit of molecule 2.
5	c3bboJ_	 Alignment		100.0	33	PDB header: ribosome Chain: J: PDB Molecule: ribosomal protein I9; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
6	d1diva1	 Alignment		99.9	30	Fold: Ribosomal protein L9 C-domain Superfamily: Ribosomal protein L9 C-domain Family: Ribosomal protein L9 C-domain
7	d2gycf1	 Alignment		99.9	35	Fold: Ribosomal protein L9 C-domain Superfamily: Ribosomal protein L9 C-domain Family: Ribosomal protein L9 C-domain
8	d2gycf2	 Alignment		99.8	44	Fold: MbtH/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
9	c4ce4I_	 Alignment		99.8	45	PDB header: ribosome Chain: I: PDB Molecule: mrpl9; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
10	d2j01i2	 Alignment		99.8	45	Fold: MbtH/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
11	d2hbaa1	 Alignment		99.8	38	Fold: MbtH/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain

12	d1cqua_		Alignment		99.8	36	Fold: MbTH/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
13	c4v19l_		Alignment		99.8	45	PDB header: ribosome Chain: I: PDB Molecule: mitoribosomal protein bl9m, mrpl9; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
14	c1pnyF_		Alignment		99.8	45	PDB header: ribosome Chain: F: PDB Molecule: 50s ribosomal protein I9; PDBTitle: crystal structure of the wild type ribosome from e. coli, 50s subunit2 of 70s ribosome. this file, 1pny, contains only molecules of the 50s3 ribosomal subunit. the 30s subunit is in the pdb file 1pnx.
15	c1sm1F_		Alignment		99.8	45	PDB header: ribosome/antibiotic Chain: F: PDB Molecule: 50s ribosomal protein I9; PDBTitle: complex of the large ribosomal subunit from deinococcus radiodurans2 with quinupristin and dalfopristin
16	d2j01i1		Alignment		99.8	27	Fold: Ribosomal protein L9 C-domain Superfamily: Ribosomal protein L9 C-domain Family: Ribosomal protein L9 C-domain
17	c1vw4G_		Alignment		98.4	21	PDB header: ribosome Chain: G: PDB Molecule: 54s ribosomal protein I50, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
18	c4qjty_		Alignment		94.7	46	PDB header: ribosome Chain: Y: PDB Molecule: PDBTitle: crystal structure of elongation factor 4 (ef4/lepa) bound to the2 thermus thermophilus 70s ribosome, 30s subunit of the 70s ribosome
19	d3ddja1		Alignment		29.3	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
20	c6nrwA_		Alignment		29.0	12	PDB header: cell adhesion Chain: A: PDB Molecule: dpr1; PDBTitle: crystal structure of dpr1 ig1 bound to dip-eta ig1
21	c3rbgB_		Alignment	not modelled	27.1	18	PDB header: immune system Chain: B: PDB Molecule: cytotoxic and regulatory t-cell molecule; PDBTitle: crystal structure analysis of class-i mhc restricted t-cell associated2 molecule
22	d2j9la1		Alignment	not modelled	23.0	27	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
23	d1vr9a3		Alignment	not modelled	22.1	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
24	c4fryA_		Alignment	not modelled	21.8	27	PDB header: signaling protein Chain: A: PDB Molecule: putative signal-transduction protein with cbs domains; PDBTitle: the structure of a putative signal-transduction protein with cbs2 domains from burkholderia ambifaria mc40-6
25	c2k50A_		Alignment	not modelled	21.4	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: replication factor a related protein; PDBTitle: solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
26	c2pfiA_		Alignment	not modelled	20.4	21	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein clc-ka; PDBTitle: crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
27	d1nksa_		Alignment	not modelled	20.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
28	c6cozB_		Alignment	not modelled	20.2	32	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic

						domain
29	c2afdA	Alignment	not modelled	20.1	16	PDB header: ligand binding protein Chain: A: PDB Molecule: protein asl1650; PDBTitle: solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
30	c2or7A	Alignment	not modelled	18.7	17	PDB header: immune system Chain: A: PDB Molecule: t-cell immunoglobulin and mucin domain- PDBTitle: tim-2
31	c1vr9B	Alignment	not modelled	18.4	18	PDB header: unknown function Chain: B: PDB Molecule: cbs domain protein/act domain protein; PDBTitle: crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
32	c6nrrA	Alignment	not modelled	18.1	21	PDB header: cell adhesion Chain: A: PDB Molecule: defective proboscis extension response 11, isoform b; PDBTitle: crystal structure of dpr11 ig1 bound to dip-gamma ig+ig2
33	d2yzia1	Alignment	not modelled	17.4	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
34	c3lqnA	Alignment	not modelled	16.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
35	c3ddjA	Alignment	not modelled	16.1	17	PDB header: amp-binding protein Chain: A: PDB Molecule: cbs domain-containing protein; PDBTitle: crystal structure of a cbs domain-containing protein in complex with2 amp (sso3205) from sulfolobus solfataricus at 1.80 a resolution
36	d1q1va	Alignment	not modelled	16.0	17	Fold: Another 3-helical bundle Superfamily: DEK C-terminal domain Family: DEK C-terminal domain
37	c4owxB	Alignment	not modelled	15.5	31	PDB header: dna binding protein/dna Chain: B: PDB Molecule: soss complex subunit b1; PDBTitle: structural basis of soss1 in complex with a 12nt ssdna
38	c3m45D	Alignment	not modelled	15.4	15	PDB header: cell adhesion Chain: D: PDB Molecule: cell adhesion molecule 2; PDBTitle: crystal structure of ig1 domain of mouse syncam 2
39	d1o50a3	Alignment	not modelled	15.0	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
40	c3kpbA	Alignment	not modelled	14.6	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mj0100; PDBTitle: crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
41	c3gbyA	Alignment	not modelled	13.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ct1051; PDBTitle: crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
42	d1b8za	Alignment	not modelled	13.7	15	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
43	c2ouxB	Alignment	not modelled	13.7	23	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
44	c3e0eA	Alignment	not modelled	13.6	43	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 large mrr110b
45	c1x37A	Alignment	not modelled	13.5	38	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease la 1; PDBTitle: structure of bacillus subtilis lon protease ssd domain
46	c4gitA	Alignment	not modelled	13.4	50	PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of alpha sub-domain of lon protease from2 brevibacillus thermoruber
47	d2ef7a1	Alignment	not modelled	12.8	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
48	d2d7oa1	Alignment	not modelled	12.6	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
49	c4nocA	Alignment	not modelled	12.5	14	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein with cbs domains; PDBTitle: the crystal structure of a cbs domain-containing protein of unknown2 function from kribbella flavida dsm 17836.
50	c2ds4A	Alignment	not modelled	12.4	19	PDB header: protein binding Chain: A: PDB Molecule: tripartite motif protein 45; PDBTitle: solution structure of the filamin domain from human2 tripartite motif protein 45
51	c2emqA	Alignment	not modelled	12.4	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
52	d1m55a	Alignment	not modelled	12.3	35	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Replication protein Rep, nuclease domain
53	c3ctuB	Alignment	not modelled	12.2	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4

54	d1j98a_	Alignment	not modelled	12.1	18	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
55	c2yvxD_	Alignment	not modelled	12.1	24	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
56	c3rghA_	Alignment	not modelled	12.0	15	PDB header: cell adhesion Chain: A: PDB Molecule: filamin-a; PDBTitle: structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
57	d1k1xa1	Alignment	not modelled	11.6	43	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: 4-alpha-glucanotransferase, domain 2
58	d1j6xa_	Alignment	not modelled	11.6	13	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
59	d1qzma_	Alignment	not modelled	11.5	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
60	c3nqrD_	Alignment	not modelled	11.3	16	PDB header: transport protein Chain: D: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: a putative cbs domain-containing protein from salmonella typhimurium2 lt2
61	d2d4za3	Alignment	not modelled	11.3	34	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
62	d1ixla_	Alignment	not modelled	11.1	33	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
63	c2p9mD_	Alignment	not modelled	11.1	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0922; PDBTitle: crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
64	c2n5iA_	Alignment	not modelled	11.0	12	PDB header: transport protein Chain: A: PDB Molecule: peptidyl carrier protein pltI; PDBTitle: pltI-pyrrolyl
65	c6cxtA_	Alignment	not modelled	10.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of fad-dependent dehydrogenase
66	c2d4zB_	Alignment	not modelled	10.6	34	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
67	c3lhhA_	Alignment	not modelled	10.6	24	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
68	c4bphA_	Alignment	not modelled	10.5	9	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 2; PDBTitle: high resolution crystal structure of bacillus subtilis dltc
69	d1o7ia_	Alignment	not modelled	10.5	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
70	c4ehxA_	Alignment	not modelled	10.5	28	PDB header: transferase Chain: A: PDB Molecule: tetraacyldisaccharide 4'-kinase; PDBTitle: crystal structure of lpxk from aquifex aeolicus at 1.9 angstrom2 resolution
71	c2yvzA_	Alignment	not modelled	10.4	29	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
72	c5iipA_	Alignment	not modelled	10.4	31	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
73	c6c4qA_	Alignment	not modelled	10.4	21	PDB header: transport protein Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis
74	c5dzoA_	Alignment	not modelled	10.1	23	PDB header: immune system Chain: A: PDB Molecule: hepatitis a virus cellular receptor 1; PDBTitle: crystal structure of human t-cell immunoglobulin and mucin domain2 protein 1
75	d2ooxe2	Alignment	not modelled	10.0	26	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
76	d1wlha1	Alignment	not modelled	9.6	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
77	c4h5sB_	Alignment	not modelled	9.5	21	PDB header: cell adhesion Chain: B: PDB Molecule: cell adhesion molecule 1; PDBTitle: complex structure of nec1-2 and crtam
78	d2e9ia1	Alignment	not modelled	9.4	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
79	c1s1i0_	Alignment	not modelled	9.4	42	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, l31i, contains 60s subunit. the 40s4 ribosomal subunit is in file l31h.

80	d1yava3	Alignment	not modelled	9.4	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
81	c2auvA	Alignment	not modelled	9.3	26	PDB header: oxidoreductase Chain: A: PDB Molecule: potential nad-reducing hydrogenase subunit; PDBTitle: solution structure of hndac : a thioredoxin-like [2fe-2s] ₂ ferredoxin involved in the nadp-reducing hydrogenase3 complex
82	d1u2ca1	Alignment	not modelled	9.3	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cadherin-like Family: Dystroglycan, N-terminal domain
83	d1zfja4	Alignment	not modelled	9.3	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
84	d1nunb2	Alignment	not modelled	9.2	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: ! set domains
85	c2qstB	Alignment	not modelled	9.1	9	PDB header: cell adhesion Chain: B: PDB Molecule: carcinoembryonic antigen-related cell adhesion PDBTitle: crystal structure of the v39c mutant of the n-terminal2 domain of carcinoembryonic antigen (cea)
86	c2ehtA	Alignment	not modelled	9.1	12	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
87	c3kxrA	Alignment	not modelled	8.9	31	PDB header: transport protein Chain: A: PDB Molecule: magnesium transporter, putative; PDBTitle: structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
88	d2b78a1	Alignment	not modelled	8.6	21	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)
89	c1z9mA	Alignment	not modelled	8.5	11	PDB header: cell adhesion Chain: A: PDB Molecule: gapa225; PDBTitle: crystal structure of nectin-like molecule-1 protein domain 1
90	c2mf4A	Alignment	not modelled	8.4	19	PDB header: transferase Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: 1h, 13c, 15n chemical shift assignments of streptomyces virginiae vira2 acp5a
91	c2l7yA	Alignment	not modelled	8.4	16	PDB header: structural protein Chain: A: PDB Molecule: putative endo-beta-n-acetylglucosaminidase; PDBTitle: solution structure of a putative surface protein
92	d2d7ma1	Alignment	not modelled	8.4	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
93	c2k75A	Alignment	not modelled	8.3	19	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein ta0387; PDBTitle: solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
94	c3ns4A	Alignment	not modelled	8.3	56	PDB header: protein binding Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 53; PDBTitle: structure of a c-terminal fragment of its vps53 subunit suggests2 similarity of garp to a family of tethering complexes
95	d1dv5a	Alignment	not modelled	8.3	6	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: apo-D-alanyl carrier protein
96	c3fioB	Alignment	not modelled	8.2	16	PDB header: nucleotide binding protein, metal bindin protein Chain: B: PDB Molecule: a cystathionine beta-synthase domain PDBTitle: crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
97	c4mz3A	Alignment	not modelled	8.1	20	PDB header: membrane protein Chain: A: PDB Molecule: sodium channel subunit beta-4; PDBTitle: crystal structure of the voltage-gated sodium channel beta 4 subunit2 extracellular domain, c131w mutant
98	d1nq4a	Alignment	not modelled	8.1	23	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
99	c5abrB	Alignment	not modelled	8.1	15	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin, 2fe-2s; PDBTitle: structure of fesi protein from azotobacter vinelandii