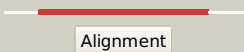

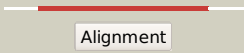

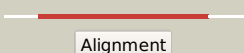

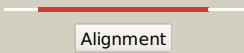

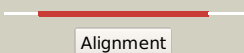
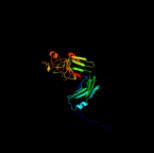
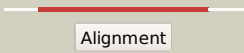

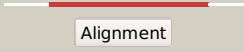

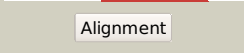



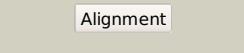
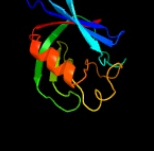
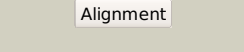
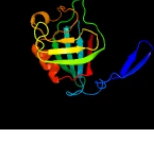


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0116c_(-)_140265_141020
Date	Tue Jul 23 14:50:15 BST 2019
Unique Job ID	a126ae3df323137e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3u1qB_	 Alignment		100.0	44	PDB header: peptidoglycan binding protein Chain: B: PDB Molecule: mycobacteria tuberculosis ld-transpeptidase type 2; PDBTitle: crystal structure of m. tuberculosis ld-transpeptidase type 2 with 2-2 mercaptoethanol
2	c4xvoB_	 Alignment		100.0	62	PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: l,d-transpeptidase from mycobacterium smegmatis
3	c4jmxA_	 Alignment		100.0	100	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable l,d-transpeptidase ldtA; PDBTitle: structure of ld transpeptidase ldtmt1 in complex with imipenem
4	c3vynB_	 Alignment		100.0	41	PDB header: transferase Chain: B: PDB Molecule: probable conserved lipoprotein lpps; PDBTitle: crystal structure of mycobacterium tuberculosis l,d-transpeptidase2 ldtmt2 n55 truncation mutant (residue 55-408)
5	c4z7aA_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: mycobacterium tuberculosis (3,3)l,d-transpeptidase type 5; PDBTitle: structural and biochemical characterization of a non-functionally2 redundant m. tuberculosis (3,3) l,d-transpeptidase, ldtmt5.
6	c4k73A_	 Alignment		100.0	57	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: x-ray crystal structure of an l,d-transpeptidase from mycobacterium2 tuberculosis h37rv
7	c2hklB_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
8	c5bmqA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of l,d-transpeptidase (yku) from stackebrandtia2 nassauensis
9	dlzata1	 Alignment		100.0	29	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
10	dlv7ma1	 Alignment		100.0	24	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
11	c1y7mB_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14040; PDBTitle: crystal structure of the b. subtilis ykud protein at 2 a2 resolution

12	c4lzhA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: l,d-transpeptidase from klebsiella pneumoniae
13	c4lpqA_	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of the l,d-transpeptidase (residues 123-326) from2 xylanimonas cellulositytica dsm 15894
14	c4y4vB_	Alignment		99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd6 in the d-ala-bound state
15	c4xxtA_	Alignment		99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: fusion of predicted zn-dependent amidase/peptidase (cell PDBTitle: crystal structure of fused zn-dependent2 amidase/peptidase/peptodoglycan-binding domain-containing protein3 from clostridium acetobutylicum atcc 824
16	c4hu2A_	Alignment		99.8	35	PDB header: unknown function Chain: A: PDB Molecule: probable conserved lipoprotein lpps; PDBTitle: crystal structure of ldtmt2, a l,d-transpeptidase from mycobacterium2 tuberculosis: domain a and b
17	c6ntwA_	Alignment		99.4	18	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable l,d-transpeptidase yccb; PDBTitle: crystal structure of e. coli yccb
18	dlcz5a1	Alignment		56.9	15	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
19	dl1x2a_	Alignment		54.3	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
20	c1eqqD_	Alignment		51.2	16	PDB header: replication/rna Chain: D: PDB Molecule: single stranded dna binding protein; PDBTitle: single stranded dna binding protein and ssdna complex
21	c6rteB_	Alignment	not modelled	48.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
22	c2vw9B_	Alignment	not modelled	45.7	16	PDB header: dna-binding protein Chain: B: PDB Molecule: single-stranded dna binding protein; PDBTitle: single stranded dna binding protein complex from2 helicobacter pylori
23	c3lgjA_	Alignment	not modelled	44.2	18	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
24	c5xgtA_	Alignment	not modelled	39.7	16	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of the n-terminal domain of staphylococcus aureus2 single-stranded dna-binding protein ssba at 1.82 angstrom resolution
25	c1z9fa_	Alignment	not modelled	39.2	24	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
26	c5gqoB_	Alignment	not modelled	37.9	28	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein; PDBTitle: structure of the second single stranded dna binding protein (ssbb)2 from mycobacterium smegmatis
27	dl1eyga_	Alignment	not modelled	36.9	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
28	c3tqyA_	Alignment	not modelled	35.1	20	PDB header: transferase Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii

29	c5odnG	Alignment	not modelled	34.3	8	PDB header: dna binding protein Chain: G: PDB Molecule: single-stranded dna-binding protein; PDBTitle: salinibacter ruber single-strand binding protein
30	c3pe9D	Alignment	not modelled	33.0	11	PDB header: unknown function Chain: D: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
31	d2piaa1	Alignment	not modelled	32.8	29	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
32	d1qvca	Alignment	not modelled	32.7	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
33	c1qvcA	Alignment	not modelled	32.7	16	PDB header: dna binding protein Chain: A: PDB Molecule: single stranded dna binding protein monomer; PDBTitle: crystal structure analysis of single stranded dna binding protein2 (ssb) from e.coli
34	d3ulla	Alignment	not modelled	32.5	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
35	c6nfgC	Alignment	not modelled	32.0	24	PDB header: metal binding protein Chain: C: PDB Molecule: copc; PDBTitle: copc from pseudomonas fluorescens
36	c4damA	Alignment	not modelled	31.4	35	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein 1; PDBTitle: crystal structure of small single-stranded dna-binding protein from2 streptomyces coelicolor
37	c1ue7A	Alignment	not modelled	31.2	24	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis
38	c3pgzB	Alignment	not modelled	30.2	14	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of a single strand binding protein (ssb) from2 bartonella henselae
39	c3vdyA	Alignment	not modelled	27.3	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded dna-binding protein sbb; PDBTitle: b. subtilis sbb/ssdna
40	d2c9qa1	Alignment	not modelled	27.2	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
41	c3eivB	Alignment	not modelled	26.3	15	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein 2; PDBTitle: crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor
42	d3btaa1	Alignment	not modelled	26.1	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Clostridium neurotoxins, the second last domain
43	c5ch7E	Alignment	not modelled	23.5	16	PDB header: oxidoreductase Chain: E: PDB Molecule: dmsO reductase family type ii enzyme, molybdopterin PDBTitle: crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
44	c4p9IA	Alignment	not modelled	22.9	26	PDB header: transport protein Chain: A: PDB Molecule: ryanodine receptor 2; PDBTitle: crystal structure of mouse ryanodine receptor 2 spry2 domain (1080-2 1253) disease mutant a1107m
45	d1gawa1	Alignment	not modelled	22.4	25	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
46	d1ue1a	Alignment	not modelled	21.6	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
47	c3ulpC	Alignment	not modelled	21.2	14	PDB header: dna binding protein/dna Chain: C: PDB Molecule: single-strand binding protein; PDBTitle: plasmodium falciparum ssb complex with ssdna
48	c2xc8B	Alignment	not modelled	20.7	23	PDB header: viral protein Chain: B: PDB Molecule: gene 22 product; PDBTitle: crystal structure of the gene 22 product of the bacillus subtilis spp12 phage
49	c5zktA	Alignment	not modelled	20.6	29	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
50	d2slla1	Alignment	not modelled	19.7	16	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Leech intramolecular trans-sialidase, N-terminal domain
51	c5icuA	Alignment	not modelled	19.5	18	PDB header: chaperone Chain: A: PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylosinus trichosporium ob3b
52	d1cqxa2	Alignment	not modelled	19.1	29	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
53	d2bmwa1	Alignment	not modelled	18.9	13	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
54	d1gvha2	Alignment	not modelled	18.4	29	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
						PDB header: oxidoreductase

55	c1h5nC_	Alignment	not modelled	18.3	21	Chain: C; PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
56	d1fnda1	Alignment	not modelled	18.2	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
57	d1tvca1	Alignment	not modelled	17.4	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
58	c5zktB_	Alignment	not modelled	17.1	29	PDB header: transcription Chain: B; PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
59	d1e1oa1	Alignment	not modelled	15.7	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
60	c2mnuB_	Alignment	not modelled	15.2	13	PDB header: cell adhesion Chain: B; PDB Molecule: apt; PDBTitle: backbone and side chain 1h, 13c, and 15n chemical shift assignments2 for edb and specific binding aptide
61	c4qt6A_	Alignment	not modelled	15.2	31	PDB header: transport protein Chain: A; PDB Molecule: probable e3 ubiquitin-protein ligase herc1; PDBTitle: crystal structure of the spry domain of human herc1
62	c3flpJ_	Alignment	not modelled	15.1	24	PDB header: sugar binding protein Chain: J; PDB Molecule: sap-like pentraxin; PDBTitle: crystal structure of native heptameric sap-like pentraxin2 from limulus polyphemus
63	c6er3B_	Alignment	not modelled	14.5	17	PDB header: sugar binding protein Chain: B; PDB Molecule: bnr/asp-box repeat protein; PDBTitle: ruminococcus gnavus it-sialidase cbm40 bound to alpha2,3 sialyllactose
64	c4ywka_	Alignment	not modelled	14.4	31	PDB header: cell cycle Chain: A; PDB Molecule: cell division control protein 21; PDBTitle: pyrococcus furiosus mcm n-terminal domain with zinc-binding subdomain2 b deleted
65	c4obiA_	Alignment	not modelled	14.3	6	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1312 family protein (ef3258) from2 enterococcus faecalis v583 at 1.73 a resolution
66	d1sm4a1	Alignment	not modelled	14.2	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
67	c2iheA_	Alignment	not modelled	14.0	27	PDB header: dna binding protein Chain: A; PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
68	d1krha1	Alignment	not modelled	13.6	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
69	d1eg7a_	Alignment	not modelled	13.4	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
70	c3pe9B_	Alignment	not modelled	13.3	12	PDB header: unknown function Chain: B; PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
71	d1wjja_	Alignment	not modelled	13.3	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
72	c5a4jC_	Alignment	not modelled	13.2	44	PDB header: ligase Chain: C; PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of fthfs1 from t. acetoxydans re1
73	c4p9jC_	Alignment	not modelled	13.0	26	PDB header: transport protein Chain: C; PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of rabbit ryanodine receptor 1 spry2 domain (1070-2 1246)
74	d1e32a1	Alignment	not modelled	12.9	22	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
75	d1bbua1	Alignment	not modelled	12.6	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
76	c3do6B_	Alignment	not modelled	12.4	33	PDB header: ligase Chain: B; PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution
77	c5n1tM_	Alignment	not modelled	12.0	21	PDB header: oxidoreductase Chain: M; PDB Molecule: copc; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
78	d1y5ia1	Alignment	not modelled	12.0	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
79	d1a8da1	Alignment	not modelled	11.8	11	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Clostridium neurotoxins, the second last domain
80	d1k78a1	Alignment	not modelled	11.8	71	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
81	c2v73B_	Alignment	not modelled	11.7	12	PDB header: sugar-binding protein Chain: B; PDB Molecule: putative exo-alpha-sialidase; PDBTitle: the structure of the family 40 cbm from c. perfringens nanj2 in complex with a sialic acid containing molecule

82	c4pogC_	Alignment	not modelled	11.5	33	PDB header: replication, dna binding protein/dna Chain: C: PDB Molecule: cell division control protein 21; PDBTitle: mcm-ssdna co-crystal structure
83	c2vf6C_	Alignment	not modelled	10.9	38	PDB header: dna binding protein Chain: C: PDB Molecule: minichromosome maintenance protein mcm; PDBTitle: structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
84	c2vdaB_	Alignment	not modelled	10.8	26	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex
85	c4owtB_	Alignment	not modelled	10.8	28	PDB header: dna binding protein Chain: B: PDB Molecule: soxs complex subunit b1; PDBTitle: structural basis of soxs1 complex assembly
86	d1lka_	Alignment	not modelled	10.6	17	Fold: Head-binding domain of phage P22 tailspike protein Superfamily: Head-binding domain of phage P22 tailspike protein Family: Head-binding domain of phage P22 tailspike protein
87	d1ogya1	Alignment	not modelled	10.4	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
88	d1qfa1	Alignment	not modelled	10.3	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
89	d6paxa1	Alignment	not modelled	10.1	57	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
90	c4me3A_	Alignment	not modelled	10.1	20	PDB header: replication Chain: A: PDB Molecule: dna replication licensing factor mcm related protein; PDBTitle: 1.8 angstrom crystal structure of the n-terminal domain of an archaeal2 mcm
91	c1ltE_	Alignment	not modelled	9.9	40	PDB header: replication Chain: E: PDB Molecule: dna replication initiator (cdc21/cdc54); PDBTitle: the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
92	c6cqoH_	Alignment	not modelled	9.6	11	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)
93	c6hinA_	Alignment	not modelled	9.5	15	PDB header: membrane protein Chain: A: PDB Molecule: 5-hydroxytryptamine receptor 3a; PDBTitle: mouse serotonin 5-HT ₃ receptor, serotonin-bound, f conformation
94	c4azzB_	Alignment	not modelled	9.5	9	PDB header: hydrolase Chain: B: PDB Molecule: levanase; PDBTitle: carbohydrate binding module cbm66 from bacillus subtilis
95	d1qksa2	Alignment	not modelled	9.4	20	Fold: 8-bladed beta-propeller Superfamily: C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase Family: C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase
96	d1c1a_	Alignment	not modelled	9.2	17	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
97	c2kd2A_	Alignment	not modelled	9.2	32	PDB header: apoptosis Chain: A: PDB Molecule: fas apoptotic inhibitory molecule 1; PDBTitle: nmr structure of faim-ctd
98	c5jiaH_	Alignment	not modelled	9.1	25	PDB header: ran-binding protein Chain: H: PDB Molecule: ran-binding protein 10; PDBTitle: the crystal structure of ius-spry domain from ranbp10
99	d1lta_	Alignment	not modelled	8.9	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA replication initiator (cdc21/cdc54) N-terminal domain