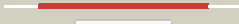



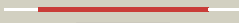
















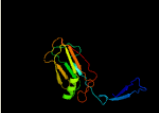


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1433_(-)_1611440_1612255
Date	Wed Jul 31 22:05:54 BST 2019
Unique Job ID	d315fd095e46c4a1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3vynB_	 Alignment		100.0	35	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)
2	c3u1qB_	 Alignment		100.0	38	PDB header: peptidoglycan binding protein Chain: B: PDB Molecule: mycobacteria tuberculosis l,d-transpeptidase type 2; PDBTitle: crystal structure of m. tuberculosis l,d-transpeptidase type 2 with 2-2 mercaptoethanol
3	c4z7aA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: mycobacterium tuberculosis (3,3),d-transpeptidase type 5; PDBTitle: structural and biochemical characterization of a non-functionally2 redundant m. tuberculosis (3,3) l,d-transpeptidase, ldtmt5.
4	c4k73A_	 Alignment		100.0	98	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: x-ray crystal structure of an l,d-transpeptidase from mycobacterium2 tuberculosis h37rv
5	c4xvoB_	 Alignment		100.0	50	PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: l,d-transpeptidase from mycobacterium smegmatis
6	c4jmxA_	 Alignment		100.0	50	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable l,d-transpeptidase ldtmt1; PDBTitle: structure of l,d-transpeptidase ldtmt1 in complex with imipenem
7	c2hklB_	 Alignment		100.0	19	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	24	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	d1y7ma1	 Alignment		99.9	19	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
10	d1zata1	 Alignment		99.9	27	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
11	c4hu2A_	 Alignment		99.9	29	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

12	c1y7mB_	Alignment		99.9	19	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
13	c4lzhA_	Alignment		99.9	23	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: l,d-transpeptidase from klebsiella pneumoniae
14	c4lpqA_	Alignment		99.8	17	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
15	c4xxtA_	Alignment		99.8	20	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	c4y4vB_	Alignment		99.7	20	PDB header: hydrolase Chain: B: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd6 in the d-ala-bound state
17	c6ntwA_	Alignment		98.9	20	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable l,d-transpeptidase yccb; PDBTitle: crystal structure of e. coli yccb
18	dlzata2	Alignment		91.7	6	Fold: L,D-transpeptidase pre-catalytic domain-like Superfamily: L,D-transpeptidase pre-catalytic domain-like Family: L,D-transpeptidase pre-catalytic domain-like
19	d6paxa1	Alignment		33.2	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
20	dlcz5a1	Alignment		31.7	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
21	c6nfgC_	Alignment	not modelled	30.6	15	PDB header: metal binding protein Chain: C: PDB Molecule: copc; PDBTitle: copc from pseudomonas fluorescens
22	c5ch7E_	Alignment	not modelled	30.3	15	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
23	d1ix2a_	Alignment	not modelled	28.2	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
24	c2mnuB_	Alignment	not modelled	27.7	20	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
25	c3kmIB_	Alignment	not modelled	26.1	18	PDB header: viral protein Chain: B: PDB Molecule: coat protein; PDBTitle: circular permutant of the tobacco mosaic virus
26	d1lka_	Alignment	not modelled	24.2	10	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
27	c5n1tM_	Alignment	not modelled	23.2	33	PDB header: oxidoreductase Chain: M: PDB Molecule: copc; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
28	d1eg7a_	Alignment	not modelled	22.8	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like

29	c5a4jC_	Alignment	not modelled	22.6	39	PDB header: ligase Chain: C: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of fthfs1 from t.acetoxydans re1
30	c5zktA_	Alignment	not modelled	19.4	29	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
31	c3do6B_	Alignment	not modelled	17.3	28	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
32	c5zktB_	Alignment	not modelled	16.8	29	PDB header: transcription Chain: B: PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
33	d1wjja_	Alignment	not modelled	16.4	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
34	c1h5nC_	Alignment	not modelled	16.1	19	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
35	c4wwxY_	Alignment	not modelled	16.0	17	PDB header: hydrolase, ligase Chain: Y: PDB Molecule: v(d)j recombination-activating protein 2; PDBTitle: crystal structure of the core rag1/2 recombinase
36	c2vkyB_	Alignment	not modelled	15.6	10	PDB header: viral protein Chain: B: PDB Molecule: tail protein, piignc4; PDBTitle: headbinding domain of phage p22 tailspike c-terminally fused to2 isoleucine zipper piignc4 (chimera i)
37	d1ogya1	Alignment	not modelled	15.5	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d1k78a1	Alignment	not modelled	15.5	71	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
39	c5cupB_	Alignment	not modelled	15.4	27	PDB header: transferase Chain: B: PDB Molecule: phosphate propanoyltransferase; PDBTitle: structure of rhodopseudomonas palustris pdul - phosphate bound form
40	c3bbnD_	Alignment	not modelled	14.6	13	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
41	d1y5ia1	Alignment	not modelled	13.2	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
42	c1s1hO_	Alignment	not modelled	12.6	38	PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s11; 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.
43	c4owtB_	Alignment	not modelled	12.6	30	PDB header: dna binding protein Chain: B: PDB Molecule: soSS complex subunit b1; PDBTitle: structural basis of soSS1 complex assembly
44	d2gy9d1	Alignment	not modelled	12.2	27	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
45	c3j6vO_	Alignment	not modelled	12.2	23	PDB header: ribosome Chain: Q: PDB Molecule: 28s ribosomal protein s17, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
46	d2gy9q1	Alignment	not modelled	12.0	46	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
47	c3lgjA_	Alignment	not modelled	11.8	15	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
48	c2vw9B_	Alignment	not modelled	11.8	21	PDB header: dna-binding protein Chain: B: PDB Molecule: single-stranded dna binding protein; PDBTitle: single stranded dna binding protein complex from2 helicobacter pylori
49	d2gp4a1	Alignment	not modelled	11.6	28	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
50	c5o5jO_	Alignment	not modelled	11.2	38	PDB header: ribosome Chain: Q: PDB Molecule: 30s ribosomal protein s17; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
51	c1r1gA_	Alignment	not modelled	11.2	67	PDB header: toxin Chain: A: PDB Molecule: neurotoxin bmk37; PDBTitle: crystal structure of the scorpion toxin bmbkttx1
52	c1r1gB_	Alignment	not modelled	11.2	67	PDB header: toxin Chain: B: PDB Molecule: neurotoxin bmk37; PDBTitle: crystal structure of the scorpion toxin bmbkttx1
53	d1r1ga_	Alignment	not modelled	11.2	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
54	c3j3aL_	Alignment	not modelled	10.9	50	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s11; PDBTitle: structure of the human 40s ribosomal proteins
						Fold: Alpha-L RNA-binding motif

55	d1c06a_	Alignment	not modelled	10.3	27	Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
56	c3bbnQ_	Alignment	not modelled	10.3	31	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein s17; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
57	c5xgtA_	Alignment	not modelled	10.2	21	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
58	d2piaa1	Alignment	not modelled	10.1	25	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
59	c3d12A_	Alignment	not modelled	10.0	38	PDB header: hydrolase/membrane protein Chain: A: PDB Molecule: hemagglutinin-neuraminidase; PDBTitle: crystal structures of nipah virus g attachment glycoprotein in complex2 with its receptor ephrin-b3
60	d1hvxal	Alignment	not modelled	10.0	13	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
61	c5o5jD_	Alignment	not modelled	9.8	27	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
62	c2zkqq_	Alignment	not modelled	9.5	46	PDB header: ribosomal protein/rna Chain: Q: 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
63	d2uubd1	Alignment	not modelled	9.5	30	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
64	d2jioa1	Alignment	not modelled	9.4	32	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
65	c2n59A_	Alignment	not modelled	9.1	19	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein csgh; PDBTitle: solution structure of r. palustris csgh
66	c5t5iL_	Alignment	not modelled	8.9	24	PDB header: oxidoreductase Chain: L: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdd; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
67	c2mn5A_	Alignment	not modelled	8.5	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: copsin; PDBTitle: nmr structure of copsin
68	c1z9fA_	Alignment	not modelled	8.4	25	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
69	c5odnG_	Alignment	not modelled	8.4	21	PDB header: dna binding protein Chain: G: PDB Molecule: single-stranded dna-binding protein; PDBTitle: salinibacter ruber single-strand binding protein
70	c1eqqD_	Alignment	not modelled	8.3	21	PDB header: replication/rna Chain: D: PDB Molecule: single stranded dna binding protein; PDBTitle: single stranded dna binding protein and ssdna complex
71	d2uubq1	Alignment	not modelled	8.3	31	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
72	d1h0ha1	Alignment	not modelled	8.0	28	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
73	d1eyga_	Alignment	not modelled	8.0	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
74	d1ripa_	Alignment	not modelled	7.8	38	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
75	d1xrsb2	Alignment	not modelled	7.4	24	Fold: Dodecin subunit-like Superfamily: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain Family: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
76	c4owxB_	Alignment	not modelled	7.1	29	PDB header: dna binding protein/dna Chain: B: PDB Molecule: ssoss complex subunit b1; PDBTitle: structural basis of soss1 in complex with a 12nt ssdna
77	c5gqoB_	Alignment	not modelled	7.1	21	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
78	c2k27A_	Alignment	not modelled	7.1	71	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
79	c3pgzB_	Alignment	not modelled	6.9	7	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
80	c5b2cA_	Alignment	not modelled	6.9	25	PDB header: viral protein Chain: A: PDB Molecule: hn protein; PDBTitle: crystal structure of mumps virus hemagglutinin-neuraminidase

81	c1qvca_	Alignment	not modelled	6.9	21	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
82	d1qvca_	Alignment	not modelled	6.9	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
83	d3ulla_	Alignment	not modelled	6.8	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
84	c3asiA_	Alignment	not modelled	6.8	14	PDB header: cell adhesion Chain: A: PDB Molecule: neurexin-1-alpha; PDBTitle: alpha-neurexin-1 ectodomain fragment; Ins5-egf3-Ins6
85	d1e32a1	Alignment	not modelled	6.6	27	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
86	d1i94q_	Alignment	not modelled	6.5	31	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
87	c4fzhD_	Alignment	not modelled	6.4	25	PDB header: hydrolase Chain: D: PDB Molecule: hemagglutinin-neuraminidase; PDBTitle: structure of the ulster strain newcastle disease virus hemagglutinin-2 neuraminidase reveals auto-inhibitory interactions associated with3 low virulence
88	d2d3na1	Alignment	not modelled	6.4	13	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
89	d1gvha2	Alignment	not modelled	6.0	31	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
90	c3u5gL_	Alignment	not modelled	5.9	45	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s11-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
91	c1z4xA_	Alignment	not modelled	5.9	25	PDB header: hydrolase Chain: A: PDB Molecule: hemagglutinin-neuraminidase; PDBTitle: parainfluenza virus 5 (sv5) hemagglutinin-neuraminidase (hn) with2 ligand sialyllactose (soaked with sialyllactose, ph8.0)
92	d1xg8a_	Alignment	not modelled	5.9	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: YuzD-like
93	d1cqxa2	Alignment	not modelled	5.8	25	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
94	c3tqyA_	Alignment	not modelled	5.7	16	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
95	d2gjp1	Alignment	not modelled	5.7	11	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
96	c3vdyA_	Alignment	not modelled	5.6	29	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded dna-binding protein ssbb; PDBTitle: b. subtilis ssbb/ssdna
97	c4inmV_	Alignment	not modelled	5.6	18	PDB header: structural protein/dna Chain: V: PDB Molecule: cenp-c; PDBTitle: crystal structure of cenp-c in complex with the nucleosome core2 particle
98	c4x23V_	Alignment	not modelled	5.6	18	PDB header: structural protein/dna Chain: V: PDB Molecule: cenp-c; PDBTitle: crystal structure of cenp-c in complex with the nucleosome core2 particle
99	c2mt4A_	Alignment	not modelled	5.5	27	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: solution structure of the n-terminal domain of nusa from b. subtilis