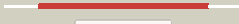



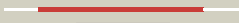






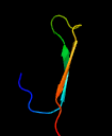

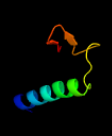







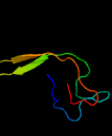
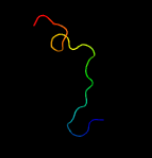
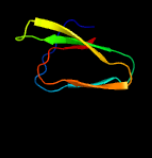
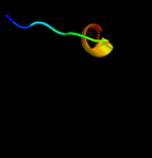
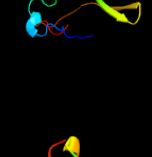
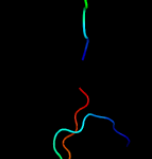

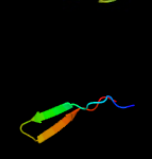
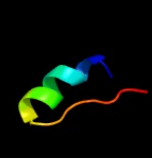
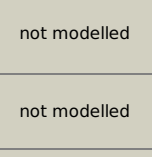


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3100c_smpB_3469298_3469780
 Date Thu Aug 8 16:20:28 BST 2019
 Unique Job ID ae904fb6a5dd8d42

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zeyC_	 Alignment		100.0	76	PDB header: ribosome Chain: C: PDB Molecule: ssra-binding protein; PDBTitle: m. smegmatis trans-translation state 70s ribosome
2	d1p6va_	 Alignment		100.0	50	Fold: Small protein B (SmpB) Superfamily: Small protein B (SmpB) Family: Small protein B (SmpB)
3	c1p6vC_	 Alignment		100.0	50	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ssra-binding protein; PDBTitle: crystal structure of the trna domain of transfer-messenger2 rna in complex with smpb
4	c1j1hA_	 Alignment		100.0	52	PDB header: rna binding protein Chain: A: PDB Molecule: small protein b; PDBTitle: solution structure of a tmrna-binding protein, smpb, from2 thermus thermophilus
5	d1wjxa_	 Alignment		100.0	53	Fold: Small protein B (SmpB) Superfamily: Small protein B (SmpB) Family: Small protein B (SmpB)
6	c6hbeA_	 Alignment		36.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: copper-containing nitrite reductase; PDBTitle: cu-containing nitrite reductase (nirk) from thermus scotoductus sa-01
7	d2ipqx1	 Alignment		31.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: STY4665 C-terminal domain-like
8	c2qnkA_	 Alignment		21.3	30	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyanthranilate 3,4-dioxygenase; PDBTitle: crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
9	d1sdwa2	 Alignment		19.0	15	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: PHM/PNGase F Family: Peptidylglycine alpha-hydroxylating monooxygenase, PHM
10	c4q28B_	 Alignment		15.9	23	PDB header: structural protein Chain: B: PDB Molecule: periplakin; PDBTitle: crystal structure of the plectin 1 and 2 repeats of the human2 periplakin. northeast structural genomics consortium (nesg) target3 hr9083a
11	c1wqsA_	 Alignment		15.5	14	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like protease; PDBTitle: crystal structure of norovirus 3c-like protease

12	dlg31a_	Alignment		15.3	27	Fold: GroES-like Superfamily: GroES-like Family: GroES
13	dlyfua1	Alignment		14.3	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
14	c4u39L_	Alignment		13.9	45	PDB header: cell cycle Chain: L: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
15	c6b6iD_	Alignment		13.4	18	PDB header: viral protein,protease Chain: D: PDB Molecule: 3c-like protease; PDBTitle: 2.4a resolution structure of human norovirus gii.4 protease
16	c4u39J_	Alignment		13.2	45	PDB header: cell cycle Chain: J: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
17	c6pqhA_	Alignment		12.8	29	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase; PDBTitle: crystal structure of asparagine-trna ligase from elizabethkingia sp.2 ccug 26117
18	c2elvA_	Alignment		12.1	38	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 6th c2h2 zinc finger of human2 zinc finger protein 406
19	c4ij2E_	Alignment		11.1	23	PDB header: oxygen transport/protein binding Chain: E: PDB Molecule: iron-regulated surface determinant protein h; PDBTitle: human methemoglobin in complex with the second and third neat domains2 of isdh from staphylococcus aureus
20	c3jsbA_	Alignment		11.0	17	PDB header: rna binding protein Chain: A: PDB Molecule: rna-directed rna polymerase; PDBTitle: crystal structure of the n-terminal domain of the lymphocytic2 choriomeningitis virus I protein
21	c5t2tB_	Alignment	not modelled	10.8	17	PDB header: transferase Chain: B: PDB Molecule: rna-directed rna polymerase I; PDBTitle: crystal structure of lymphocytic choriomeningitis mammarenavirus2 endonuclease bound to compound I742001
22	c1hf9B_	Alignment	not modelled	10.2	29	PDB header: atpase inhibitor Chain: B: PDB Molecule: atpase inhibitor (mitochondrial); PDBTitle: c-terminal coiled-coil domain from bovine if1
23	c4i1tA_	Alignment	not modelled	10.2	28	PDB header: viral protein Chain: A: PDB Molecule: rna-directed rna polymerase I; PDBTitle: crystal structure of the cap-snatching endonuclease from pichinde2 virus
24	c6nwoD_	Alignment	not modelled	9.7	12	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator bgar; PDBTitle: structures of the transcriptional regulator bgar, a lactose sensor.
25	d1zvfa1	Alignment	not modelled	9.6	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
26	c2quoA_	Alignment	not modelled	9.3	27	PDB header: toxin Chain: A: PDB Molecule: heat-labile enterotoxin b chain; PDBTitle: crystal structure of c terminal fragment of clostridium perfringens2 enterotoxin
27	c5hgqD_	Alignment	not modelled	9.3	30	PDB header: ligase/ligase inhibitor Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: loa loa lysyl-trna synthetase in complex with cladosporin.
28	c4u39N_	Alignment	not modelled	9.1	36	PDB header: cell cycle Chain: N: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
						Fold: Reductase/isomerase/elongation factor common domain

29	d1d1na_	Alignment	not modelled	8.8	20	Superfamily: Translation proteins Family: Elongation factors
30	c5xumA_	Alignment	not modelled	8.8	22	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of thermotoga maritima holo-[acyl-carrier-protein]2 synthase (acps)
31	c2oa9B_	Alignment	not modelled	8.7	24	PDB header: hydrolase Chain: B: PDB Molecule: r.mvai; PDBTitle: restriction endonuclease mvai in the absence of dna
32	c4miwA_	Alignment	not modelled	8.6	22	PDB header: viral protein, transferase Chain: A: PDB Molecule: rna-directed rna polymerase I; PDBTitle: high-resolution structure of the n-terminal endonuclease domain of the2 lassa virus I polymerase
33	c3mjdB_	Alignment	not modelled	8.5	31	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
34	c2w3zA_	Alignment	not modelled	8.0	12	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
35	c4tq0D_	Alignment	not modelled	7.6	29	PDB header: protein binding Chain: D: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
36	c4tq0B_	Alignment	not modelled	7.5	29	PDB header: protein binding Chain: B: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
37	d2c0ha1	Alignment	not modelled	7.3	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
38	d2cc0a1	Alignment	not modelled	7.3	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
39	d2c1ia1	Alignment	not modelled	7.1	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
40	d2nlya1	Alignment	not modelled	7.1	23	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase
41	c4l1gB_	Alignment	not modelled	6.6	24	PDB header: hydrolase Chain: B: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus
42	c5npvB_	Alignment	not modelled	6.6	29	PDB header: cell cycle Chain: B: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16l1(atg5bd) complex (i4)
43	c4m1bA_	Alignment	not modelled	6.5	20	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
44	c5npvD_	Alignment	not modelled	6.4	29	PDB header: cell cycle Chain: D: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16l1(atg5bd) complex (i4)
45	c5npwF_	Alignment	not modelled	6.4	29	PDB header: cell cycle Chain: F: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16l1(atg5bd) complex (c2)
46	c3rpmA_	Alignment	not modelled	6.4	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetyl-hexosaminidase; PDBTitle: crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
47	c2ylaA_	Alignment	not modelled	6.3	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
48	c4u1eB_	Alignment	not modelled	6.3	35	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: crystal structure of the eif3b-ctd/eif3i/eif3g-ntd translation2 initiation complex
49	c5jp6A_	Alignment	not modelled	6.3	11	PDB header: hydrolase Chain: A: PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
50	d1im3d_	Alignment	not modelled	6.2	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytomegalovirus protein US2
51	d1h2ca_	Alignment	not modelled	6.1	9	Fold: EV matrix protein Superfamily: EV matrix protein Family: EV matrix protein
52	d1kk1a1	Alignment	not modelled	6.1	32	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
53	d8ohma2	Alignment	not modelled	6.1	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
54	c2r2yA_	Alignment	not modelled	6.1	29	PDB header: protein binding Chain: A: PDB Molecule: protein adrm1; PDBTitle: crystal structure of the proteasomal rpn13 pru-domain
55	c2z59A_	Alignment	not modelled	6.1	29	PDB header: protein transport Chain: A: PDB Molecule: protein adrm1; PDBTitle: complex structures of mouse rpn13 (22-130aa) and

					ubiquitin
56	c5x8r8_	Alignment	not modelled	6.1	25 PDB header: ribosome Chain: 8; PDB Molecule: 30s ribosomal protein s1, chloroplastic; PDBTitle: structure of the 30s small subunit of chloroplast ribosome from2 spinach
57	c1h2dA_	Alignment	not modelled	6.1	9 PDB header: virus/viral protein Chain: A; PDB Molecule: matrix protein vp40; PDBTitle: ebola virus matrix protein vp40 n-terminal domain in complex with rna2 (low-resolution vp40[31-212] variant).
58	d2ieca1	Alignment	not modelled	5.9	71 Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
59	c1gmjD_	Alignment	not modelled	5.9	29 PDB header: atpase inhibitor Chain: D; PDB Molecule: atpase inhibitor; PDBTitle: the structure of bovine if1, the regulatory subunit of mitochondrial2 f-atpase
60	d2i52a1	Alignment	not modelled	5.6	71 Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
61	c4uecB_	Alignment	not modelled	5.6	29 PDB header: translation Chain: B; PDB Molecule: eukaryotic translation initiation factor 4g, isoform a; PDBTitle: complex of d. melanogaster eif4e with eif4g and cap analog
62	c4h3wB_	Alignment	not modelled	5.5	47 PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative secreted protein (bdi_1231) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
63	c4ah6B_	Alignment	not modelled	5.5	24 PDB header: ligase Chain: B; PDB Molecule: aspartate--trna ligase, mitochondrial; PDBTitle: human mitochondrial aspartyl-trna synthetase
64	d1jaka1	Alignment	not modelled	5.3	15 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
65	c2ogfD_	Alignment	not modelled	5.2	57 PDB header: structural genomics, unknown function Chain: D; PDB Molecule: hypothetical protein mj0408; PDBTitle: crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
66	d1yhta1	Alignment	not modelled	5.2	25 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
67	c3wzhA_	Alignment	not modelled	5.2	18 PDB header: transcription Chain: A; PDB Molecule: uncharacterized protein af_1864; PDBTitle: crystal structure of afcsx3
68	d1mkya3	Alignment	not modelled	5.2	25 Fold: Alpha-lytic protease prodomain-like Superfamily: Probable GTPase Der, C-terminal domain Family: Probable GTPase Der, C-terminal domain
69	d2qfaa1	Alignment	not modelled	5.2	23 Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
70	d2gjxa1	Alignment	not modelled	5.1	5 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain