



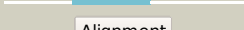
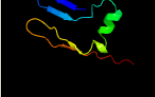
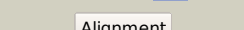







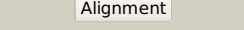
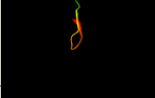
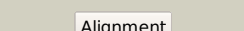
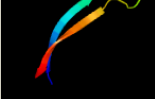
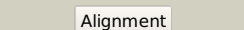


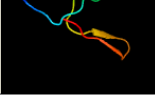


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2290_(lppO)_2562609_2563124
 Date Mon Aug 5 13:25:43 BST 2019
 Unique Job ID 2183f00dd31a89fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zimA_	 Alignment		97.4	21	PDB header: unknown function Chain: A; PDB Molecule: lipoprotein lpqh; PDBTitle: crystal structure of mycobacterium tuberculosis lpqh (rv3763)
2	c4xinB_	 Alignment		97.1	24	PDB header: unknown function Chain: B; PDB Molecule: lpqh orthologue; PDBTitle: x-ray crystal structure of an lpqh orthologue from mycobacterium avium
3	c2e6pA_	 Alignment		30.8	24	PDB header: structural protein Chain: A; PDB Molecule: obscurin-like protein 1; PDBTitle: solution structure of the ig-like domain (714-804) from 2 human obscurin-like protein 1
4	c2f8vY_	 Alignment		26.4	67	PDB header: contractile protein/contractile protein Chain: Y; PDB Molecule: telethonin; PDBTitle: structure of full length telethonin in complex with the n-terminus of 2 titin
5	d2i cha1	 Alignment		23.4	21	Fold: AttH-like Superfamily: AttH-like Family: AttH-like
6	c1ya5T_	 Alignment		23.3	67	PDB header: structural protein Chain: T; PDB Molecule: telethonin; PDBTitle: crystal structure of the titin domains z1z2 in complex with telethonin
7	c4b4rA_	 Alignment		18.0	34	PDB header: cell adhesion Chain: A; PDB Molecule: f18 fimbrial adhesin ac; PDBTitle: crystal structure of the lectin domain of f18 fimbrial2 adhesin fedf in complex with blood group b type 13 hexasaccharide
8	c1ye9A_	 Alignment		16.1	21	PDB header: oxidoreductase Chain: A; PDB Molecule: catalase hpii; PDBTitle: crystal structure of proteolytically truncated catalase2 hpii from e. coli
9	d1je5a_	 Alignment		15.8	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Phage ssDNA-binding proteins
10	c3lr4A_	 Alignment		13.5	44	PDB header: transferase Chain: A; PDB Molecule: sensor protein; PDBTitle: periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
11	d1vlf n1	 Alignment		10.9	45	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain

12	d1pfsa_	Alignment		9.4	34	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Phage ssDNA-binding proteins
13	c3cglF_	Alignment		9.0	70	PDB header: fluorescent protein Chain: F: PDB Molecule: gfp-like fluorescent chromoprotein dsfp483; PDBTitle: crystal structure and raman studies of dsfp483, a cyan fluorescent2 protein from discosoma striata
14	d1y0ua_	Alignment		8.9	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
15	c4cabA_	Alignment		8.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase; PDBTitle: the refined structure of catalase dr1998 from deinococcus radiodurans2 at 2.6 a resolution
16	c2pd0D_	Alignment		8.6	22	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: protein cgd2_2020 from cryptosporidium parvum
17	d1m7sa_	Alignment		8.3	21	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
18	d1jmx5	Alignment		8.3	24	Fold: Streptavidin-like Superfamily: Quinohemoprotein amine dehydrogenase A chain, domain 3 Family: Quinohemoprotein amine dehydrogenase A chain, domain 3
19	d1gwea_	Alignment		7.7	29	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
20	c6fx6A_	Alignment		7.3	19	PDB header: unknown function Chain: A: PDB Molecule: satie-ted; PDBTitle: thioester domain of the staphylococcus aureus tie protein
21	c4hwmA_	Alignment	not modelled	7.2	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yedd; PDBTitle: crystal structure of a lipoprotein yedd (kpn_02420) from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 at 1.38 a resolution
22	d1wwbx_	Alignment	not modelled	6.9	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
23	c2rriA_	Alignment	not modelled	6.3	21	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik
24	d1p80a2	Alignment	not modelled	6.3	17	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
25	d1a4ea_	Alignment	not modelled	6.2	21	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
26	c1p81A_	Alignment	not modelled	6.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
27	d1v8ka_	Alignment	not modelled	5.9	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Motor proteins
28	c3hi2C_	Alignment	not modelled	5.9	30	PDB header: dna binding protein/toxin Chain: C: PDB Molecule: hth-type transcriptional regulator mqsA(ygit); PDBTitle: structure of the n-terminal domain of the e. coli antitoxin mqsA2 (ygit/b3021) in complex with the e. coli toxin mqsR

					(ygiu/b3022)
29	c4wrrnB_	Alignment	not modelled	5.7	16 PDB header: structural protein Chain: B: PDB Molecule: maltose-binding periplasmic protein, uromodulin; PDBTitle: crystal structure of the polymerization region of human2 uromodulin/tamm-horsfall protein
30	c3pn1A_	Alignment	not modelled	5.6	18 PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: dna ligase; PDBTitle: novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
31	d4blca_	Alignment	not modelled	5.5	21 Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
32	d1dgfa_	Alignment	not modelled	5.4	21 Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
33	c3ej6D_	Alignment	not modelled	5.3	25 PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: neurospora crassa catalase-3 crystal structure
34	c4f78A_	Alignment	not modelled	5.3	11 PDB header: hydrolase Chain: A: PDB Molecule: d,d-dipeptidase/d,d-carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-dipeptidase vanxyg
35	d1wv3a1	Alignment	not modelled	5.2	44 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: EssC N-terminal domain-like
36	c3j60I_	Alignment	not modelled	5.2	50 PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8e; PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
37	d2ivda2	Alignment	not modelled	5.2	36 Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
38	c1sy7B_	Alignment	not modelled	5.2	25 PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
39	c2vrsC_	Alignment	not modelled	5.2	24 PDB header: viral protein Chain: C: PDB Molecule: sigma-c capsid protein; PDBTitle: structure of avian reovirus sigmac117-326, c2 crystal form