








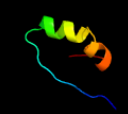





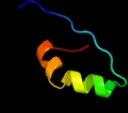








Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0835_(lpqQ)_930956_931600
 Date Fri Jul 26 01:50:42 BST 2019
 Unique Job ID ba651b25a36e3da2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4esqA_	 Alignment		100.0	16	PDB header: transferase Chain: A; PDB Molecule: serine/threonine protein kinase; PDBTitle: crystal structure of the extracellular domain of pknh from2 mycobacterium tuberculosis
2	c3lo3E_	 Alignment		37.2	24	PDB header: structure genomics, unknown function Chain: E; PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 colwellia psychrerythraea 34h.
3	d2fiua1	 Alignment		35.6	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
4	c3dcaC_	 Alignment		20.8	22	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: rpa0582; PDBTitle: crystal structure of the rpa0582- protein of unknown2 function from rhodospseudomonas palustris- a structural3 genomics target
5	d1kr4a_	 Alignment		17.1	18	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
6	c2b3gB_	 Alignment		14.4	26	PDB header: replication Chain: B; PDB Molecule: cellular tumor antigen p53; PDBTitle: p53n (fragment 33-60) bound to rpa70n
7	d1vhfa_	 Alignment		11.5	19	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
8	c4iyqB_	 Alignment		10.0	25	PDB header: protein binding Chain: B; PDB Molecule: divalent ion tolerance protein cuta1; PDBTitle: crystal structure of divalent ion tolerance protein cuta1 from2 ehrlichia chaffeensis
9	d2zfha1	 Alignment		9.7	26	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
10	c1xk8A_	 Alignment		9.7	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: divalent cation tolerant protein cuta; PDBTitle: divalent cation tolerant protein cuta from homo sapiens o60888
11	c3i08D_	 Alignment		9.6	12	PDB header: signaling protein Chain: D; PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)

12	d1lmma_	Alignment		9.5	22	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
13	d1lukua_	Alignment		9.3	27	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
14	c6oswA_	Alignment		9.0	16	PDB header: cell cycle Chain: A: PDB Molecule: forkhead box m1; PDBTitle: an order-to-disorder structural switch activates the foxm12 transcription factor
15	c6gdxA_	Alignment		8.5	16	PDB header: metal binding protein Chain: A: PDB Molecule: periplasmic divalent cation tolerance protein; PDBTitle: structure of cuta from synechococcus elongatus pcc7942 complexed with2 3 molecules of bis-tris
16	d1j1ta_	Alignment		8.3	38	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Alginate lyase
17	d1osce_	Alignment		8.1	26	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
18	c4e98C_	Alignment		7.7	16	PDB header: signaling protein Chain: C: PDB Molecule: cuta1 divalent ion tolerance protein; PDBTitle: crystal structure of possible cuta1 divalent ion tolerance protein2 from cryptosporidium parvum iowa ii
19	c2mzdB_	Alignment		7.6	29	PDB header: protein binding Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: characterization of the p300 taz2-p53 tad2 complex and comparison with2 the p300 taz2-p53 tad1 complex
20	c2ly4B_	Alignment		6.8	29	PDB header: nuclear protein/antitumour protein Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: hmgb1-facilitated p53 dna binding occurs via hmgb1/p53 transactivation domain interaction and is regulated by the acidic3 tail
21	c2zfhA_	Alignment	not modelled	6.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cuta; PDBTitle: crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
22	d1p1la_	Alignment	not modelled	6.4	31	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
23	c5k8qB_	Alignment	not modelled	6.4	30	PDB header: metal binding protein Chain: B: PDB Molecule: zgc:136689; PDBTitle: crystal structure of calcium-loaded calmodulin in complex with stra62 camp2-site peptide.
24	c2nuhA_	Alignment	not modelled	6.2	18	PDB header: unknown function Chain: A: PDB Molecule: periplasmic divalent cation tolerance protein; PDBTitle: crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosa
25	c3oqcB_	Alignment	not modelled	6.1	40	PDB header: hydrolase Chain: B: PDB Molecule: ufm1-specific protease 2; PDBTitle: ubiquitin-fold modifier 1 specific protease, ufsp2
26	c5hb8B_	Alignment	not modelled	5.7	9	PDB header: transport protein Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of chaetomium thermophilum nup53 rrm (space group2 p3121)
27	c3ahpA_	Alignment	not modelled	5.7	15	PDB header: electron transport Chain: A: PDB Molecule: cuta1; PDBTitle: crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
28	c5eijA_	Alignment	not modelled	5.3	40	PDB header: hydrolase Chain: A: PDB Molecule: ufm1-specific protease; PDBTitle: crystal structure of ufsp from c.elegans