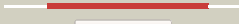

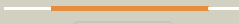
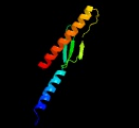









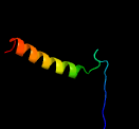

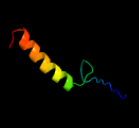

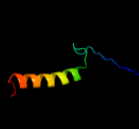



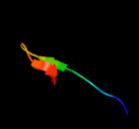


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0030 (-)_33224_33553
Date	Tue Jul 23 14:50:05 BST 2019
Unique Job ID	e5539e569c0d02a5

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ybxA_	 Alignment		91.5	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved hypothetical protein; PDBTitle: conserved hypothetical protein cth-383 from clostridium thermocellum
2	d1j8ba_	 Alignment		81.6	11	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
3	d1puga_	 Alignment		79.7	18	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
4	d1pugb_	 Alignment		51.0	18	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
5	c5yrxA_	 Alignment		43.1	21	PDB header: dna binding protein Chain: A; PDB Molecule: nucleoid-associated protein rv3716c; PDBTitle: crystal structure of a hypothetical protein rv3716c from mycobacterium2 tuberculosis
6	c3f42A_	 Alignment		15.1	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein hp0035; PDBTitle: crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
7	d2p02a2	 Alignment		14.4	28	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
8	d1mxaa2	 Alignment		13.9	32	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
9	d1qm4a2	 Alignment		13.0	28	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
10	c2vlqD_	 Alignment		10.4	26	PDB header: transferase Chain: D; PDB Molecule: sporulation kinase a; PDBTitle: kina pas-a domain, homodimer
11	c2nncB_	 Alignment		8.2	23	PDB header: ligand binding protein Chain: B; PDB Molecule: sulfur covalently-binding protein; PDBTitle: structure of the sulfur carrier protein soxy from chlorobium limicola2 f thiosulfatophilum

12	c3iwcD_		Alignment		7.4	13	PDB header: lyase Chain: D: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with s-adenosylmethionine methyl ester
13	c4xi7A_		Alignment		7.3	25	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mzm-rep domains of mind bomb 1 in complex2 with jagged1 n-box peptide
14	c5gy6A_		Alignment		6.4	33	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease t1; PDBTitle: ribonuclease from hericium erinaceus (rnase he1)
15	c5z08C_		Alignment		6.4	41	PDB header: cell cycle Chain: C: PDB Molecule: cenp-k; PDBTitle: the crystal structure of kinetochore subunits cenp-h/i/k triple2 complex
16	c2lf0A_		Alignment		5.9	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yib1; PDBTitle: solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scattering, nesg4 target sfr339/ocsp target sf3636
17	c5u0sO_		Alignment		5.9	22	PDB header: transcription/transferase Chain: Q: PDB Molecule: mediator complex subunit 17; PDBTitle: cryo-em structure of the mediator-rnapii complex
18	c2l3hA_		Alignment		5.9	27	PDB header: hydrolase Chain: A: PDB Molecule: prostatic acid phosphatase; PDBTitle: nmr structure in a membrane environment reveals putative amyloidogenic2 regions of the sevi precursor peptide pap248-286
19	d1dy2a_		Alignment		5.8	40	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Endostatin
20	c4odjA_		Alignment		5.7	25	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of a putative s-adenosylmethionine synthetase from2 cryptosporidium hominis in complex with s-adenosyl-methionine
21	c4wo1C_		Alignment	not modelled	5.6	39	PDB header: signaling protein Chain: C: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
22	c4wo1A_		Alignment	not modelled	5.6	39	PDB header: signaling protein Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
23	c4wo1B_		Alignment	not modelled	5.6	39	PDB header: signaling protein Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
24	c4wo1D_		Alignment	not modelled	5.6	39	PDB header: signaling protein Chain: D: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
25	c4le5A_		Alignment	not modelled	5.6	22	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: structure of an unusual s-adenosylmethionine synthetase from2 campylobacter jejuni
26	c5c6hN_		Alignment	not modelled	5.0	100	PDB header: apoptosis/apoptosis regulator Chain: N: PDB Molecule: mule bh3 peptide from e3 ubiquitin-protein ligase huwe1; PDBTitle: mcl-1 complexed with mule