




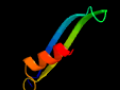

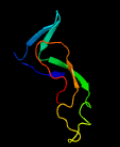





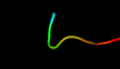







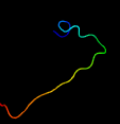

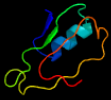







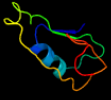





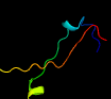








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0307c (-)_376573_377055
Date	Tue Jul 23 14:50:37 BST 2019
Unique Job ID	f12feb21878cdb23

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2g3wa1	 Alignment		45.2	27	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: YaeQ-like
2	c3c0uA	 Alignment		39.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yaeq; PDBTitle: crystal structure of e.coli yaeq protein
3	d2ot9a1	 Alignment		39.1	20	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: YaeQ-like
4	c4ldxB	 Alignment		25.8	29	PDB header: transcription/dna Chain: B: PDB Molecule: auxin response factor 1; PDBTitle: crystal structure of the dna binding domain of arabidopsis thaliana2 auxin response factor 1 (arf1) in complex with protomor-like sequence3 er7
5	c3zeyl	 Alignment		12.0	33	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s15, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
6	d1t95a3	 Alignment		9.8	20	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain
7	c3lgeF	 Alignment		9.4	56	PDB header: lyase/protein binding Chain: F: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
8	c3lgeG	 Alignment		9.4	56	PDB header: lyase/protein binding Chain: G: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
9	c2m9uA	 Alignment		9.4	29	PDB header: viral protein Chain: A: PDB Molecule: integrase p46; PDBTitle: solution nmr structure of the c-terminal domain (ctd) of moloney2 murine leukemia virus integrase, northeast structural genomics target3 or41a
10	d3bz6a1	 Alignment		9.2	58	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PSPTO2686-like
11	d1wjna	 Alignment		8.7	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related

12	c5ze4A_	 Alignment		7.7	32	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
13	c6gcsj_	 Alignment		7.6	67	PDB header: oxidoreductase Chain: J: PDB Molecule: nujm subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
14	c3gxvD_	 Alignment		6.3	70	PDB header: hydrolase/replication Chain: D: PDB Molecule: replicative dna helicase; PDBTitle: three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
15	c2qldA_	 Alignment		6.3	24	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 1; PDBTitle: human hsp40 hdj1
16	c5ym0A_	 Alignment		6.1	30	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the crystal structure of dhad
17	c3gxvC_	 Alignment		6.0	70	PDB header: hydrolase/replication Chain: C: PDB Molecule: replicative dna helicase; PDBTitle: three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
18	d1c5ea_	 Alignment		5.8	55	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
19	d2a0ua1	 Alignment		5.6	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: lF2B-like
20	c4wfdA_	 Alignment		5.5	5	PDB header: hydrolase Chain: A: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of the rrp6-rrp47-mtr4 interaction
21	d1td4a_	 Alignment	not modelled	5.5	55	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
22	d1yq2a4	 Alignment	not modelled	5.5	19	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: beta-Galactosidase, domain 5
23	c2ro5B_	 Alignment	not modelled	5.4	35	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: rdc-refined solution structure of the n-terminal dna recognition2 domain of the bacillus subtilis transition-state regulator spovt
24	c1h7dA_	 Alignment	not modelled	5.2	50	PDB header: acyltransferase Chain: A: PDB Molecule: aminolevulinic acid synthase 2, erythroid; PDBTitle: solution structure of the 49 aa presequence of 5-alas