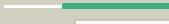
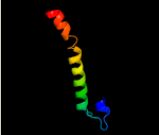
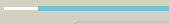







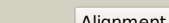
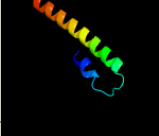
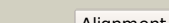

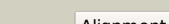










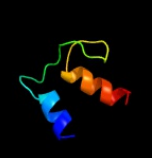




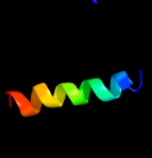


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0463 (-) _554019_554312
Date	Tue Jul 23 14:50:54 BST 2019
Unique Job ID	8f0f8a89cfe6d986

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3vr6G_	 Alignment		46.0	16	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: G; PDB Molecule: cytochrome b-large subunit; PDBTitle: mitochondrial rhoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
2	c4rfsS_	 Alignment		32.6	19	PDB header: hydrolase, transport protein Chain: S; PDB Molecule: substrate binding prtein s; PDBTitle: structure of a pantothenate energy coupling factor transporter
3	c5ir6A_	 Alignment		21.6	20	PDB header: oxidoreductase Chain: A; PDB Molecule: bd-type quinol oxidase subunit i; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
4	c2l2ta_	 Alignment		20.7	58	PDB header: membrane protein Chain: A; PDB Molecule: receptor tyrosine-protein kinase erbB-4; PDBTitle: solution nmr structure of the erbB4 dimeric membrane domain
5	c2l2cxB_	 Alignment		20.7	58	PDB header: transferase Chain: B; PDB Molecule: receptor tyrosine-protein kinase erbB-4; PDBTitle: spatial structure of the erbB4 dimeric tm domain
6	c6adqP_	 Alignment		17.7	13	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
7	c2k9yA_	 Alignment		16.0	45	PDB header: transferase Chain: A; PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
8	c2k9yB_	 Alignment		14.1	36	PDB header: transferase Chain: B; PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
9	c3zd0A_	 Alignment		13.3	46	PDB header: transport protein Chain: A; PDB Molecule: p7 protein; PDBTitle: the solution structure of monomeric hepatitis c virus p72 yields potent inhibitors of virion release
10	c2m6xC_	 Alignment		9.8	23	PDB header: membrane protein Chain: C; PDB Molecule: p7; PDBTitle: structure of the p7 channel of hepatitis c virus, genotype 5a
11	c1k82D_	 Alignment		9.7	13	PDB header: hydrolase/dna Chain: D; PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna

12	d1q59a_	Alignment		8.5	13	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
13	c2opfA_	Alignment		8.0	17	PDB header: hydrolase/dna Chain: A: PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
14	c5tzipA_	Alignment		7.3	13	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein fpv039; PDBTitle: crystal structure of fpv039:bik bh3 complex
15	c6m97A_	Alignment		7.1	19	PDB header: transport protein Chain: A: PDB Molecule: chimera protein of high affinity copper uptake protein 1 PDBTitle: crystal structure of the high-affinity copper transporter ctr1
16	d1ic8a2	Alignment		6.5	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
17	c2a5yA_	Alignment		6.5	21	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator ced-9; PDBTitle: structure of a ced-4/ced-9 complex
18	c3twkB_	Alignment		6.0	20	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
19	c5vf3Z_	Alignment		6.0	20	PDB header: virus Chain: Z: PDB Molecule: highly immunogenic outer capsid protein; PDBTitle: bacteriophage t4 isometric capsid
20	c4cdiC_	Alignment		5.8	35	PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; PDBTitle: crystal structure of acrb-acrz complex
21	d1ee8a1	Alignment	not modelled	5.8	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
22	d1k3xa1	Alignment	not modelled	5.6	14	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
23	c3rq9B_	Alignment	not modelled	5.6	38	PDB header: tse2-binding protein Chain: B: PDB Molecule: type vi secretion immunity protein; PDBTitle: structure of tsi2, a tse2-immunity protein from pseudomonas aeruginosa
24	c5wosA_	Alignment	not modelled	5.6	27	PDB header: viral protein Chain: A: PDB Molecule: cnpv058 bcl-2 like protein; PDBTitle: structural and functional insights into canarypox virus cnp0582 regulation of apoptosis
25	d1k3ka_	Alignment	not modelled	5.4	27	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
26	c4hzuS_	Alignment	not modelled	5.4	12	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: predicted membrane protein; PDBTitle: structure of a bacterial energy-coupling factor transporter
27	c2n2aA_	Alignment	not modelled	5.1	30	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the presence of cytoplasmic juxtamembrane domains