










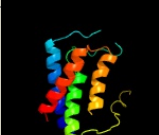



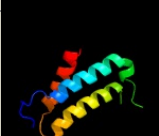


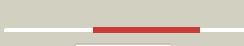



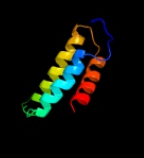

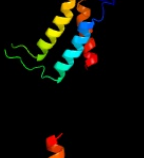
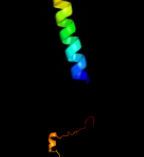
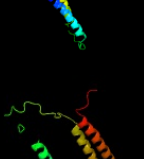
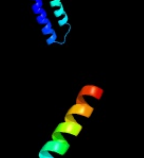


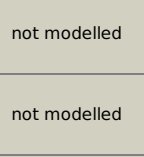


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0308 (-)_377113_377829
Date	Tue Jul 23 14:50:37 BST 2019
Unique Job ID	e8277f8c035daff0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5jkiA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: putative lipid phosphate phosphatase yodm; PDBTitle: crystal structure of the first transmembrane pap2 type2 phosphatidylglycerolphosphate phosphatase from bacillus subtilis
2	c4px7A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pgpb
3	c6ebuA_	 Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: lpxe; PDBTitle: crystal structure of aquifex aeolicus lppe
4	d1d2ta_	 Alignment		99.7	19	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Type 2 phosphatidic acid phosphatase, PAP2
5	c2akcC_	 Alignment		99.7	23	PDB header: hydrolase Chain: C: PDB Molecule: class a nonspecific acid phosphatase phon; PDBTitle: crystal structure of tungstate complex of the phon protein from s.2 typhimurium
6	c4uszA_	 Alignment		99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: vanadium-dependent haloperoxidase; PDBTitle: crystal structure of the first bacterial vanadium dependant2 iodoperoxidase
7	c3w36A_	 Alignment		98.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: naph1; PDBTitle: crystal structure of holo-type bacterial vanadium-dependent2 chloroperoxidase
8	d1qi9a_	 Alignment		97.6	23	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
9	d1vnsa_	 Alignment		97.5	21	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Chloroperoxidase
10	c1vngA_	 Alignment		97.5	20	PDB header: haloperoxidase Chain: A: PDB Molecule: vanadium chloroperoxidase; PDBTitle: chloroperoxidase from the fungus curvularia inaequalis: mutant h404a
11	c5aa6F_	 Alignment		96.7	29	PDB header: oxidoreductase Chain: F: PDB Molecule: vanadium-dependent bromoperoxidase 2; PDBTitle: homohexameric structure of the second vanadate-dependent2 bromoperoxidase (anii) from ascophyllum nodosum

12	d1up8a_	Alignment		96.3	22	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
13	d1qhba_	Alignment		96.0	25	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
14	c5lpcA_	Alignment		95.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: vanadium-dependent bromoperoxidase; PDBTitle: crystal structure of vanadium-dependent haloperoxidase from a. marina
15	c6hu9u_	Alignment		25.9	25	PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
16	c6hwhB_	Alignment		25.3	18	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
17	c6hwhX_	Alignment		25.1	17	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
18	c6mitC_	Alignment		18.0	20	PDB header: lipid transport Chain: C: PDB Molecule: lipopolysaccharide export system protein lptc; PDBTitle: lptbfgc from enterobacter cloacae
19	c2rddB_	Alignment		13.6	11	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
20	c6fosK_	Alignment		12.4	32	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x; PDBTitle: cyanidioschyzon merolae photosystem i
21	c5w87B_	Alignment	not modelled	8.1	6	PDB header: transferase/ligase Chain: B: PDB Molecule: probable e3 ubiquitin-protein ligase herc6; PDBTitle: crystal structure of the c-terminal lobe of the human herc6 hect2 domain
22	c6cfwl_	Alignment	not modelled	7.6	19	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
23	c2mc7A_	Alignment	not modelled	7.4	20	PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgtr
24	d1dsva_	Alignment	not modelled	6.0	14	Fold: Retrovirus zinc finger-like domains Superfamily: Retrovirus zinc finger-like domains Family: Retrovirus zinc finger-like domains
25	c5zghK_	Alignment	not modelled	5.5	24	PDB header: photosynthesis Chain: K: PDB Molecule: psak; PDBTitle: cryo-em structure of the red algal psi-lhcr
26	c2plxB_	Alignment	not modelled	5.5	33	PDB header: hydrolase Chain: B: PDB Molecule: peptide inhibitor; PDBTitle: trypsin complexed to a synthetic peptide from veronica hederifolia
27	c5ykhH_	Alignment	not modelled	5.3	9	PDB header: membrane protein Chain: H: PDB Molecule: atp-binding cassette sub-family c member 8 isoform x2; PDBTitle: structure of pancreatic atp-sensitive potassium channel bound with2 glibenclamide and atpgammas (3d class1 at 4.33a)
28	c6ithA_	Alignment	not modelled	5.1	40	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles