

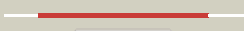














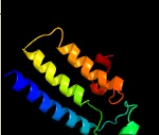





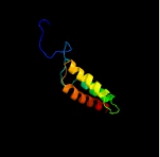

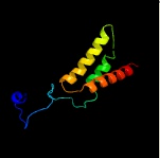
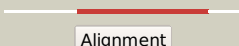
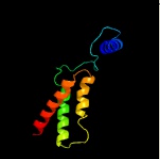
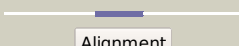
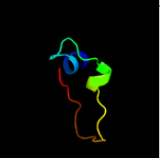
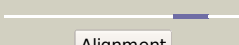
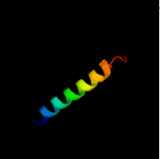
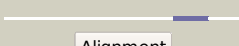
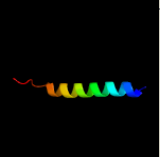
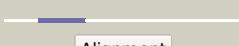
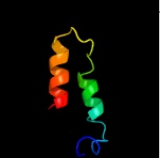

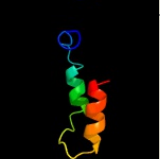

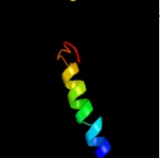







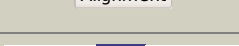


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3807c_(-)_4270018_4270515
Date	Fri Aug 9 18:20:51 BST 2019
Unique Job ID	165eda69ad43e2e3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5jkiA_	 Alignment		100.0	22	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	c6ebuA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: !pxe; PDBTitle: crystal structure of aquifex aeolicus !pxe
3	c4px7A_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pggp
4	c2akcC_	 Alignment		99.9	20	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
5	d1d2ta_	 Alignment		99.9	16	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Type 2 phosphatidic acid phosphatase, PAP2
6	c4uszA_	 Alignment		99.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: vanadium-dependent haloperoxidase; PDBTitle: crystal structure of the first bacterial vanadium dependant2 iodoperoxidase
7	c3w36A_	 Alignment		99.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: naph1; PDBTitle: crystal structure of holo-type bacterial vanadium-dependent2 chloroperoxidase
8	d1qi9a_	 Alignment		98.8	32	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
9	c1vngA_	 Alignment		98.6	29	PDB header: haloperoxidase Chain: A: PDB Molecule: vanadium chloroperoxidase; PDBTitle: chloroperoxidase from the fungus curvularia inaequalis: mutant h404a
10	d1vnsa_	 Alignment		98.6	30	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Chloroperoxidase
11	d1up8a_	 Alignment		98.3	27	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)

12	c5lpcA_		Alignment		98.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: vanadium-dependent bromoperoxidase; PDBTitle: crystal structure of vanadium-dependent haloperoxidase from a. marina
13	d1qhba_		Alignment		98.3	23	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
14	c5aa6F_		Alignment		98.2	20	PDB header: oxidoreductase Chain: F: PDB Molecule: vanadium-dependent bromoperoxidase 2; PDBTitle: homo-hexameric structure of the second vanadate-dependent 2 bromoperoxidase (anii) from ascophyllum nodosum
15	c3pt3A_		Alignment		17.8	14	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase ubr5; PDBTitle: crystal structure of the c-terminal lobe of the human ubr5 hect domain
16	c2momB_		Alignment		16.6	22	PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
17	c2momC_		Alignment		16.6	22	PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
18	c1p58F_		Alignment		16.0	16	PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2.95 angstrom cryo-em reconstruction
19	c1p58E_		Alignment		16.0	16	PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2.95 angstrom cryo-em reconstruction
20	c2micA_		Alignment		9.9	15	PDB header: membrane protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
21	c2micB_		Alignment	not modelled	9.9	15	PDB header: membrane protein Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
22	c6ithA_		Alignment	not modelled	8.6	20	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
23	c6mluA_		Alignment	not modelled	8.2	35	PDB header: membrane protein Chain: A: PDB Molecule: seipin; PDBTitle: cryo-em structure of lipid droplet formation protein seipin/bscl2
24	d1dsva_		Alignment	not modelled	6.6	43	Fold: Retrovirus zinc finger-like domains Superfamily: Retrovirus zinc finger-like domains Family: Retrovirus zinc finger-like domains
25	c5lp8A_		Alignment	not modelled	6.5	17	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: crystal structure of an asymmetric dimer of the ubiquitin ligase huwe1
26	d1c4za_		Alignment	not modelled	6.2	11	Fold: Hect, E3 ligase catalytic domain Superfamily: Hect, E3 ligase catalytic domain Family: Hect, E3 ligase catalytic domain
27	c3j2pD_		Alignment	not modelled	5.9	16	PDB header: viral protein Chain: D: PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer
28	c1zvdA_		Alignment	not modelled	5.7	23	PDB header: ligase Chain: A: PDB Molecule: smad ubiquitination regulatory factor 2; PDBTitle: regulation of smurf2 ubiquitin ligase activity by anchoring the e2 to the hect domain

29	d2a65a1	Alignment	not modelled	5.4	13	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
30	c5ireD_	Alignment	not modelled	5.4	16	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus