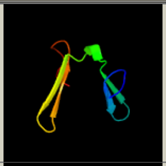
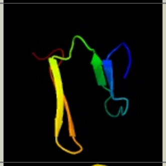
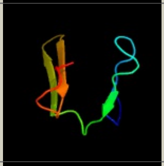
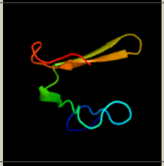
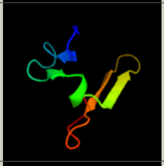
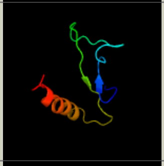
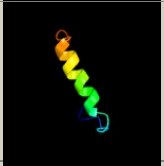
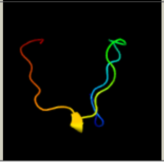
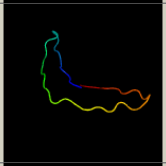
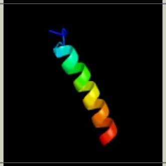
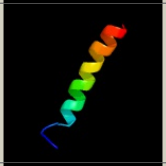
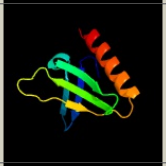
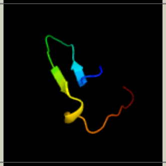
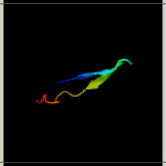
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1417_(-)_1592156_1592620
Date	Wed Jul 31 22:05:52 BST 2019
Unique Job ID	e2cac915b571de47

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ef1a2	Alignment		47.9	20	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
2	d1gg3a2	Alignment		39.6	26	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
3	d1e5wa2	Alignment		38.4	18	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
4	d1j19a2	Alignment		36.7	18	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
5	d1isna2	Alignment		34.2	14	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
6	c1e5wA_	Alignment		31.7	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** structure of isolated ferm domain and first long helix of moesin
7	d3bzka5	Alignment		26.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
8	c6adqP_	Alignment		23.7	18	**PDB header:**electron transport **Chain:** P: **PDB Molecule:**prokaryotic respiratory supercomplex associate factor 1 **PDBTitle:** respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
9	d1iwga2	Alignment		20.9	20	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
10	c2kl4A_	Alignment		18.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2032 protein; **PDBTitle:** nmr structure of the protein nb7804a
11	c2i1jA_	Alignment		17.1	26	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution

12	d1h4ra2	Alignment		15.9	17	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
13	c4gioA_	Alignment		15.4	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of campylobacter jejuni cj0090
14	c6ijjK_	Alignment		12.2	36	**PDB header:**membrane protein **Chain:** K: **PDB Molecule:**psak; **PDBTitle:** photosystem i of chlamydomonas reinhardtii
15	c6d2qA_	Alignment		11.9	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ferm, rhogef (arhgef) and pleckstrin domain protein 1 **PDBTitle:** crystal structure of the ferm domain of zebrafish farp1
16	c6igzK_	Alignment		11.7	24	**PDB header:**plant protein **Chain:** K: **PDB Molecule:**psak; **PDBTitle:** structure of psi-lhci
17	d2zpya2	Alignment		11.6	20	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
18	c2i1kA_	Alignment		10.8	27	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda reveals the coiled-coil domain at2 3.0 angstrom resolution
19	c6odih_	Alignment		10.3	24	**PDB header:**translocase **Chain:** H: **PDB Molecule:** **PDBTitle:** structure of cagy from a cryo-em reconstruction of a t4ss
20	c5n76C_	Alignment		9.8	22	**PDB header:**nickel-binding protein **Chain:** C: **PDB Molecule:**coot; **PDBTitle:** crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
21	c3u8zD_	Alignment	not modelled	8.4	17	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**merlin; **PDBTitle:** human merlin ferm domain
22	c6ijoG_	Alignment	not modelled	8.1	36	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**psag; **PDBTitle:** photosystem i of chlamydomonas reinhardtii
23	d2gf3a2	Alignment	not modelled	7.8	20	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**D-aminoacid oxidase-like
24	c3nqnB_	Alignment	not modelled	7.7	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function. (dr_2006) from2 deinococcus radiodurans at 1.88 a resolution
25	c2emtB_	Alignment	not modelled	7.7	20	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**radixin; **PDBTitle:** crystal structure analysis of the radixin ferm domain complexed with2 adhesion molecule psgl-1
26	c3lw5K_	Alignment	not modelled	6.0	30	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem i reaction center subunit x psak; **PDBTitle:** improved model of plant photosystem i
27	c3uc0B_	Alignment	not modelled	6.0	38	**PDB header:**viral protein/immune system **Chain:** B: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
28	c2mckA_	Alignment	not modelled	5.7	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus cr6 ns1/2 protein

29	c5xu1A_	Alignment	not modelled	5.5	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
30	d1ei5a2	Alignment	not modelled	5.4	36	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains