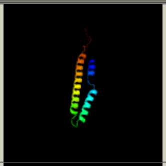
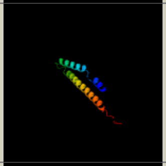
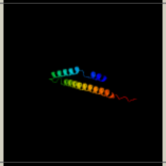
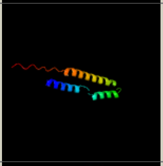
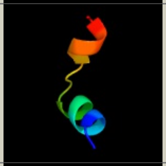
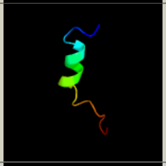
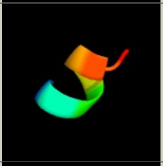
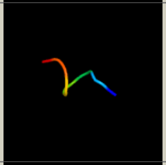
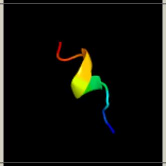
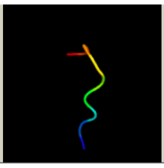
Email	mdejesus@rockefeller.edu
Description	RVBD3738c_(PPE66)_4189463_4190410
Date	Fri Aug 9 18:20:43 BST 2019
Unique Job ID	3be3bc59885cde4c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	Alignment		100.0	39	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**ppe family protein ppe15; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
2	d2g38b1	Alignment		100.0	23	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PPE
3	c2g38B_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ppe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
4	c4xy3A_	Alignment		99.9	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**esx-1 secretion-associated protein espb; **PDBTitle:** structure of esx-1 secreted protein espb
5	c4xb6D_	Alignment		43.4	35	**PDB header:**transferase **Chain:** D: **PDB Molecule:**alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; **PDBTitle:** structure of the e. coli c-p lyase core complex
6	c6aokA_	Alignment		21.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ceg4; **PDBTitle:** crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
7	d1zeea1	Alignment		20.8	38	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Indoleamine 2,3-dioxygenase-like
8	c6cgjA_	Alignment		19.8	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**effector protein lem4 (lpg1101); **PDBTitle:** structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
9	c1bzgA_	Alignment		14.5	14	**PDB header:**hormone **Chain:** A: **PDB Molecule:**parathyroid hormone-related protein; **PDBTitle:** the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
10	c2nvjA_	Alignment		12.8	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**25mer peptide from vacuolar atp synthase subunit **PDBTitle:** nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
11	c3sjrB_	Alignment		11.5	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved unkown function protein cv_1783 from2 chromobacterium violaceum atcc 12472

12	d1vlfn1	Alignment		10.7	100	**Fold:**Prealbumin-like **Superfamily:**Cna protein B-type domain **Family:**Cna protein B-type domain
13	c5l85B_	Alignment		10.2	36	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**nuclear fragile x mental retardation-interacting protein 1; **PDBTitle:** solution structure of the complex between human znhit3 and nufip12 proteins
14	c6nbiP_	Alignment		9.5	80	**PDB header:**signaling protein **Chain:** P: **PDB Molecule:**long-acting parathyroid hormone analog; **PDBTitle:** cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
15	c2jtwA_	Alignment		8.4	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**transmembrane helix 7 of yeast vatpase; **PDBTitle:** solution structure of tm7 bound to dpc micelles
16	d1fcda3	Alignment		8.1	29	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
17	c6qpiA_	Alignment		7.0	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**anoctamin-6; **PDBTitle:** cryo-em structure of calcium-free mtmem16f lipid scramblase in2 nanodisc

18	c4c47B_	Alignment		6.0	22	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**inner membrane lipoprotein; **PDBTitle:** salmonella enterica trimeric lipoprotein sadb