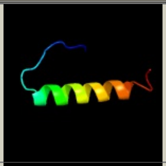
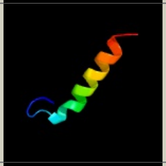
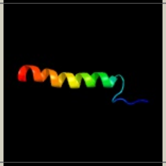
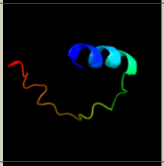
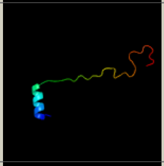
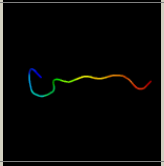
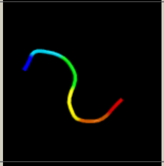
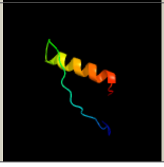
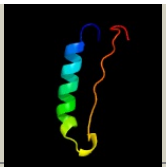
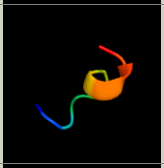
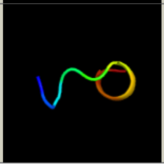
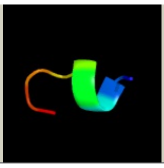
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2395A_(RVBD2395A)_2692234_2692449
Date	Mon Aug 5 13:25:55 BST 2019
Unique Job ID	8dd17f294bd488e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gcsP_	Alignment		50.8	19	**PDB header:**oxidoreductase **Chain:** P: **PDB Molecule:**nb4m subunit; **PDBTitle:** cryo-em structure of respiratory complex i from yarrowia lipolytica
2	d2vkva2	Alignment		31.1	24	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
3	c5lc5W_	Alignment		24.2	31	**PDB header:**oxidoreductase **Chain:** W: **PDB Molecule:**nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit **PDBTitle:** structure of mammalian respiratory complex i, class2
4	c2mt3A_	Alignment		15.4	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-54 factor; **PDBTitle:** structure of -24 dna binding domain of sigma 54 from e.coli
5	c5w7dA_	Alignment		12.4	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyloxyacyl hydrolase; **PDBTitle:** murine acyloxyacyl hydrolase (aoah), s262a mutant
6	d1gnya_	Alignment		9.1	69	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**CBM15
7	c3w1sC_	Alignment		8.6	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**ubiquitin-like protein atg12; **PDBTitle:** crystal structure of saccharomyces cerevisiae atg12-atg5 conjugate2 bound to the n-terminal domain of atg16
8	c6f0gD_	Alignment		6.9	67	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**ip3; **PDBTitle:** crystal structure asf1-ip3
9	c6f0gC_	Alignment		6.9	67	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**ip3; **PDBTitle:** crystal structure asf1-ip3
10	c6adqP_	Alignment		6.8	67	**PDB header:**electron transport **Chain:** P: **PDB Molecule:**prokaryotic respiratory supercomplex associate factor 1 **PDBTitle:** respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
11	c6r1eC_	Alignment		5.8	22	**PDB header:**flavoprotein **Chain:** C: **PDB Molecule:**dodecin; **PDBTitle:** structure of dodecin from streptomyces coelicolor

12	c2rilA_	Alignment		5.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**antibiotic biosynthesis monooxygenase; **PDBTitle:** crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
13	c4hedA_	Alignment		5.4	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** zebrafish chemokine cxl1
14	c5l3xB_	Alignment		5.4	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**negative elongation factor c/d; **PDBTitle:** crystal structure of negative elongation factor subcomplex nelf-ac

15	c2m4eA_	Alignment		5.3	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution nmr structure of vv2_0175 from vibrio vulnificus, nesg target2 vnr1 and csgid target idp91333