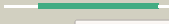
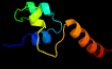
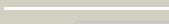


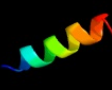


















Phyre2

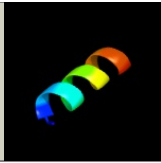
Email	mdejesus@rockefeller.edu
Description	RVBD1924c (-)_2176557_2176937
Date	Fri Aug 2 13:30:54 BST 2019
Unique Job ID	a1891b8907d456cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4a0zA_	 Alignment		42.0	30	PDB header: transcription Chain: A; PDB Molecule: transcription factor fapr; PDBTitle: structure of the global transcription regulator fapr from2 staphylococcus aureus in complex with malonyl-coa
2	c5lc5d_	 Alignment		24.5	41	PDB header: oxidoreductase Chain: D; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class2
3	c5ldwd_	 Alignment		22.3	41	PDB header: oxidoreductase Chain: D; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class1
4	c5ldxd_	 Alignment		22.3	41	PDB header: oxidoreductase Chain: D; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class3.
5	c5h35C_	 Alignment		19.9	17	PDB header: immune system/membrane protein Chain: C; PDB Molecule: membrane protein tric; PDBTitle: crystal structures of the tric trimeric intracellular cation channel2 orthologue from sulfolobus solfataricus
6	d1uj8a1	 Alignment		16.9	50	Fold: Another 3-helical bundle Superfamily: lscX-like Family: lscX-like
7	c2jynA_	 Alignment		13.3	50	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: upf0368 protein ypl225w; PDBTitle: a novel solution nmr structure of protein yst0336 from2 saccharomyces cerevisiae. northeast structural genomics3 consortium target yt51/ontario centre for structural4 proteomics target yst0336
8	d1fiua_	 Alignment		12.8	50	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease NgoIV
9	c6jo5I_	 Alignment		8.4	53	PDB header: photosynthesis Chain: I; PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: structure of the green algal photosystem i supercomplex with light-2 harvesting complex i
10	c6jjoI_	 Alignment		7.9	53	PDB header: photosynthesis Chain: I; PDB Molecule: psai; PDBTitle: photosystem i of chlamydomonas reinhardtii
11	d1o82a_	 Alignment		6.2	45	Fold: Sapoin-like Superfamily: Bacteriocin AS-48 Family: Bacteriocin AS-48

12 [c4h1wB](#)

Alignment



5.0

54

PDB header:hydrolase/hydrolase regulator
Chain: B: **PDB Molecule:**sarcolipin;
PDBTitle: e1 structure of the (sr) ca2+-atpase in complex with sarcolipin