
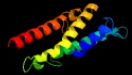



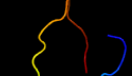



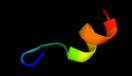











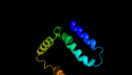
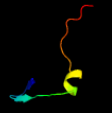

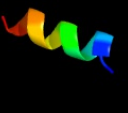







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1735c_(-)_1961298_1961795
Date	Fri Aug 2 13:30:33 BST 2019
Unique Job ID	0e3a2a111ffe17bc

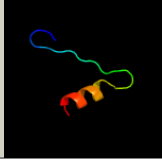
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3m7bA_</a>	 Alignment		99.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein teha homolog; <b>PDBTitle:</b> crystal structure of plant slac1 homolog teha
2	<a href="#">c3m7eA_</a>	 Alignment		99.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein teha homolog; <b>PDBTitle:</b> crystal structure of plant slac1 homolog teha
3	<a href="#">c5klcA_</a>	 Alignment		49.5	28	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding module e1; <b>PDBTitle:</b> structure of cbm_e1, a novel carbohydrate-binding module found by2 sugar cane soil metagenome
4	<a href="#">c6adqP_</a>	 Alignment		20.3	12	<b>PDB header:</b> electron transport <b>Chain:</b> P: <b>PDB Molecule:</b> prokaryotic respiratory supercomplex associate factor 1 <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
5	<a href="#">c6hu9t_</a>	 Alignment		15.8	13	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 9; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
6	<a href="#">d2ciwa2</a>	 Alignment		15.3	19	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> Cloroperoxidase <b>Family:</b> Cloroperoxidase
7	<a href="#">c2rrfA_</a>	 Alignment		11.8	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 21; <b>PDBTitle:</b> the solution structure of the c-terminal region of zinc finger fyve2 domain-containing protein 21
8	<a href="#">c1z65A_</a>	 Alignment		10.2	27	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> prion-like protein doppel; <b>PDBTitle:</b> mouse doppel 1-30 peptide
9	<a href="#">c4hxcC_</a>	 Alignment		8.8	33	<b>PDB header:</b> rna/rna binding protein/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> histone rna hairpin-binding protein; <b>PDBTitle:</b> structure of mrna stem-loop, human stem-loop binding protein and2 3'hexo ternary complex
10	<a href="#">c2k1aA_</a>	 Alignment		8.5	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiib; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iiib) transmembrane segment
11	<a href="#">c5yq7L_</a>	 Alignment		7.2	13	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> precursor for l subunits of photosynthetic reaction center; <b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii

12	<a href="#">d2bjqa2</a>	Alignment		7.0	22	<b>Fold:</b> MFPT repeat-like <b>Superfamily:</b> MFPT repeat-like <b>Family:</b> MFPT repeat
13	<a href="#">c5ldwc_</a>	Alignment		6.7	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
14	<a href="#">c5lc5c_</a>	Alignment		6.7	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
15	<a href="#">c6c24A_</a>	Alignment		6.6	60	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> polycomb protein suz12; <b>PDBTitle:</b> cryo-em structure of prc2 bound to cofactors aebp2 and jarid2 in the2 extended active state
16	<a href="#">d2p5ma1</a>	Alignment		6.5	32	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
17	<a href="#">c5a63D_</a>	Alignment		5.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> gamma-secretase subunit pen-2; <b>PDBTitle:</b> cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
18	<a href="#">d2v4ja2</a>	Alignment		5.4	44	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
19	<a href="#">c3aygA_</a>	Alignment		5.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric oxide reductase; <b>PDBTitle:</b> crystal structure of nitric oxide reductase complex with hqno

20 [dlxaa\\_](#)

Alignment



5.1

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**Fold:**DCoH-like  
**Superfamily:**C-terminal domain of arginine repressor  
**Family:**C-terminal domain of arginine repressor