


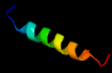



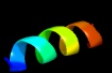

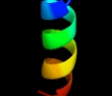










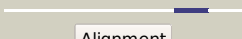



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3852\_(hns)\_4325252\_4325656  
 Date Sat Aug 10 22:05:03 BST 2019  
 Unique Job ID 7613b6f20c76164f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2lonA_</a>	 Alignment		34.5	29	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> hig1 domain family member 1b; <b>PDBTitle:</b> backbone structure of human membrane protein higd1b
2	<a href="#">c2lomA_</a>	 Alignment		33.2	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> hig1 domain family member 1a; <b>PDBTitle:</b> backbone structure of human membrane protein higd1a
3	<a href="#">c6ithA_</a>	 Alignment		26.3	42	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> syndecan-2; <b>PDBTitle:</b> structure of the transmembrane domain of syndecan 2 in micelles
4	<a href="#">c2cq8A_</a>	 Alignment		22.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> solution structure of rsgi ruh-033, a pp-binding domain of 2 10-ftfhdh from human cdna
5	<a href="#">c5mtiA_</a>	 Alignment		10.0	50	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> phosphopantetheine-binding protein; <b>PDBTitle:</b> bamb_5917 acyl-carrier protein
6	<a href="#">c5xsyB_</a>	 Alignment		9.0	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> voltage-gated sodium channel beta subunit 1; <b>PDBTitle:</b> structure of the nav1.4-beta1 complex from electric eel
7	<a href="#">c2o01j_</a>	 Alignment		8.5	35	<b>PDB header:</b> photosynthesis <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem i reaction center subunit ix; <b>PDBTitle:</b> the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
8	<a href="#">c6igzj_</a>	 Alignment		8.3	43	<b>PDB header:</b> plant protein <b>Chain:</b> J; <b>PDB Molecule:</b> psaj; <b>PDBTitle:</b> structure of psi-lhci
9	<a href="#">d2pnga1</a>	 Alignment		8.2	29	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
10	<a href="#">c2mr7A_</a>	 Alignment		7.8	43	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> apo structure of the peptidyl carrier protein domain 7 of the2 teicoplanin producing non-ribosomal peptide synthetase
11	<a href="#">c2roqA_</a>	 Alignment		6.6	50	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> enterobactin synthetase component f; <b>PDBTitle:</b> solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f

12	<a href="#">c3w1sB_</a>	Alignment		6.3	46	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae atg12-atg5 conjugate2 bound to the n-terminal domain of atg16
13	<a href="#">d2gnoa1</a>	Alignment		6.3	40	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
14	<a href="#">c2dymH_</a>	Alignment		6.3	46	<b>PDB header:</b> protein turnover/protein turnover <b>Chain:</b> H; <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
15	<a href="#">c2dymD_</a>	Alignment		6.3	46	<b>PDB header:</b> protein turnover/protein turnover <b>Chain:</b> D; <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
16	<a href="#">c2dymF_</a>	Alignment		6.3	46	<b>PDB header:</b> protein turnover/protein turnover <b>Chain:</b> F; <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
17	<a href="#">c2dymB_</a>	Alignment		6.3	46	<b>PDB header:</b> protein turnover/protein turnover <b>Chain:</b> B; <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
18	<a href="#">d1hrua_</a>	Alignment		5.5	20	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
19	<a href="#">c2m59A_</a>	Alignment		5.3	33	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
20	<a href="#">c2m59B_</a>	Alignment		5.3	33	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
21	<a href="#">c4pxhF_</a>	Alignment	not modelled	5.3	36	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> F; <b>PDB Molecule:</b> peptide synthetase; <b>PDBTitle:</b> structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis in complex with a peptidyl carrier protein domain
22	<a href="#">c2dyoB_</a>	Alignment	not modelled	5.3	46	<b>PDB header:</b> protein turnover/protein turnover <b>Chain:</b> B; <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex