
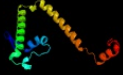













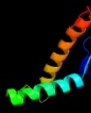



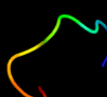

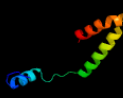
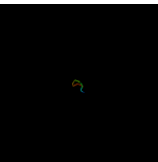



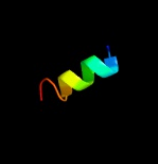


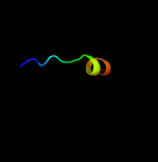



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0649\_(fabD2)\_746366\_747040  
 Date Fri Jul 26 01:50:21 BST 2019  
 Unique Job ID 497a81bc48085249

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3rfwA_</a>	 Alignment		82.4	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> cell-binding factor 2; <b>PDBTitle:</b> the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally-related sura-like chaperones in the human pathogen3 campylobacter jejuni
2	<a href="#">d1m5ya1</a>	 Alignment		80.6	15	<b>Fold:</b> Triger factor/SurA peptide-binding domain-like <b>Superfamily:</b> Triger factor/SurA peptide-binding domain-like <b>Family:</b> Porin chaperone SurA, peptide-binding domain
3	<a href="#">c3nrkA_</a>	 Alignment		65.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lic12922; <b>PDBTitle:</b> the crystal structure of the leptospiral hypothetical protein lic12922
4	<a href="#">c1nauA_</a>	 Alignment		26.1	38	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> glucagon; <b>PDBTitle:</b> nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of 3 perdeuterated dodecylphosphocholine micelles
5	<a href="#">c5yqzP_</a>	 Alignment		26.0	38	<b>PDB header:</b> signaling protein/hydrolase <b>Chain:</b> P: <b>PDB Molecule:</b> glucagon analogue; <b>PDBTitle:</b> structure of the glucagon receptor in complex with a glucagon analogue
6	<a href="#">d1k7ia2</a>	 Alignment		25.7	44	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
7	<a href="#">c1m5yB_</a>	 Alignment		22.6	15	<b>PDB header:</b> isomerase, cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> survival protein sura; <b>PDBTitle:</b> crystallographic structure of sura, a molecular chaperone2 that facilitates outer membrane porin folding
8	<a href="#">c2pv3B_</a>	 Alignment		21.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone sura; <b>PDBTitle:</b> crystallographic structure of sura fragment lacking the second2 peptidyl-prolyl isomerase domain complexed with peptide nftlkfwdifrk
9	<a href="#">c1bh0A_</a>	 Alignment		20.5	31	<b>PDB header:</b> synthetic hormone <b>Chain:</b> A: <b>PDB Molecule:</b> glucagon; <b>PDBTitle:</b> structure of a glucagon analog
10	<a href="#">c5miyA_</a>	 Alignment		18.0	55	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin ligase ravn; <b>PDBTitle:</b> crystal structure of the e3 ubiquitin ligase ravn from legionella2 pneumophila
11	<a href="#">d1kyqa2</a>	 Alignment		17.2	17	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like

12	<a href="#">d1kapp2</a>	Alignment		15.1	56	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
13	<a href="#">d1sata2</a>	Alignment		14.3	56	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
14	<a href="#">d1g9ka2</a>	Alignment		13.8	56	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
15	<a href="#">c1kyqC_</a>	Alignment		11.6	17	<b>PDB header:</b> oxidoreductase, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> siroheme biosynthesis protein met8; <b>PDBTitle:</b> met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelataase involved in siroheme synthesis.
16	<a href="#">c2h3oA_</a>	Alignment		10.0	40	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> structure of merft, a membrane protein with two trans-2 membrane helices
17	<a href="#">c2oyyF_</a>	Alignment		9.8	22	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> hexameric cytochrome; <b>PDBTitle:</b> hthp: a hexameric tyrosine-coordinated heme protein
18	<a href="#">c3c4rC_</a>	Alignment		9.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein encoded by2 cryptic prophage
19	<a href="#">c2k4vA_</a>	Alignment		8.9	43	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa1076; <b>PDBTitle:</b> solution structure of uncharacterized protein pa1076 from pseudomonas2 aeruginosa. northeast structural genomics consortium (nesg) target3 pat3, ontario center for structural proteomics target pa1076 .
20	<a href="#">c5z7bB_</a>	Alignment		7.3	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> padr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the vanr transcription factor in complex with2 vanillate
21	<a href="#">c5ez1B_</a>	Alignment	not modelled	6.2	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative peptidyl-prolyl cis-trans isomerase hp_0175; <b>PDBTitle:</b> crystal structure of cell binding factor 2 from helicobacter pylori in2 complex with i2ca
22	<a href="#">c2jh3C_</a>	Alignment	not modelled	6.2	9	<b>PDB header:</b> ribosomal protein <b>Chain:</b> C: <b>PDB Molecule:</b> ribosomal protein s2-related protein; <b>PDBTitle:</b> the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
23	<a href="#">c5camC_</a>	Alignment	not modelled	5.8	26	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> pupr protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of the pseudomonas putida2 anti-sigma factor pupr (semet)
24	<a href="#">c1d0rA_</a>	Alignment	not modelled	5.6	27	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> glucagon-like peptide-1-(7-36)-amide; <b>PDBTitle:</b> solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water
25	<a href="#">d1mska_</a>	Alignment	not modelled	5.6	29	<b>Fold:</b> Methionine synthase activation domain-like <b>Superfamily:</b> Methionine synthase activation domain-like <b>Family:</b> Methionine synthase SAM-binding domain
26	<a href="#">c3rgcB_</a>	Alignment	not modelled	5.4	14	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> possible periplasmic protein; <b>PDBTitle:</b> the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally related sura-like chaperones in the human pathogen3 campylobacter jejuni