



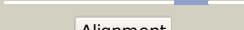
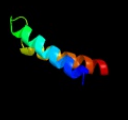
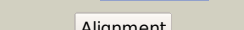

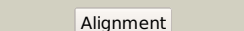





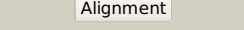

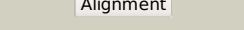

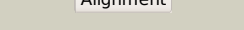

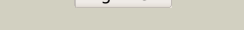
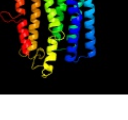


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0529\_ccsA\_619894\_620868  
 Date Fri Jul 26 01:50:08 BST 2019  
 Unique Job ID 244ef2b9c6a37f82

Detailed template information

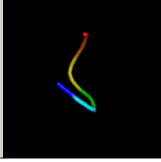
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ir6B_</a>	 Alignment		46.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bd-type quinol oxidase subunit ii; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans
2	<a href="#">c3aygA_</a>	 Alignment		31.9	11	<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
3	<a href="#">c5azcA_</a>	 Alignment		29.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> prolipoprotein diacylglycerol transferase; <b>PDBTitle:</b> crystal structure of escherichia coli lgt in complex with 2 phosphatidylglycerol
4	<a href="#">c6o7ua_</a>	 Alignment		28.9	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
5	<a href="#">c3mk7K_</a>	 Alignment		25.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit n; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
6	<a href="#">c6gcsX_</a>	 Alignment		19.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> nuxm subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
7	<a href="#">c3ol4B_</a>	 Alignment		19.6	18	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from 2 mycobacterium smegmatis, an ortholog of rv0543c
8	<a href="#">c2lkyA_</a>	 Alignment		19.3	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of msmeq_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
9	<a href="#">c2m0nA_</a>	 Alignment		16.7	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
10	<a href="#">c6o7xa_</a>	 Alignment		14.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a; <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3
11	<a href="#">c3o0rB_</a>	 Alignment		14.0	12	<b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitric oxide reductase subunit b; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment

12	<a href="#">c2kvcA_</a>	Alignment		12.8	14	<p><b>PDB header:</b>unknown function  <b>Chain:</b> A; <b>PDB Molecule:</b>putative uncharacterized protein;  <b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a</p>
13	<a href="#">c5xnmj_</a>	Alignment		9.5	28	<p><b>PDB header:</b>membrane protein  <b>Chain:</b> J; <b>PDB Molecule:</b>photosystem ii reaction center protein j;  <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum</p>
14	<a href="#">c3jcu_</a>	Alignment		9.3	28	<p><b>PDB header:</b>membrane protein  <b>Chain:</b> J; <b>PDB Molecule:</b>photosystem ii reaction center protein j;  <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution</p>
15	<a href="#">d1u7ga_</a>	Alignment		7.1	18	<p><b>Fold:</b>Ammonium transporter  <b>Superfamily:</b>Ammonium transporter  <b>Family:</b>Ammonium transporter</p>
16	<a href="#">d2axtj1</a>	Alignment		6.6	67	<p><b>Fold:</b>Single transmembrane helix  <b>Superfamily:</b>Photosystem II reaction center protein J, Psbj  <b>Family:</b>Psbj-like</p>

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[c3a0hj\\_](#)

Alignment



6.6

67

**PDB header:** electron transport

**Chain:** J; **PDB Molecule:** photosystem ii reaction center protein j;

**PDB Title:** crystal structure of i-substituted photosystem ii complex