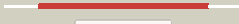



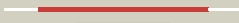



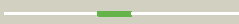

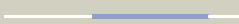




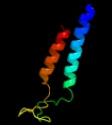

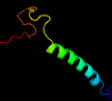



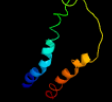
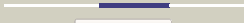

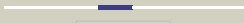



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2684\_arsA\_3000624\_3001913  
 Date Wed Aug 7 12:50:33 BST 2019  
 Unique Job ID 360a12b9d670b6d1

Detailed template information

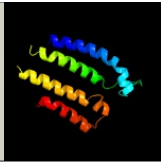
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4f35C_</a>	 Alignment		100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transporter, nadc family; <b>PDBTitle:</b> crystal structure of a bacterial dicarboxylate/sodium symporter
2	<a href="#">c4r1iB_</a>	 Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> aminobenzoyl-glutamate transporter; <b>PDBTitle:</b> structure and function of neisseria gonorrhoeae mtrf illuminates a2 class of antimetabolite efflux pumps
3	<a href="#">c4r0cB_</a>	 Alignment		99.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> abgt putative transporter family; <b>PDBTitle:</b> crystal structure of the alcanivorax borkumensis ydah transporter2 reveals an unusual topology
4	<a href="#">c5a1sB_</a>	 Alignment		93.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> citrate-sodium symporter; <b>PDBTitle:</b> crystal structure of the sodium-dependent citrate symporter secits2 form salmonella enterica.
5	<a href="#">c3qngD_</a>	 Alignment		54.8	8	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
6	<a href="#">c4kppA_</a>	 Alignment		25.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax
7	<a href="#">c2b6pA_</a>	 Alignment		15.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
8	<a href="#">c3mk7F_</a>	 Alignment		8.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
9	<a href="#">c6nbxG_</a>	 Alignment		8.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
10	<a href="#">c2bbjB_</a>	 Alignment		7.0	20	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
11	<a href="#">d1fftb2</a>	 Alignment		6.9	12	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region

12	<a href="#">d1y5ic1</a>  Alignment		6.6	9 <b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Respiratory nitrate reductase 1 gamma chain <b>Family:</b> Respiratory nitrate reductase 1 gamma chain
13	<a href="#">c4djiA</a>  Alignment		6.4	14 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc

14

[c5levA\\_](#)

Alignment



5.6

12

**PDB header:**transferase

**Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine--dolichyl-phosphate n-

**PDBTitle:** crystal structure of human udp-n-acetylglucosamine-dolichyl-phosphate2 n-acetylglucosaminephosphotransferase (dpagt1) (v264g mutant)