Phyre2

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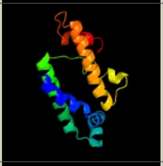
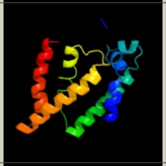
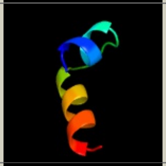
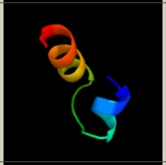
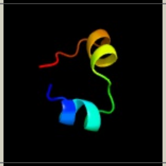
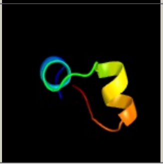
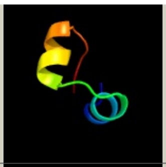
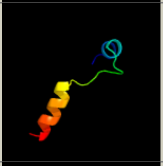
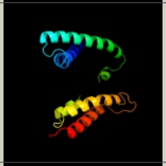
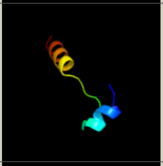
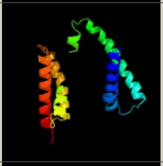
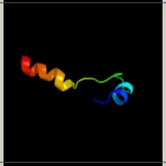
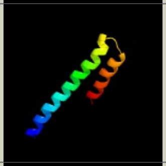
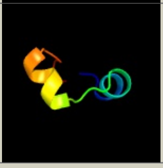
Description	RVBD2060_(-)_2316287_2316688
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	c2b97f960e1c375a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5b57B_	Alignment		99.7	15	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**putative hemin abc transport system, membrane protein; **PDBTitle:** inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
2	c4g1uB_	Alignment		99.7	16	**PDB header:**transport protein/hydrolase **Chain:** B: **PDB Molecule:**hemin transport system permease protein hmuu; **PDBTitle:** x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
3	c2nq2A_	Alignment		99.5	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**hypothetical abc transporter permease protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
4	c4dblB_	Alignment		99.5	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**vitamin b12 import system permease protein btuc; **PDBTitle:** crystal structure of e159q mutant of btucdf
5	d1l7va_	Alignment		99.1	18	**Fold:**ABC transporter involved in vitamin B12 uptake, BtuC **Superfamily:**ABC transporter involved in vitamin B12 uptake, BtuC **Family:**ABC transporter involved in vitamin B12 uptake, BtuC
6	c2bbjB_	Alignment		19.1	8	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
7	d1pn2a2	Alignment		14.0	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
8	c1q1hA_	Alignment		13.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor e; **PDBTitle:** an extended winged helix domain in general transcription2 factor e/iie alpha
9	d1q1ha_	Alignment		13.7	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcription factor E/IIe-alpha, N-terminal domain
10	c3j3bL_	Alignment		13.4	25	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l13; **PDBTitle:** structure of the human 60s ribosomal proteins
11	c3u5eL_	Alignment		11.5	17	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l13-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a

12	c3zf7N_	Alignment		11.2	29	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l13; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
13	c4a18U_	Alignment		11.1	21	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**rpl13; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
14	d1s9ca1	Alignment		9.7	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
15	c2xq2A_	Alignment		9.5	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
16	c4w7bD_	Alignment		9.3	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**hydratase chsh2; **PDBTitle:** crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
17	c3dh4A_	Alignment		9.3	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
18	d2b3na1	Alignment		8.8	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
19	c5gasN_	Alignment		8.4	24	**PDB header:**hydrolase **Chain:** N: **PDB Molecule:**archaeal/vacuolar-type h+-atpase subunit i; **PDBTitle:** thermus thermophilus v/a-atpase, conformation 2
20	c3j39L_	Alignment		7.2	21	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l13; **PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins
21	c4rv2B_	Alignment	not modelled	7.1	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**maoc family protein; **PDBTitle:** crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
22	d2iuba2	Alignment	not modelled	6.7	14	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
23	c5n9yB_	Alignment	not modelled	6.6	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**zinc transport protein zntb; **PDBTitle:** the full-length structure of zntb
24	c2kr6A_	Alignment	not modelled	6.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**presenilin-1; **PDBTitle:** solution structure of presenilin-1 ctf subunit
25	c2odbB_	Alignment	not modelled	6.2	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
26	c3cmwA_	Alignment	not modelled	5.9	33	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-ssdna/dsdna2 structures