Phyre2

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Description	RVBD1217c_(-)_1360161_1361807
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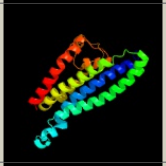
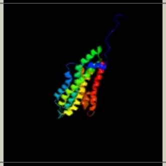
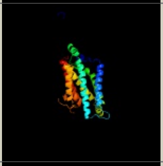
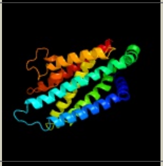
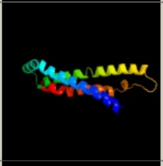
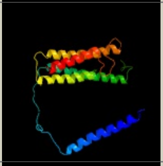
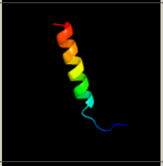
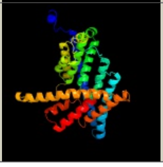
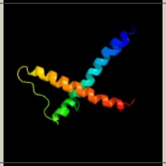
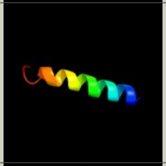
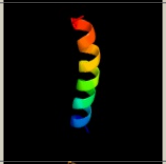
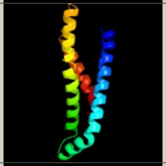
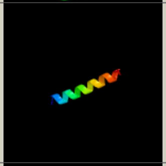
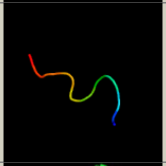
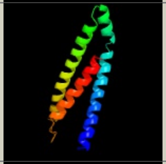
Unique Job ID	e538e326a7eb3495

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6an7D_	Alignment		99.2	10	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport permease protein; **PDBTitle:** crystal structure of o-antigen polysaccharide abc-transporter
2	c6an7C_	Alignment		99.1	9	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transport permease protein; **PDBTitle:** crystal structure of o-antigen polysaccharide abc-transporter
3	c5do7A_	Alignment		98.9	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family g member 5; **PDBTitle:** crystal structure of the human sterol transporter abcg5/abcg8
4	c5do7B_	Alignment		98.9	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**atp-binding cassette sub-family g member 8; **PDBTitle:** crystal structure of the human sterol transporter abcg5/abcg8
5	c5nj3B_	Alignment		98.4	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**atp-binding cassette sub-family g member 2; **PDBTitle:** structure of an abc transporter: complete structure
6	c5njgB_	Alignment		98.4	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**atp-binding cassette sub-family g member 2; **PDBTitle:** structure of an abc transporter: part of the structure that could be2 built de novo
7	c5xjyA_	Alignment		95.8	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family a member 1; **PDBTitle:** cryo-em structure of human abca1
8	c5ws4A_	Alignment		45.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**macrolide export atp-binding/permease protein macb; **PDBTitle:** crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
9	c6elhA_	Alignment		25.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide reductase; **PDBTitle:** low resolution structure of neisseria meningitidis qnor
10	c6hwhX_	Alignment		12.7	29	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**cytochrome c oxidase polypeptide 4; **PDBTitle:** structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
11	d1otsa_	Alignment		9.0	16	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel

12	d1jqna_	Alignment		8.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
13	c3hzqA_	Alignment		7.8	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate state
14	c2jp3A_	Alignment		7.6	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
15	c2jo1A_	Alignment		7.5	36	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
16	c5xu1M_	Alignment		7.4	14	**PDB header:**transport protein **Chain:** M: **PDB Molecule:**abc transporter permeae; **PDBTitle:** structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
17	c2mkvA_	Alignment		7.3	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/potassium-transporting atpase subunit gamma; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd2b in micelles
18	d1atxa_	Alignment		7.2	36	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
19	c5lj7B_	Alignment		6.9	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**macrolide export atp-binding/permease protein macb; **PDBTitle:** structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
20	c2h9xA_	Alignment		6.9	24	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin cgna; **PDBTitle:** nmr structure for the cgna toxin from the sea anemone2 condylactis gigantea
21	c2bbjB_	Alignment	not modelled	6.4	17	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
22	c5lm4A_	Alignment	not modelled	6.3	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**excitatory amino acid transporter 1,neutral amino acid **PDBTitle:** structure of the thermostalilized eaat1 cryst-ii mutant in complex2 with l-asp and the allosteric inhibitor ucph101
23	d1grja2	Alignment	not modelled	6.3	27	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
24	c1grjA_	Alignment	not modelled	6.1	27	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
25	d2ezla_	Alignment	not modelled	6.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
26	c2h7dB_	Alignment	not modelled	6.0	45	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**chimera of 24-mer peptide from integrin beta-3 **PDBTitle:** solution structure of the talin f3 domain in complex with a2 chimeric beta3 integrin-pip kinase peptide
27	d2adra2	Alignment	not modelled	5.9	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
28	c2jpwA_	Alignment	not modelled	5.8	25	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin i, cardiac muscle; **PDBTitle:** solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i

29	c4ev6E_	Alignment	not modelled	5.6	14	**PDB header:**metal transport **Chain:** E: **PDB Molecule:**magnesium transport protein cora; **PDBTitle:** the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
30	d2oz4a1	Alignment	not modelled	5.6	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C2 set domains
31	c5nikK_	Alignment	not modelled	5.3	12	**PDB header:**transport protein **Chain:** K: **PDB Molecule:**macrolide export atp-binding/permease protein macb; **PDBTitle:** structure of the macab-tolc abc-type tripartite multidrug efflux pump
32	c5ld1D_	Alignment	not modelled	5.1	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**polyphosphate:amp phosphotransferase; **PDBTitle:** crystal structure of polyphosphate kinase from meiothermus ruber bound2 to atp