Phyre2

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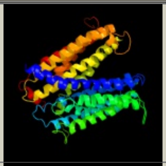
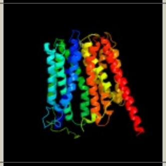
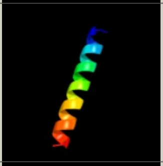
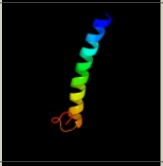
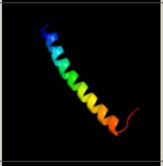
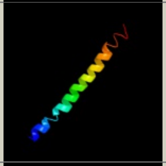
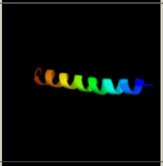
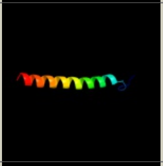
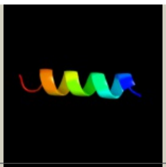
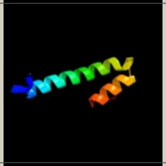
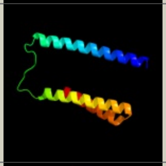
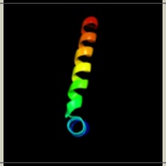
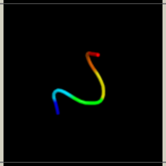
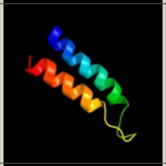
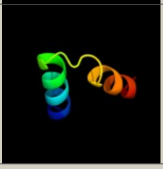
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mkuA_	Alignment		100.0	55	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
2	d1pw4a_	Alignment		18.8	12	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
3	d2iuba2	Alignment		10.0	18	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
4	c3g43F_	Alignment		9.7	8	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel subunit **PDBTitle:** crystal structure of the calmodulin-bound cav1.2 c-terminal2 regulatory domain dimer
5	c1wrgA_	Alignment		9.6	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
6	d1lghb_	Alignment		8.8	8	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
7	c3ipdB_	Alignment		8.7	10	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
8	c3hzqA_	Alignment		8.3	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state
9	c2ketA_	Alignment		7.9	8	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**cathelicidin-6; **PDBTitle:** solution structure of bmap-27
10	d1m56d_	Alignment		7.7	11	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
11	c1novE_	Alignment		7.5	15	**PDB header:**virus **Chain:** E: **PDB Molecule:**nodamura virus coat proteins; **PDBTitle:** nodamura virus

12	c2z2qF_	Alignment		7.4	0	**PDB header:**virus/rna **Chain:** F: **PDB Molecule:**coat protein gamma; **PDBTitle:** crystal structure of flock house virus
13	d2d5ba1	Alignment		7.2	8	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
14	d1u61a_	Alignment		7.1	13	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**RNase III catalytic domain-like
15	d1v54c_	Alignment		6.9	10	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
16	d1jo5a_	Alignment		6.7	16	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
17	c2hydB_	Alignment		6.6	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
18	d1w7ab4	Alignment		6.3	50	**Fold:**MutS N-terminal domain-like **Superfamily:**DNA repair protein MutS, domain I **Family:**DNA repair protein MutS, domain I
19	c2l35A_	Alignment		6.3	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dap12-nkg2c_tm; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
20	c2gslE_	Alignment		6.3	11	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**hypothetical protein; **PDBTitle:** x-ray crystal structure of protein fn1578 from fusobacterium2 nucleatum. northeast structural genomics consortium target nr1.
21	c2k6xA_	Alignment	not modelled	6.2	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
22	d1pf4a2	Alignment	not modelled	6.0	13	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
23	c1m46B_	Alignment	not modelled	5.8	22	**PDB header:**cell cycle protein **Chain:** B: **PDB Molecule:**iq4 motif from myo2p, a class v myosin; **PDBTitle:** crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
24	c1tiiC_	Alignment	not modelled	5.7	10	**PDB header:**enterotoxin **Chain:** C: **PDB Molecule:**heat labile enterotoxin type iib; **PDBTitle:** escherichia coli heat labile enterotoxin type iib
25	d1kbhb_	Alignment	not modelled	5.5	40	**Fold:**Nuclear receptor coactivator interlocking domain **Superfamily:**Nuclear receptor coactivator interlocking domain **Family:**Nuclear receptor coactivator interlocking domain
26	d1eysh2	Alignment	not modelled	5.4	7	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
27	d1nvpb_	Alignment	not modelled	5.4	17	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
28	c1nvpB_	Alignment	not modelled	5.4	17	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription initiation factor iia alpha chain; **PDBTitle:** human tfiia/tbp/dna complex

29	c1b9uA_	Alignment	not modelled	5.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
30	d1nkzb_	Alignment	not modelled	5.2	12	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
31	c1unyA_	Alignment	not modelled	5.2	15	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
32	d1qlec_	Alignment	not modelled	5.1	13	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
33	d1zoqc1	Alignment	not modelled	5.1	40	**Fold:**Nuclear receptor coactivator interlocking domain **Superfamily:**Nuclear receptor coactivator interlocking domain **Family:**Nuclear receptor coactivator interlocking domain
34	c2i7uA_	Alignment	not modelled	5.1	42	**PDB header:**de novo protein/ligand binding protein **Chain:** A: **PDB Molecule:**four-alpha-helix bundle; **PDBTitle:** structural and dynamical analysis of a four-alpha-helix2 bundle with designed anesthetic binding pockets
35	d2cqna1	Alignment	not modelled	5.1	23	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
36	c1iojA_	Alignment	not modelled	5.1	43	**PDB header:**apolipoprotein **Chain:** A: **PDB Molecule:**apoc-i; **PDBTitle:** human apolipoprotein c-i, nmr, 18 structures
37	c2khgA_	Alignment	not modelled	5.0	22	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in tfe
38	c2khfA_	Alignment	not modelled	5.0	22	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in dpc-micelles