Phyre2

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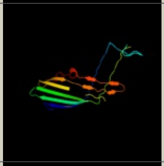
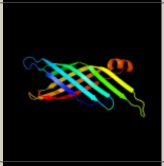
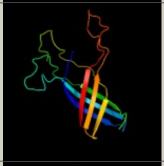
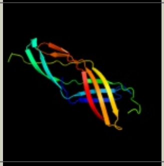
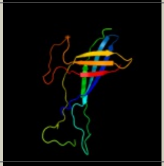
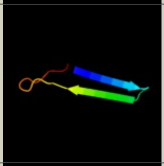
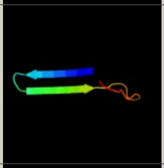
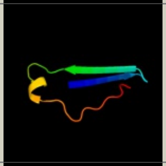
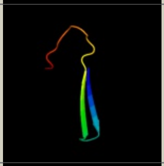
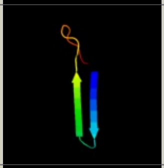
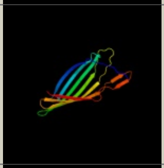
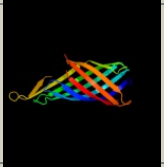
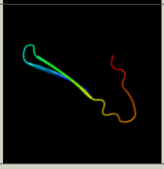
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t16a_	Alignment		94.7	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
2	c3dwoX_	Alignment		90.1	18	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
3	c2x4mD_	Alignment		88.9	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
4	d1i78a_	Alignment		88.6	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
5	d1qj8a_	Alignment		87.1	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
6	d1g90a_	Alignment		85.4	10	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
7	c2f1tB_	Alignment		81.7	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
8	d1qjpa_	Alignment		72.9	11	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
9	c2x27X_	Alignment		70.8	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
10	c2k0lA_	Alignment		67.5	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
11	d1p4ta_	Alignment		60.5	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein

12	c2iwvD_	Alignment		50.6	14	**PDB header:**ion channel **Chain:** D: **PDB Molecule:**outer membrane protein g; **PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
13	d1pama3	Alignment		50.0	22	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
14	d1qhoa3	Alignment		43.2	22	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
15	d3bmva3	Alignment		42.0	24	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
16	d1cyga3	Alignment		39.8	22	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
17	d1cxla3	Alignment		38.7	30	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
18	c3aehB_	Alignment		37.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
19	c3nb3C_	Alignment		37.1	12	**PDB header:**virus **Chain:** C: **PDB Molecule:**outer membrane protein a; **PDBTitle:** the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
20	d1cgta3	Alignment		34.8	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
21	c3qraA_	Alignment	not modelled	34.5	15	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**attachment invasion locus protein; **PDBTitle:** the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis
22	c2hb0B_	Alignment	not modelled	30.1	24	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**cfa/i fimbrial subunit e; **PDBTitle:** crystal structure of cfae, the adhesive subunit of cfa/i2 fimbria of enterotoxigenic escherichia coli
23	c1o75A_	Alignment	not modelled	20.3	25	**PDB header:**lipoproteinullntigen **Chain:** A: **PDB Molecule:**47 kda membrane antigen; **PDBTitle:** tp47, the 47-kilodalton lipoprotein of treponema pallidum
24	d1osma_	Alignment	not modelled	18.3	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
25	c3bryB_	Alignment	not modelled	17.7	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
26	d1o75a1	Alignment	not modelled	15.4	32	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains
27	c1qd6C_	Alignment	not modelled	14.0	18	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein (outer membrane phospholipase (ompla)); **PDBTitle:** outer membrane phospholipase a from escherichia coli
28	d2vdfa1	Alignment	not modelled	13.7	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
						PDB header:rna binding protein

29	c2dgwA_	Alignment	not modelled	13.5	7	**Chain:** A: **PDB Molecule:**probable rna-binding protein 19; **PDBTitle:** solution structure of the second rna recognition motif in2 rna-binding protein 19
30	d1tlya_	Alignment	not modelled	12.7	21	**Fold:**Transmembrane beta-barrels **Superfamily:**Tsx-like channel **Family:**Tsx-like channel
31	c3f83A_	Alignment	not modelled	11.2	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fusion of the minor pilin cfae and major pilin cfab; **PDBTitle:** structure of fusion complex of the minor pilin cfae and major pilin2 cfab of cfa/i pili from etec e. coli
32	c2ostC_	Alignment	not modelled	10.5	45	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**putative endonuclease; **PDBTitle:** the structure of a bacterial homing endonuclease : i-ssp6803i
33	d1b24a2	Alignment	not modelled	10.4	26	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
34	c2e12B_	Alignment	not modelled	8.8	25	**PDB header:**translation **Chain:** B: **PDB Molecule:**hypothetical protein xcc3642; **PDBTitle:** the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif
35	c2hyiJ_	Alignment	not modelled	8.3	43	**PDB header:**hydrolase/rna binding protein/rna **Chain:** J: **PDB Molecule:**protein casc3; **PDBTitle:** structure of the human exon junction complex with a trapped2 dead-box helicase bound to rna
36	d2akja3	Alignment	not modelled	8.2	22	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
37	c1fw3A_	Alignment	not modelled	6.2	17	**PDB header:**hydrolase, membrane protein **Chain:** A: **PDB Molecule:**outer membrane phospholipase a; **PDBTitle:** outer membrane phospholipase a from escherichia coli
38	d2icya1	Alignment	not modelled	6.0	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
39	d1weza_	Alignment	not modelled	5.8	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
40	d1x40a1	Alignment	not modelled	5.4	20	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
41	d2dcfa1	Alignment	not modelled	5.3	27	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
42	d3cdda2	Alignment	not modelled	5.2	14	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like