Phyre^2

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Description	P77286
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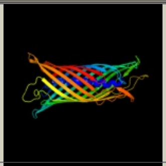
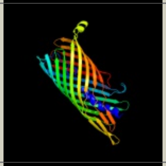
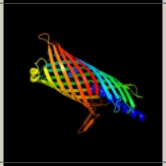
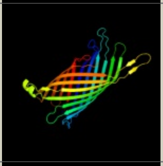
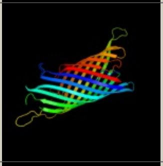
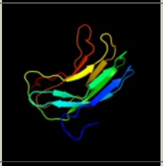
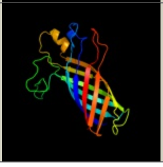
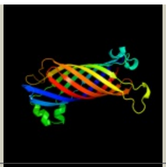
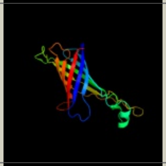
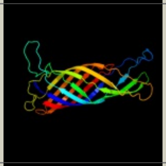
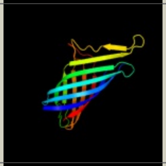
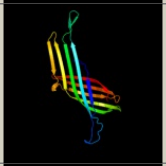
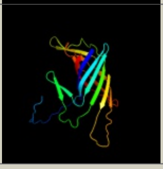
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kvnA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
2	c3sljA_	Alignment		100.0	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
3	c3aehB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
4	c3qq2C_	Alignment		100.0	23	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
5	c2qomB_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
6	d1uynx_	Alignment		100.0	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
7	c3ml3A_	Alignment		99.8	34	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**outer membrane protein icsa autotransporter; **PDBTitle:** crystal structure of the icsa autochaperone region
8	d1daba_	Alignment		99.5	28	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Virulence factor P.69 pertactin
9	c3h09B_	Alignment		98.6	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**immunoglobulin a1 protease; **PDBTitle:** the structure of haemophilus influenzae iga1 protease
10	c3syjA_	Alignment		98.5	34	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesion and penetration protein autotransporter; **PDBTitle:** crystal structure of the haemophilus influenzae hap adhesin
11	d1g90a_	Alignment		98.4	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein

12	d1p4ta_	Alignment		98.4	18	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
13	c2jmmA_	Alignment		98.3	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein
14	c2x27X_	Alignment		98.3	15	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
15	c2k0lA_	Alignment		98.3	13	**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.
16	c2f1tB_	Alignment		98.1	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
17	d1qjpa_	Alignment		98.1	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
18	c3nb3C_	Alignment		98.1	15	**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
19	d1qj8a_	Alignment		97.8	9	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
20	c2lhfA_	Alignment		97.8	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein h1; **PDBTitle:** solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles
21	c3qraA_	Alignment	not modelled	97.6	11	**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	c3ak5B_	Alignment	not modelled	97.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp; **PDBTitle:** hemoglobin protease (hbp) passenger missing domain-2
23	c2iwvD_	Alignment	not modelled	96.2	13	**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
24	d2zfga1	Alignment	not modelled	95.0	24	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
25	c1wxrA_	Alignment	not modelled	94.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haemoglobin protease; **PDBTitle:** crystal structure of heme binding protein, an2 autotransporter hemoglobine protease from pathogenic3 escherichia coli
26	d1osma_	Alignment	not modelled	94.7	26	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
27	d1phoa_	Alignment	not modelled	94.3	21	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
28	c2x4mD_	Alignment	not modelled	94.2	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
						PDB header:membrane protein

29	c3nsgA_	Alignment	not modelled	93.4	27	**Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
30	c2wjqA_	Alignment	not modelled	91.6	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
31	d3prna_	Alignment	not modelled	91.6	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
32	d1i78a_	Alignment	not modelled	90.8	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
33	d2pora_	Alignment	not modelled	90.7	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
34	c3brzA_	Alignment	not modelled	90.1	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
35	c3dwoX_	Alignment	not modelled	88.2	16	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
36	c3bryB_	Alignment	not modelled	87.1	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
37	c3a2rX_	Alignment	not modelled	83.4	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
38	d2fgqx1	Alignment	not modelled	82.5	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
39	d1t16a_	Alignment	not modelled	68.9	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
40	c3cslB_	Alignment	not modelled	45.4	11	**PDB header:**membrane protein/heme binding protein **Chain:** B: **PDB Molecule:**hasr protein; **PDBTitle:** structure of the serratia marcescens hemophore receptor hasr in2 complex with its hemophore hasa and heme
41	c2hdiA_	Alignment	not modelled	45.1	16	**PDB header:**protein transport,antimicrobial protein **Chain:** A: **PDB Molecule:**colicin i receptor; **PDBTitle:** crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
42	c3dzmB_	Alignment	not modelled	44.3	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
43	d2vdfa1	Alignment	not modelled	38.8	11	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
44	c2ervA_	Alignment	not modelled	25.4	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
45	c2o4vA_	Alignment	not modelled	20.4	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
46	d1cyga1	Alignment	not modelled	19.7	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
47	c2iahA_	Alignment	not modelled	19.1	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
48	d2gufa1	Alignment	not modelled	18.0	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
49	c2wkdA_	Alignment	not modelled	14.3	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf34p2; **PDBTitle:** crystal structure of a double ile-to-met mutant of protein2 orf34 from lactococcus phage p2
50	c1xkwA_	Alignment	not modelled	12.9	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
51	d2gr8a1	Alignment	not modelled	12.7	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
52	d2icwj1	Alignment	not modelled	10.7	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
53	d1n7va_	Alignment	not modelled	9.7	16	**Fold:**Adsorption protein p2 **Superfamily:**Adsorption protein p2 **Family:**Adsorption protein p2
54	d2icya1	Alignment	not modelled	9.7	10	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
55	d1ahsa_	Alignment	not modelled	9.5	40	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein

56	c3emoA_	Alignment	not modelled	9.4	19	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
57	d1bvp12	Alignment	not modelled	8.8	33	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
58	d2dd8l1	Alignment	not modelled	8.6	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
59	c2gr7C_	Alignment	not modelled	8.3	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
60	d2gr7a1	Alignment	not modelled	8.3	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
61	c1xkhC_	Alignment	not modelled	7.7	15	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
62	d1cgta1	Alignment	not modelled	7.4	47	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
63	d1fepa_	Alignment	not modelled	6.8	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
64	d1lila1	Alignment	not modelled	6.4	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
65	d1mfal1	Alignment	not modelled	6.3	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
66	d1qhoa1	Alignment	not modelled	6.2	41	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
67	d3bmva1	Alignment	not modelled	6.2	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
68	c2gjhA_	Alignment	not modelled	6.2	36	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
69	c1al0B_	Alignment	not modelled	6.1	31	**PDB header:**virus **Chain:** B: **PDB Molecule:**scaffolding protein gpb; **PDBTitle:** procapsid of bacteriophage phix174
70	d1w72l1	Alignment	not modelled	5.9	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
71	c2fqhA_	Alignment	not modelled	5.9	57	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0938; **PDBTitle:** nmr structure of hypothetical protein ta0938 from2 termoplasma acidophilum
72	c3orjA_	Alignment	not modelled	5.9	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar-binding protein; **PDBTitle:** crystal structure of a sugar-binding protein (bacova_04391) from2 bacteroides ovatus at 2.16 a resolution
73	d1adql1	Alignment	not modelled	5.6	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
74	d1nsnh1	Alignment	not modelled	5.5	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
75	c2f6iG_	Alignment	not modelled	5.5	50	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp-dependent clp protease, putative; **PDBTitle:** crystal structure of the clpp protease catalytic domain from2 plasmodium falciparum
76	d2ooja1	Alignment	not modelled	5.4	15	**Fold:**AOC barrel-like **Superfamily:**SO1590-like **Family:**SO1590-like
77	c3ir3B_	Alignment	not modelled	5.4	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-thioester dehydratase 2; **PDBTitle:** crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
78	c2k4tA_	Alignment	not modelled	5.3	9	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
79	c3duiB_	Alignment	not modelled	5.3	32	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**beta-galactoside-binding lectin; **PDBTitle:** crystal structure of the oxidized cg-1b: an adhesion/growth-2 regulatory lectin from chicken