Phyre^2

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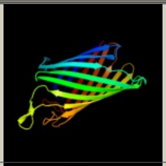
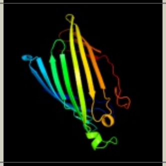
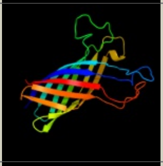
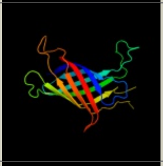
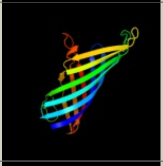
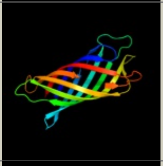
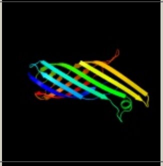
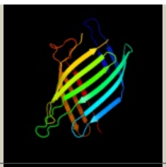
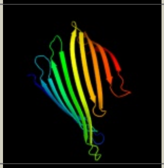
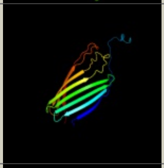
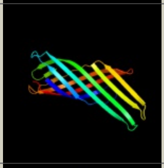
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wjqA_	Alignment		100.0	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
2	c2iwvD_	Alignment		98.3	16	**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
3	c2f1tB_	Alignment		97.8	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
4	d1g90a_	Alignment		97.7	9	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
5	c3aehB_	Alignment		97.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
6	c2jmmA_	Alignment		97.3	12	**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
7	d1qjpa_	Alignment		97.0	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
8	d1p4ta_	Alignment		97.0	7	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
9	c3a2rX_	Alignment		97.0	8	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
10	c3qraA_	Alignment		96.8	12	**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
11	c2k0lA_	Alignment		96.5	8	**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.

12	c3qq2C_	Alignment		96.4	17	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
13	c3sljA_	Alignment		96.4	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
14	c3nb3C_	Alignment		95.9	13	**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
15	c2qomB_	Alignment		95.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
16	d2fgqx1	Alignment		95.3	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
17	d1t16a_	Alignment		94.8	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
18	d1qj8a_	Alignment		93.0	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
19	c2hdiA_	Alignment		91.9	11	**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.
20	d1phoa_	Alignment		89.9	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
21	d1osma_	Alignment	not modelled	89.0	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
22	c3dwoX_	Alignment	not modelled	88.7	18	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
23	c2ervA_	Alignment	not modelled	85.6	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
24	c2x27X_	Alignment	not modelled	83.5	16	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
25	c3nsgA_	Alignment	not modelled	81.3	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
26	c1fw3A_	Alignment	not modelled	79.6	12	**PDB header:**hydrolase, membrane protein **Chain:** A: **PDB Molecule:**outer membrane phospholipase a; **PDBTitle:** outer membrane phospholipase a from escherichia coli
27	c3brzA_	Alignment	not modelled	69.8	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
28	c2lhfA_	Alignment	not modelled	67.7	15	**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
						PDB header:transport protein

29	c2y0kA_	Alignment	not modelled	65.7	8	**Chain:** A: **PDB Molecule:**pyroglutatmate porin opdo; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
30	c3rbhC_	Alignment	not modelled	61.0	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
31	c3kvnA_	Alignment	not modelled	58.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
32	d2zfga1	Alignment	not modelled	53.4	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
33	d3prna_	Alignment	not modelled	51.4	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
34	c1qd6C_	Alignment	not modelled	45.4	12	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein (outer membrane phospholipase (ompla)); **PDBTitle:** outer membrane phospholipase a from escherichia coli
35	d1a0tp_	Alignment	not modelled	45.2	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
36	d2jnaa1	Alignment	not modelled	42.8	38	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
37	c3bryB_	Alignment	not modelled	39.6	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
38	c2o4vA_	Alignment	not modelled	38.7	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
39	c2odjA_	Alignment	not modelled	38.3	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin d; **PDBTitle:** crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
40	d1k28d2	Alignment	not modelled	32.6	14	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
41	d1uynx_	Alignment	not modelled	30.0	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
42	c2x4mD_	Alignment	not modelled	22.5	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
43	c1pdjF_	Alignment	not modelled	19.4	14	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**baseplate structural protein gp27; **PDBTitle:** fitting of gp27 into cryoem reconstruction of bacteriophage2 t4 baseplate
44	d2vdfa1	Alignment	not modelled	17.6	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
45	c2qtkB_	Alignment	not modelled	17.3	8	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
46	d1i78a_	Alignment	not modelled	16.1	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
47	d1af6a_	Alignment	not modelled	15.8	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
48	c2k4tA_	Alignment	not modelled	12.4	11	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
49	c2k3aA_	Alignment	not modelled	11.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chap domain protein; **PDBTitle:** nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
50	d2noca1	Alignment	not modelled	11.2	17	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
51	c1e1hC_	Alignment	not modelled	10.4	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**botulinum neurotoxin type a light chain; **PDBTitle:** crystal structure of recombinant botulinum neurotoxin type2 a light chain, self-inhibiting zn endopeptidase.
52	c1xkwA_	Alignment	not modelled	10.1	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
53	d2gufa1	Alignment	not modelled	9.9	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
54	c3k3qB_	Alignment	not modelled	9.9	29	**PDB header:**immune system **Chain:** B: **PDB Molecule:**botulinum neurotoxin type a; **PDBTitle:** crystal structure of a llama antibody complexed with the c.2 botulinum neurotoxin serotype a catalytic domain
55	d2idib2	Alignment	not modelled	9.8	32	**Fold:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Superfamily:**Epsilon subunit of F1F0-ATP synthase N-terminal

		Alignment	not modelled			domain **Family:**Epsilon subunit of F1F0-ATP synthase N-terminal domain
56	c2kx7A_	Alignment	not modelled	7.7	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sensor-like histidine kinase yojn; **PDBTitle:** solution structure of the e.coli rcsd-abl domain (residues 688-795)
57	d1fepa_	Alignment	not modelled	7.2	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
58	d1wdds_	Alignment	not modelled	7.2	24	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
59	c3jtyB_	Alignment	not modelled	7.2	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**benf-like porin; **PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
60	d2mpra_	Alignment	not modelled	6.7	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
61	d1jeta_	Alignment	not modelled	6.7	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
62	c2y0lA_	Alignment	not modelled	6.2	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
63	d3bona1	Alignment	not modelled	5.9	29	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
64	c2ilpA_	Alignment	not modelled	5.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin a light-chain; **PDBTitle:** clostridium botulinum serotype a light chain inhibited by 4-2 chlorocinnamic hydroxamate
65	c1z7hA_	Alignment	not modelled	5.4	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tetanus toxin light chain; **PDBTitle:** 2.3 angstrom crystal structure of tetanus neurotoxin light2 chain
66	c2a97B_	Alignment	not modelled	5.4	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**botulinum neurotoxin type f; **PDBTitle:** crystal structure of catalytic domain of clostridium2 botulinum neurotoxin serotype f
67	c2qn0A_	Alignment	not modelled	5.4	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin; **PDBTitle:** structure of botulinum neurotoxin serotype c1 light chain2 protease