Phyre2

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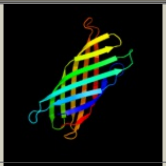
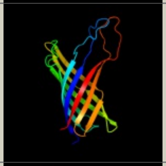
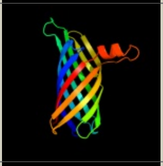
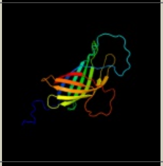
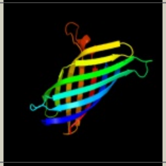
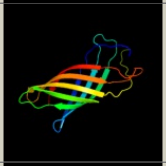
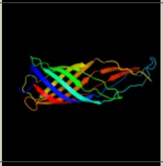
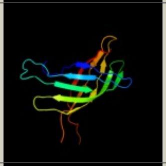
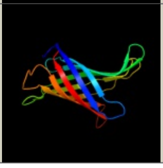
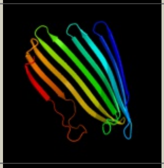
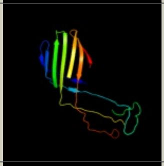
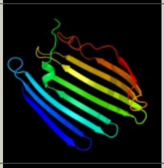
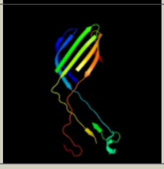
Description	P76471
Date	Thu Jan 5 12:23:16 GMT 2012
Unique Job ID	4604dd69dfa4d403

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qj8a_	Alignment		99.4	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
2	c3qraA_	Alignment		99.4	17	**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
3	d1g90a_	Alignment		99.3	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
4	c3nb3C_	Alignment		99.3	14	**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
5	c2k0lA_	Alignment		99.3	15	**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.
6	d1qjpa_	Alignment		99.2	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
7	d1p4ta_	Alignment		99.2	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
8	c2f1tB_	Alignment		98.9	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
9	c2x27X_	Alignment		98.9	12	**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	c2lhfA_	Alignment		98.8	21	**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
11	c2jmmA_	Alignment		98.6	13	**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

12	d1osma_	Alignment		98.3	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
13	d1phoa_	Alignment		98.2	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
14	d2fgqx1	Alignment		98.1	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
15	d2zfga1	Alignment		98.1	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
16	c2x4mD_	Alignment		97.7	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
17	c3dwoX_	Alignment		97.5	17	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
18	c3nsgA_	Alignment		97.4	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
19	c3a2rX_	Alignment		97.3	15	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
20	d1i78a_	Alignment		97.2	18	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
21	d1t16a_	Alignment	not modelled	97.2	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
22	c3aehB_	Alignment	not modelled	96.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
23	c3bryB_	Alignment	not modelled	96.5	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
24	d1uynx_	Alignment	not modelled	96.2	20	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
25	c3brzA_	Alignment	not modelled	95.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
26	c3qq2C_	Alignment	not modelled	95.4	14	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
27	c3sljA_	Alignment	not modelled	95.3	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
28	d3prna_	Alignment	not modelled	94.9	20	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
						PDB header:ion channel

29	c2iwvD_	Alignment	not modelled	93.2	16	**Chain:** D: **PDB Molecule:**outer membrane protein g; **PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
30	c2wjqA_	Alignment	not modelled	92.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
31	c2qomB_	Alignment	not modelled	91.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
32	c2o4vA_	Alignment	not modelled	90.8	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
33	c2odjA_	Alignment	not modelled	88.5	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin d; **PDBTitle:** crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
34	d2pora_	Alignment	not modelled	87.7	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
35	c3kvnA_	Alignment	not modelled	87.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
36	c2hdiA_	Alignment	not modelled	83.7	20	**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.
37	c3rbhC_	Alignment	not modelled	57.7	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
38	c2y0hA_	Alignment	not modelled	38.2	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
39	c2iahA_	Alignment	not modelled	34.8	13	**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.
40	c2ervA_	Alignment	not modelled	32.5	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
41	c3efmA_	Alignment	not modelled	31.6	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferric alcaligin siderophore receptor; **PDBTitle:** structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
42	c1xkwA_	Alignment	not modelled	28.5	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
43	d2jnaa1	Alignment	not modelled	28.3	33	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
44	c2k4tA_	Alignment	not modelled	21.0	18	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
45	c2vdaB_	Alignment	not modelled	17.7	30	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**maltoporin; **PDBTitle:** solution structure of the seca-signal peptide complex
46	c2nncB_	Alignment	not modelled	15.9	13	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**sulfur covalently-binding protein; **PDBTitle:** structure of the sulfur carrier protein soxy from chlorobium limicola2 f thiosulfatophilum
47	d1of5b_	Alignment	not modelled	14.2	29	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**NTF2-like
48	c3fhhA_	Alignment	not modelled	13.6	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane heme receptor shua; **PDBTitle:** crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae
49	c3jtyB_	Alignment	not modelled	12.6	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**benf-like porin; **PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
50	c2y0lA_	Alignment	not modelled	9.1	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
51	d2gufa1	Alignment	not modelled	7.8	21	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel