Phyre2

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Description	P69856
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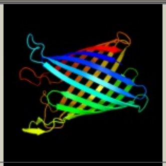
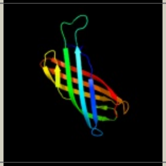
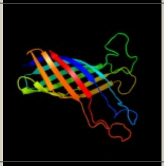
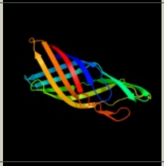
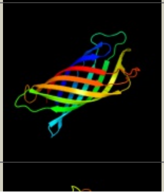
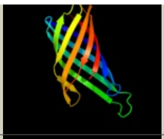
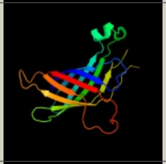
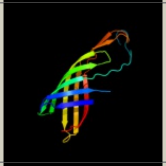
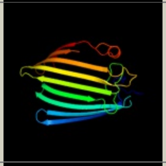
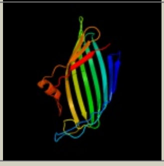
Unique Job ID	e51a5339a317d2ec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wjqA_	Alignment		100.0	100	**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	12	**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	c3qraA_	Alignment		97.8	14	**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
4	d1g90a_	Alignment		97.6	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
5	c2f1tB_	Alignment		97.5	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
6	d1t16a_	Alignment		97.5	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
7	c2k0lA_	Alignment		97.4	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.
8	c3dwoX_	Alignment		97.3	12	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
9	c3aehB_	Alignment		97.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
10	c3sljA_	Alignment		96.8	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
11	d1p4ta_	Alignment		96.8	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein

12	c3nb3C_	Alignment		96.4	9	**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
13	c3qq2C_	Alignment		96.3	9	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
14	d1qjpa_	Alignment		96.2	9	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
15	c2jmmA_	Alignment		96.0	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
16	d2fgqx1	Alignment		95.9	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
17	c3brzA_	Alignment		95.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
18	c2x27X_	Alignment		95.5	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
19	d1osma_	Alignment		94.8	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
20	c2qomB_	Alignment		93.7	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
21	d1qj8a_	Alignment	not modelled	93.2	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
22	c2hdiA_	Alignment	not modelled	93.1	13	**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.
23	c3rbhC_	Alignment	not modelled	92.5	16	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
24	d1a0tp_	Alignment	not modelled	92.5	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
25	c3a2rX_	Alignment	not modelled	92.4	10	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
26	d1phoa_	Alignment	not modelled	92.2	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
27	d2vdfa1	Alignment	not modelled	91.4	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
28	c3bryB_	Alignment	not modelled	90.2	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
29	c3efmA_	Alignment	not modelled	88.8	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferric alcaligin siderophore receptor; **PDBTitle:** structure of the alcaligin outer membrane recepteur faua

						from2 bordetella pertussis
30	c2lhfA_	Alignment	not modelled	88.3	10	**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
31	c3nsgA_	Alignment	not modelled	85.7	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
32	c2y0kA_	Alignment	not modelled	84.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pyroglutatmate porin opdo; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
33	c3kvnA_	Alignment	not modelled	82.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
34	d3prna_	Alignment	not modelled	82.5	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
35	c2y0hA_	Alignment	not modelled	81.0	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
36	d1uynx_	Alignment	not modelled	78.0	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
37	d1af6a_	Alignment	not modelled	74.7	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
38	d2zfga1	Alignment	not modelled	59.8	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
39	c3jtyB_	Alignment	not modelled	59.2	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**benf-like porin; **PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
40	d2mpra_	Alignment	not modelled	56.8	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
41	c1fw3A_	Alignment	not modelled	56.2	17	**PDB header:**hydrolase, membrane protein **Chain:** A: **PDB Molecule:**outer membrane phospholipase a; **PDBTitle:** outer membrane phospholipase a from escherichia coli
42	c1xkwA_	Alignment	not modelled	55.9	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
43	d1fepa_	Alignment	not modelled	49.9	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
44	d2gufa1	Alignment	not modelled	49.0	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
45	c2odjA_	Alignment	not modelled	47.6	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin d; **PDBTitle:** crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
46	d1by5a_	Alignment	not modelled	44.9	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
47	c2qtkB_	Alignment	not modelled	39.9	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
48	c2o4vA_	Alignment	not modelled	36.9	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
49	d1k28d2	Alignment	not modelled	35.3	15	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
50	c2y0lA_	Alignment	not modelled	31.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
51	d2jnaa1	Alignment	not modelled	24.9	20	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
52	c1pdjF_	Alignment	not modelled	23.9	15	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**baseplate structural protein gp27; **PDBTitle:** fitting of gp27 into cryoem reconstruction of bacteriophage2 t4 baseplate
53	c2ervA_	Alignment	not modelled	20.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
54	c2eeyA_	Alignment	not modelled	20.1	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis; **PDBTitle:** structure of gk0241 protein from geobacillus kaustophilus
55	c2k4tA_	Alignment	not modelled	19.0	17	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
56	c3fhhA_	Alignment	not modelled	18.5	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane heme receptor shua;

56	[illegible]	Alignment	not modelled	18.5	8	**PDBTitle:** crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae
57	c3cslB_	Alignment	not modelled	17.4	17	**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
58	d2jdih2	Alignment	not modelled	15.2	33	**Fold:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Superfamily:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Family:**Epsilon subunit of F1F0-ATP synthase N-terminal domain
59	c2iahA_	Alignment	not modelled	14.0	11	**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.
60	d1jeta_	Alignment	not modelled	13.6	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
61	c3t66A_	Alignment	not modelled	9.4	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
62	d1uqwa_	Alignment	not modelled	7.7	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
63	c3o9pA_	Alignment	not modelled	7.3	11	**PDB header:**peptide binding protein/peptide **Chain:** A: **PDB Molecule:**periplasmic murein peptide-binding protein; **PDBTitle:** the structure of the escherichia coli murein tripeptide binding2 protein mppa
64	c3rqtA_	Alignment	not modelled	6.9	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines
65	d1kmoa_	Alignment	not modelled	6.9	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
66	c1xkhC_	Alignment	not modelled	6.4	9	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
67	d1zlqa1	Alignment	not modelled	6.2	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
68	c1qd6C_	Alignment	not modelled	6.2	16	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein (outer membrane phospholipase (ompla)); **PDBTitle:** outer membrane phospholipase a from escherichia coli
69	c3ftoA_	Alignment	not modelled	6.2	5	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**oligopeptide-binding protein oppa; **PDBTitle:** crystal structure of oppa in a open conformation
70	d1ks9a2	Alignment	not modelled	6.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
71	c2djmA_	Alignment	not modelled	6.0	12	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**glucoamylase a; **PDBTitle:** solution structure of n-terminal starch-binding domain of2 glucoamylase from rhizopus oryzae
72	c3lznA_	Alignment	not modelled	5.9	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**p19 protein; **PDBTitle:** crystal structure analysis of the apo p19 protein from campylobacter2 jejuni at 1.59 a at ph 9
73	c1ztyA_	Alignment	not modelled	5.9	3	**PDB header:**sugar binding protein, signaling protein **Chain:** A: **PDB Molecule:**chitin oligosaccharide binding protein; **PDBTitle:** crystal structure of the chitin oligasaccharide binding2 protein
74	d1xoca1	Alignment	not modelled	5.8	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
75	c3ry3B_	Alignment	not modelled	5.8	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative solute-binding protein; **PDBTitle:** putative solute-binding protein from yersinia pestis.
76	d1wdds_	Alignment	not modelled	5.7	19	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
77	d1ynha1	Alignment	not modelled	5.6	29	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Succinylarginine dihydrolase-like
78	d1d5ra1	Alignment	not modelled	5.3	11	**Fold:**C2 domain-like **Superfamily:**C2 domain (Calcium/lipid-binding domain, CaLB) **Family:**PLC-like (P variant)
79	c2grxB_	Alignment	not modelled	5.2	10	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrichrome-iron receptor; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
80	c3na3A_	Alignment	not modelled	5.2	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
81	d1ej7s_	Alignment	not modelled	5.1	19	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit