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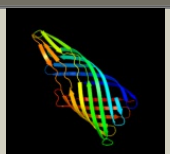
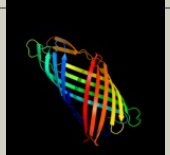
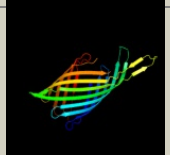
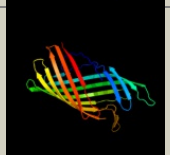
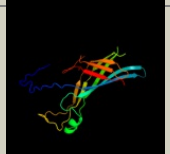
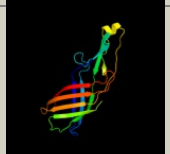
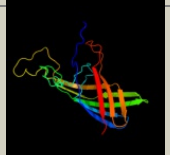
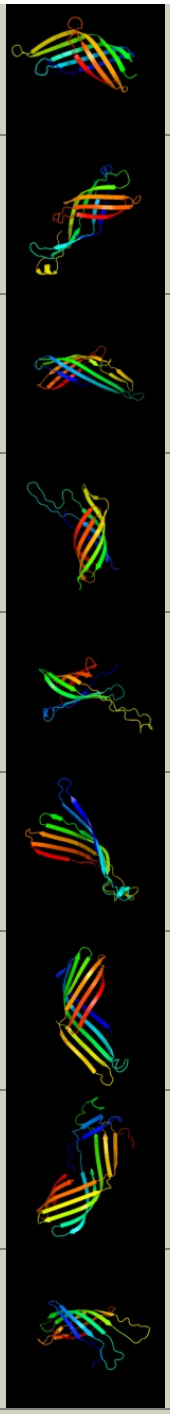
Description	P37663
Date	Thu Jan 5 11:56:36 GMT 2012
Unique Job ID	ae294f432af407ad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sljA_	Alignment		100.0	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
2	c3kvnA_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
3	c2qomB_	Alignment		100.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
4	c3qq2C_	Alignment		100.0	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
5	d1uynx_	Alignment		100.0	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
6	c3aehB_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
7	c2k0lA_	Alignment		98.8	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	d1qjpa_	Alignment		98.7	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
9	c2f1tB_	Alignment		98.7	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
10	d1g90a_	Alignment		98.7	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
11	c3qraA_	Alignment		98.6	8	**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

12	c3nb3C_	Alignment		98.6	18	**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	c2x27X_	Alignment		98.6	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
14	d1qj8a_	Alignment		98.6	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
15	d1p4ta_	Alignment		98.5	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
16	c2jmmA_	Alignment		98.2	16	**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
17	c2iwvD_	Alignment		98.0	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
18	d1i78a_	Alignment		97.9	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
19	c2x4mD_	Alignment		97.7	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
20	c2lhfA_	Alignment		97.7	11	**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	c2wjqA_	Alignment	not modelled	97.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
22	c3a2rX_	Alignment	not modelled	97.1	15	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
23	d2fgqx1	Alignment	not modelled	97.1	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
24	d2pora_	Alignment	not modelled	96.8	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
25	d3prna_	Alignment	not modelled	96.5	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
26	d1osma_	Alignment	not modelled	96.1	23	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
27	d1t16a_	Alignment	not modelled	95.7	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
28	d1phoa_	Alignment	not modelled	95.4	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
29	c3dwoX_	Alignment	not modelled	94.9	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue

30	c3nsgA_	Alignment	not modelled	94.7	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
31	d2zfga1	Alignment	not modelled	93.7	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
32	c2iahA_	Alignment	not modelled	90.1	8	**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.
33	c3brzA_	Alignment	not modelled	89.2	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
34	c3dzmB_	Alignment	not modelled	89.0	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
35	c2hdiA_	Alignment	not modelled	82.0	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.
36	c1xkhC_	Alignment	not modelled	81.8	8	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
37	c1xkwA_	Alignment	not modelled	69.9	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
38	d2gufa1	Alignment	not modelled	31.9	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
39	c2o4vA_	Alignment	not modelled	28.5	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
40	d1fepa_	Alignment	not modelled	26.5	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
41	d2gr7a1	Alignment	not modelled	24.7	14	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
42	c2gr7C_	Alignment	not modelled	24.7	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
43	c3cslB_	Alignment	not modelled	23.1	10	**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
44	c3bryB_	Alignment	not modelled	18.6	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
45	d2gr8a1	Alignment	not modelled	15.2	14	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
46	c1fw3A_	Alignment	not modelled	14.3	14	**PDB header:**hydrolase, membrane protein **Chain:** A: **PDB Molecule:**outer membrane phospholipase a; **PDBTitle:** outer membrane phospholipase a from escherichia coli
47	c3qlbA_	Alignment	not modelled	12.8	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**enantio-pyochelin receptor; **PDBTitle:** enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
48	c3emoA_	Alignment	not modelled	9.5	16	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
49	d1kmoa_	Alignment	not modelled	7.8	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
50	c2k4tA_	Alignment	not modelled	7.6	10	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
51	d1by5a_	Alignment	not modelled	7.3	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
52	d2cxaa1	Alignment	not modelled	6.3	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**LFTR-like
53	c2cxaA_	Alignment	not modelled	6.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucyl/phenylalanyl-trna-protein transferase; **PDBTitle:** crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
54	c3qteA_	Alignment	not modelled	6.3	57	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**defensin-6; **PDBTitle:** crystal structure of human alpha-defensin 6 (h27w mutant)