Phyre^2

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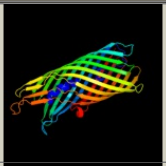
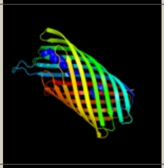
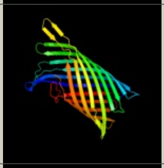
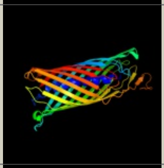
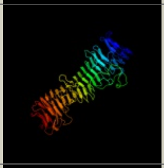
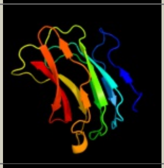
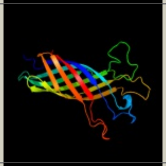
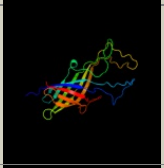
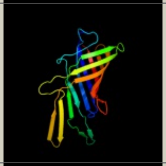
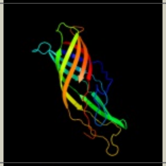
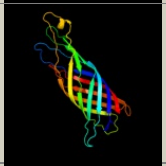
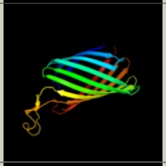
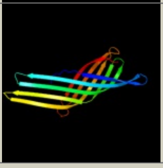
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sljA_	Alignment		100.0	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
2	c3aehB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
3	d1uynx_	Alignment		100.0	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
4	c3qq2C_	Alignment		100.0	19	**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	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
6	c3kvnA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
7	d1daba_	Alignment		99.5	13	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Virulence factor P.69 pertactin
8	c3ml3A_	Alignment		99.1	26	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**outer membrane protein icsa autotransporter; **PDBTitle:** crystal structure of the icsa autochaperone region
9	d1g90a_	Alignment		99.0	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
10	c2k0lA_	Alignment		98.9	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.
11	c3h09B_	Alignment		98.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**immunoglobulin a1 protease; **PDBTitle:** the structure of haemophilus influenzae iga1 protease

12	c3nb3C_	Alignment		98.8	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
13	d1p4ta_	Alignment		98.8	19	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
14	d1qjpa_	Alignment		98.6	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
15	c2jmmA_	Alignment		98.5	15	**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	c2f1tB_	Alignment		98.4	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
17	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
18	c3qraA_	Alignment		98.3	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
19	c2wjqA_	Alignment		97.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
20	d1qj8a_	Alignment		97.7	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
21	c3syjA_	Alignment	not modelled	97.6	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesion and penetration protein autotransporter; **PDBTitle:** crystal structure of the haemophilus influenzae hap adhesin
22	c2iwvD_	Alignment	not modelled	96.9	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
23	c2x4mD_	Alignment	not modelled	96.7	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
24	c3a2rX_	Alignment	not modelled	96.5	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
25	c2lhfA_	Alignment	not modelled	95.8	14	**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
26	d1i78a_	Alignment	not modelled	95.5	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
27	d3prna_	Alignment	not modelled	91.8	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
28	d2zfga1	Alignment	not modelled	90.6	5	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
						Fold: Transmembrane beta-barrels

29	d1phoa_	Alignment	not modelled	88.6	9	**Superfamily:**Porins **Family:**Porin
30	d2pora_	Alignment	not modelled	87.8	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	c3brzA_	Alignment	not modelled	80.7	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
32	d1t16a_	Alignment	not modelled	77.4	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
33	d2fgqx1	Alignment	not modelled	76.5	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
34	d1osma_	Alignment	not modelled	73.9	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
35	c3dwoX_	Alignment	not modelled	60.7	17	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
36	d1g5aa1	Alignment	not modelled	53.9	32	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
37	c3bryB_	Alignment	not modelled	49.6	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
38	d2vdfa1	Alignment	not modelled	45.2	11	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
39	c1qd6C_	Alignment	not modelled	38.3	18	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein (outer membrane phospholipase (ompla)); **PDBTitle:** outer membrane phospholipase a from escherichia coli
40	d3ulla_	Alignment	not modelled	37.7	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
41	c2ihfA_	Alignment	not modelled	32.7	44	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
42	c3rbhC_	Alignment	not modelled	27.7	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
43	c2ervA_	Alignment	not modelled	25.4	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
44	c3nsgA_	Alignment	not modelled	22.8	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
45	d1pm6a_	Alignment	not modelled	18.1	6	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
46	d1wv8a1	Alignment	not modelled	16.9	22	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like **Family:**TTHA1013-like
47	d1gxya_	Alignment	not modelled	16.8	11	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Ecto-ART
48	c3alzB_	Alignment	not modelled	14.7	17	**PDB header:**viral protein/membrane protein **Chain:** B: **PDB Molecule:**cdw150; **PDBTitle:** crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (form i)
49	c2z5vA_	Alignment	not modelled	14.1	7	**PDB header:**immune system **Chain:** A: **PDB Molecule:**myeloid differentiation primary response protein **PDBTitle:** solution structure of the tir domain of human myd88
50	d2hrva_	Alignment	not modelled	13.8	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
51	c1fw3A_	Alignment	not modelled	13.2	18	**PDB header:**hydrolase, membrane protein **Chain:** A: **PDB Molecule:**outer membrane phospholipase a; **PDBTitle:** outer membrane phospholipase a from escherichia coli
52	c3fmfA_	Alignment	not modelled	12.8	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
53	d1nrja_	Alignment	not modelled	12.2	33	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**SRP alpha N-terminal domain-like
54	c2hw2A_	Alignment	not modelled	12.2	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
55	d1rh6a_	Alignment	not modelled	11.2	6	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like

56	c2hdiA_	Alignment	not modelled	10.7	17	**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.
57	c2wvyA_	Alignment	not modelled	10.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
58	c3jtyB_	Alignment	not modelled	9.9	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
59	c2ww1B_	Alignment	not modelled	9.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
60	c2pe4A_	Alignment	not modelled	8.8	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-1; **PDBTitle:** structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
61	d1jmxa4	Alignment	not modelled	8.3	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
62	c1fdfA_	Alignment	not modelled	8.3	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhodopsin; **PDBTitle:** helix 7 bovine rhodopsin
63	d2f15a1	Alignment	not modelled	8.2	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
64	c2gr7C_	Alignment	not modelled	8.1	11	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
65	d2gr7a1	Alignment	not modelled	8.1	11	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
66	c3fidA_	Alignment	not modelled	8.0	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein (lpxr); **PDBTitle:** lpxr from salmonella typhimurium
67	d1qqga2	Alignment	not modelled	7.7	10	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Phosphotyrosine-binding domain (PTB)
68	d2gr8a1	Alignment	not modelled	7.7	11	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
69	c1z8rA_	Alignment	not modelled	7.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coxsackievirus b4 polyprotein; **PDBTitle:** 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschoten / new york / 51)
70	d1euza2	Alignment	not modelled	7.3	21	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
71	d2gc9a1	Alignment	not modelled	7.1	31	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Phenolic acid decarboxylase (PAD)
72	d1bgva2	Alignment	not modelled	6.9	42	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
73	c1ahuB_	Alignment	not modelled	6.8	18	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
74	d2pi0a1	Alignment	not modelled	6.8	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Interferon regulatory factor
75	d1cm7a_	Alignment	not modelled	6.6	13	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
76	c2dllA_	Alignment	not modelled	6.5	27	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**interferon regulatory factor 4; **PDBTitle:** solution structure of the irf domain of human interferon2 regulatory factors 4
77	d1k0ra4	Alignment	not modelled	6.3	50	**Fold:**Transcription factor NusA, N-terminal domain **Superfamily:**Transcription factor NusA, N-terminal domain **Family:**Transcription factor NusA, N-terminal domain
78	d1zrua1	Alignment	not modelled	6.3	13	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Lactophage receptor-binding protein head domain
79	d1tf3a3	Alignment	not modelled	6.3	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
80	c2atmA_	Alignment	not modelled	6.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure of the recombinant allergen ves v 2
81	c1kq8A_	Alignment	not modelled	6.3	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 3 forkhead homolog 1; **PDBTitle:** solution structure of winged helix protein hfh-1
82	d1kq8a_	Alignment	not modelled	6.3	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain

83	d2zkmx2	Alignment	not modelled	6.3	13	**Fold:**C2 domain-like **Superfamily:**C2 domain (Calcium/lipid-binding domain, CaLB) **Family:**PLC-like (P variant)
84	c3dvkB_	Alignment	not modelled	6.3	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**voltage-dependent r-type calcium channel subunit alpha-1e; **PDBTitle:** crystal structure of ca2+/cam-cav2.3 iq domain complex
85	d1dcea2	Alignment	not modelled	6.3	29	**Fold:**C2 domain-like **Superfamily:**Rab geranylgeranyltransferase alpha-subunit, insert domain **Family:**Rab geranylgeranyltransferase alpha-subunit, insert domain
86	d1bvua2	Alignment	not modelled	6.3	21	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
87	c3s2xB_	Alignment	not modelled	6.2	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
88	d1hwxa2	Alignment	not modelled	6.2	16	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
89	d1qvca_	Alignment	not modelled	6.1	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
90	d1dwka1	Alignment	not modelled	6.1	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
91	c3o7vX_	Alignment	not modelled	6.1	27	**PDB header:**rna binding protein/rna **Chain:** X: **PDB Molecule:**piwi-like protein 1; **PDBTitle:** crystal structure of human hiwi1 (v361m) paz domain (residues 277-399)2 in complex with 14-mer rna (12-bp + 2-nt overhang) containing 2'-och33 at its 3'-end
92	c2ic7A_	Alignment	not modelled	6.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltose transacetylase; **PDBTitle:** crystal structure of maltose transacetylase from2 geobacillus kaustophilus
93	c1z1sA_	Alignment	not modelled	6.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa3332; **PDBTitle:** crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
94	c3nadB_	Alignment	not modelled	5.9	31	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ferulate decarboxylase; **PDBTitle:** crystal structure of phenolic acid decarboxylase from bacillus pumilus2 ui-670
95	d1jx4a1	Alignment	not modelled	5.9	38	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
96	c2lakA_	Alignment	not modelled	5.8	8	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**ahsa1-like protein rhe_ch02687; **PDBTitle:** solution nmr structure of the ahsa1-like protein rhe_ch02687 (1-152)2 from rhizobium etli, northeast structural genomics consortium target3 rer242
97	d2irfg_	Alignment	not modelled	5.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Interferon regulatory factor
98	c1qqgA_	Alignment	not modelled	5.8	15	**PDB header:**signal transduction **Chain:** A: **PDB Molecule:**insulin receptor substrate 1; **PDBTitle:** crystal structure of the ph-ptb targeting region of irs-1
99	c3qu3A_	Alignment	not modelled	5.7	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**interferon regulatory factor 7; **PDBTitle:** crystal structure of irf-7 dbd apo form