Phyre2

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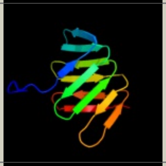
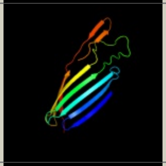
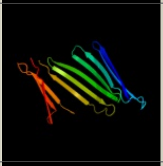
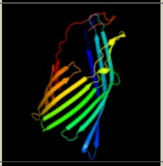
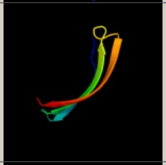
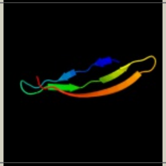
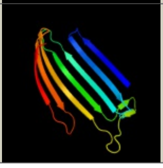
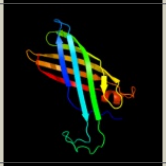
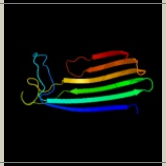
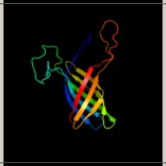
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r1aD_	Alignment		99.3	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**protein yhbn; **PDBTitle:** crystal structure of the periplasmic lipopolysaccharide transport2 protein lpta (yhbn), trigonal form
2	c3my2A_	Alignment		98.7	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipopolysaccharide export system protein lptc; **PDBTitle:** crystal structure of lptc
3	d1t16a_	Alignment		97.0	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
4	c2k4tA_	Alignment		95.9	16	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
5	c3brzA_	Alignment		95.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
6	c3bryB_	Alignment		95.4	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
7	c2wjqA_	Alignment		81.7	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
8	c3dwoX_	Alignment		81.2	15	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
9	d1p4ta_	Alignment		71.6	18	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
10	c2lhfA_	Alignment		70.1	23	**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	d1osma_	Alignment		63.5	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin

12	c2f1tB_	Alignment		62.5	9	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
13	c2k0lA_	Alignment		58.3	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.
14	c3qraA_	Alignment		45.5	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
15	d2zfga1	Alignment		40.9	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
16	c2iwvD_	Alignment		39.2	11	**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
17	d1g90a_	Alignment		37.6	19	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
18	c2x27X_	Alignment		34.8	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	d1qjpa_	Alignment		28.9	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
20	d1qj8a_	Alignment		26.1	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
21	d1fepa_	Alignment	not modelled	23.9	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
22	c1xkhC_	Alignment	not modelled	22.3	10	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
23	c3nb3C_	Alignment	not modelled	22.1	16	**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
24	c2iahA_	Alignment	not modelled	21.5	10	**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.
25	d1x1na1	Alignment	not modelled	16.8	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
26	c1dgrX_	Alignment	not modelled	14.5	9	**PDB header:**plant protein **Chain:** X: **PDB Molecule:**canavalin; **PDBTitle:** refined crystal structure of canavalin from jack bean
27	d1od5a2	Alignment	not modelled	12.2	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
28	d1m1ca_	Alignment	not modelled	12.1	19	**Fold:**L-A virus major coat protein **Superfamily:**L-A virus major coat protein **Family:**L-A virus major coat protein

29	c2eaaB_	Alignment	not modelled	12.1	14	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
30	c3aqjQ_	Alignment	not modelled	10.2	19	**PDB header:**metal binding protein **Chain:** Q: **PDB Molecule:**baseplate assembly protein v; **PDBTitle:** crystal structure of a c-terminal domain of the bacteriophage p2 tail2 spike protein, gpv
31	d2pora_	Alignment	not modelled	9.9	19	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
32	c2cauA_	Alignment	not modelled	9.8	10	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
33	d2bbkl_	Alignment	not modelled	8.5	28	**Fold:**Methylamine dehydrogenase, L chain **Superfamily:**Methylamine dehydrogenase, L chain **Family:**Methylamine dehydrogenase, L chain
34	d1mdal_	Alignment	not modelled	8.0	35	**Fold:**Methylamine dehydrogenase, L chain **Superfamily:**Methylamine dehydrogenase, L chain **Family:**Methylamine dehydrogenase, L chain
35	c3c75L_	Alignment	not modelled	7.9	28	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**methylamine dehydrogenase light chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
36	c2jmbA_	Alignment	not modelled	7.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu4866; **PDBTitle:** solution structure of the protein atu4866 from agrobacterium2 tumefaciens
37	c2o6dB_	Alignment	not modelled	7.2	9	**PDB header:**membrane protein, protein binding **Chain:** B: **PDB Molecule:**34 kda membrane antigen; **PDBTitle:** structure of native rtp34 from treponema pallidum
38	c2iurD_	Alignment	not modelled	7.1	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aromatic amine dehydrogenase beta subunit; **PDBTitle:** crystal structure of n-quinol form of aromatic amine2 dehydrogenase (aadh) from alcaligenes faecalis, form a3 cocrystal
39	c3c3vA_	Alignment	not modelled	7.0	12	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
40	c2d5fB_	Alignment	not modelled	7.0	12	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**glycinin a3b4 subunit; **PDBTitle:** crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
41	d1phoa_	Alignment	not modelled	6.8	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
42	c1uijA_	Alignment	not modelled	6.8	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta subunit of beta conglycinin; **PDBTitle:** crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
43	d1fxza2	Alignment	not modelled	6.8	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
44	c1m1cB_	Alignment	not modelled	6.4	40	**PDB header:**virus **Chain:** B: **PDB Molecule:**major coat protein; **PDBTitle:** structure of the l-a virus
45	d2fgqx1	Alignment	not modelled	6.3	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
46	d1c8ua1	Alignment	not modelled	6.2	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
47	c2vqaC_	Alignment	not modelled	6.1	10	**PDB header:**metal-binding protein **Chain:** C: **PDB Molecule:**sll1358 protein; **PDBTitle:** protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
48	c3kglB_	Alignment	not modelled	5.9	12	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
49	c3kscD_	Alignment	not modelled	5.8	16	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
50	c2cveA_	Alignment	not modelled	5.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
51	d1tbua1	Alignment	not modelled	5.7	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
52	c3rd7A_	Alignment	not modelled	5.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coa thioesterase; **PDBTitle:** crystal structure of acyl-coa thioesterase from mycobacterium avium
53	c3ehkC_	Alignment	not modelled	5.6	20	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
54	c2e9qA_	Alignment	not modelled	5.5	12	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
						Fold:TIM beta/alpha-barrel

55	d1tz7a1	Alignment	not modelled	5.2	16	**Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain