Phyre^{2}

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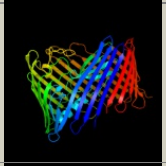
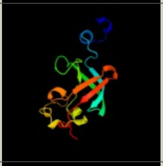
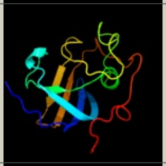
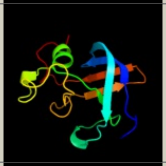
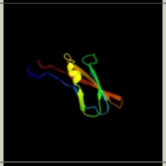
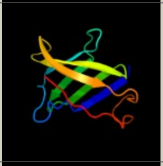
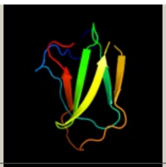
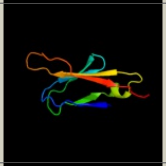
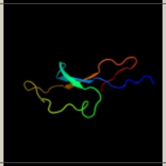
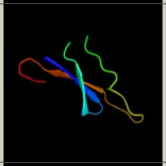
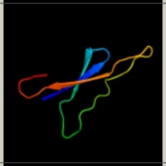
Description	P77468
Date	Thu Jan 5 12:29:32 GMT 2012
Unique Job ID	e4d3a048f955a734

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfzB_	Alignment		100.0	48	**PDB header:**cell adhesion/transport/chaperone **Chain:** B: **PDB Molecule:**outer membrane usher protein, type 1 fimbrial synthesis; **PDBTitle:** crystal structure of the fimd usher bound to its cognate fimc:fimh2 substrate
2	c3ohnA_	Alignment		100.0	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane usher protein fimd; **PDBTitle:** crystal structure of the fimd translocation domain
3	c2vqiA_	Alignment		100.0	25	**PDB header:**transport **Chain:** A: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** structure of the p pilus usher (papc) translocation pore
4	d3bwud1	Alignment		100.0	39	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
5	d1zdva1	Alignment		100.0	39	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
6	d1zdxa1	Alignment		99.9	34	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
7	c3fcgB_	Alignment		99.9	43	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher
8	c2xetB_	Alignment		99.8	35	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
9	c3l48B_	Alignment		99.7	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** crystal structure of the c-terminal domain of the papc usher
10	c3pe9B_	Alignment		94.5	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
11	c3pdgA_	Alignment		94.4	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules

12	d1w0na_	Alignment		88.3	20	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
13	c3pe9D_	Alignment		88.0	13	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
14	c1d2pA_	Alignment		85.6	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen adhesin; **PDBTitle:** crystal structure of two b repeat units (b1b2) of the2 collagen binding protein (cna) of staphylococcus aureus
15	c3pe9A_	Alignment		84.7	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
16	c3pe9C_	Alignment		84.7	14	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
17	c2nsmA_	Alignment		78.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
18	c1h8lA_	Alignment		73.3	8	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
19	c2boiA_	Alignment		72.8	13	**PDB header:**lectin **Chain:** A: **PDB Molecule:**cv-iil lectin; **PDBTitle:** 1.1a structure of chromobacterium violaceum lectin cv2l in2 complex with alpha-methyl-fucoside
20	c2vnvC_	Alignment		70.5	11	**PDB header:**sugar-binding protein **Chain:** C: **PDB Molecule:**bcla; **PDBTitle:** crystal structure of bcla lectin from burkholderia2 cenocepacia in complex with alpha-methyl-mannoside at 1.73 angstrom resolution
21	c3c12A_	Alignment	not modelled	68.5	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**flagellar protein; **PDBTitle:** crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
22	d1h8la1	Alignment	not modelled	67.9	6	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
23	c3bryB_	Alignment	not modelled	65.8	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
24	c2pz4A_	Alignment	not modelled	65.3	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein gbs052; **PDBTitle:** crystal structure of spab (gbs52), the minor pilin in gram-positive2 pathogen streptococcus agalactiae
25	c1uwyA_	Alignment	not modelled	58.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
26	c2xr4A_	Alignment	not modelled	57.7	12	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
27	c1ug9A_	Alignment	not modelled	56.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
28	c1u00A_	Alignment	not modelled	54.8	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
						PDB header:hydrolase

29	c3fn9B_	Alignment	not modelled	53.0	11	**Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
30	d1uwya1	Alignment	not modelled	52.5	14	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
31	c2bpbA_	Alignment	not modelled	51.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit a; **PDBTitle:** sulfite dehydrogenase from starkeya novella
32	c2x5pA_	Alignment	not modelled	51.3	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
33	c3n8eA_	Alignment	not modelled	51.3	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stress-70 protein, mitochondrial; **PDBTitle:** substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
34	c1bprA_	Alignment	not modelled	49.9	20	**PDB header:**molecular chaperone **Chain:** A: **PDB Molecule:**dnak; **PDBTitle:** nmr structure of the substrate binding domain of dnak,2 minimized average structure
35	c2op6A_	Alignment	not modelled	49.7	16	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**heat shock 70 kda protein d; **PDBTitle:** peptide-binding domain of heat shock 70 kda protein d precursor from2 c.elegans
36	c3cmgA_	Alignment	not modelled	49.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
37	c3dpqE_	Alignment	not modelled	48.8	20	**PDB header:**chaperone, peptide binding protein **Chain:** E: **PDB Molecule:**chaperone protein dnak; **PDBTitle:** crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrhocoricin-derived3 inhibitor peptide (form b)
38	d1uzva_	Alignment	not modelled	46.5	10	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
39	d1u00a2	Alignment	not modelled	44.3	19	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
40	c2r32A_	Alignment	not modelled	40.8	27	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
41	c3mn8A_	Alignment	not modelled	39.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
42	d1dkza2	Alignment	not modelled	36.7	21	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
43	d1yuwa1	Alignment	not modelled	35.9	16	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
44	d1aoza2	Alignment	not modelled	34.4	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
45	c3brzA_	Alignment	not modelled	33.2	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
46	d1v8ha1	Alignment	not modelled	31.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
47	c3dqgC_	Alignment	not modelled	31.7	20	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock 70 kda protein f; **PDBTitle:** peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.
48	c3b9eA_	Alignment	not modelled	30.6	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
49	c3dwoX_	Alignment	not modelled	28.9	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
50	d1ci3m2	Alignment	not modelled	26.1	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
51	d2dj4a1	Alignment	not modelled	25.4	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
52	c3pddA_	Alignment	not modelled	25.0	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
53	d1edqa1	Alignment	not modelled	24.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
54	d2a9da1	Alignment	not modelled	24.8	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
						Fold: Galactose-binding domain-like

55	d2vzsa4	Alignment	not modelled	24.8	8	**Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
56	d2dmca1	Alignment	not modelled	24.7	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
57	c3rghA_	Alignment	not modelled	23.4	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
58	d2chha1	Alignment	not modelled	23.4	9	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
59	c2oxgE_	Alignment	not modelled	23.0	18	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
60	d2dmba1	Alignment	not modelled	22.7	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
61	d2e9ia1	Alignment	not modelled	22.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
62	d1wlha1	Alignment	not modelled	22.3	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
63	d1e2wa2	Alignment	not modelled	21.4	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
64	d1yq2a3	Alignment	not modelled	19.6	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
65	d2je8a4	Alignment	not modelled	18.4	8	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
66	c2lgeA_	Alignment	not modelled	18.2	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the calcium-bound form of the protein yp_001302112.12 from parabacteroides distasonis
67	d2j3sa2	Alignment	not modelled	17.9	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
68	c2ww8A_	Alignment	not modelled	17.8	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell wall surface anchor family protein; **PDBTitle:** structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
69	c2a9dB_	Alignment	not modelled	17.7	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite oxidase; **PDBTitle:** crystal structure of recombinant chicken sulfite oxidase with arg at2 residue 161
70	d2d7oa1	Alignment	not modelled	17.4	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
71	d2d7pa1	Alignment	not modelled	16.7	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
72	c3d33B_	Alignment	not modelled	16.6	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**domain of unknown function with an immunoglobulin-like **PDBTitle:** crystal structure of a duf3244 family protein with an immunoglobulin-2 like beta-sandwich fold (bvu_0276) from bacteroides vulgatus atcc3 8482 at 1.70 a resolution
73	d2dica1	Alignment	not modelled	16.5	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
74	c2e9jA_	Alignment	not modelled	16.1	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 14th filamin domain from human2 filamin-b
75	c3k1dA_	Alignment	not modelled	16.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme; **PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
76	c2ds4A_	Alignment	not modelled	16.0	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 45; **PDBTitle:** solution structure of the filamin domain from human2 tripartite motif protein 45
77	d2d7na1	Alignment	not modelled	15.8	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
78	d1uura3	Alignment	not modelled	15.8	17	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
79	d2di8a1	Alignment	not modelled	15.8	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
80	c1w2tE_	Alignment	not modelled	15.6	18	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**beta fructosidase; **PDBTitle:** beta-fructosidase from thermotoga maritima in complex with2 raffinose
81	d1qfha2	Alignment	not modelled	15.5	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains

						Family: Filamin repeat (rod domain)
82	d2w0pa1	Alignment	not modelled	15.5	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
83	c2dcjA_	Alignment	not modelled	15.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xylanase j; **PDBTitle:** a two-domain structure of alkaliphilic xynj from bacillus sp. 41m-1
84	d1qfha1	Alignment	not modelled	15.1	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
85	d1d2oa1	Alignment	not modelled	14.8	19	**Fold:**Prealbumin-like **Superfamily:**Cna protein B-type domain **Family:**Cna protein B-type domain
86	c2jf1A_	Alignment	not modelled	14.5	40	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta2 cytoplasmic tail peptide
87	d2ja9a2	Alignment	not modelled	14.2	26	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
88	d2d7ma1	Alignment	not modelled	14.2	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
89	d1jjcb5	Alignment	not modelled	14.1	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
90	d1v05a_	Alignment	not modelled	14.0	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
91	d2diaa1	Alignment	not modelled	13.9	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
92	d2diba1	Alignment	not modelled	13.8	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
93	d2je6i3	Alignment	not modelled	13.6	17	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
94	d2di9a1	Alignment	not modelled	13.1	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
95	c3cnkB_	Alignment	not modelled	13.1	27	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the dimerization domain of human2 filamin a
96	d2ag4a1	Alignment	not modelled	12.7	15	**Fold:**Ganglioside M2 (gm2) activator **Superfamily:**Ganglioside M2 (gm2) activator **Family:**Ganglioside M2 (gm2) activator
97	c2w0pB_	Alignment	not modelled	12.6	40	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the migfilin peptide
98	c2brqA_	Alignment	not modelled	12.6	40	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
99	d1y4wa1	Alignment	not modelled	12.5	11	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 32 C-terminal domain