Phyre^2

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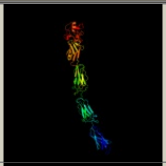
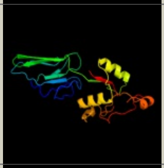
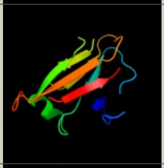
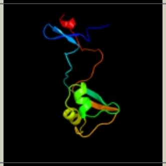
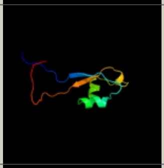
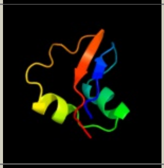
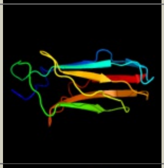
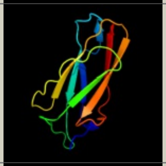
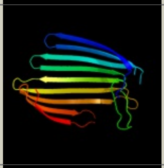
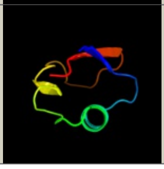
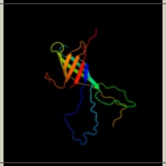
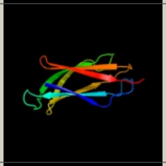
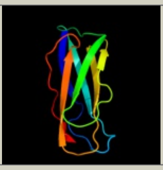
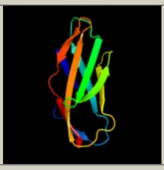
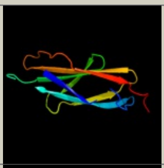
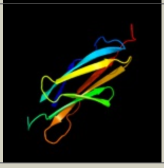
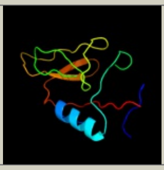
Detailed template information

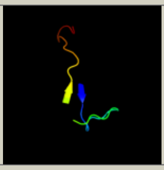
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cwvA_	Alignment		100.0	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**invasin; **PDBTitle:** crystal structure of invasin: a bacterial integrin-binding protein
2	c1e5uI_	Alignment		99.9	23	**PDB header:**intimin **Chain:** I: **PDB Molecule:**intimin; **PDBTitle:** nmr representative structure of intimin-190 (int190) from2 enteropathogenic e. coli
3	c1f00I_	Alignment		99.6	18	**PDB header:**cell adhesion **Chain:** I: **PDB Molecule:**intimin; **PDBTitle:** crystal structure of c-terminal 282-residue fragment of2 enteropathogenic e. coli intimin
4	d1cwva4	Alignment		98.8	34	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
5	c2l9yA_	Alignment		98.0	14	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
6	c2djpA_	Alignment		98.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
7	d1e0ga_	Alignment		97.8	25	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
8	d1cwva3	Alignment		97.7	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
9	d1cwva2	Alignment		97.5	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
10	d2zfga1	Alignment		97.5	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
11	d1y7ma2	Alignment		97.5	24	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain

12	d1phoa_	Alignment		97.3	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
13	d1cwva5	Alignment		97.2	23	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Invasin/intimin cell-adhesion fragment, C-terminal domain
14	c2gu1A_	Alignment		97.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
15	c3nb3C_	Alignment		96.8	19	**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
16	c2qomB_	Alignment		96.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
17	c2k0lA_	Alignment		96.6	19	**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.
18	d1cwva1	Alignment		96.5	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
19	c3aehB_	Alignment		96.5	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
20	d1osma_	Alignment		96.4	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
21	d1t16a_	Alignment	not modelled	96.4	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
22	c1y7mB_	Alignment	not modelled	96.4	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
23	d1qj8a_	Alignment	not modelled	96.4	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
24	c2x4mD_	Alignment	not modelled	96.2	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
25	d1f00i1	Alignment		96.1	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
26	c3qq2C_	Alignment	not modelled	96.1	12	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
27	d1qjpa_	Alignment	not modelled	96.0	19	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
						PDB header:transport protein

28	c3bryB_	Alignment	not modelled	96.0	13	**Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
29	c3pdgA_	Alignment		95.9	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
30	c3qraA_	Alignment	not modelled	95.8	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
31	c2f1tB_	Alignment	not modelled	95.8	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
32	c3kvnA_	Alignment	not modelled	95.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
33	c2jmmA_	Alignment	not modelled	95.4	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
34	c3pe9C_	Alignment		95.0	15	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
35	c3pe9A_	Alignment		95.0	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
36	d1g90a_	Alignment	not modelled	94.8	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
37	c3pddA_	Alignment	not modelled	94.3	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
38	c3pe9D_	Alignment	not modelled	94.0	13	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
39	c2x27X_	Alignment	not modelled	93.4	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
40	c3nsgA_	Alignment	not modelled	92.9	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
41	c3brzA_	Alignment	not modelled	92.5	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
42	d1uynx_	Alignment	not modelled	91.8	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
43	d3prna_	Alignment	not modelled	91.8	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
44	c3pe9B_	Alignment	not modelled	91.8	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
45	d1i78a_	Alignment	not modelled	91.3	10	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
46	d2pora_	Alignment	not modelled	91.3	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
47	c2vqiA_	Alignment	not modelled	91.1	15	**PDB header:**transport **Chain:** A: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** structure of the p pilus usher (papc) translocation pore
48	c3sljA_	Alignment	not modelled	90.7	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
49	d1p4ta_	Alignment	not modelled	90.3	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
50	d2fgqx1	Alignment	not modelled	89.4	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
51	c2o4vA_	Alignment	not modelled	87.3	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific

						transfer across2 the outer membrane
52	c3a2rX_	Alignment	not modelled	81.8	10	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
53	d1pama3	Alignment	not modelled	80.4	30	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
54	d1ja3a_	Alignment	not modelled	78.4	16	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
55	d1qhoa3	Alignment	not modelled	77.8	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
56	d1cyga3	Alignment	not modelled	76.3	33	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
57	d3bmva3	Alignment	not modelled	75.9	33	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
58	d1rdl1_	Alignment	not modelled	75.8	17	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
59	d1cxla3	Alignment	not modelled	75.8	30	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
60	d1byfa_	Alignment	not modelled	75.7	29	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
61	d1cgta3	Alignment	not modelled	75.6	33	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
62	d2afpa_	Alignment	not modelled	75.6	14	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
63	c3c8jB_	Alignment	not modelled	75.5	16	**PDB header:**immune system **Chain:** B: **PDB Molecule:**natural killer cell receptor ly49c; **PDBTitle:** the crystal structure of natural killer cell receptor ly49c
64	c2wjqA_	Alignment	not modelled	75.2	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
65	c2lhfA_	Alignment	not modelled	74.9	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
66	c3k7bA_	Alignment	not modelled	74.8	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein a33; **PDBTitle:** the structure of the poxvirus a33 protein reveals a dimer of unique c-2 type lectin-like domains.
67	c2dcjA_	Alignment	not modelled	74.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xylanase j; **PDBTitle:** a two-domain structure of alkaliphilic xynj from bacillus sp. 41m-1
68	c3dwoX_	Alignment	not modelled	73.5	11	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
69	d1wk1a_	Alignment	not modelled	72.6	24	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
70	c1eslA_	Alignment	not modelled	72.1	28	**PDB header:**cell adhesion protein **Chain:** A: **PDB Molecule:**human e-selectin; **PDBTitle:** insight into e-selectin(slash)ligand interaction from the2 crystal structure and mutagenesis of the lec(slash)egf3 domains
71	d1l0qa1	Alignment	not modelled	71.2	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PKD domain **Family:**PKD domain
72	d3c8ja1	Alignment	not modelled	70.8	16	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
73	c2bpdB_	Alignment		70.7	17	**PDB header:**receptor **Chain:** B: **PDB Molecule:**dectin-1; **PDBTitle:** structure of murine dectin-1
74	d1tlya_	Alignment	not modelled	69.5	23	**Fold:**Transmembrane beta-barrels **Superfamily:**Tsx-like channel **Family:**Tsx-like channel
75	d1yu3a2	Alignment	not modelled	68.7	19	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Mtd variable domain
76	c2lfcA_	Alignment	not modelled	68.5	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
77	c2iwvD	Alignment	not modelled	67.7	21	**PDB header:**ion channel **Chain:** D: **PDB Molecule:**outer membrane protein g;

77	c2iwvD_	Alignment	not modelled	67.7	21	**PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
78	c2zwkA_	Alignment	not modelled	66.5	30	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**intimin; **PDBTitle:** crystal structure of intimin-tir90 complex
79	d1y4ja1	Alignment	not modelled	66.4	23	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Sulfatase-modifying factor-like
80	c2q17C_	Alignment	not modelled	66.3	17	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**formylglycine generating enzyme; **PDBTitle:** formylglycine generating enzyme from streptomyces coelicolor
81	d1yu0a2	Alignment	not modelled	65.7	19	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Mtd variable domain
82	d1z70x1	Alignment	not modelled	65.1	20	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Sulfatase-modifying factor-like
83	d2msba_	Alignment	not modelled	64.2	26	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
84	d1rjha_	Alignment	not modelled	63.9	10	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
85	c1y1fX_	Alignment	not modelled	61.5	23	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**c-alpha-formyglycine-generating enzyme; **PDBTitle:** human formylglycine generating enzyme with cysteine sulfenic acid
86	d2gufa1	Alignment	not modelled	61.2	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
87	c2kzwA_	Alignment	not modelled	60.6	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q8psa4 from methanosarcina mazei, northeast2 structural genomics consortium target mar143a
88	c2zibA_	Alignment	not modelled	59.7	15	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**type ii antifreeze protein; **PDBTitle:** crystal structure analysis of calcium-independent type ii2 antifreeze protein
89	d1g1ta1	Alignment	not modelled	58.9	22	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
90	c1hupA_	Alignment	not modelled	58.5	13	**PDB header:**c-type lectin **Chain:** A: **PDB Molecule:**mannose-binding protein; **PDBTitle:** human mannose binding protein carbohydrate recognition domain2 trimerizes through a triple alpha-helical coiled-coil
91	c2k53A_	Alignment	not modelled	58.2	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
92	c3dbzB_	Alignment	not modelled	58.1	16	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** human surfactant protein d
93	d1g1sa1	Alignment	not modelled	57.7	9	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
94	d1r13a1	Alignment	not modelled	57.6	9	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
95	d1xpha1	Alignment	not modelled	57.5	6	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
96	c2iouC_	Alignment	not modelled	57.1	17	**PDB header:**viral protein/membrane protein **Chain:** C: **PDB Molecule:**major tropism determinant p1; **PDBTitle:** major tropism determinant p1 (mtd-p1) variant complexed with2 bordetella brochiseptica virulence factor pertactin extracellular3 domain (prn-e).
97	d1rr7a_	Alignment	not modelled	56.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
98	c1rr7A_	Alignment	not modelled	56.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
99	c1fm5A_	Alignment	not modelled	56.4	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**early activation antigen cd69; **PDBTitle:** crystal structure of human cd69
100	c3cfwA_	Alignment	not modelled	56.2	30	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**l-selectin; **PDBTitle:** l-selectin lectin and egf domains
101	c2yrlA_	Alignment	not modelled	54.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1837 protein; **PDBTitle:** solution structure of the pkd domain from kiaa 1837 protein
102	c1l0qC_	Alignment	not modelled	53.8	17	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**surface layer protein; **PDBTitle:** tandem yvtn beta-propeller and pkd domains from an archaeal surface2 layer protein
						PDB header:dna binding protein

103	c2elhA_	Alignment	not modelled	53.5	33	**Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
104	c3rfzB_	Alignment	not modelled	52.9	12	**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
105	d1egga_	Alignment	not modelled	52.5	14	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
106	d1fepa_	Alignment	not modelled	52.3	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
107	c3m9zA_	Alignment	not modelled	52.1	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**killer cell lectin-like receptor subfamily b member 1a; **PDBTitle:** crystal structure of extracellular domain of mouse nkr-p1a
108	c2c5uA_	Alignment		51.7	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**rna ligase; **PDBTitle:** t4 rna ligase (rnl1) crystal structure
109	d1by5a_	Alignment	not modelled	51.7	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
110	c2py2E_	Alignment	not modelled	51.3	13	**PDB header:**antifreeze protein **Chain:** E: **PDB Molecule:**antifreeze protein type ii; **PDBTitle:** structure of herring type ii antifreeze protein
111	d1f00i3	Alignment	not modelled	51.2	30	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Invasin/intimin cell-adhesion fragment, C-terminal domain
112	c1kwwC_	Alignment	not modelled	50.3	16	**PDB header:**immune system, sugar binding protein **Chain:** C: **PDB Molecule:**mannose-binding protein a; **PDBTitle:** rat mannose protein a complexed with a-me-fuc.
113	d1o75a1	Alignment	not modelled	49.7	35	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains
114	d1y0pa3	Alignment	not modelled	48.9	17	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
115	c3orjA_	Alignment	not modelled	48.8	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar-binding protein; **PDBTitle:** crystal structure of a sugar-binding protein (bacova_04391) from2 bacteroides ovatus at 2.16 a resolution
116	d1fifa1	Alignment	not modelled	48.7	27	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
117	c2ostC_	Alignment	not modelled	47.7	40	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**putative endonuclease; **PDBTitle:** the structure of a bacterial homing endonuclease : i-ssp6803i
118	d2jn6a1	Alignment	not modelled	46.6	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
119	c1g1qD_	Alignment	not modelled	45.9	21	**PDB header:**immune system, membrane protein **Chain:** D: **PDB Molecule:**p-selectin; **PDBTitle:** crystal structure of p-selectin lectin/egf domains
120	c2pmzV_	Alignment	not modelled	45.6	18	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus