Phyre^2

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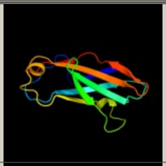
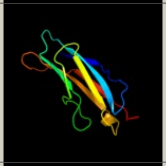
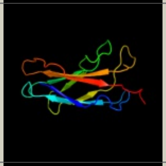
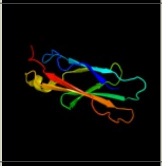
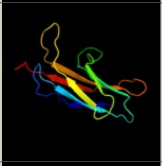
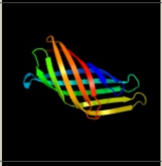
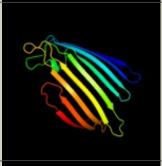
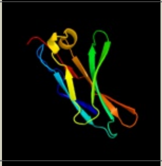
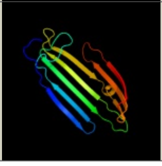
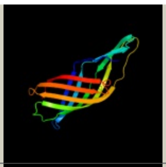
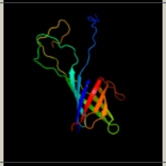
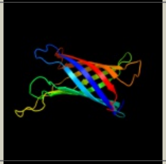
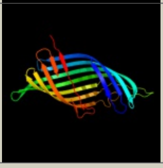
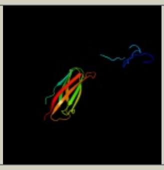
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pdgA_	Alignment		97.0	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
2	c3pe9A_	Alignment		97.0	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
3	c3pe9C_	Alignment		96.9	8	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
4	c3pe9D_	Alignment		96.5	9	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
5	c3pe9B_	Alignment		96.1	8	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
6	c3nb3C_	Alignment		95.9	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
7	d1qj8a_	Alignment		95.7	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
8	c3qraA_	Alignment		94.6	15	**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
9	d1phoa_	Alignment		94.2	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
10	c3pddA_	Alignment		93.0	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
11	d1osma_	Alignment		92.9	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin

12	c2f1tB_	Alignment		92.6	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
13	c2x4mD_	Alignment		92.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
14	d2zfga1	Alignment		91.9	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
15	c2k0lA_	Alignment		91.6	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.
16	c2jmmA_	Alignment		90.9	14	**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	d1t16a_	Alignment		90.1	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
18	d1g90a_	Alignment		89.8	18	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
19	d1qjpa_	Alignment		89.8	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
20	c2qomB_	Alignment		89.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
21	c3bryB_	Alignment	not modelled	88.4	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
22	c3brzA_	Alignment	not modelled	87.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
23	c3aehB_	Alignment	not modelled	87.3	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
24	d1uynx_	Alignment	not modelled	81.7	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
25	c2yrlA_	Alignment	not modelled	81.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1837 protein; **PDBTitle:** solution structure of the pkd domain from kiaa 1837 protein
26	c2x27X_	Alignment	not modelled	80.7	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
27	d1p4ta_	Alignment	not modelled	79.2	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
28	d1i78a_	Alignment	not modelled	77.2	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
						Fold: Immunoglobulin-like beta-sandwich

29	d1wgoa_	Alignment	not modelled	75.7	18	**Superfamily:**PKD domain **Family:**PKD domain
30	d2fcba2	Alignment	not modelled	72.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
31	d1l0qa1	Alignment	not modelled	71.8	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PKD domain **Family:**PKD domain
32	c3dwoX_	Alignment	not modelled	71.5	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
33	c2kzwA_	Alignment	not modelled	68.5	18	**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
34	d1fnla2	Alignment	not modelled	67.9	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
35	d1f2qa2	Alignment	not modelled	65.4	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
36	c3nsgA_	Alignment	not modelled	61.5	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
37	c3qq2C_	Alignment	not modelled	61.4	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
38	c2lhfA_	Alignment	not modelled	59.1	16	**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
39	c2e7mA_	Alignment	not modelled	58.0	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein kiaa0319; **PDBTitle:** solution structure of the pkd domain (329-428) from human2 kiaa0319
40	c3o3uN_	Alignment	not modelled	57.5	15	**PDB header:**transport protein, signaling protein **Chain:** N: **PDB Molecule:**maltose-binding periplasmic protein, advanced glycosylation **PDBTitle:** crystal structure of human receptor for advanced glycation endproducts2 (rage)
41	d1epfa1	Alignment	not modelled	56.2	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
42	c2a74B_	Alignment	not modelled	55.8	9	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement component c3c; **PDBTitle:** human complement component c3c
43	d1pama3	Alignment	not modelled	55.6	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
44	d1w8oa1	Alignment	not modelled	55.5	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
45	c2xwxB_	Alignment		53.3	17	**PDB header:**chitin-binding protein **Chain:** B: **PDB Molecule:**glcnac-binding protein a; **PDBTitle:** vibrio cholerae colonization factor gbpa crystal structure
46	c2e7bA_	Alignment	not modelled	51.4	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**obscurin; **PDBTitle:** solution structure of the 6th ig-like domain from human2 kiaa1556
47	c2c26A_	Alignment	not modelled	50.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** structural basis for the promiscuous specificity of the2 carbohydrate-binding modules from the beta-sandwich super3 family
48	c2ensA_	Alignment	not modelled	50.5	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**advanced glycosylation end product-specific **PDBTitle:** solution structure of the third ig-like domain from human2 advanced glycosylation end product-specific receptor
49	d3bmva3	Alignment	not modelled	50.5	24	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
50	d1qhoa3	Alignment	not modelled	49.7	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
51	c3ubfA_	Alignment	not modelled	49.1	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**neural-cadherin; **PDBTitle:** crystal structure of drosophila n-cadherin ec1-3, i
52	c3jquA_	Alignment	not modelled	48.5	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**collagenase; **PDBTitle:** crystal structure of clostridium histolyticum colg collagenase2 polycystic kidney disease domain at 1.4 angstrom resolution
53	d1cyga3	Alignment	not modelled	47.2	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain

54	d1cxla3	Alignment	not modelled	46.4	22	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
55	d1biha3	Alignment	not modelled	46.1	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
56	d1tiua_	Alignment	not modelled	45.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
57	c2ee0A_	Alignment	not modelled	45.1	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protocadherin-9; **PDBTitle:** solution structures of the ca domain of human protocadherin2 9
58	d2fdbp2	Alignment	not modelled	44.6	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
59	d1cgta3	Alignment	not modelled	43.8	15	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
60	c3ottB_	Alignment	not modelled	43.0	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two-component system sensor histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative one2 component system bt4673 from b. thetaiotaomicron
61	c2wjqA_	Alignment	not modelled	41.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
62	d1fcga2	Alignment	not modelled	41.9	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
63	c2k1mA_	Alignment	not modelled	41.4	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**myosin-binding protein c, cardiac-type; **PDBTitle:** 3d nmr structure of domain cc0 of cardiac myosin binding2 protein c (mybpc)
64	c2o4vA_	Alignment	not modelled	40.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
65	c3ff7B_	Alignment	not modelled	40.6	16	**PDB header:**cell adhesion/immunue system **Chain:** B: **PDB Molecule:**epithelial cadherin; **PDBTitle:** structure of nk cell receptor klrg1 bound to e-cadherin
66	c1l0qC_	Alignment	not modelled	40.0	10	**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
67	c3s37X_	Alignment	not modelled	39.8	12	**PDB header:**immune system/transferase **Chain:** X: **PDB Molecule:**vascular endothelial growth factor receptor 2; **PDBTitle:** structural basis for the function of two anti-vegf receptor antibodies
68	c2enyA_	Alignment	not modelled	39.6	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**obscurin; **PDBTitle:** solution structure of the ig-like domain (2735-2825) of2 human obscurin
69	c3ppeB_	Alignment	not modelled	39.6	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**vascular endothelial cadherin; **PDBTitle:** crystal structure of chicken ve-cadherin ec1-2
70	c2cr6A_	Alignment	not modelled	37.9	13	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**kiaa1556 protein; **PDBTitle:** solution structure of the ig domain (2998-3100) of human2 obscurin
71	c2gqhA_	Alignment	not modelled	37.4	12	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**kiaa1556 protein; **PDBTitle:** solution structure of the 15th ig-like domain of human2 kiaa1556 protein
72	c2jjsB_	Alignment	not modelled	37.4	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type **PDBTitle:** structure of human cd47 in complex with human signal2 regulatory protein (sirp) alpha
73	d2fgqx1	Alignment	not modelled	36.9	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
74	d1epfa2	Alignment	not modelled	36.8	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
75	c2cknA_	Alignment	not modelled	36.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**basic fibroblast growth factor receptor 1; **PDBTitle:** nmr structure of the first ig module of mouse fgfr1
76	c2dkuA_	Alignment	not modelled	36.6	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**kiaa1556 protein; **PDBTitle:** solution structure of the third ig-like domain of human2 kiaa1556 protein
77	d1gl4b_	Alignment	not modelled	36.1	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
78	d2nqda1	Alignment	not modelled	35.2	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ICP-like **Family:**ICP-like
79	c2nmsA_	Alignment	not modelled	34.3	9	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cmrf35-like-molecule 1; **PDBTitle:** the crystal structure of the extracellular domain of the2 inhibitor receptor expressed on myeloid cells irem-1

80	d1l3wa5	Alignment	not modelled	33.5	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cadherin-like **Family:**Cadherin
81	c2e6pA_	Alignment	not modelled	32.9	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**obscurin-like protein 1; **PDBTitle:** solution structure of the ig-like domain (714-804) from2 human obscurin-like protein 1
82	d1pd6a_	Alignment	not modelled	31.9	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
83	d1l3wa4	Alignment	not modelled	31.9	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cadherin-like **Family:**Cadherin
84	c3hs0B_	Alignment	not modelled	31.8	11	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cobra venom factor; **PDBTitle:** cobra venom factor (cvf) in complex with human factor b
85	c2bk8A_	Alignment	not modelled	31.2	14	**PDB header:**ig domain **Chain:** A: **PDB Molecule:**titin heart isoform n2-b; **PDBTitle:** m1 domain from titin
86	c1ncjA_	Alignment	not modelled	30.4	13	**PDB header:**cell adhesion protein **Chain:** A: **PDB Molecule:**protein (n-cadherin); **PDBTitle:** n-cadherin, two-domain fragment
87	c1gzpA_	Alignment	not modelled	30.1	15	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd1b; **PDBTitle:** cd1b in complex with gm2 ganglioside
88	d1o75a1	Alignment	not modelled	29.4	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains
89	c1nchB_	Alignment	not modelled	28.8	16	**PDB header:**cell adhesion protein **Chain:** B: **PDB Molecule:**n-cadherin; **PDBTitle:** structural basis of cell-cell adhesion by cadherins
90	d1f97a2	Alignment	not modelled	28.8	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
91	c3m86B_	Alignment	not modelled	28.6	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**amoebiasin-2; **PDBTitle:** crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica
92	c1bqsA_	Alignment	not modelled	27.6	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein (mucosal addressin cell adhesion **PDBTitle:** the crystal structure of mucosal addressin cell adhesion2 molecule-1 (madcam-1)
93	c3ff8B_	Alignment	not modelled	27.6	14	**PDB header:**cell adhesion/immune system **Chain:** B: **PDB Molecule:**epithelial cadherin; **PDBTitle:** structure of nk cell receptor klrg1 bound to e-cadherin
94	c1q5cA_	Alignment	not modelled	26.6	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ep-cadherin; **PDBTitle:** s-s-lambda-shaped trans and cis interactions of cadherins model based2 on fitting c-cadherin (1l3w) to 3d map of desmosomes obtained by3 electron tomography
95	c2edoA_	Alignment	not modelled	26.0	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cd48 antigen; **PDBTitle:** solution structure of the first ig-like domain from human2 cd48 antigen
96	c3a2rX_	Alignment	not modelled	25.9	15	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
97	d1tlya_	Alignment	not modelled	25.7	19	**Fold:**Transmembrane beta-barrels **Superfamily:**Tsx-like channel **Family:**Tsx-like channel
98	c2y25C_	Alignment	not modelled	25.7	14	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**myomesin; **PDBTitle:** crystal structure of the myomesin domains my11-my13
99	c2oxgE_	Alignment	not modelled	25.1	19	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
100	c2yuvA_	Alignment	not modelled	25.0	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**myosin-binding protein c, slow-type; **PDBTitle:** solution structure of 2nd immunoglobulin domain of slow2 type myosin-binding protein c
101	d1l3wa1	Alignment	not modelled	24.9	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cadherin-like **Family:**Cadherin
102	c2nplX_	Alignment	not modelled	24.7	13	**PDB header:**cell adhesion **Chain:** X: **PDB Molecule:**coxsackievirus and adenovirus receptor; **PDBTitle:** nmr structure of card d2 domain
103	d1b4ra_	Alignment	not modelled	24.5	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PKD domain **Family:**PKD domain
104	d1biha1	Alignment	not modelled	23.1	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
105	c3g6jB_	Alignment	not modelled	23.0	9	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement c3 alpha chain; **PDBTitle:** c3b in complex with a c3b specific fab
106	c2if7C_	Alignment	not modelled	22.8	21	**PDB header:**immune system **Chain:** C: **PDB Molecule:**slam family member 6; **PDBTitle:** crystal structure of ntb-a

107	d1u2ca1	Alignment	not modelled	22.6	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cadherin-like **Family:**Dystroglycan, N-terminal domain
108	c1zvnA_	Alignment	not modelled	22.2	13	**PDB header:**---- **Chain:** A: **PDB Molecule:**mn-cadherin; **PDBTitle:** crystal structure of chick mn-cadherin ec1
109	c2yuzA_	Alignment	not modelled	21.7	7	**PDB header:**immune system **Chain:** A: **PDB Molecule:**myosin-binding protein c, slow-type; **PDBTitle:** solution structure of 4th immunoglobulin domain of slow2 type myosin-binding protein c
110	c1hngB_	Alignment	not modelled	21.5	15	**PDB header:**t lymphocyte adhesion glycoprotein **Chain:** B: **PDB Molecule:**cd2; **PDBTitle:** crystal structure at 2.8 angstroms resolution of a soluble2 form of the cell adhesion molecule cd2
111	c2a73B_	Alignment	not modelled	21.3	10	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement c3; **PDBTitle:** human complement component c3
112	c3lndC_	Alignment	not modelled	21.2	19	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**cdh6 protein; **PDBTitle:** crystal structure of cadherin-6 ec12 w4a
113	c3mpcB_	Alignment	not modelled	20.9	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fn3-like protein; **PDBTitle:** the crystal structure of a fn3-like protein from clostridium2 thermocellum
114	c1nciA_	Alignment	not modelled	20.8	16	**PDB header:**cell adhesion protein **Chain:** A: **PDB Molecule:**n-cadherin; **PDBTitle:** structural basis of cell-cell adhesion by cadherins
115	d1ncia_	Alignment	not modelled	20.8	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cadherin-like **Family:**Cadherin
116	c2wd0C_	Alignment	not modelled	20.2	9	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**cadherin-23; **PDBTitle:** crystal structure of nonsyndromic deafness (dfnb12)2 associated mutant d124g of mouse cadherin-23 ec1-2