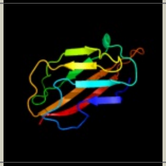
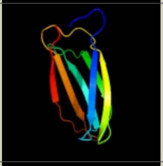
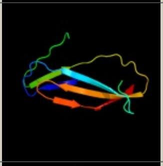
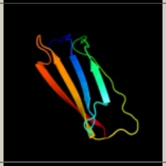
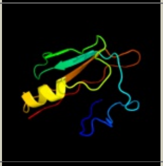
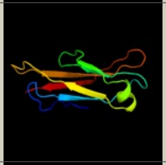
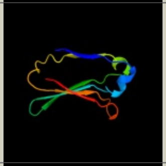
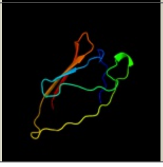
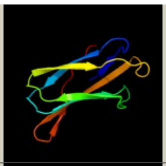
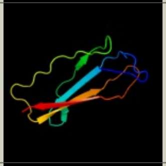
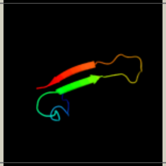
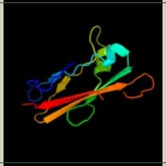
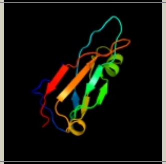
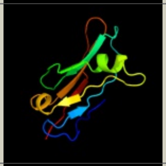
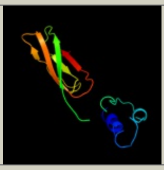
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AA57
Date	Thu Jan 5 11:12:00 GMT 2012
Unique Job ID	433c7faa6aeec8c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2c9qa1	Alignment		99.9	39	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
2	d1ix2a_	Alignment		99.9	41	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
3	c3isyA_	Alignment		96.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
4	c2xwxB_	Alignment		96.3	12	**PDB header:**chitin-binding protein **Chain:** B: **PDB Molecule:**glcnac-binding protein a; **PDBTitle:** vibrio cholerae colonization factor gbpa crystal structure
5	c2r5oA_	Alignment		95.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative atp binding component of abc- **PDBTitle:** crystal structure of the c-terminal domain of wzt
6	c3c12A_	Alignment		95.4	19	**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
7	c2p9rA_	Alignment		95.1	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**alpha-2-macroglobulin; **PDBTitle:** human alpha2-macroglogulin is composed of multiple domains,2 as predicted by homology with complement component c3
8	c2x5pA_	Alignment		94.6	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
9	c3pe9B_	Alignment		94.2	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
10	c3d33B_	Alignment		93.3	15	**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
11	c2e59A_	Alignment		93.0	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**lymphocyte antigen 96; **PDBTitle:** crystal structure of human md-2 in complex with lipid iva

12	c3osvC_	Alignment		92.3	9	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**flagellar basal-body rod modification protein flgd; **PDBTitle:** the crytsal structure of flgd from p. aeruginosa
13	c3pdgA_	Alignment		91.3	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
14	c3cu7A_	Alignment		91.2	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement c5; **PDBTitle:** human complement component 5
15	c3jqxA_	Alignment		90.1	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**colh protein; **PDBTitle:** crystal structure of clostridium histolyticum colh collagenase2 collagen binding domain 3 at 2.2 angstrom resolution in the presence3 of calcium and cademium
16	c3mu3A_	Alignment		89.6	22	**PDB header:**immune system **Chain:** A: **PDB Molecule:**protein md-1; **PDBTitle:** crystal structure of chicken md-1 complexed with lipid iva
17	c3pe9D_	Alignment		88.3	13	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
18	c3pe9C_	Alignment		88.1	12	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
19	c3pe9A_	Alignment		88.1	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
20	c2pn5A_	Alignment		87.9	20	**PDB header:**immune system **Chain:** A: **PDB Molecule:**thioester-containing protein i; **PDBTitle:** crystal structure of tep1r
21	d1nepa_	Alignment	not modelled	87.9	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**ML domain
22	d1w8oa1	Alignment	not modelled	87.8	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
23	d1nqjb_	Alignment	not modelled	87.1	20	**Fold:**CUB-like **Superfamily:**Collagen-binding domain **Family:**Collagen-binding domain
24	c2b39B_	Alignment	not modelled	86.8	15	**PDB header:**immune system **Chain:** B: **PDB Molecule:**c3; **PDBTitle:** structure of mammalian c3 with an intact thioester at 3a resolution
25	c2kpnA_	Alignment	not modelled	85.5	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillolysin; **PDBTitle:** solution nmr structure of a bacterial ig-like (big_3) domain from2 bacillus cereus. northeast structural genomics consortium target3 bcr147a
26	c2ra1A_	Alignment	not modelled	84.5	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**surface layer protein; **PDBTitle:** crystal structure of the n-terminal part of the bacterial s-layer2 protein sbsc
27	c2qkiA_	Alignment	not modelled	83.8	13	**PDB header:**immune system/hydrolase inhibitor **Chain:** A: **PDB Molecule:**complement c3; **PDBTitle:** human c3c in complex with the inhibitor compstatin
28	c3ottB_	Alignment	not modelled	83.4	16	**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

29	c3m7oB_	Alignment	not modelled	81.9	10	**PDB header:**immune system **Chain:** B: **PDB Molecule:**lymphocyte antigen 86; **PDBTitle:** crystal structure of mouse md-1 in complex with phosphatidylcholine
30	c3kptA_	Alignment	not modelled	81.2	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**collagen adhesion protein; **PDBTitle:** crystal structure of bcpa, the major pilin subunit of2 bacillus cereus
31	d2a9da1	Alignment	not modelled	80.1	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
32	c2k7pA_	Alignment	not modelled	79.7	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 16-17
33	c3pddA_	Alignment	not modelled	75.6	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
34	d1owwa_	Alignment	not modelled	75.6	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
35	c2z64C_	Alignment	not modelled	74.7	11	**PDB header:**immune system **Chain:** C: **PDB Molecule:**lymphocyte antigen 96; **PDBTitle:** crystal structure of mouse tlr4 and mouse md-2 complex
36	c2bpbA_	Alignment	not modelled	73.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit a; **PDBTitle:** sulfite dehydrogenase from starkeya novella
37	d1nqja_	Alignment	not modelled	73.8	20	**Fold:**CUB-like **Superfamily:**Collagen-binding domain **Family:**Collagen-binding domain
38	c3sd2A_	Alignment	not modelled	70.9	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative member of duf3244 protein family; **PDBTitle:** crystal structure of a putative member of duf3244 protein family2 (bt_3571) from bacteroides thetaiotaomicron vpi-5482 at 1.40 a3 resolution
39	d2bvya1	Alignment	not modelled	70.7	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
40	d1pfsa_	Alignment	not modelled	68.7	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
41	d2diba1	Alignment	not modelled	64.7	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
42	c2di7A_	Alignment	not modelled	64.6	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**bk158_1; **PDBTitle:** solution structure of the filamin domain from human bk158_12 protein
43	c3hrzA_	Alignment	not modelled	64.0	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cobra venom factor; **PDBTitle:** cobra venom factor (cvf) in complex with human factor b
44	c3qhtC_	Alignment	not modelled	63.3	13	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**monobody ysmb-1; **PDBTitle:** crystal structure of the monobody ysmb-1 bound to yeast sumo
45	c2yrlA_	Alignment	not modelled	62.9	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1837 protein; **PDBTitle:** solution structure of the pkd domain from kiaa 1837 protein
46	c3payB_	Alignment	not modelled	60.8	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**putative adhesin; **PDBTitle:** crystal structure of a putative adhesin (bacova_04077) from2 bacteroides ovatus at 2.50 a resolution
47	c3nmeA_	Alignment		59.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
48	c2ds4A_	Alignment	not modelled	57.0	18	**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
49	c3a0oB_	Alignment	not modelled	56.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oligo alginate lyase; **PDBTitle:** crystal structure of alginate lyase from agrobacterium tumefaciens c58
50	c3gf8A_	Alignment	not modelled	56.2	10	**PDB header:**carbohydrate binding protein **Chain:** A: **PDB Molecule:**putative polysaccharide binding proteins (duf1812); **PDBTitle:** crystal structure of putative polysaccharide binding proteins2 (duf1812) (np_809975.1) from bacteroides thetaiotaomicron vpi-5482 at3 2.20 a resolution
51	c3irpX_	Alignment	not modelled	54.9	16	**PDB header:**cell adhesion **Chain:** X: **PDB Molecule:**uro-adherence factor a; **PDBTitle:** crystal structure of functional region of uafa from staphylococcus2 saprophyticus at 1.50 angstrom resolution
52	d3csba1	Alignment	not modelled	54.7	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
53	c1ttfA_	Alignment	not modelled	54.5	17	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**fibronectin;

		Alignment	not modelled			**PDBTitle:** the three-dimensional structure of the tenth type iii2 module of fibronectin: an insight into rgd-mediated3 interactions
54	c1ttgA_	Alignment	not modelled	54.5	17	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**fibronectin; **PDBTitle:** the three-dimensional structure of the tenth type iii2 module of fibronectin: an insight into rgd-mediated3 interactions
55	d2d7na1	Alignment	not modelled	54.3	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
56	c3pvmB_	Alignment	not modelled	53.3	10	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cobra venom factor; **PDBTitle:** structure of complement c5 in complex with cvf
57	c2w1wB_	Alignment	not modelled	52.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipolytic enzyme, g-d-s-l; **PDBTitle:** native structure of a family 35 carbohydrate binding module2 from clostridium thermocellum
58	d1uwya1	Alignment	not modelled	51.7	11	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
59	c3jquA_	Alignment	not modelled	50.0	32	**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
60	c2yetB_	Alignment	not modelled	50.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**gh61 isozyme a; **PDBTitle:** thermoascus gh61 isozyme a
61	d2diaa1	Alignment	not modelled	49.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
62	c3l48B_	Alignment	not modelled	49.1	14	**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
63	c1qfhB_	Alignment	not modelled	48.8	25	**PDB header:**actin binding protein **Chain:** B: **PDB Molecule:**protein (gelation factor); **PDBTitle:** dimerization of gelation factor from dictyostelium2 discoideum: crystal structure of rod domains 5 and 6
64	d1xwva_	Alignment	not modelled	48.6	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**ML domain
65	c3rzwA_	Alignment	not modelled	48.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**monobody ysmb-9; **PDBTitle:** crystal structure of the monobody ysmb-9 bound to human sumo1
66	d2ag4a1	Alignment	not modelled	48.0	24	**Fold:**Ganglioside M2 (gm2) activator **Superfamily:**Ganglioside M2 (gm2) activator **Family:**Ganglioside M2 (gm2) activator
67	c2xetB_	Alignment	not modelled	47.6	16	**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
68	c3ejaB_	Alignment	not modelled	47.4	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**protein gh61e; **PDBTitle:** magnesium-bound glycoside hydrolase 61 isoform e from thielavia2 terrestris
69	c3mn8A_	Alignment	not modelled	46.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
70	d1fnfa2	Alignment	not modelled	46.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
71	d1lmia_	Alignment	not modelled	46.5	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Antigen MPT63/MPB63 (immunoprotective extracellular protein) **Family:**Antigen MPT63/MPB63 (immunoprotective extracellular protein)
72	c2o6dB_	Alignment	not modelled	46.3	20	**PDB header:**membrane protein, protein binding **Chain:** B: **PDB Molecule:**34 kda membrane antigen; **PDBTitle:** structure of native rtp34 from treponema pallidum
73	c2o0i1_	Alignment	not modelled	46.0	15	**PDB header:**surface active protein **Chain:** 1: **PDB Molecule:**c protein alpha-antigen; **PDBTitle:** crystal structure of the r185a mutant of the n-terminal domain of the2 group b streptococcus alpha c protein
74	d1tdqa2	Alignment	not modelled	44.9	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
75	d1v5ja_	Alignment	not modelled	43.1	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
76	c2v4vA_	Alignment	not modelled	42.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gh59 galactosidase; **PDBTitle:** crystal structure of a family 6 carbohydrate-binding module2 from clostridium cellulolyticum in complex with xylose
77	d2dmca1	Alignment	not modelled	41.4	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
78	d1ex0a1	Alignment	not modelled	41.2	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
79		Alignment	not modelled	41.1	17	**PDB header:**hormone/growth factor **Chain:** D: **PDB Molecule:**fibronectin;

79	c2ocfD_	Alignment	not modelled	41.1	17	**PDBTitle:** human estrogen receptor alpha ligand-binding domain in complex with2 estradiol and the e2#23 fn3 monobody
80	c2a9dB_	Alignment	not modelled	40.3	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite oxidase; **PDBTitle:** crystal structure of recombinant chicken sulfite oxidase with arg at2 residue 161
81	c2k7qA_	Alignment	not modelled	39.6	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 18-19
82	c2e9jA_	Alignment	not modelled	39.6	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 14th filamin domain from human2 filamin-b
83	c2vtcB_	Alignment	not modelled	39.4	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cel61b; **PDBTitle:** the structure of a glycoside hydrolase family 61 member,2 cel61b from the hypocrea jecorina.
84	d1ktja_	Alignment	not modelled	39.2	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**ML domain
85	d1qfha1	Alignment	not modelled	38.9	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
86	c2dtgE_	Alignment	not modelled	38.8	17	**PDB header:**hormone receptor/immune system **Chain:** E: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (ir) ectodomain in complex with fab's
87	d2fnba_	Alignment	not modelled	37.6	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
88	d1tfpa_	Alignment	not modelled	36.9	8	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
89	d1cwva3	Alignment	not modelled	36.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
90	c2xtsC_	Alignment	not modelled	35.9	9	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**sulfite dehydrogenase; **PDBTitle:** crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
91	d1fnha3	Alignment	not modelled	35.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
92	d2d7oa1	Alignment	not modelled	34.2	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
93	c2jxpA_	Alignment	not modelled	34.2	8	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein b; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
94	c3qhtD_	Alignment	not modelled	33.6	13	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**monobody ysmb-1; **PDBTitle:** crystal structure of the monobody ysmb-1 bound to yeast sumo
95	c3nrqB_	Alignment	not modelled	33.3	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**periplasmic protein-probably involved in high-affinity fe2+ **PDBTitle:** crystal structure of copper-reconstituted fetp from uropathogenic2 escherichia coli strain f11
96	c2kzwA_	Alignment	not modelled	32.9	16	**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
97	c3iswA_	Alignment	not modelled	32.9	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cftr
98	c1uwyA_	Alignment	not modelled	32.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
99	d1ut9a2	Alignment	not modelled	31.2	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
100	c3rghA_	Alignment	not modelled	31.2	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
101	c2xicB_	Alignment	not modelled	30.7	25	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**ancillary protein 1; **PDBTitle:** pilus-presented adhesin, spy0125 (cpa), p212121 form (esrf data)
102	c3lxuX_	Alignment	not modelled	30.6	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**tripeptidyl-peptidase 2; **PDBTitle:** crystal structure of tripeptidyl peptidase 2 (tpp ii)
103	c2lllA_	Alignment	not modelled	28.4	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-b2; **PDBTitle:** solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
104	d1qfha2	Alignment	not modelled	28.2	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
105	d1oqpa1	Alignment	not modelled	27.8	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains

105	d1ogpa1	Alignment	not modelled	27.8	14	**Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
106	d1w9sa_	Alignment	not modelled	27.3	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 6 carbohydrate binding module, CBM6
107	d2qfra1	Alignment	not modelled	26.7	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Purple acid phosphatase, N-terminal domain **Family:**Purple acid phosphatase, N-terminal domain
108	c2gpzC_	Alignment	not modelled	26.7	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** transthyretin-like protein from salmonella dublin
109	c3gzkA_	Alignment	not modelled	26.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulase; **PDBTitle:** structure of a. acidocaldarius cellulase cela
110	c3uyoD_	Alignment	not modelled	26.5	15	**PDB header:**signaling protein/protein binding **Chain:** D: **PDB Molecule:**monobody sh13; **PDBTitle:** crystal structure of monobody sh13/abl1 sh2 domain complex
111	d2e9ia1	Alignment	not modelled	26.3	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
112	d2dj4a1	Alignment	not modelled	25.9	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
113	c2nsmA_	Alignment	not modelled	25.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
114	d1ufga_	Alignment	not modelled	25.8	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
115	c2e7mA_	Alignment	not modelled	25.0	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein kiaa0319; **PDBTitle:** solution structure of the pkd domain (329-428) from human2 kiaa0319
116	d1tdqa1	Alignment	not modelled	24.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
117	c2w3jA_	Alignment	not modelled	24.4	15	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**carbohydrate binding module; **PDBTitle:** structure of a family 35 carbohydrate binding module from2 an environmental isolate
118	c3d30A_	Alignment	not modelled	23.8	30	**PDB header:**peptidoglycan-binding protein **Chain:** A: **PDB Molecule:**expansin like protein; **PDBTitle:** structure of an expansin like protein from bacillus subtilis at 1.9a2 resolution
119	d1kmta_	Alignment	not modelled	23.7	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
120	d1doab_	Alignment	not modelled	22.9	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like