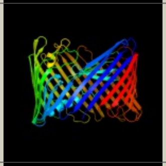
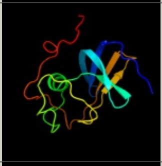
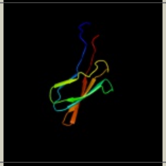
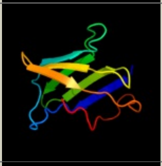
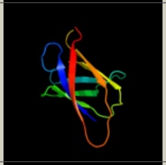
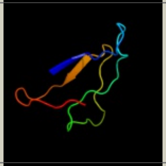
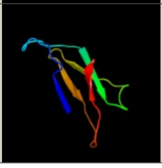
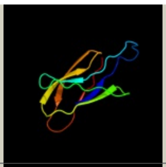
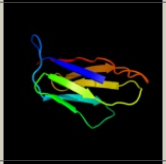
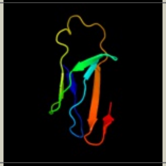
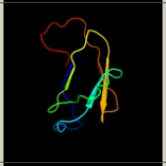
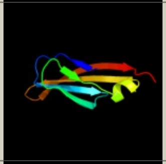
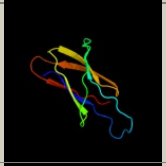
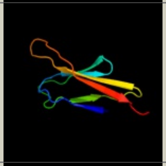
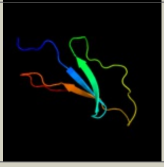
Email	l.a.kelley@imperial.ac.uk
Description	P76655
Date	Thu Jan 5 12:25:14 GMT 2012
Unique Job ID	249b8d5f9bb9944f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfzB_	Alignment		100.0	28	**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	c2vqiA_	Alignment		100.0	41	**PDB header:**transport **Chain:** A: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** structure of the p pilus usher (papc) translocation pore
3	c3ohnA_	Alignment		100.0	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane usher protein fimd; **PDBTitle:** crystal structure of the fimd translocation domain
4	d3bwud1	Alignment		100.0	24	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
5	d1zdva1	Alignment		100.0	26	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
6	c3fcgB_	Alignment		99.9	34	**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
7	d1zdxa1	Alignment		99.9	22	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
8	c3l48B_	Alignment		99.7	38	**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
9	c2xetB_	Alignment		99.7	25	**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
10	d1uwya1	Alignment		90.8	10	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
11	c3mn8A_	Alignment		88.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short

12	d1h8la1	Alignment		88.3	14	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
13	c2nsmA_	Alignment		88.3	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
14	c3pdgA_	Alignment		87.3	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
15	c1uwyA_	Alignment		87.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
16	c3pe9B_	Alignment		86.9	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
17	c1h8lA_	Alignment		82.9	14	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
18	d1w0na_	Alignment		82.5	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
19	c3pe9D_	Alignment		76.7	11	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
20	c1d2pA_	Alignment		75.8	12	**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
21	c1u00A_	Alignment	not modelled	75.6	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
22	c3dpqE_	Alignment	not modelled	72.4	22	**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)
23	c2op6A_	Alignment	not modelled	71.9	20	**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
24	c3n8eA_	Alignment	not modelled	70.8	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stress-70 protein, mitochondrial; **PDBTitle:** substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
25	c3d33B_	Alignment	not modelled	70.5	7	**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
26	c1bprA_	Alignment	not modelled	67.2	20	**PDB header:**molecular chaperone **Chain:** A: **PDB Molecule:**dnak; **PDBTitle:** nmr structure of the substrate binding domain of dnak,2 minimized average structure
27	c3pe9A_	Alignment	not modelled	66.8	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
						PDB header:unknown function

28	c3pe9C_	Alignment	not modelled	66.8	11	**Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
29	c2r32A_	Alignment	not modelled	58.6	25	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
30	d1ci3m2	Alignment	not modelled	58.2	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
31	d1u00a2	Alignment	not modelled	57.6	22	**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
32	c3dqgC_	Alignment	not modelled	57.3	24	**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.
33	c3e8vA_	Alignment	not modelled	56.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible transglutaminase-family protein; **PDBTitle:** crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis
34	d1yuwa1	Alignment	not modelled	55.1	22	**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
35	d1v8ha1	Alignment	not modelled	53.3	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
36	d2ag4a1	Alignment	not modelled	53.2	9	**Fold:**Ganglioside M2 (gm2) activator **Superfamily:**Ganglioside M2 (gm2) activator **Family:**Ganglioside M2 (gm2) activator
37	d1dkza2	Alignment	not modelled	51.3	22	**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
38	c3k1dA_	Alignment	not modelled	47.1	16	**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
39	d1e2wa2	Alignment	not modelled	46.2	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
40	c3c12A_	Alignment	not modelled	39.1	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
41	c2oxgE_	Alignment	not modelled	31.5	15	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
42	d2vzsa4	Alignment	not modelled	29.3	22	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
43	d1cxla1	Alignment	not modelled	27.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
44	c2x5pA_	Alignment	not modelled	27.4	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
45	c1e2vB_	Alignment	not modelled	24.8	17	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
46	d2je8a4	Alignment	not modelled	22.5	11	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
47	c2jxmB_	Alignment	not modelled	21.9	15	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
48	c1q90A_	Alignment	not modelled	21.8	19	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
49	c3rghA_	Alignment	not modelled	21.1	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
50	c3bryB_	Alignment	not modelled	21.0	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
51	d1wlha1	Alignment	not modelled	20.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
52	d2dj4a1	Alignment	not modelled	20.3	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
53	d2bp3a1	Alignment	not modelled	19.8	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
						PDB header:transcription

54	c2xk0A_	Alignment	not modelled	19.8	23	**Chain:** A: **PDB Molecule:**polycomb protein pcl; **PDBTitle:** solution structure of the tudor domain from drosophila2 polycomblike (pcl)
55	c3iswA_	Alignment	not modelled	19.3	31	**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
56	c2ww8A_	Alignment	not modelled	18.5	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell wall surface anchor family protein; **PDBTitle:** structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
57	c2pz4A_	Alignment	not modelled	18.4	14	**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
58	c2eqjA_	Alignment	not modelled	18.2	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
59	c3b9eA_	Alignment	not modelled	18.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
60	d2a9da1	Alignment	not modelled	17.8	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
61	d2di8a1	Alignment	not modelled	17.3	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
62	d1edqa1	Alignment	not modelled	17.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
63	d2dmca1	Alignment	not modelled	16.8	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
64	c2k78A_	Alignment	not modelled	16.6	12	**PDB header:**heme-binding protein **Chain:** A: **PDB Molecule:**iron-regulated surface determinant protein c; **PDBTitle:** solution structure of the isdc neat domain bound to zinc2 protoporphyrin
65	d1pfsa_	Alignment	not modelled	16.1	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
66	d2o6pa1	Alignment	not modelled	16.0	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**NEAT domain-like **Family:**NEAT domain
67	c2o6pA_	Alignment	not modelled	15.3	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-regulated surface determinant protein c; **PDBTitle:** crystal structure of the heme-isdc complex
68	d2gr7a1	Alignment	not modelled	14.6	22	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
69	c2gr7C_	Alignment	not modelled	14.6	22	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
70	c2brqB_	Alignment	not modelled	14.6	31	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
71	d2dica1	Alignment	not modelled	14.1	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
72	d2w0pa1	Alignment	not modelled	14.0	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
73	d2vmha1	Alignment	not modelled	13.8	10	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**NPCBM-like
74	d1qfha1	Alignment	not modelled	13.7	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
75	c2ds4A_	Alignment	not modelled	13.6	19	**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
76	c3brzA_	Alignment	not modelled	13.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
77	d1psoe_	Alignment	not modelled	13.4	10	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
78	c3lemA_	Alignment	not modelled	13.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructosyltransferase; **PDBTitle:** crystal structure of fructosyltransferase (d191a) from a. japonicus in2 complex with nystose
79	c2jf1A_	Alignment	not modelled	13.1	31	**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
						Fold: Immunoglobulin-like beta-sandwich

80	d2d7oa1	Alignment	not modelled	13.0	21	**Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
81	d2e9ia1	Alignment	not modelled	13.0	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
82	d1qfha2	Alignment	not modelled	13.0	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
83	c3nm7C_	Alignment	not modelled	12.8	16	**PDB header:**nucleic acid binding protein **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
84	d2dmba1	Alignment	not modelled	12.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
85	d1yq2a3	Alignment	not modelled	12.1	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
86	d2diaa1	Alignment	not modelled	12.0	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
87	d1v05a_	Alignment	not modelled	11.9	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
88	c2e5pA_	Alignment	not modelled	11.9	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
89	c2k7pA_	Alignment	not modelled	11.5	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 16-17
90	d2diba1	Alignment	not modelled	11.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
91	d2je6i3	Alignment	not modelled	11.3	25	**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)
92	c2brqA_	Alignment	not modelled	11.2	31	**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
93	c2w0pB_	Alignment	not modelled	11.2	31	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the migfilin peptide
94	c3iswB_	Alignment	not modelled	11.2	31	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cftr
95	c1ksrA_	Alignment	not modelled	11.2	13	**PDB header:**actin binding protein **Chain:** A: **PDB Molecule:**gelation factor; **PDBTitle:** the repeating segments of the f-actin cross-linking2 gelation factor (abp-120) have an immunoglobulin fold, nmr,3 20 structures
96	c2e9jA_	Alignment	not modelled	11.2	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 14th filamin domain from human2 filamin-b
97	d2d7ma1	Alignment	not modelled	10.9	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
98	c3cnkB_	Alignment	not modelled	10.9	25	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the dimerization domain of human2 filamin a
99	c2vnvC_	Alignment	not modelled	10.7	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