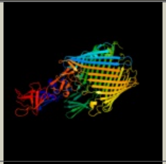
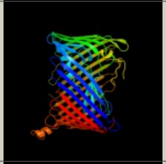
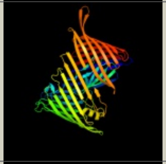
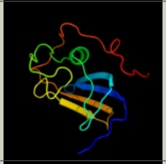
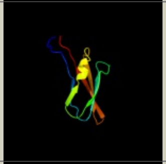
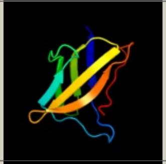
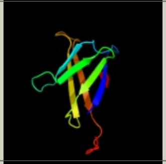
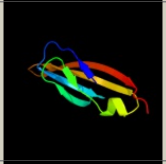
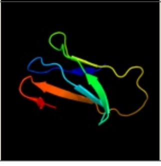
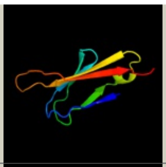
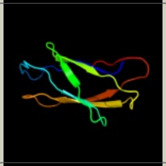
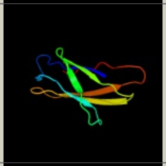
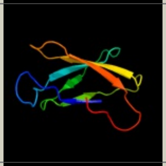
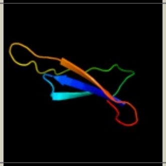
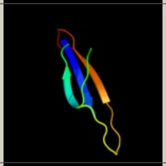
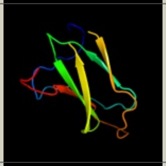
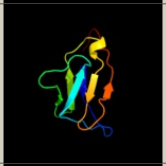
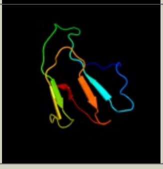
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P33341
Date	Thu Jan 5 11:51:41 GMT 2012
Unique Job ID	e19a5c012ebd726a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfzB_	Alignment		100.0	31	**PDB header:**cell adhesion/transport/chaperone **Chain:** B: **PDB Molecule:**outer membrane usher protein, type 1 fimbrial synthesis; **PDBTitle:** crystal structure of the fimd usher bound to its cognate fimc:fimh2 substrate
2	c3ohnA_	Alignment		100.0	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane usher protein fimd; **PDBTitle:** crystal structure of the fimd translocation domain
3	c2vqiA_	Alignment		100.0	27	**PDB header:**transport **Chain:** A: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** structure of the p pilus usher (papc) translocation pore
4	d1zdva1	Alignment		99.9	31	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
5	d3bwud1	Alignment		99.9	23	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
6	c3fcgB_	Alignment		99.9	39	**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		99.8	26	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
8	c3l48B_	Alignment		99.7	18	**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	18	**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	c3pe9B_	Alignment		95.0	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
11	c3pdgA_	Alignment		94.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules

12	c3pe9D_	Alignment		90.5	16	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
13	c1h8lA_	Alignment		90.4	11	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
14	d1h8la1	Alignment		90.2	10	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
15	c2nsmA_	Alignment		89.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
16	c3pe9C_	Alignment		86.9	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
17	c3pe9A_	Alignment		86.9	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
18	d1w0na_	Alignment		85.5	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
19	d1uwya1	Alignment		85.4	7	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
20	c2x5pA_	Alignment		84.1	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
21	c1d2pA_	Alignment	not modelled	82.5	20	**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
22	c3mn8A_	Alignment	not modelled	82.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
23	c1uwyA_	Alignment	not modelled	81.8	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
24	c2vnvC_	Alignment	not modelled	79.4	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
25	d3pccm_	Alignment	not modelled	64.9	17	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
26	d2burb1	Alignment	not modelled	63.6	20	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
27	c2boiA_	Alignment	not modelled	63.2	13	**PDB header:**lectin **Chain:** A: **PDB Molecule:**cv-iil lectin; **PDBTitle:** 1.1a structure of chromobacterium violaceum lectin cv2l in2 complex with alpha-methyl-fucoside
28	c2xr4A_	Alignment	not modelled	63.1	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** c-terminal domain of bc2l-c lectin from burkholderia cenocepacia

29	d1uzva_	Alignment	not modelled	54.0	14	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
30	c1u00A_	Alignment	not modelled	52.6	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
31	c3e8vA_	Alignment	not modelled	50.7	14	**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
32	c3bryB_	Alignment	not modelled	50.0	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
33	c3dpqE_	Alignment	not modelled	49.8	21	**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)
34	c1bprA_	Alignment	not modelled	49.5	21	**PDB header:**molecular chaperone **Chain:** A: **PDB Molecule:**dnak; **PDBTitle:** nmr structure of the substrate binding domain of dnak,2 minimized average structure
35	c3b9eA_	Alignment	not modelled	49.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
36	c2bpbA_	Alignment	not modelled	49.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit a; **PDBTitle:** sulfite dehydrogenase from starkeya novella
37	d1nkga1	Alignment	not modelled	48.5	7	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Rhamnogalacturonase B, RhgB, middle domain
38	c1ug9A_	Alignment	not modelled	48.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
39	c3c12A_	Alignment	not modelled	47.1	22	**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
40	c2op6A_	Alignment	not modelled	46.4	18	**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
41	c3n8eA_	Alignment	not modelled	45.3	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stress-70 protein, mitochondrial; **PDBTitle:** substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
42	c3fn9B_	Alignment	not modelled	42.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
43	d1v8ha1	Alignment	not modelled	41.7	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
44	c3cmgA_	Alignment	not modelled	40.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
45	d1edqa1	Alignment	not modelled	39.5	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
46	c1nkgA_	Alignment	not modelled	37.8	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rhamnogalacturonase b; **PDBTitle:** rhamnogalacturonan lyase from aspergillus aculeatus
47	d1u00a2	Alignment	not modelled	36.8	23	**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
48	d2chha1	Alignment	not modelled	34.3	13	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
49	d1dkza2	Alignment	not modelled	33.0	21	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
50	c2a9dB_	Alignment	not modelled	32.2	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite oxidase; **PDBTitle:** crystal structure of recombinant chicken sulfite oxidase with arg at2 residue 161
51	c3dqgC_	Alignment	not modelled	32.2	19	**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.
52	d2vzsa4	Alignment	not modelled	31.3	19	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
53	d1yuwa1	Alignment	not modelled	31.2	20	**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
54	d1ci3m2	Alignment	not modelled	31.1	10	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain

55	d1aoza2	Alignment	not modelled	28.7	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
56	c2r32A_	Alignment	not modelled	28.6	29	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
57	d1e2wa2	Alignment	not modelled	27.3	11	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
58	c2oxgE_	Alignment	not modelled	26.7	25	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
59	d2a9da1	Alignment	not modelled	26.2	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
60	c3pddA_	Alignment	not modelled	25.1	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
61	c2ww8A_	Alignment	not modelled	24.7	6	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell wall surface anchor family protein; **PDBTitle:** structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
62	c3k1dA_	Alignment	not modelled	23.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme; **PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
63	d2dj4a1	Alignment	not modelled	22.0	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
64	d3pcca_	Alignment	not modelled	21.9	11	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
65	d1o75a2	Alignment	not modelled	21.2	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains
66	c3rghA_	Alignment	not modelled	21.2	33	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
67	c2lgeA_	Alignment	not modelled	21.0	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the calcium-bound form of the protein yp_001302112.12 from parabacteroides distasonis
68	d2je8a4	Alignment	not modelled	21.0	13	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
69	d1wlha1	Alignment	not modelled	20.2	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
70	d2bp3a1	Alignment	not modelled	20.2	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
71	c3hj8A_	Alignment	not modelled	20.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
72	c2yujA_	Alignment	not modelled	19.5	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
73	c2l3bA_	Alignment	not modelled	19.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
74	d1ogpa1	Alignment	not modelled	18.7	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
75	c2pdtD_	Alignment	not modelled	17.5	20	**PDB header:**circadian clock protein **Chain:** D: **PDB Molecule:**vivid pas protein vvd; **PDBTitle:** 2.3 angstrom structure of phosphodiesterase treated vivid
76	d2d7oa1	Alignment	not modelled	16.8	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
77	d2e9ia1	Alignment	not modelled	16.7	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
78	d2dmca1	Alignment	not modelled	16.5	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
79	c1zc1A_	Alignment	not modelled	16.4	13	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
80	c3d33B		not modelled	16.3	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**domain of unknown function with an immunoglobulin-like

80	c3d33B_	Alignment	not modelled	16.3	14	**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
81	c2jxmB_	Alignment	not modelled	16.1	12	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
82	d1ulva2	Alignment	not modelled	16.1	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
83	c2crvA_	Alignment	not modelled	15.5	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
84	d1qfha1	Alignment	not modelled	15.5	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
85	d1yq2a3	Alignment	not modelled	15.4	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
86	d2slia1	Alignment	not modelled	15.4	16	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Leech intramolecular trans-sialidase, N-terminal domain
87	d1uura3	Alignment	not modelled	15.2	26	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
88	c3girA_	Alignment	not modelled	14.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of glycine cleavage system2 aminomethyltransferase t from bartonella henselae
89	d2dica1	Alignment	not modelled	14.3	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
90	c2brqB_	Alignment	not modelled	14.1	27	**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
91	c2ds4A_	Alignment	not modelled	13.8	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 45; **PDBTitle:** solution structure of the filamin domain from human2 tripartite motif protein 45
92	d2j3sa2	Alignment	not modelled	13.6	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
93	d2di8a1	Alignment	not modelled	13.5	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
94	d2w0pa1	Alignment	not modelled	13.4	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
95	d2nn6i1	Alignment	not modelled	13.4	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
96	d2diaa1	Alignment	not modelled	13.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
97	d2d7pa1	Alignment	not modelled	13.3	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
98	d2dmba1	Alignment	not modelled	13.2	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
99	c1w2tE_	Alignment	not modelled	13.2	16	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**beta fructosidase; **PDBTitle:** beta-fructosidase from thermotoga maritima in complex with2 raffinose