Phyre^2

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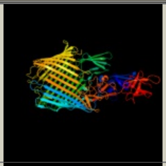
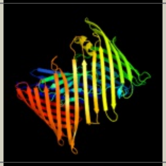
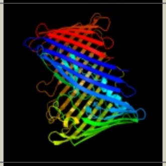
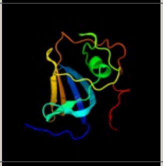
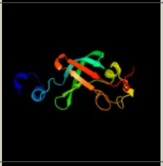
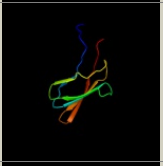
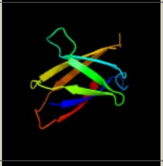
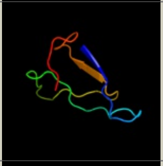
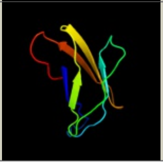
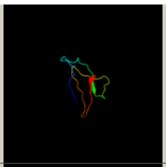
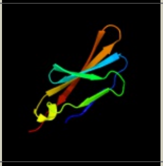
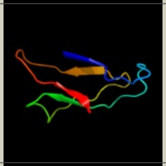
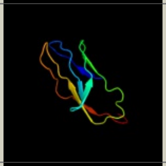
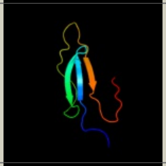
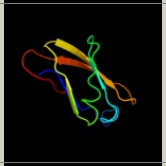
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfzB_	Alignment		100.0	29	**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	36	**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	31	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane usher protein fimd; **PDBTitle:** crystal structure of the fimd translocation domain
4	d1zdva1	Alignment		99.9	22	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
5	d3bwud1	Alignment		99.9	22	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
6	c3fcgB_	Alignment		99.9	33	**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	21	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
8	c3l48B_	Alignment		99.7	40	**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	22	**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		91.4	8	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
11	c2nsmA_	Alignment		85.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain

12	c1uwyA_	Alignment		85.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
13	c3pe9B_	Alignment		84.1	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
14	c3mn8A_	Alignment		84.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
15	c3pdgA_	Alignment		79.9	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
16	c1d2pA_	Alignment		77.3	16	**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
17	c1u00A_	Alignment		74.6	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
18	c1h8lA_	Alignment		74.4	15	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
19	d1h8la1	Alignment		74.0	16	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
20	d1w0na_	Alignment		73.7	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
21	c3dpqE_	Alignment	not modelled	73.5	24	**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)
22	c3pe9D_	Alignment	not modelled	72.3	14	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
23	c2op6A_	Alignment	not modelled	71.6	17	**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	c1bprA_	Alignment	not modelled	71.2	24	**PDB header:**molecular chaperone **Chain:** A: **PDB Molecule:**dnak; **PDBTitle:** nmr structure of the substrate binding domain of dnak,2 minimized average structure
25	c3n8eA_	Alignment	not modelled	71.1	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stress-70 protein, mitochondrial; **PDBTitle:** substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
26	c3d33B_	Alignment	not modelled	64.8	19	**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
27	c2x5pA_	Alignment	not modelled	64.3	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
						Fold: Heat shock protein 70kD (HSP70), peptide-binding domain

28	d1u00a2	Alignment	not modelled	63.6	21	**Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
29	c3pe9A_	Alignment	not modelled	63.0	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
30	c3pe9C_	Alignment	not modelled	63.0	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
31	d1v8ha1	Alignment	not modelled	61.8	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
32	d1yuwa1	Alignment	not modelled	59.5	19	**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
33	c3dqgC_	Alignment	not modelled	59.0	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.
34	c2r32A_	Alignment	not modelled	50.9	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
35	d1dkza2	Alignment	not modelled	50.9	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
36	d2ag4a1	Alignment	not modelled	49.8	11	**Fold:**Ganglioside M2 (gm2) activator **Superfamily:**Ganglioside M2 (gm2) activator **Family:**Ganglioside M2 (gm2) activator
37	c3bryB_	Alignment	not modelled	46.7	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
38	c2oxgE_	Alignment	not modelled	40.7	19	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
39	c3k1dA_	Alignment	not modelled	39.6	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
40	d1ci3m2	Alignment	not modelled	29.9	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
41	d2burb1	Alignment	not modelled	29.2	18	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
42	c2xk0A_	Alignment	not modelled	26.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein pcl; **PDBTitle:** solution structure of the tudor domain from drosophila2 polycomblike (pcl)
43	c3c12A_	Alignment	not modelled	26.2	20	**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
44	d2vmha1	Alignment	not modelled	23.9	7	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**NPCBM-like
45	d2dj4a1	Alignment	not modelled	23.8	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
46	d2e9ia1	Alignment	not modelled	22.6	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
47	c3rghA_	Alignment	not modelled	22.5	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
48	d2bp3a1	Alignment	not modelled	21.5	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
49	d2je8a4	Alignment	not modelled	21.5	5	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
50	c3hizB_	Alignment	not modelled	21.5	15	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
51	d1wlha1	Alignment	not modelled	21.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
52	d3pcca_	Alignment	not modelled	20.6	15	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
53	c2ww8A_	Alignment	not modelled	20.3	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
54	c3iswA	Alignment	not modelled	20.2	53	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a;

54	c3iswA_	Alignment	not modelled	20.2	53	**PDBTitle:** crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cftr
55	c1nkgA_	Alignment	not modelled	19.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rhamnogalacturonase b; **PDBTitle:** rhamnogalacturonan lyase from aspergillus aculeatus
56	d3pccm_	Alignment	not modelled	19.9	14	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
57	c2jxmB_	Alignment	not modelled	18.7	24	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
58	d2dmca1	Alignment	not modelled	18.4	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
59	c3gxxB_	Alignment	not modelled	17.8	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
60	c2k78A_	Alignment	not modelled	17.6	8	**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
61	c3cmgA_	Alignment	not modelled	17.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
62	c3b9eA_	Alignment	not modelled	17.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
63	d2j3sa2	Alignment	not modelled	17.4	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
64	d2d7oa1	Alignment	not modelled	17.2	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
65	d2o6pa1	Alignment	not modelled	17.1	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**NEAT domain-like **Family:**NEAT domain
66	c3fn9B_	Alignment	not modelled	17.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
67	d2je6i3	Alignment	not modelled	16.8	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)
68	c2o6pA_	Alignment	not modelled	16.6	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-regulated surface determinant protein c; **PDBTitle:** crystal structure of the heme-isdc complex
69	c2boyC_	Alignment	not modelled	16.4	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp
70	d2dica1	Alignment	not modelled	16.3	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
71	d2a9da1	Alignment	not modelled	16.1	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
72	d1cwva1	Alignment	not modelled	15.9	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
73	c2brqB_	Alignment	not modelled	15.9	53	**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
74	d2w0pa1	Alignment	not modelled	15.9	53	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
75	d2dmba1	Alignment	not modelled	15.8	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
76	c3dwoX_	Alignment	not modelled	15.6	16	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
77	c2jf1A_	Alignment	not modelled	15.6	53	**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
78	d2di8a1	Alignment	not modelled	15.4	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
79	c2e9jA_	Alignment	not modelled	15.1	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 14th filamin domain from human2 filamin-b
80	d1qfha2	Alignment	not modelled	15.0	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)

81	d2ja9a2	Alignment	not modelled	14.9	16	**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)
82	d2d7ma1	Alignment	not modelled	14.5	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
83	d1v05a_	Alignment	not modelled	14.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
84	d1e2wa2	Alignment	not modelled	14.4	15	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
85	c2ds4A_	Alignment	not modelled	14.4	33	**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
86	d1qfha1	Alignment	not modelled	14.3	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
87	c2vnvC_	Alignment	not modelled	14.2	8	**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
88	c3o82B_	Alignment	not modelled	14.1	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
89	d2diaa1	Alignment	not modelled	13.9	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
90	d2diba1	Alignment	not modelled	13.8	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
91	c3cnkB_	Alignment	not modelled	13.0	33	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the dimerization domain of human2 filamin a
92	d1cxla1	Alignment	not modelled	13.0	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
93	c3brzA_	Alignment	not modelled	12.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
94	d2di9a1	Alignment	not modelled	12.6	47	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
95	c2w0pB_	Alignment	not modelled	12.4	53	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the migfilin peptide
96	c3iswB_	Alignment	not modelled	12.4	53	**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
97	c2brqA_	Alignment	not modelled	12.4	53	**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
98	d1lnza1	Alignment	not modelled	12.3	21	**Fold:**Obg-fold **Superfamily:**Obg GTP-binding protein N-terminal domain **Family:**Obg GTP-binding protein N-terminal domain
99	d1udxa1	Alignment	not modelled	12.1	29	**Fold:**Obg-fold **Superfamily:**Obg GTP-binding protein N-terminal domain **Family:**Obg GTP-binding protein N-terminal domain