Phyre2

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Description	P77196
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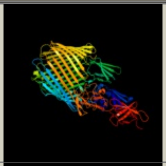
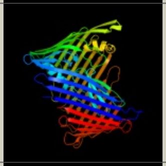
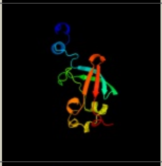
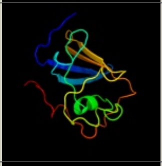
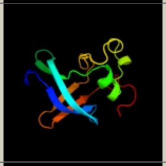
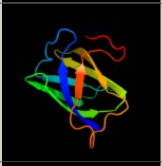
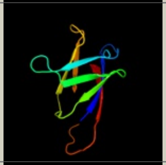
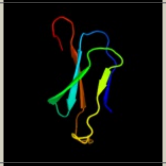
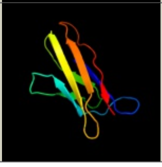
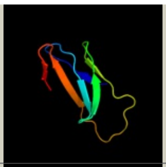
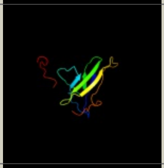
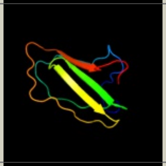
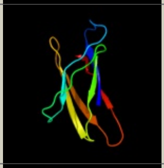
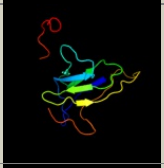
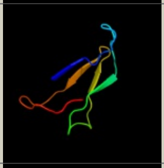
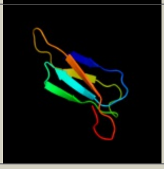
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfzB_	Alignment		100.0	27	**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	42	**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	27	**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	24	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
6	c3fcgB_	Alignment		99.9	30	**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		99.8	48	**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		99.8	27	**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		90.8	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
11	c2nsmA_	Alignment		90.2	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	c3pdgA_	Alignment		88.6	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
13	c1uwyA_	Alignment		86.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
14	c2x5pA_	Alignment		84.8	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
15	d1w0na_	Alignment		84.4	11	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
16	d1h8la1	Alignment		83.6	11	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
17	d1uwya1	Alignment		83.3	17	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
18	c3mn8A_	Alignment		82.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
19	c1h8lA_	Alignment		81.7	11	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
20	c3pe9D_	Alignment		80.6	11	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
21	c1d2pA_	Alignment	not modelled	79.4	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
22	c1u00A_	Alignment	not modelled	78.6	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
23	c3dpqE_	Alignment	not modelled	75.2	14	**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)
24	c3n8eA_	Alignment	not modelled	74.5	19	**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	c2op6A_	Alignment	not modelled	73.7	13	**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
26	c3pe9A_	Alignment	not modelled	73.3	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
27	c3pe9C_	Alignment	not modelled	73.3	14	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
28	c3e8vA_	Alignment	not modelled	72.9	21	**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
29	d1v8ha1	Alignment	not modelled	72.6	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
30	c1bprA_	Alignment	not modelled	71.1	13	**PDB header:**molecular chaperone **Chain:** A: **PDB Molecule:**dnak; **PDBTitle:** nmr structure of the substrate binding domain of dnak,2 minimized average structure
31	c2r32A_	Alignment	not modelled	63.4	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
32	d1u00a2	Alignment	not modelled	62.0	15	**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	c3d33B_	Alignment	not modelled	60.5	14	**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
34	c3dqgC_	Alignment	not modelled	60.2	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.
35	d1yuwa1	Alignment	not modelled	60.0	13	**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	d1dkza2	Alignment	not modelled	55.1	14	**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
37	c3k1dA_	Alignment	not modelled	49.9	10	**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
38	c2oxgE_	Alignment	not modelled	47.0	17	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
39	d2ag4a1	Alignment	not modelled	41.4	13	**Fold:**Ganglioside M2 (gm2) activator **Superfamily:**Ganglioside M2 (gm2) activator **Family:**Ganglioside M2 (gm2) activator
40	c2vnvC_	Alignment	not modelled	36.9	10	**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
41	d1ci3m2	Alignment	not modelled	31.7	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
42	c3b9eA_	Alignment	not modelled	31.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
43	d1uzva_	Alignment	not modelled	28.3	13	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
44	d2vzsa4	Alignment	not modelled	28.1	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
45	c3girA_	Alignment	not modelled	27.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of glycine cleavage system2 aminomethyltransferase t from bartonella henselae
46	c1pj6A_	Alignment	not modelled	27.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n,n-dimethylglycine oxidase; **PDBTitle:** crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
47	c3acgA_	Alignment	not modelled	26.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-1,4-endoglucanase; **PDBTitle:** crystal structure of carbohydrate-binding module family 282 from clostridium josui cel5a in complex with cellobiose
48	d2dj4a1	Alignment	not modelled	25.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
49	d1e2wa2	Alignment	not modelled	24.7	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
50	c3rghA_	Alignment	not modelled	24.0	33	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
51	c3brzA_	Alignment	not modelled	23.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
52	d2e9ia1	Alignment	not modelled	23.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
53	c3iswA_	Alignment	not modelled	23.3	33	**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

54	d1wlha1	Alignment	not modelled	23.2	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
55	d2bp3a1	Alignment	not modelled	22.2	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
56	d2vmha1	Alignment	not modelled	22.0	7	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**NPCBM-like
57	c3gxxB_	Alignment	not modelled	21.6	24	**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
58	c3hizB_	Alignment	not modelled	20.7	18	**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
59	d2je8a4	Alignment	not modelled	20.4	11	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
60	c1ug9A_	Alignment	not modelled	19.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
61	d1gyva_	Alignment	not modelled	19.0	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**gamma-adaptin C-terminal appendage domain-like
62	d2a9da1	Alignment	not modelled	18.8	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
63	c2ww8A_	Alignment	not modelled	18.7	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell wall surface anchor family protein; **PDBTitle:** structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
64	c2l1tA_	Alignment	not modelled	18.1	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of the n-terminal domain of np_954075.1
65	d1uwwa_	Alignment	not modelled	18.1	15	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 28 carbohydrate binding module, CBM28
66	c2brqB_	Alignment	not modelled	17.9	33	**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
67	c2xr4A_	Alignment	not modelled	17.9	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
68	c2bpbA_	Alignment	not modelled	17.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit a; **PDBTitle:** sulfite dehydrogenase from starkeya novella
69	c2e9jA_	Alignment	not modelled	17.5	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 14th filamin domain from human2 filamin-b
70	d1edqa1	Alignment	not modelled	17.1	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
71	c2ds4A_	Alignment	not modelled	16.9	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
72	c2vzvB_	Alignment	not modelled	16.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
73	c1worA_	Alignment	not modelled	16.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of t-protein of the glycine cleavage2 system
74	d2dmba1	Alignment	not modelled	16.4	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
75	d1qfha2	Alignment	not modelled	16.2	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
76	c3dnhB_	Alignment	not modelled	16.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein atu2129; **PDBTitle:** the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58
77	d2dica1	Alignment	not modelled	15.8	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
78	d2j3sa2	Alignment	not modelled	15.8	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
79	d2dmca1	Alignment	not modelled	15.7	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
						Fold: Immunoglobulin-like beta-sandwich

80	d2di9a1	Alignment	not modelled	15.6	20	**Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
81	d2burb1	Alignment	not modelled	15.5	30	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
82	d2d7ma1	Alignment	not modelled	15.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
83	d1qfha1	Alignment	not modelled	15.3	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
84	d2w0pa1	Alignment	not modelled	15.1	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
85	d1v05a_	Alignment	not modelled	15.1	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
86	d2diba1	Alignment	not modelled	15.0	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
87	c2jf1A_	Alignment	not modelled	14.9	33	**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
88	d2di8a1	Alignment	not modelled	14.9	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
89	d2p0la1	Alignment	not modelled	14.8	16	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
90	c3iswB_	Alignment	not modelled	14.7	33	**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
91	c2brqA_	Alignment	not modelled	14.7	33	**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
92	d2diaa1	Alignment	not modelled	14.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
93	c2e8oA_	Alignment	not modelled	14.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** solution structure of the n-terminal sam-domain of the sam2 domain and hd domain containing protein 1 (dendritic cell-3 derived ifng-induced protein) (dcip) (monocyte protein 5)4 (mop-5)
94	c2w0pB_	Alignment	not modelled	13.7	33	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the migfilin peptide
95	d2d7oa1	Alignment	not modelled	13.7	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
96	d2ns0a1	Alignment	not modelled	13.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
97	c2boiA_	Alignment	not modelled	13.2	14	**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
98	d2d7pa1	Alignment	not modelled	13.1	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
99	c1ksrA_	Alignment	not modelled	12.9	18	**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