



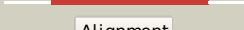

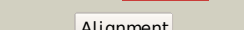

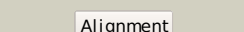







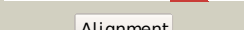

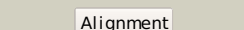

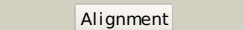


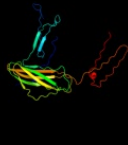
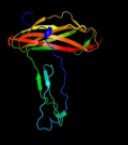





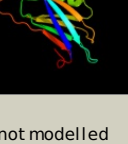


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pn5A_	 Alignment		100.0	14	PDB header: immune system Chain: A: PDB Molecule: thioester-containing protein i; PDBTitle: crystal structure of tep1r
2	c3cu7A_	 Alignment		100.0	14	PDB header: immune system Chain: A: PDB Molecule: complement c5; PDBTitle: human complement component 5
3	c2b39B_	 Alignment		100.0	16	PDB header: immune system Chain: B: PDB Molecule: c3; PDBTitle: structure of mammalian c3 with an intact thioester at 3a resolution
4	c2a73B_	 Alignment		100.0	15	PDB header: immune system Chain: B: PDB Molecule: complement c3; PDBTitle: human complement component c3
5	c3g6jB_	 Alignment		100.0	15	PDB header: immune system Chain: B: PDB Molecule: complement c3 alpha chain; PDBTitle: c3b in complex with a c3b specific fab
6	c3pvmB_	 Alignment		100.0	18	PDB header: immune system Chain: B: PDB Molecule: cobra venom factor; PDBTitle: structure of complement c5 in complex with cvf
7	d1hzfa_	 Alignment		100.0	19	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
8	c1hzfA_	 Alignment		100.0	19	PDB header: immune system Chain: A: PDB Molecule: complement factor c4a; PDBTitle: c4adg fragment of human complement factor c4a
9	d1c3da_	 Alignment		100.0	19	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
10	c3hrzA_	 Alignment		100.0	13	PDB header: immune system Chain: A: PDB Molecule: cobra venom factor; PDBTitle: cobra venom factor (cvf) in complex with human factor b
11	d1qqfa_	 Alignment		100.0	16	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components

12	c2qkiA_	Alignment		100.0	14	PDB header: immune system/hydrolase inhibitor Chain: A: PDB Molecule: complement c3; PDBTitle: human c3c in complex with the inhibitor compstatin
13	c3hs0B_	Alignment		100.0	14	PDB header: immune system Chain: B: PDB Molecule: cobra venom factor; PDBTitle: cobra venom factor (cvf) in complex with human factor b
14	c2a74B_	Alignment		99.9	11	PDB header: immune system Chain: B: PDB Molecule: complement component c3c; PDBTitle: human complement component c3c
15	c2p9rA_	Alignment		99.7	23	PDB header: signaling protein Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: human alpha2-macroglobulin is composed of multiple domains,2 as predicted by homology with complement component c3
16	d2sqca1	Alignment		99.6	16	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
17	c3hrzC_	Alignment		99.6	10	PDB header: immune system Chain: C: PDB Molecule: cobra venom factor; PDBTitle: cobra venom factor (cvf) in complex with human factor b
18	c1o79A_	Alignment		99.6	20	PDB header: isomerase Chain: A: PDB Molecule: squalene--hopene cyclase; PDBTitle: structures of human oxidosqualene cyclase inhibitors bound2 to a homologous enzyme
19	c1w6kA_	Alignment		99.4	18	PDB header: isomerase Chain: A: PDB Molecule: lanosterol synthase; PDBTitle: structure of human osc in complex with lanosterol
20	d1ledya_	Alignment		99.4	15	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Alpha-macroglobulin receptor domain Family: Alpha-macroglobulin receptor domain
21	d1ayoa_	Alignment	not modelled	99.4	16	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Alpha-macroglobulin receptor domain Family: Alpha-macroglobulin receptor domain
22	d1bv8a_	Alignment	not modelled	99.4	14	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Alpha-macroglobulin receptor domain Family: Alpha-macroglobulin receptor domain
23	d3es6b1	Alignment	not modelled	99.4	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: SVA-like
24	d2sqca2	Alignment	not modelled	99.3	15	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
25	d1w6ka1	Alignment	not modelled	99.3	18	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
26	c2qkiC_	Alignment	not modelled	99.2	7	PDB header: immune system/hydrolase inhibitor Chain: C: PDB Molecule: complement c3; PDBTitle: human c3c in complex with the inhibitor compstatin
27	d3dssb1	Alignment	not modelled	98.6	17	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases
28	c3e37B_	Alignment	not modelled	98.2	13	PDB header: transferase Chain: B: PDB Molecule: protein farnesyltransferase subunit beta; PDBTitle: protein farnesyltransferase complexed with bisubstrate2 ethylenediamine scaffold inhibitor 5
						Fold: alpha/alpha toroid

29	d2h6fb1	Alignment	not modelled	98.1	13	Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases
30	c1cwvA	Alignment	not modelled	97.8	10	PDB header: structural protein Chain: A: PDB Molecule: invasin; PDBTitle: crystal structure of invasins: a bacterial integrin-binding protein
31	c3q7aB	Alignment	not modelled	97.7	14	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: farnesyltransferase beta subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpp and l-778,123
32	c2pmvB	Alignment	not modelled	97.4	11	PDB header: transport protein Chain: B: PDB Molecule: gastric intrinsic factor; PDBTitle: crystal structure of human intrinsic factor- cobalamin complex at 2.62 a resolution
33	c1tnuL	Alignment	not modelled	97.4	12	PDB header: transferase Chain: L: PDB Molecule: geranylgeranyl transferase type i beta subunit; PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a gcinckvvl peptide derived from rhob
34	d1n4qb	Alignment	not modelled	97.4	12	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases
35	d1w6ka2	Alignment	not modelled	97.1	19	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
36	c3draB	Alignment	not modelled	97.0	10	PDB header: transferase Chain: B: PDB Molecule: geranylgeranyltransferase type i beta subunit; PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
37	d1w8oa1	Alignment	not modelled	96.8	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
38	c1l9mB	Alignment	not modelled	96.6	15	PDB header: transferase Chain: B: PDB Molecule: protein-glutamine glutamyltransferase e3; PDBTitle: three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
39	d1r76a	Alignment	not modelled	96.5	23	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
40	d1gxma	Alignment	not modelled	96.5	23	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
41	c2v3nA	Alignment	not modelled	96.1	13	PDB header: transport protein Chain: A: PDB Molecule: transcobalamin-2; PDBTitle: crystallographic analysis of upper axial ligand2 substitutions in cobalamin bound to transcobalamin
42	d2afaa1	Alignment	not modelled	95.1	17	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: N-acylglucosamine (NAG) epimerase
43	c2kl6A	Alignment	not modelled	94.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
44	c3e8vA	Alignment	not modelled	93.1	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
45	d1cwva1	Alignment	not modelled	92.5	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
46	c1wlhA	Alignment	not modelled	91.7	12	PDB header: structural protein Chain: A: PDB Molecule: gelation factor; PDBTitle: molecular structure of the rod domain of dictyostelium2 filamin
47	d1h8la1	Alignment	not modelled	91.5	13	Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Carboxypeptidase regulatory domain
48	c3irpX	Alignment	not modelled	90.5	36	PDB header: cell adhesion Chain: X: PDB Molecule: uro-adherence factor a; PDBTitle: crystal structure of functional region of uafa from staphylococcus2 saprophyticus at 1.50 angstrom resolution
49	c3kptA	Alignment	not modelled	89.9	18	PDB header: cell adhesion Chain: A: PDB Molecule: collagen adhesion protein; PDBTitle: crystal structure of bcpa, the major pilin subunit of2 bacillus cereus
50	c2h0eA	Alignment	not modelled	89.4	12	PDB header: hydrolase Chain: A: PDB Molecule: transthyretin-like protein pucm; PDBTitle: crystal structure of pucm in the absence of substrate
51	d1qfha1	Alignment	not modelled	89.3	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
52	d1f00i1	Alignment	not modelled	88.9	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
53	c1kv3F	Alignment	not modelled	88.8	9	PDB header: transferase Chain: F: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: human tissue transglutaminase in gdp bound form
						PDB header: cell adhesion Chain: A: PDB Molecule: cell surface protein;

54	c2l0dA	Alignment	not modelled	88.8	14	PDBTitle: solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
55	c3qvaB	Alignment	not modelled	87.5	33	PDB header: hydrolase Chain: B: PDB Molecule: tranthyrelin-like protein; PDBTitle: structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
56	c1g0dA	Alignment	not modelled	86.6	15	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of red sea bream transglutaminase
57	d1cwva2	Alignment	not modelled	86.3	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
58	c2pz4A	Alignment	not modelled	85.2	16	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
59	d1kgia	Alignment	not modelled	85.0	11	Fold: Prealbumin-like Superfamily: Tranthyrelin (synonym: prealbumin) Family: Tranthyrelin (synonym: prealbumin)
60	d2q3za3	Alignment	not modelled	84.8	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
61	c1h8lA	Alignment	not modelled	84.8	13	PDB header: carboxypeptidase Chain: A: PDB Molecule: carboxypeptidase gp180 residues 503-882; PDBTitle: duck carboxypeptidase d domain ii in complex with gemsA
62	d1uwya1	Alignment	not modelled	84.6	13	Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Carboxypeptidase regulatory domain
63	d2diba1	Alignment	not modelled	84.4	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
64	c2r39A	Alignment	not modelled	83.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fixg-related protein; PDBTitle: crystal structure of fixg-related protein from vibrio parahaemolyticus
65	c3mn8A	Alignment	not modelled	83.4	10	PDB header: hydrolase Chain: A: PDB Molecule: lp15968p; PDBTitle: structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
66	c1uwya	Alignment	not modelled	82.9	11	PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase m; PDBTitle: crystal structure of human carboxypeptidase m
67	c2h1xB	Alignment	not modelled	82.7	18	PDB header: hydrolase Chain: B: PDB Molecule: 5-hydroxyisourate hydrolase (formerly known as PDBTitle: crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, tranthyretin related protein)
68	d1vjja3	Alignment	not modelled	82.6	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
69	d1f86a	Alignment	not modelled	82.6	13	Fold: Prealbumin-like Superfamily: Tranthyrelin (synonym: prealbumin) Family: Tranthyrelin (synonym: prealbumin)
70	d2e9ia1	Alignment	not modelled	82.3	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
71	c1f13A	Alignment	not modelled	81.7	10	PDB header: coagulation factor Chain: A: PDB Molecule: cellular coagulation factor xiii zymogen; PDBTitle: recombinant human cellular coagulation factor xiii
72	c3saeA	Alignment	not modelled	81.7	9	PDB header: lyase Chain: A: PDB Molecule: alpha-bisabolene synthase; PDBTitle: structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
73	d1tfpa	Alignment	not modelled	81.3	16	Fold: Prealbumin-like Superfamily: Tranthyrelin (synonym: prealbumin) Family: Tranthyrelin (synonym: prealbumin)
74	d1ttaa	Alignment	not modelled	80.8	11	Fold: Prealbumin-like Superfamily: Tranthyrelin (synonym: prealbumin) Family: Tranthyrelin (synonym: prealbumin)
75	d1g0da3	Alignment	not modelled	80.7	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
76	d1oo2a	Alignment	not modelled	80.6	18	Fold: Prealbumin-like Superfamily: Tranthyrelin (synonym: prealbumin) Family: Tranthyrelin (synonym: prealbumin)
77	c2k7pA	Alignment	not modelled	80.4	14	PDB header: structural protein Chain: A: PDB Molecule: filamin-a; PDBTitle: filamin a ig-like domains 16-17
78	c2gpzC	Alignment	not modelled	80.2	24	PDB header: hydrolase Chain: C: PDB Molecule: tranthyrelin-like protein; PDBTitle: tranthyretin-like protein from salmonella dublin
79	d1vjja2	Alignment	not modelled	79.8	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
80	d1ex0a2	Alignment	not modelled	77.5	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains

81	d2q3za2	Alignment	not modelled	77.4	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
82	d2d7ma1	Alignment	not modelled	77.0	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
83	d1qfha2	Alignment	not modelled	76.6	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
84	d1ex0a3	Alignment	not modelled	76.2	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
85	c2xzzA_	Alignment	not modelled	74.1	14	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase k; PDBTitle: crystal structure of the human transglutaminase 1 beta-barrel domain
86	c2nsmA_	Alignment	not modelled	73.5	20	PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase n catalytic chain; PDBTitle: crystal structure of the human carboxypeptidase n (kinase i)2 catalytic domain
87	d2dmca1	Alignment	not modelled	71.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
88	c2ww8A_	Alignment	not modelled	71.8	24	PDB header: cell adhesion Chain: A: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
89	c2e9jA_	Alignment	not modelled	71.7	21	PDB header: structural protein Chain: A: PDB Molecule: filamin-b; PDBTitle: solution structure of the 14th filamin domain from human2 filamin-b
90	d2dmba1	Alignment	not modelled	70.9	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
91	c2k7qA_	Alignment	not modelled	69.3	13	PDB header: structural protein Chain: A: PDB Molecule: filamin-a; PDBTitle: filamin a ig-like domains 18-19
92	d1cwva3	Alignment	not modelled	67.9	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
93	d1v05a_	Alignment	not modelled	67.4	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
94	d1g0da2	Alignment	not modelled	67.0	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
95	c3k11A_	Alignment	not modelled	67.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative glycosyl hydrolase; PDBTitle: crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
96	c1ksrA_	Alignment	not modelled	65.8	15	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
97	c1qfhB_	Alignment	not modelled	65.1	13	PDB header: actin binding protein Chain: B: PDB Molecule: protein (gelation factor); PDBTitle: dimerization of gelation factor from dictyostelium2 discoideum: crystal structure of rod domains 5 and 6
98	c3n6yA_	Alignment	not modelled	65.1	18	PDB header: unknown function Chain: A: PDB Molecule: immunoglobulin-like protein; PDBTitle: crystal structure of an immunoglobulin-like protein (pa1606) from2 pseudomonas aeruginosa at 1.50 a resolution
99	c2kutA_	Alignment	not modelled	63.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
100	c3ogrA_	Alignment	not modelled	62.1	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: complex structure of beta-galactosidase from trichoderma reesei with2 galactose
101	c1xc6A_	Alignment	not modelled	62.0	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
102	c3qe5A_	Alignment	not modelled	60.5	14	PDB header: cell adhesion Chain: A: PDB Molecule: major cell-surface adhesin pac; PDBTitle: complete structure of streptococcus mutans antigen i/ii carboxy-2 terminus
103	d2dj4a1	Alignment	not modelled	60.1	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
104	d1vjja1	Alignment	not modelled	59.8	6	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
105	c2ds4A_	Alignment	not modelled	59.4	17	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
106	d1wlha1	Alignment	not modelled	58.3	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains

					Family: Filamin repeat (rod domain)
107	c3pmmA_	Alignment	not modelled	56.5	16 PDB header: hydrolase Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
108	c2zxcA_	Alignment	not modelled	54.5	11 PDB header: hydrolase Chain: A: PDB Molecule: neutral ceramidase; PDBTitle: seramidase complexed with c2
109	d2d7na1	Alignment	not modelled	54.3	13 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
110	d2diaa1	Alignment	not modelled	52.3	21 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
111	c2x5pA_	Alignment	not modelled	51.8	15 PDB header: protein binding Chain: A: PDB Molecule: fibronectin binding protein; PDBTitle: crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
112	c1f00I_	Alignment	not modelled	49.2	10 PDB header: cell adhesion Chain: I: PDB Molecule: intimin; PDBTitle: crystal structure of c-terminal 282-residue fragment of2 enteropathogenic e. coli intimin
113	c2di7A_	Alignment	not modelled	49.2	9 PDB header: structural protein Chain: A: PDB Molecule: bk158_1; PDBTitle: solution structure of the filamin domain from human bk158_12 protein
114	d1g4ma2	Alignment	not modelled	49.1	14 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
115	d2d7pa1	Alignment	not modelled	48.9	18 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
116	c2e6jA_	Alignment	not modelled	48.0	15 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hydin protein; PDBTitle: solution structure of the c-terminal papd-like domain from2 human hydin protein
117	d1ayra2	Alignment	not modelled	47.4	9 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
118	c2okmA_	Alignment	not modelled	46.1	11 PDB header: cell adhesion Chain: A: PDB Molecule: collagen adhesin; PDBTitle: crystal structure of ace19, the collagen binding subdomain2 of enterococcus faecalis surface protein ace
119	c2z1pA_	Alignment	not modelled	45.4	12 PDB header: cell adhesion Chain: A: PDB Molecule: collagen adhesin protein; PDBTitle: the enterococcus faecalis mscramm ace binds its ligands by2 the collagen hug model
120	c3n9tA_	Alignment	not modelled	45.0	14 PDB header: oxidoreductase Chain: A: PDB Molecule: pnpcc; PDBTitle: cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4