Phyre^2

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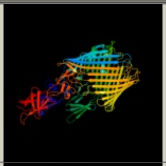
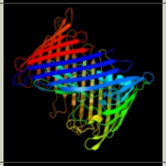
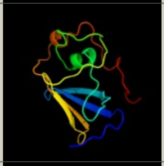
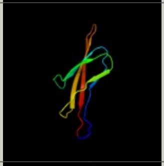
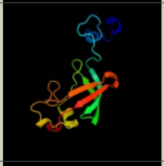
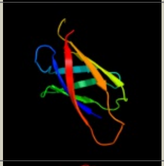
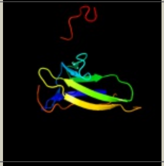
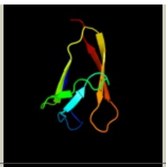
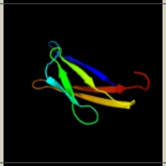
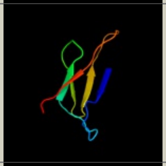
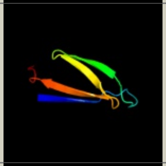
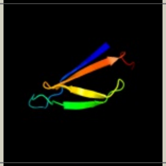
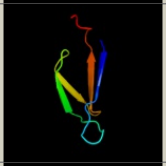
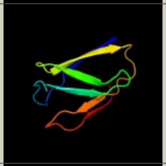
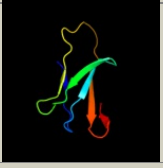
Description	P77802
Date	Thu Jan 5 12:32:57 GMT 2012
Unique Job ID	185dcf661c768f26

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfzB_	Alignment		100.0	12	**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	12	**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	15	**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	18	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
5	c3fcgB_	Alignment		99.8	18	**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
6	d3bwud1	Alignment		99.7	16	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
7	d1zdxa1	Alignment		99.7	19	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
8	c3l48B_	Alignment		99.4	16	**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		99.3	10	**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	c1uwyA_	Alignment		95.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
11	d1h8la1	Alignment		95.3	15	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain

12	d1uwya1	Alignment		94.8	21	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
13	c2nsmA_	Alignment		94.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
14	c1h8lA_	Alignment		94.6	15	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
15	c3mn8A_	Alignment		94.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
16	d2burb1	Alignment		91.8	43	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
17	d3pccm_	Alignment		91.5	27	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
18	c2azqA_	Alignment		89.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
19	c3n9tA_	Alignment		88.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pnpc; **PDBTitle:** cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
20	c3pdgA_	Alignment		87.6	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
21	c3hj8A_	Alignment	not modelled	87.0	30	**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
22	d1nkga1	Alignment	not modelled	87.0	15	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Rhamnogalacturonase B, RhgB, middle domain
23	d1s9aa_	Alignment	not modelled	86.8	25	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
24	c1tmxA_	Alignment	not modelled	86.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e
25	c3pe9B_	Alignment	not modelled	86.4	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
26	c3e8vA_	Alignment	not modelled	86.3	20	**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
27	c2xsuA_	Alignment	not modelled	86.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2 dioxygenase; **PDBTitle:** crystal structure of the a72g mutant of acinetobacter2 radioresistens catechol 1,2 dioxygenase
28	c2boyC_	Alignment	not modelled	82.0	26	**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
29	d1dmha_	Alignment	not modelled	80.6	32	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
30	c3pe9D_	Alignment	not modelled	80.2	15	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
31	c2vnvC_	Alignment	not modelled	71.4	14	**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
32	d3pcca_	Alignment	not modelled	64.3	23	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
33	d2q9oa2	Alignment	not modelled	62.1	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
34	c1d2pA_	Alignment	not modelled	55.4	15	**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
35	d1w0na_	Alignment	not modelled	55.2	15	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
36	c3pe9A_	Alignment	not modelled	52.1	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
37	c3pe9C_	Alignment	not modelled	52.1	14	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
38	d2bura1	Alignment	not modelled	51.8	20	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
39	d1kyaa2	Alignment	not modelled	49.8	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
40	d1hfua2	Alignment	not modelled	48.7	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
41	c2w87B_	Alignment	not modelled	44.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase d; **PDBTitle:** xyl-cbm35 in complex with glucuronic acid containing2 disaccharide.
42	d1aoza2	Alignment	not modelled	42.1	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
43	d1v10a2	Alignment	not modelled	41.8	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
44	d1cwva2	Alignment	not modelled	41.0	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
45	c2r32A_	Alignment	not modelled	40.0	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
46	d1cwva1	Alignment	not modelled	38.9	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
47	d1gyca2	Alignment	not modelled	36.9	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
48	d1edqa1	Alignment	not modelled	35.4	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
49	c3d33B_	Alignment	not modelled	32.9	13	**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
50	c2x5pA_	Alignment	not modelled	25.4	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
51	c3ottB_	Alignment	not modelled	24.6	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two-component system sensor histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative one2 component system bt4673 from b. thetaiotaomicron
52	c2crvA_	Alignment	not modelled	24.6	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
53	c3c12A_	Alignment	not modelled	21.7	18	**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
54	c3h9eA	Alignment	not modelled	21.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a;

54	c3b9eA_	Alignment	not modelled	21.5	13	**PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
55	c1bprA_	Alignment	not modelled	21.4	21	**PDB header:**molecular chaperone **Chain:** A: **PDB Molecule:**dnak; **PDBTitle:** nmr structure of the substrate binding domain of dnak,2 minimized average structure
56	c3uotB_	Alignment	not modelled	20.4	12	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
57	d1f00i1	Alignment	not modelled	20.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
58	c1u00A_	Alignment	not modelled	20.1	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
59	d1u00a2	Alignment	not modelled	19.6	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
60	c3osvC_	Alignment	not modelled	19.6	18	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**flagellar basal-body rod modification protein flgd; **PDBTitle:** the crytsal structure of flgd from p. aeruginosa
61	c3n8eA_	Alignment	not modelled	19.0	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stress-70 protein, mitochondrial; **PDBTitle:** substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
62	c3pddA_	Alignment	not modelled	18.2	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
63	c3dpqE_	Alignment	not modelled	16.3	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)
64	d1thqa_	Alignment	not modelled	15.9	6	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane enzyme PagP
65	d1cwva3	Alignment	not modelled	15.8	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
66	d1ulva2	Alignment	not modelled	15.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
67	d1o75a2	Alignment	not modelled	14.0	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains
68	d1d1na_	Alignment	not modelled	13.6	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
69	c1cwvA_	Alignment	not modelled	12.1	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**invasin; **PDBTitle:** crystal structure of invasin: a bacterial integrin-binding protein
70	c3dqgC_	Alignment	not modelled	11.4	16	**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.
71	d1yuwa1	Alignment	not modelled	11.3	17	**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
72	d1zata1	Alignment	not modelled	10.7	18	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
73	d2o14a1	Alignment	not modelled	10.1	40	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**YxiM N-terminal domain-like
74	d2i02a1	Alignment	not modelled	9.9	8	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
75	c2hklB_	Alignment	not modelled	9.5	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l,d-transpeptidase; **PDBTitle:** crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
76	c2qkiA_	Alignment	not modelled	9.1	11	**PDB header:**immune system/hydrolase inhibitor **Chain:** A: **PDB Molecule:**complement c3; **PDBTitle:** human c3c in complex with the inhibitor compstatin
77	c1motA_	Alignment	not modelled	9.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glycine receptor alpha-1 chain; **PDBTitle:** nmr structure of extended second transmembrane domain of2 glycine receptor alpha1 subunit in sds micelles
78	c2xr4A_	Alignment	not modelled	9.0	19	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
79	c2op6A_	Alignment	not modelled	8.9	21	**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
80	c1cvrA	Alignment	not modelled	8.6	12	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**gingipain r;

80	c1cvrA_	Alignment	not modelled	8.6	12	**PDBTitle:** crystal structure of the arg specific cysteine proteinase gingipain r2 (rgpb)
81	c2kppA_	Alignment	not modelled	8.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0431 protein; **PDBTitle:** solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
82	c2w3jA_	Alignment	not modelled	8.3	10	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**carbohydrate binding module; **PDBTitle:** structure of a family 35 carbohydrate binding module from2 an environmental isolate
83	d2je8a4	Alignment	not modelled	8.2	10	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
84	d1v8ha1	Alignment	not modelled	7.9	4	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
85	c3k1dA_	Alignment	not modelled	7.9	22	**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
86	c1ug9A_	Alignment	not modelled	7.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
87	c1vryA_	Alignment	not modelled	7.4	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glycine receptor alpha-1 chain; **PDBTitle:** second and third transmembrane domains of the alpha-12 subunit of human glycine receptor
88	d1yq2a3	Alignment	not modelled	7.4	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
89	d1c8ua1	Alignment	not modelled	7.4	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
90	d3btaa1	Alignment	not modelled	7.3	15	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Clostridium neurotoxins, the second last domain
91	c2nn6I_	Alignment	not modelled	7.2	12	**PDB header:**hydrolase/transferase **Chain:** I: **PDB Molecule:**3'-5' exoribonuclease csl4 homolog; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
92	d1dkza2	Alignment	not modelled	7.2	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
93	c3dnoC_	Alignment	not modelled	7.2	13	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**hiv-1 envelope glycoprotein gp120; **PDBTitle:** molecular structure for the hiv-1 gp120 trimer in the cd4-2 bound state
94	c3pvmB_	Alignment	not modelled	7.2	13	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cobra venom factor; **PDBTitle:** structure of complement c5 in complex with cvf
95	c2w1wB_	Alignment	not modelled	7.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipolytic enzyme, g-d-s-l; **PDBTitle:** native structure of a family 35 carbohydrate binding module2 from clostridium thermocellum
96	d1qbea_	Alignment	not modelled	6.8	12	**Fold:**RNA bacteriophage capsid protein **Superfamily:**RNA bacteriophage capsid protein **Family:**RNA bacteriophage capsid protein
97	c2xwxB_	Alignment	not modelled	6.8	11	**PDB header:**chitin-binding protein **Chain:** B: **PDB Molecule:**glcnac-binding protein a; **PDBTitle:** vibrio cholerae colonization factor gbpa crystal structure
98	c3kptA_	Alignment	not modelled	6.7	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**collagen adhesion protein; **PDBTitle:** crystal structure of bcpa, the major pilin subunit of2 bacillus cereus
99	d2vmha1	Alignment	not modelled	6.6	12	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**NPCBM-like