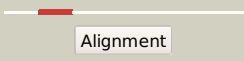
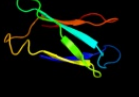
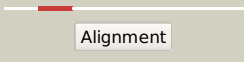

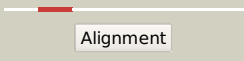

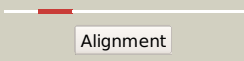

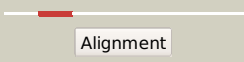

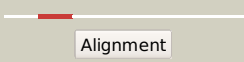

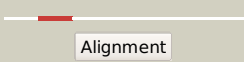

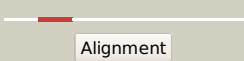

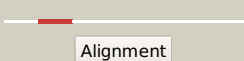

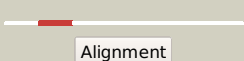
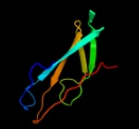
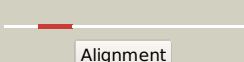



# Phyre2

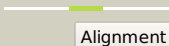
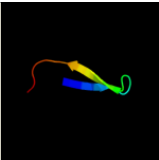
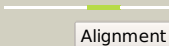

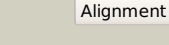
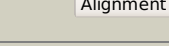
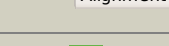


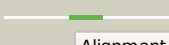



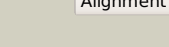
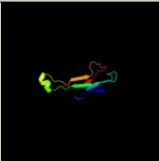


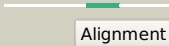
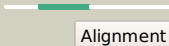
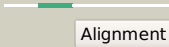

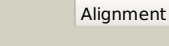
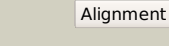
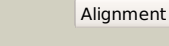
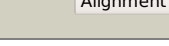
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Description	A2A699
Date	Wed Jul 10 14:20:28 BST 2013
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1h8lA_</a>	 Alignment		97.6	23	<b>PDB header:</b> carboxypeptidase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxypeptidase gp180 residues 503-882; <b>PDBTitle:</b> duck carboxypeptidase d domain ii in complex with gemsA
2	<a href="#">d1h8la1</a>	 Alignment		97.5	21	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Carboxypeptidase regulatory domain-like <b>Family:</b> Carboxypeptidase regulatory domain
3	<a href="#">c3mn8A_</a>	 Alignment		97.4	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lp15968p; <b>PDBTitle:</b> structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
4	<a href="#">c1uwvA_</a>	 Alignment		97.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxypeptidase m; <b>PDBTitle:</b> crystal structure of human carboxypeptidase m
5	<a href="#">c2nsmA_</a>	 Alignment		97.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxypeptidase n catalytic chain; <b>PDBTitle:</b> crystal structure of the human carboxypeptidase n (kinase i)2 catalytic domain
6	<a href="#">d1uwvA1</a>	 Alignment		96.8	25	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Carboxypeptidase regulatory domain-like <b>Family:</b> Carboxypeptidase regulatory domain
7	<a href="#">c3e8vA_</a>	 Alignment		96.5	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible transglutaminase-family protein; <b>PDBTitle:</b> crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis
8	<a href="#">d1cwva1</a>	 Alignment		96.0	28	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Invasin/intimin cell-adhesion fragments <b>Family:</b> Invasin/intimin cell-adhesion fragments
9	<a href="#">d1cwva2</a>	 Alignment		96.0	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Invasin/intimin cell-adhesion fragments <b>Family:</b> Invasin/intimin cell-adhesion fragments
10	<a href="#">d1f00i1</a>	 Alignment		95.7	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Invasin/intimin cell-adhesion fragments <b>Family:</b> Invasin/intimin cell-adhesion fragments
11	<a href="#">d1cwva3</a>	 Alignment		94.8	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Invasin/intimin cell-adhesion fragments <b>Family:</b> Invasin/intimin cell-adhesion fragments

12	<a href="#">c2ww8A_</a>	Alignment		94.6	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell wall surface anchor family protein; <b>PDBTitle:</b> structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
13	<a href="#">c2gpzC_</a>	Alignment		94.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> transthyretin-like protein; <b>PDBTitle:</b> transthyretin-like protein from salmonella dublin
14	<a href="#">c3qvaB_</a>	Alignment		93.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transthyretin-like protein; <b>PDBTitle:</b> structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
15	<a href="#">c1cwvA_</a>	Alignment		93.3	32	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> invasin; <b>PDBTitle:</b> crystal structure of invasin: a bacterial integrin-binding protein
16	<a href="#">c3kptA_</a>	Alignment		93.2	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> collagen adhesion protein; <b>PDBTitle:</b> crystal structure of bcpa, the major pilin subunit of2 bacillus cereus
17	<a href="#">c4ilvB_</a>	Alignment		92.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> intradiol ring-cleavage dioxygenase; <b>PDBTitle:</b> structure of the dioxygenase domain of sacte_2871, a novel dioxygenase2 carbohydrate-binding protein fusion from the cellulolytic bacterium3 streptomyces sp. sirexaa-e
18	<a href="#">d1ttaa_</a>	Alignment		92.2	27	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
19	<a href="#">d1f86a_</a>	Alignment		92.0	27	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
20	<a href="#">d3pccm_</a>	Alignment		92.0	25	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
21	<a href="#">d1oo2a_</a>	Alignment	not modelled	91.9	27	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
22	<a href="#">d1kgia_</a>	Alignment	not modelled	91.9	30	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
23	<a href="#">d1tfpa_</a>	Alignment	not modelled	91.5	32	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
24	<a href="#">c3hj8A_</a>	Alignment	not modelled	91.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
25	<a href="#">c2xsuA_</a>	Alignment	not modelled	90.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 1,2 dioxygenase; <b>PDBTitle:</b> crystal structure of the a72g mutant of acinetobacter2 radioresistens catechol 1,2 dioxygenase
26	<a href="#">c2yewl_</a>	Alignment		90.2	34	<b>PDB header:</b> virus <b>Chain:</b> I: <b>PDB Molecule:</b> e2 envelope glycoprotein; <b>PDBTitle:</b> modeling barmah forest virus structural proteins
27	<a href="#">c2boyC_</a>	Alignment	not modelled	90.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-chlorocatechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp

28	<a href="#">c2h0eA_</a>	Alignment	not modelled	90.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> transthyretin-like protein pucm; <b>PDBTitle:</b> crystal structure of pucm in the absence of substrate
29	<a href="#">c2h1xB_</a>	Alignment	not modelled	89.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-hydroxyisourate hydrolase (formerly known as <b>PDBTitle:</b> crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
30	<a href="#">d2burb1</a>	Alignment	not modelled	89.2	21	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
31	<a href="#">c3n9tA_</a>	Alignment	not modelled	89.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pnpq; <b>PDBTitle:</b> cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
32	<a href="#">d1nkgal</a>	Alignment	not modelled	88.8	10	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Rhamnogalacturonase B, RhgB, middle domain
33	<a href="#">c3th1C_</a>	Alignment	not modelled	88.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> chlorocatechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of chlorocatechol 1,2-dioxygenase from pseudomonas2 putida
34	<a href="#">c2x5pA_</a>	Alignment	not modelled	87.8	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fibronectin binding protein; <b>PDBTitle:</b> crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
35	<a href="#">d1s9aa_</a>	Alignment	not modelled	87.7	18	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
36	<a href="#">c2azqA_</a>	Alignment	not modelled	87.2	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
37	<a href="#">c2xicB_</a>	Alignment	not modelled	87.1	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> ancillary protein 1; <b>PDBTitle:</b> pilus-presented adhesin, spy0125 (cpa), p212121 form (esrf data)
38	<a href="#">d2bura1</a>	Alignment	not modelled	87.1	19	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
39	<a href="#">d2b59b2</a>	Alignment	not modelled	87.0	22	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Carboxypeptidase regulatory domain-like <b>Family:</b> Pre-dockerin domain
40	<a href="#">c1tmxA_</a>	Alignment	not modelled	86.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyquinol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e
41	<a href="#">d1dmha_</a>	Alignment	not modelled	84.8	20	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
42	<a href="#">c3j2wS_</a>	Alignment	not modelled	84.6	21	<b>PDB header:</b> virus <b>Chain:</b> S: <b>PDB Molecule:</b> glycoprotein e2; <b>PDBTitle:</b> electron cryo-microscopy of chikungunya virus
43	<a href="#">c4jdzA_</a>	Alignment	not modelled	83.5	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> ser-asp rich fibrinogen/bone sialoprotein-binding protein <b>PDBTitle:</b> structures of sdrd from staphylococcus aureus reveal the molecular2 mechanism of how the cell surface receptors recognize their ligands
44	<a href="#">c3irpX_</a>	Alignment	not modelled	82.7	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> X: <b>PDB Molecule:</b> uro-adherence factor a; <b>PDBTitle:</b> crystal structure of functional region of uafa from staphylococcus2 saprophyticus at 1.50 angstrom resolution
45	<a href="#">c2qkiA_</a>	Alignment	not modelled	80.8	22	<b>PDB header:</b> immune system/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> complement c3; <b>PDBTitle:</b> human c3c in complex with the inhibitor compstatin
46	<a href="#">d3pcca_</a>	Alignment	not modelled	80.3	23	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
47	<a href="#">c2pz4A_</a>	Alignment	not modelled	79.6	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> protein gbs052; <b>PDBTitle:</b> crystal structure of spab (gbs52), the minor pilin in gram-positive2 pathogen streptococcus agalactiae
48	<a href="#">c3j0fK_</a>	Alignment	not modelled	77.9	24	<b>PDB header:</b> virus <b>Chain:</b> K: <b>PDB Molecule:</b> e2 envelope glycoprotein; <b>PDBTitle:</b> sindbis virion
49	<a href="#">c2zyiB_</a>	Alignment	not modelled	76.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase, putative; <b>PDBTitle:</b> a. fulgidus lipase with fatty acid fragment and calcium
50	<a href="#">c2kluA_</a>	Alignment		76.1	27	<b>PDB header:</b> immune system, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
51	<a href="#">d1xkea1</a>	Alignment		69.8	30	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Ran-binding domain

52	<a href="#">d2crfa1</a>	 Alignment		66.4	40	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Ran-binding domain
53	<a href="#">c2m20B_</a>	 Alignment	not modelled	64.1	31	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
54	<a href="#">d1qc6a_</a>	 Alignment	not modelled	62.9	25	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
55	<a href="#">c1afoB_</a>	 Alignment	not modelled	62.8	38	<b>PDB header:</b> integral membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycophorin a; <b>PDBTitle:</b> dimeric transmembrane domain of human glycophorin a, nmr, 2 20 structures
56	<a href="#">c1f00I_</a>	 Alignment	not modelled	62.4	22	<b>PDB header:</b> cell adhesion <b>Chain:</b> I: <b>PDB Molecule:</b> intimin; <b>PDBTitle:</b> crystal structure of c-terminal 282-residue fragment of 2 enteropathogenic e. coli intimin
57	<a href="#">c3uxfA_</a>	 Alignment	not modelled	61.0	23	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> fimbrial subunit type 1; <b>PDBTitle:</b> structure of the fimbrial protein fimp from actinomyces oris
58	<a href="#">c3m1iB_</a>	 Alignment	not modelled	59.5	35	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ran-specific gtpase-activating protein 1; <b>PDBTitle:</b> crystal structure of yeast crm1 (xpo1p) in complex with yeast ranbp12 (yrb1p) and yeast rangtp (gsp1pgtp)
59	<a href="#">c3pvmB_</a>	 Alignment	not modelled	59.0	26	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> structure of complement c5 in complex with cvf
60	<a href="#">d1rrpb_</a>	 Alignment	not modelled	56.9	35	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Ran-binding domain
61	<a href="#">c4I6eA_</a>	 Alignment	not modelled	55.9	30	<b>PDB header:</b> ligase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 sumo-protein ligase ranbp2; <b>PDBTitle:</b> crystal structure of the ranbd1 fourth domain of e3 sumo-protein2 ligase ranbp2. northeast structural genomics consortium (nesg) target3 hr9193b
62	<a href="#">c2xetB_</a>	 Alignment	not modelled	55.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> f1 capsule-anchoring protein; <b>PDBTitle:</b> conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
63	<a href="#">c4gptB_</a>	 Alignment	not modelled	54.3	35	<b>PDB header:</b> protein transport/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> ran-specific gtpase-activating protein 1; <b>PDBTitle:</b> crystal structure of kpt251 in complex with crm1-ran-ranbp1
64	<a href="#">c3ud2C_</a>	 Alignment		51.1	24	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> ankyrin-1; <b>PDBTitle:</b> crystal structure of selenomethionine zu5a-zu5b protein domains of 2 human erythrocyte ankyrin
65	<a href="#">c4e9Ia_</a>	 Alignment	not modelled	47.9	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> attaching and effacing protein, pathogenesis factor; <b>PDBTitle:</b> fdec, a novel broadly conserved escherichia coli adhesin eliciting 2 protection against urinary tract infections
66	<a href="#">c2kncA_</a>	 Alignment	not modelled	46.4	26	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic 2 heterocomplex
67	<a href="#">c2k1aA_</a>	 Alignment	not modelled	45.0	30	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iiB) transmembrane segment
68	<a href="#">c3gm8A_</a>	 Alignment	not modelled	43.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 2, candidate beta-glycosidase; <b>PDBTitle:</b> crystal structure of a beta-glycosidase from bacteroides vulgatus
69	<a href="#">c3hrzA_</a>	 Alignment	not modelled	42.0	23	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> cobra venom factor (cvf) in complex with human factor b
70	<a href="#">c3cmgA_</a>	 Alignment	not modelled	37.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative beta-galactosidase; <b>PDBTitle:</b> crystal structure of putative beta-galactosidase from bacteroides 2 fragilis
71	<a href="#">c1m57H_</a>	 Alignment	not modelled	36.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter 2 sphaeroides (eq(i-286) mutant)
72	<a href="#">c2yiuE_</a>	 Alignment	not modelled	35.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome c1, heme protein; <b>PDBTitle:</b> x-ray structure of the dimeric cytochrome bc1 complex from 2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
73	<a href="#">d1jb0I_</a>	 Alignment	not modelled	32.7	32	<b>Fold:</b> Photosystem I reaction center subunit XI, PsaL <b>Superfamily:</b> Photosystem I reaction center subunit XI, PsaL <b>Family:</b> Photosystem I reaction center subunit XI, PsaL
74	<a href="#">c4b8cH_</a>	 Alignment	not modelled	30.9	9	<b>PDB header:</b> hydrolase/cell cycle <b>Chain:</b> H: <b>PDB Molecule:</b> general negative regulator of transcription subunit 1; <b>PDBTitle:</b> nuclease module of the yeast ccr4-not complex

75	<a href="#">c3waiA_</a>	Alignment	not modelled	30.6	20	<b>PDB header:</b> transferase, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, transmembrane <b>PDBTitle:</b> crystal structure of the c-terminal globular domain of 2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
76	<a href="#">c3uafA_</a>	Alignment	not modelled	29.5	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ttr-52; <b>PDBTitle:</b> crystal structure of a ttr-52 mutant of c. elegans
77	<a href="#">d1g6xa_</a>	Alignment	not modelled	29.2	23	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
78	<a href="#">d3dtub2</a>	Alignment	not modelled	29.1	17	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
79	<a href="#">c4a02A_</a>	Alignment	not modelled	29.0	14	<b>PDB header:</b> chitin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin binding protein; <b>PDBTitle:</b> x-ray crystallographic structure of efcbm33a
80	<a href="#">d1dema_</a>	Alignment	not modelled	28.4	29	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
81	<a href="#">c2jp2A_</a>	Alignment	not modelled	28.2	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sprouty-related, evh1 domain-containing protein <b>PDBTitle:</b> solution structure and resonance assignment of the n-2 terminal evh1 domain from the human spred2 protein3 (sprouty-related protein with evh1 domain isoform 2)
82	<a href="#">c2b59B_</a>	Alignment	not modelled	28.2	23	<b>PDB header:</b> hydrolase/structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> cellulosomal scaffolding protein a; <b>PDBTitle:</b> the type ii cohesin dockerin complex
83	<a href="#">c4acqC_</a>	Alignment	not modelled	27.6	13	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> alpha-2-macroglobulin; <b>PDBTitle:</b> alpha-2 macroglobulin
84	<a href="#">d1xoda1</a>	Alignment	not modelled	27.5	29	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
85	<a href="#">c3fn9B_</a>	Alignment	not modelled	27.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative beta-galactosidase; <b>PDBTitle:</b> crystal structure of putative beta-galactosidase from bacteroides2 fragilis
86	<a href="#">d1i2ha_</a>	Alignment	not modelled	26.1	19	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
87	<a href="#">d1dtxa_</a>	Alignment	not modelled	26.1	29	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
88	<a href="#">d1uuba_</a>	Alignment	not modelled	25.6	23	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
89	<a href="#">c2odyF_</a>	Alignment	not modelled	25.5	31	<b>PDB header:</b> blood clotting/blood clotting inhibitor <b>Chain:</b> F: <b>PDB Molecule:</b> boophilin; <b>PDBTitle:</b> thrombin-bound boophilin displays a functional and accessible2 reactive-site loop
90	<a href="#">d1bika1</a>	Alignment	not modelled	25.2	7	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
91	<a href="#">d1bpia_</a>	Alignment	not modelled	25.2	23	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
92	<a href="#">d1brbi_</a>	Alignment	not modelled	24.7	23	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
93	<a href="#">d1ejmb_</a>	Alignment	not modelled	24.6	23	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
94	<a href="#">c2q8iB_</a>	Alignment	not modelled	24.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase component of <b>PDBTitle:</b> pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
95	<a href="#">d1p2ji_</a>	Alignment	not modelled	23.6	21	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
96	<a href="#">c2pn5A_</a>	Alignment	not modelled	23.5	17	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> thioester-containing protein i; <b>PDBTitle:</b> crystal structure of tep1r
97	<a href="#">c2l8sA_</a>	Alignment	not modelled	23.5	33	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of 2 integrin alpha1 in detergent micelles
98	<a href="#">d1egxa_</a>	Alignment	not modelled	23.4	10	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
99	<a href="#">c1z8yN_</a>	Alignment	not modelled	23.3	23	<b>PDB header:</b> virus <b>Chain:</b> N: <b>PDB Molecule:</b> spike glycoprotein e2; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
100	<a href="#">c1z8yj_</a>	Alignment	not modelled	23.3	23	<b>PDB header:</b> virus <b>Chain:</b> J: <b>PDB Molecule:</b> spike glycoprotein e2; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses

101	<a href="#">c1z8yP_</a>	Alignment	not modelled	23.3	23	<b>PDB header:</b> virus <b>Chain:</b> P: <b>PDB Molecule:</b> spike glycoprotein e2; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
102	<a href="#">c1z8yL_</a>	Alignment	not modelled	23.3	23	<b>PDB header:</b> virus <b>Chain:</b> L: <b>PDB Molecule:</b> spike glycoprotein e2; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
103	<a href="#">d1irha_</a>	Alignment	not modelled	22.3	8	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
104	<a href="#">c2k1iA_</a>	Alignment	not modelled	22.2	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> mucosal alpha-defensin; <b>PDBTitle:</b> synthesis, structure and activities of an oral mucosal alpha-defensin2 from rhesus macaque
105	<a href="#">c3cwbQ_</a>	Alignment	not modelled	21.5	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> mitochondrial cytochrome c1, heme protein; <b>PDBTitle:</b> chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
106	<a href="#">c3kioB_</a>	Alignment	not modelled	21.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease h2 subunit b; <b>PDBTitle:</b> mouse rnase h2 complex
107	<a href="#">c1nt9G_</a>	Alignment	not modelled	21.3	17	<b>PDB header:</b> transcription, transferase <b>Chain:</b> G: <b>PDB Molecule:</b> dna-directed rna polymerase ii 19 kd polypeptide; <b>PDBTitle:</b> complete 12-subunit rna polymerase ii
108	<a href="#">c1yc0I_</a>	Alignment	not modelled	20.7	36	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> I: <b>PDB Molecule:</b> kunitz-type protease inhibitor 1; <b>PDBTitle:</b> short form hgfa with first kunitz domain from hai-1
109	<a href="#">d1tfxc_</a>	Alignment	not modelled	20.4	7	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Small Kunitz-type inhibitors & BPTI-like toxins
110	<a href="#">c3uamD_</a>	Alignment	not modelled	20.2	29	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> chitin binding domain; <b>PDBTitle:</b> crystal structure of a chitin binding domain from burkholderia2 pseudomallei