








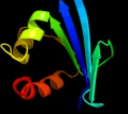






















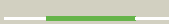




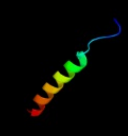








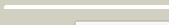


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlikta_</a>	 Alignment		98.8	15	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Sterol carrier protein, SCP
2	<a href="#">c3bn8A_</a>	 Alignment		98.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sterol carrier protein 2; <b>PDBTitle:</b> crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
3	<a href="#">c3bdqB_</a>	 Alignment		98.8	16	<b>PDB header:</b> lipid transport <b>Chain:</b> B: <b>PDB Molecule:</b> sterol carrier protein 2-like 2; <b>PDBTitle:</b> room temperture crystal structure of sterol carrier protein-2 2 like-2
4	<a href="#">d1c44a_</a>	 Alignment		98.6	16	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Sterol carrier protein, SCP
5	<a href="#">d1pz4a_</a>	 Alignment		98.4	10	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Sterol carrier protein, SCP
6	<a href="#">d2cfua1</a>	 Alignment		98.4	15	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Alkylsulfatase C-terminal domain-like
7	<a href="#">c3bkrA_</a>	 Alignment		98.2	18	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sterol carrier protein-2 like-3; <b>PDBTitle:</b> crystal structure of sterol carrier protein-2 like-3 (scp2-2 l3) from aedes aegypti
8	<a href="#">d1wfra_</a>	 Alignment		97.9	19	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Sterol carrier protein, SCP
9	<a href="#">c2cfuA_</a>	 Alignment		97.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sdsa1; <b>PDBTitle:</b> crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
10	<a href="#">d2i00a1</a>	 Alignment		92.7	13	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> EF1021 C-terminal domain-like
11	<a href="#">d2hv2a1</a>	 Alignment		91.2	16	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> EF1021 C-terminal domain-like

12	<a href="#">c2i00D_</a>	 Alignment		86.3	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
13	<a href="#">c2wukD_</a>	 Alignment		66.9	22	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> septum site-determining protein diviva; <b>PDBTitle:</b> diviva n-terminal domain, f17a mutant
14	<a href="#">d2ozga1</a>	 Alignment		61.2	18	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> EF1021 C-terminal domain-like
15	<a href="#">c1aq5C_</a>	 Alignment		58.4	35	<b>PDB header:</b> coiled-coil <b>Chain:</b> C: <b>PDB Molecule:</b> cartilage matrix protein; <b>PDBTitle:</b> high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
16	<a href="#">c1m1jA_</a>	 Alignment		56.1	15	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> fibrinogen alpha subunit; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen with two different2 bound ligands
17	<a href="#">c2hv2D_</a>	 Alignment		56.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function from2 enterococcus faecalis v583 at 2.4 a resolution, probable n-3 acyltransferase
18	<a href="#">c2xdjF_</a>	 Alignment		54.5	3	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein ybgf; <b>PDBTitle:</b> crystal structure of the n-terminal domain of e.coli ybgf
19	<a href="#">c1t3jA_</a>	 Alignment		51.2	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitofusin 1; <b>PDBTitle:</b> mitofusin domain hr2 v686nm/i 708m mutant
20	<a href="#">c1go4F_</a>	 Alignment		46.3	15	<b>PDB header:</b> cell cycle <b>Chain:</b> F: <b>PDB Molecule:</b> mad1 (mitotic arrest deficient)-like 1; <b>PDBTitle:</b> crystal structure of mad1-mad2 reveals a conserved mad22 binding motif in mad1 and cdc20.
21	<a href="#">c1dipA_</a>	 Alignment	not modelled	43.4	24	<b>PDB header:</b> acetylation <b>Chain:</b> A: <b>PDB Molecule:</b> delta-sleep-inducing peptide immunoreactive <b>PDBTitle:</b> the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
22	<a href="#">c2pnvA_</a>	 Alignment	not modelled	42.7	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> small conductance calcium-activated potassium <b>PDBTitle:</b> crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
23	<a href="#">c2yy0D_</a>	 Alignment	not modelled	38.9	27	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> c-myc-binding protein; <b>PDBTitle:</b> crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
24	<a href="#">c1m7lA_</a>	 Alignment	not modelled	35.7	29	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pulmonary surfactant-associated protein d; <b>PDBTitle:</b> solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d
25	<a href="#">c3n7zD_</a>	 Alignment	not modelled	34.3	8	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> crystal structure of acetyltransferase from bacillus anthracis
26	<a href="#">c2akfC_</a>	 Alignment	not modelled	34.0	29	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
27	<a href="#">c2akfA_</a>	 Alignment	not modelled	34.0	29	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
						<b>PDB header:</b> protein binding

28	<a href="#">c2akfB_</a>	Alignment	not modelled	34.0	29	<b>Chain:</b> B: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
29	<a href="#">c3igtA_</a>	Alignment	not modelled	29.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> signal transduction histidine-protein kinase bara; <b>PDBTitle:</b> structure of the hpt domain of sensor protein bara from escherichia2 coli cft073.
30	<a href="#">c1coiA_</a>	Alignment	not modelled	25.3	43	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> A: <b>PDB Molecule:</b> coil-vald; <b>PDBTitle:</b> designed trimeric coiled coil-vald
31	<a href="#">c3rylB_</a>	Alignment	not modelled	25.2	13	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> protein vpa1370; <b>PDBTitle:</b> dimerization domain of vibrio parahemolyticus vopl
32	<a href="#">c2ozgA_</a>	Alignment	not modelled	24.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of gcn5-related n-acetyltransferase (yp_325469.1)2 from anabaena variabilis atcc 29413 at 2.00 a resolution
33	<a href="#">c3qh9A_</a>	Alignment	not modelled	24.0	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> liprin-beta-2; <b>PDBTitle:</b> human liprin-beta2 coiled-coil
34	<a href="#">d1rf8b_</a>	Alignment	not modelled	23.1	13	<b>Fold:</b> Eukaryotic initiation factor 4f subunit eIF4g, eIF4e-binding domain <b>Superfamily:</b> Eukaryotic initiation factor 4f subunit eIF4g, eIF4e-binding domain <b>Family:</b> Eukaryotic initiation factor 4f subunit eIF4g, eIF4e-binding domain
35	<a href="#">c3ghgD_</a>	Alignment	not modelled	21.7	9	<b>PDB header:</b> blood clotting <b>Chain:</b> D: <b>PDB Molecule:</b> fibrinogen alpha chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
36	<a href="#">c1lq0A_</a>	Alignment	not modelled	19.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitotriosidase; <b>PDBTitle:</b> crystal structure of human chitotriosidase at 2.2 angstrom2 resolution
37	<a href="#">c3gw6F_</a>	Alignment	not modelled	18.2	31	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> endo-n-acetylneuraminidase; <b>PDBTitle:</b> intramolecular chaperone
38	<a href="#">d1wb0a1</a>	Alignment	not modelled	15.0	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Type II chitinase
39	<a href="#">c3r1kA_</a>	Alignment	not modelled	15.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> enhanced intracellular survival protein; <b>PDBTitle:</b> crystal structure of acetyltransferase eis from mycobacterium2 tuberculosis h37rv in complex with coa and an acetamide moiety
40	<a href="#">c1ci6B_</a>	Alignment	not modelled	14.9	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor c/ebp beta; <b>PDBTitle:</b> transcription factor atf4-c/ebp beta bzip heterodimer
41	<a href="#">c3ojaB_</a>	Alignment	not modelled	14.6	10	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of Irim1/apl1c complex
42	<a href="#">c3p8cD_</a>	Alignment	not modelled	14.5	19	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> wiskott-aldrich syndrome protein family member 1; <b>PDBTitle:</b> structure and control of the actin regulatory wave complex
43	<a href="#">c1hf9B_</a>	Alignment	not modelled	13.8	17	<b>PDB header:</b> atpase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> atpase inhibitor (mitochondrial); <b>PDBTitle:</b> c-terminal coiled-coil domain from bovine if1
44	<a href="#">c1gk7A_</a>	Alignment	not modelled	13.6	24	<b>PDB header:</b> vimentin <b>Chain:</b> A: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> human vimentin coil 1a fragment (1a)
45	<a href="#">c1kddC_</a>	Alignment	not modelled	13.3	25	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16i; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
46	<a href="#">c1kddF_</a>	Alignment	not modelled	13.0	25	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16i; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
47	<a href="#">c1kddA_</a>	Alignment	not modelled	13.0	25	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16i; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
48	<a href="#">c2o1mB_</a>	Alignment	not modelled	12.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable amino-acid abc transporter <b>PDBTitle:</b> crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytnk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
49	<a href="#">c3ctwB_</a>	Alignment	not modelled	12.7	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rcda; <b>PDBTitle:</b> crystal structure of rcda from caulobacter crescentus cb15
50	<a href="#">d1bgfa_</a>	Alignment	not modelled	12.6	7	<b>Fold:</b> Transcription factor STAT-4 N-domain <b>Superfamily:</b> Transcription factor STAT-4 N-domain <b>Family:</b> Transcription factor STAT-4 N-domain
51	<a href="#">c1u0iA_</a>	Alignment	not modelled	12.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> iaal-e3; <b>PDBTitle:</b> iaal-e3/k3 heterodimer
52	<a href="#">c1wh0A_</a>	Alignment	not modelled	12.5	10	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> chitotriosidase 1;

52	<a href="#">c1w0vA_</a>	Alignment	not modelled	12.9	10	<b>PDBTitle:</b> specificity and affinity of natural product cyclopentapeptide2 inhibitor argifin against human chitinase
53	<a href="#">c3he4A_</a>	Alignment	not modelled	11.6	30	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> synzip6; <b>PDBTitle:</b> heterospecific coiled-coil pair synzip5:synzip6
54	<a href="#">d1rp3a2</a>	Alignment	not modelled	11.2	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
55	<a href="#">d1sxje1</a>	Alignment	not modelled	11.1	14	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
56	<a href="#">c3fxyA_</a>	Alignment	not modelled	10.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acidic mammalian chitinase; <b>PDBTitle:</b> acidic mammalian chitinase, catalytic domain
57	<a href="#">c2dt7A_</a>	Alignment	not modelled	10.1	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> splicing factor 3a subunit 3; <b>PDBTitle:</b> solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
58	<a href="#">d1vf8a1</a>	Alignment	not modelled	9.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Type II chitinase
59	<a href="#">d1kfta_</a>	Alignment	not modelled	9.5	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Excinuclease UvrC C-terminal domain
60	<a href="#">c1kftA_</a>	Alignment	not modelled	9.5	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit c; <b>PDBTitle:</b> solution structure of the c-terminal domain of uvrC from e-2 coli
61	<a href="#">c3iynR_</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> virus <b>Chain:</b> R: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
62	<a href="#">c1kd9C_</a>	Alignment	not modelled	8.2	25	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16l; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
63	<a href="#">c1kd9A_</a>	Alignment	not modelled	8.2	25	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16l; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
64	<a href="#">c1kd9F_</a>	Alignment	not modelled	8.2	25	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12la16l; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
65	<a href="#">d1ivsa1</a>	Alignment	not modelled	7.9	19	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Valyl-tRNA synthetase (ValRS) C-terminal domain
66	<a href="#">d1st6a3</a>	Alignment	not modelled	7.8	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
67	<a href="#">c3myfB_</a>	Alignment	not modelled	7.7	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of the hpt domain from the hpt sensor hybrid2 histidine kinase from shewanella to 1.80a
68	<a href="#">c2l5gB_</a>	Alignment	not modelled	7.1	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ncor2; <b>PDBTitle:</b> co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
69	<a href="#">c3t97B_</a>	Alignment	not modelled	6.8	6	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54
70	<a href="#">c2lqxA_</a>	Alignment	not modelled	6.5	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> fermitin family homolog 2; <b>PDBTitle:</b> nmr structure for kindle-2 n-terminus
71	<a href="#">c1jekA_</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> env polyprotein; <b>PDBTitle:</b> visna tm core structure
72	<a href="#">c1kd8F_</a>	Alignment	not modelled	6.4	29	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12ia16v; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
73	<a href="#">c1kd8A_</a>	Alignment	not modelled	6.4	29	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12ia16v; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
74	<a href="#">c1kd8C_</a>	Alignment	not modelled	6.4	29	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4 acid base heterodimer acid-d12ia16v; <b>PDBTitle:</b> x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
75	<a href="#">c3a7pB_</a>	Alignment	not modelled	6.3	8	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg16
76	<a href="#">c3hugA_</a>	Alignment	not modelled	5.9	6	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl

77	<a href="#">c3ljmB_</a>	Alignment	not modelled	5.5	41	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> structure of de novo designed apo peptide coil ser I9c
78	<a href="#">c2jgoC_</a>	Alignment	not modelled	5.5	41	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> stucture of the arsenated de novo designed peptide coil ser2 I9c
79	<a href="#">c1cosB_</a>	Alignment	not modelled	5.4	41	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> B: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
80	<a href="#">c1e9IA_</a>	Alignment	not modelled	5.3	10	<b>PDB header:</b> macrophage secretory protein <b>Chain:</b> A: <b>PDB Molecule:</b> ym1 secretory protein; <b>PDBTitle:</b> the crystal structure of novel mammalian lectin ym12 suggests a saccharide binding site
81	<a href="#">c2jgoB_</a>	Alignment	not modelled	5.3	39	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> stucture of the arsenated de novo designed peptide coil ser2 I9c
82	<a href="#">c3ljmC_</a>	Alignment	not modelled	5.3	39	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> structure of de novo designed apo peptide coil ser I9c
83	<a href="#">c3ljmA_</a>	Alignment	not modelled	5.3	39	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> structure of de novo designed apo peptide coil ser I9c
84	<a href="#">c2jgoA_</a>	Alignment	not modelled	5.3	39	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser I9c; <b>PDBTitle:</b> stucture of the arsenated de novo designed peptide coil ser2 I9c
85	<a href="#">c1u2uA_</a>	Alignment	not modelled	5.3	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> nmr solution structure of a designed heterodimeric leucine2 zipper
86	<a href="#">d1ii5a_</a>	Alignment	not modelled	5.2	9	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
87	<a href="#">c1cosA_</a>	Alignment	not modelled	5.2	39	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> A: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
88	<a href="#">c1cosC_</a>	Alignment	not modelled	5.2	39	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> C: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
89	<a href="#">d1u00a1</a>	Alignment	not modelled	5.2	11	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain <b>Family:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain
90	<a href="#">c2xzfA_</a>	Alignment	not modelled	5.1	8	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-binding protein eibd; <b>PDBTitle:</b> escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
91	<a href="#">d2hvma_</a>	Alignment	not modelled	5.1	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Type II chitinase