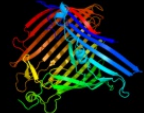
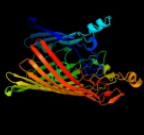
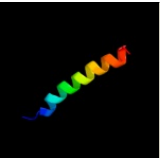
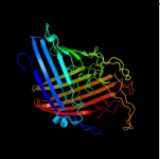
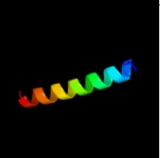
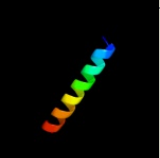
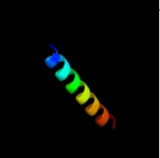
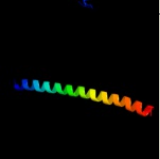
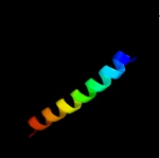
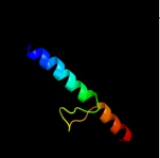


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1af6a_	 Alignment		100.0	28	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
2	d2mpa_	 Alignment		100.0	26	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
3	d1a0tp_	 Alignment		100.0	22	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
4	d2zfga1	 Alignment		94.5	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
5	c3qra_	 Alignment		93.7	16	PDB header: cell invasion Chain: A: PDB Molecule: attachment invasion locus protein; PDBTitle: the crystal structure of ail, the attachment invasion locus protein of <i>Yersinia pestis</i>
6	d1qj8a_	 Alignment		91.4	7	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
7	d1phoa_	 Alignment		90.5	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
8	c2k0IA_	 Alignment		88.2	10	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein a; PDBTitle: nmr structure of the transmembrane domain of the outer2 membrane protein a from <i>Klebsiella pneumoniae</i> in dhpc3 micelles.
9	d1g90a_	 Alignment		85.0	9	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
10	c1cosB_	 Alignment		81.1	24	PDB header: alpha-helical bundle Chain: B: PDB Molecule: coiled serine; PDBTitle: crystal structure of a synthetic triple-stranded alpha-2 helical bundle
11	c1cosA_	 Alignment		81.1	24	PDB header: alpha-helical bundle Chain: A: PDB Molecule: coiled serine; PDBTitle: crystal structure of a synthetic triple-stranded alpha-2 helical bundle

12	c1cosC_	Alignment		80.7	24	PDB header: alpha-helical bundle Chain: C: PDB Molecule: coiled serine; PDBTitle: crystal structure of a synthetic triple-stranded alpha-2 helical bundle
13	c3nsgA_	Alignment		79.9	13	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
14	c2x6pC_	Alignment		76.8	24	PDB header: de novo protein Chain: C: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c
15	c2x6pA_	Alignment		76.8	24	PDB header: de novo protein Chain: A: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c
16	c2x6pB_	Alignment		76.8	24	PDB header: de novo protein Chain: B: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c
17	c3n4xB_	Alignment		76.2	15	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
18	c3mkxC_	Alignment		74.4	9	PDB header: antiviral protein Chain: C: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: crystal structure of bst2/tetherin
19	c1zxaB_	Alignment		73.0	37	PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 1, alpha isozyme; PDBTitle: solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
20	c1aq5C_	Alignment		72.6	29	PDB header: coiled-coil Chain: C: PDB Molecule: cartilage matrix protein; PDBTitle: high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
21	c3u1aC_	Alignment	not modelled	66.1	15	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
22	c2a3dA_	Alignment	not modelled	65.9	32	PDB header: three-helix bundle Chain: A: PDB Molecule: protein (de novo three-helix bundle); PDBTitle: solution structure of a de novo designed single chain three-2 helix bundle (a3d)
23	c1y4cA_	Alignment	not modelled	63.7	10	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
24	c2x7aB_	Alignment	not modelled	63.3	9	PDB header: immune system Chain: B: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
25	c3m9bK_	Alignment	not modelled	60.5	11	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
26	c2xzrA_	Alignment	not modelled	59.8	10	PDB header: cell adhesion Chain: A: PDB Molecule: immunoglobulin-binding protein eibd; PDBTitle: escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
27	c3cveC_	Alignment	not modelled	59.3	16	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
28	c2jgoB_	Alignment	not modelled	58.8	20	PDB header: de novo protein Chain: B: PDB Molecule: coil ser l9c; PDBTitle: stucture of the arsenated de novo designed peptide coil ser2 l9c

29	c3ljmA	Alignment	not modelled	58.8	20	PDB header: de novo protein Chain: A: PDB Molecule: coil ser 19c; PDBTitle: structure of de novo designed apo peptide coil ser 19c
30	c2jgoC	Alignment	not modelled	58.8	20	PDB header: de novo protein Chain: C: PDB Molecule: coil ser 19c; PDBTitle: stucture of the arsenated de novo designed peptide coil ser2 19c
31	c3ljmB	Alignment	not modelled	58.8	20	PDB header: de novo protein Chain: B: PDB Molecule: coil ser 19c; PDBTitle: structure of de novo designed apo peptide coil ser 19c
32	c3ljmC	Alignment	not modelled	58.8	20	PDB header: de novo protein Chain: C: PDB Molecule: coil ser 19c; PDBTitle: structure of de novo designed apo peptide coil ser 19c
33	c2jgoA	Alignment	not modelled	58.8	20	PDB header: de novo protein Chain: A: PDB Molecule: coil ser 19c; PDBTitle: stucture of the arsenated de novo designed peptide coil ser2 19c
34	c2wjgA	Alignment	not modelled	58.2	16	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
35	c3cvfA	Alignment	not modelled	57.9	24	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
36	c1ca9D	Alignment	not modelled	57.8	6	PDB header: tnf signaling Chain: D: PDB Molecule: protein (tnf receptor associated factor 2); PDBTitle: structure of tnf receptor associated factor 2 in complex2 with a peptide from tnf-r2
37	c2zvfg	Alignment	not modelled	56.3	12	PDB header: ligase Chain: G: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain
38	c3ni0A	Alignment	not modelled	56.2	19	PDB header: immune system Chain: A: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: crystal structure of mouse bst-2/tetherin ectodomain
39	c3e98B	Alignment	not modelled	54.1	21	PDB header: unknown function Chain: B: PDB Molecule: gaf domain of unknown function; PDBTitle: crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
40	c1u0iA	Alignment	not modelled	51.9	24	PDB header: de novo protein Chain: A: PDB Molecule: iaal-e3; PDBTitle: iaal-e3/k3 heterodimer
41	c3nb3C	Alignment	not modelled	51.7	11	PDB header: virus Chain: C: PDB Molecule: outer membrane protein a; PDBTitle: the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
42	c1kzzA	Alignment	not modelled	48.7	16	PDB header: signaling protein Chain: A: PDB Molecule: tnf receptor associated factor 3; PDBTitle: downstream regulator tank binds to the cd40 recognition2 site on traf3
43	c3iynR	Alignment	not modelled	48.1	14	PDB header: virus Chain: R: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
44	c1coiA	Alignment	not modelled	47.4	12	PDB header: alpha-helical bundle Chain: A: PDB Molecule: coil-vald; PDBTitle: designed trimeric coiled coil-vald
45	c1abzA	Alignment	not modelled	46.6	30	PDB header: de novo design Chain: A: PDB Molecule: alpha-t-alpha; PDBTitle: alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
46	c1g6uB	Alignment	not modelled	46.1	26	PDB header: de novo protein Chain: B: PDB Molecule: domain swapped dimer; PDBTitle: crystal structure of a domain swapped dimer
47	dli78a	Alignment	not modelled	46.1	18	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
48	dlvp7b	Alignment	not modelled	46.0	15	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
49	c1kwwC	Alignment	not modelled	44.4	21	PDB header: immune system, sugar binding protein Chain: C: PDB Molecule: mannose-binding protein a; PDBTitle: rat mannose protein a complexed with a-me-fuc.
50	c2xdjF	Alignment	not modelled	43.4	18	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
51	c1ei3E	Alignment	not modelled	39.6	9	PDB header: PDB COMPND:
52	d1osma	Alignment	not modelled	39.5	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
53	c2iwvD	Alignment	not modelled	39.0	9	PDB header: ion channel Chain: D: PDB Molecule: outer membrane protein g; PDBTitle: structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
54	c2x27X	Alignment	not modelled	38.8	10	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein oprg; PDBTitle: crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
						PDB header: structural genomics, unknown function

55	c3efgA_	Alignment	not modelled	38.3	14	Chain: A: PDB Molecule: protein slyx homolog; PDBTitle: structure of slyx protein from xanthomonas campestris pv. campestris2 str. atcc 33913
56	c1rb1A_	Alignment	not modelled	36.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
57	c3k7zA_	Alignment	not modelled	36.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
58	c1rb1B_	Alignment	not modelled	36.8	19	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
59	c3k7zB_	Alignment	not modelled	36.8	19	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
60	c1swiA_	Alignment	not modelled	36.8	19	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4p1; PDBTitle: gcn4-leucine zipper core mutant as n16a complexed with2 benzene
61	c1rb6C_	Alignment	not modelled	36.8	19	PDB header: dna binding protein Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
62	c2yy0D_	Alignment	not modelled	36.7	15	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
63	d1t3ua_	Alignment	not modelled	35.4	15	Fold: Cell division protein ZapA-like Superfamily: Cell division protein ZapA-like Family: Cell division protein ZapA-like
64	d1fxka_	Alignment	not modelled	34.5	9	Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
65	c2zdiA_	Alignment	not modelled	34.4	18	PDB header: chaperone Chain: A: PDB Molecule: prefoldin subunit beta; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
66	c2ykcC_	Alignment	not modelled	34.0	16	PDB header: rna-binding protein Chain: C: PDB Molecule: line-1 orf1p; PDBTitle: structure of the human line-1 orf1p trimer
67	c1ztaA_	Alignment	not modelled	32.8	22	PDB header: dna-binding motif Chain: A: PDB Molecule: leucine zipper monomer; PDBTitle: the solution structure of a leucine-zipper motif peptide
68	d1seda_	Alignment	not modelled	32.7	40	Fold: Hypothetical protein Yha1 Superfamily: Hypothetical protein Yha1 Family: Hypothetical protein Yha1
69	c1deqF_	Alignment	not modelled	32.6	15	PDB header: PDB COMPND:
70	d1ykhb1	Alignment	not modelled	32.2	14	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
71	c3ipkA_	Alignment	not modelled	32.0	10	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
72	c1ce0B_	Alignment	not modelled	31.2	25	PDB header: hiv-1 envelope protein Chain: B: PDB Molecule: protein (leucine zipper model h38-p1); PDBTitle: trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
73	c2f1tB_	Alignment	not modelled	31.2	9	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
74	c2o7hF_	Alignment	not modelled	30.4	16	PDB header: transcription Chain: F: PDB Molecule: general control protein gcn4; PDBTitle: crystal structure of trimeric coiled coil gcn4 leucine zipper
75	c2l8aA_	Alignment	not modelled	30.0	14	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: structure of a novel cbm3 lacking the calcium-binding site
76	c2x4mD_	Alignment	not modelled	29.4	12	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
77	c2zv4O_	Alignment	not modelled	28.8	10	PDB header: structural protein Chain: O: PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
78	c1l6nA_	Alignment	not modelled	28.3	20	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
79	c1d7mA_	Alignment	not modelled	27.6	26	PDB header: contractile protein Chain: A: PDB Molecule: cortexillin i; PDBTitle: coiled-coil dimerization domain from cortexillin i
80	c3dbzB_	Alignment	not modelled	27.4	24	PDB header: sugar binding protein Chain: B: PDB Molecule: pulmonary surfactant-associated protein d; PDBTitle: human surfactant protein d
81	c1ij2C_	Alignment	not modelled	27.4	19	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2

						position
82	c1n73C_	Alignment	not modelled	27.1	8	PDB header: blood clotting Chain: C: PDB Molecule: fibrin gamma chain; PDBTitle: fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
83	c1ij3B_	Alignment	not modelled	27.0	19	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
84	c1ij3C_	Alignment	not modelled	27.0	19	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
85	c3bvhE_	Alignment	not modelled	26.9	15	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
86	c3kqgC_	Alignment	not modelled	26.6	18	PDB header: immune system Chain: C: PDB Molecule: c-type lectin domain family 4 member k; PDBTitle: trimeric structure of langerin
87	c2z5hB_	Alignment	not modelled	26.1	21	PDB header: contractile protein Chain: B: PDB Molecule: general control protein gcn4 and tropomyosin PDBTitle: crystal structure of the head-to-tail junction of2 tropomyosin complexed with a fragment of tnt
88	c2zdiC_	Alignment	not modelled	25.9	15	PDB header: chaperone Chain: C: PDB Molecule: prefoldin subunit alpha; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
89	c1ij2B_	Alignment	not modelled	25.7	19	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with threonine at the a(16)2 position
90	dlivsa1	Alignment	not modelled	25.6	23	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
91	c2zshB_	Alignment	not modelled	24.4	40	PDB header: hormone receptor Chain: B: PDB Molecule: della protein gai; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
92	d1qjpa_	Alignment	not modelled	24.4	11	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
93	c2wamB_	Alignment	not modelled	24.0	17	PDB header: unknown function Chain: B: PDB Molecule: conserved hypothetical alanine and leucine rich PDBTitle: crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
94	c3h5gB_	Alignment	not modelled	23.8	21	PDB header: de novo protein Chain: B: PDB Molecule: coil ser l16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
95	c3h5fA_	Alignment	not modelled	23.8	21	PDB header: de novo protein Chain: A: PDB Molecule: coil ser l16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
96	c3h5gC_	Alignment	not modelled	23.8	21	PDB header: de novo protein Chain: C: PDB Molecule: coil ser l16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
97	c3h5fB_	Alignment	not modelled	23.8	21	PDB header: de novo protein Chain: B: PDB Molecule: coil ser l16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
98	c3h5fC_	Alignment	not modelled	23.8	21	PDB header: de novo protein Chain: C: PDB Molecule: coil ser l16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
99	c3h5gA_	Alignment	not modelled	23.8	21	PDB header: de novo protein Chain: A: PDB Molecule: coil ser l16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
100	c2rjzA_	Alignment	not modelled	23.6	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pilo protein; PDBTitle: crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
101	d2ao9a1	Alignment	not modelled	23.4	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
102	c2hpcH_	Alignment	not modelled	21.6	15	PDB header: blood clotting Chain: H: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
103	c2hpcF_	Alignment	not modelled	20.6	9	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen, gamma polypeptide; PDBTitle: crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
104	c3ojaB_	Alignment	not modelled	20.6	8	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex