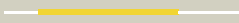
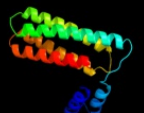
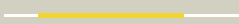
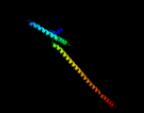

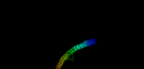

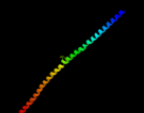

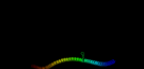

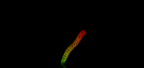



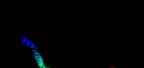

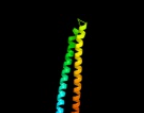

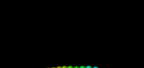

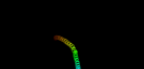







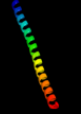
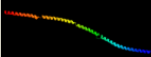


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y4cA_	 Alignment		75.4	9	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
2	c3ojaB_	 Alignment		72.9	14	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
3	c2fxmB_	 Alignment		70.7	12	PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
4	c3u59C_	 Alignment		66.9	12	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
5	c2efrB_	 Alignment		66.3	11	PDB header: contractile protein Chain: B: PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal tropomyosin fragment with n- and 2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
6	c2d3eD_	 Alignment		53.6	16	PDB header: contractile protein Chain: D: PDB Molecule: general control protein gcn4 and tropomyosin 1 PDBTitle: crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
7	c2y3aB_	 Alignment		40.2	13	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit beta; PDBTitle: crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
8	c1deaF_	 Alignment		37.3	11	PDB header: PDB COMPND:
9	c4a55B_	 Alignment		35.6	13	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
10	c3cvfA_	 Alignment		34.4	15	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
11	c2b9cA_	 Alignment		30.8	12	PDB header: contractile protein Chain: A: PDB Molecule: striated-muscle alpha tropomyosin; PDBTitle: structure of tropomyosin's mid-region: bending and binding2 sites for actin

12	c3ghgK_	Alignment		27.3	8	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
13	c3ol1A_	Alignment		25.4	12	PDB header: structural protein Chain: A: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin (fragment 144-251) from homo sapiens, 2 northeast structural genomics consortium target hr4796b
14	c1ei3E_	Alignment		25.1	10	PDB header: PDB COMPND:
15	c1l8dB_	Alignment		23.6	11	PDB header: replication Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: rad50 coiled-coil zn hook
16	c3hizB_	Alignment		22.8	13	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit PDBTitle: crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
17	c3ipkA_	Alignment		20.3	11	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
18	c2rd0B_	Alignment		19.4	9	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a human p110alpha/p85alpha complex
19	c3cveC_	Alignment		19.3	15	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
20	c3o0zD_	Alignment		16.8	11	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
21	c2gl2B_	Alignment	not modelled	16.2	18	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
22	c2v71A_	Alignment	not modelled	16.1	13	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
23	c3dtpA_	Alignment	not modelled	15.8	13	PDB header: contractile protein Chain: A: PDB Molecule: myosin 2 heavy chain chimera of smooth and PDBTitle: tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
24	c3na7A_	Alignment	not modelled	15.5	8	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
25	c3ojaA_	Alignment	not modelled	14.6	9	PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/apl1c complex
26	c3a5tB_	Alignment	not modelled	14.5	15	PDB header: transcription regulator/dna Chain: B: PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
27	c3cwgA_	Alignment	not modelled	13.6	11	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
28	c1deqO_	Alignment	not modelled	13.0	8	PDB header: PDB COMPND:

29	c3u1aC	Alignment	not modelled	11.8	19	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
30	c3ajwA	Alignment	not modelled	11.5	15	PDB header: protein transport Chain: A: PDB Molecule: flagellar fliJ protein; PDBTitle: structure of fliJ, a soluble component of flagellar type iii export2 apparatus
31	c1c1gA	Alignment	not modelled	11.5	16	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
32	d2obpa1	Alignment	not modelled	11.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ReutB4095-like
33	c1ei3C	Alignment	not modelled	11.0	21	PDB header: PDB COMPND:
34	c2jziB	Alignment	not modelled	11.0	18	PDB header: metal binding protein Chain: B: PDB Molecule: serine/threonine-protein phosphatase 2b PDBTitle: structure of calmodulin complexed with the calmodulin2 binding domain of calcineurin
35	c2v66C	Alignment	not modelled	10.8	13	PDB header: structural protein Chain: C: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: crystal structure of the coiled-coil domain of ndel1 (a.a.2 58 to 169)c
36	c1jchC	Alignment	not modelled	10.6	10	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
37	c1ic2B	Alignment	not modelled	10.5	18	PDB header: contractile protein Chain: B: PDB Molecule: tropomyosin alpha chain, skeletal muscle; PDBTitle: deciphering the design of the tropomyosin molecule
38	c1g8xB	Alignment	not modelled	10.4	13	PDB header: structural protein Chain: B: PDB Molecule: myosin ii heavy chain fused to alpha-actinin 3; PDBTitle: structure of a genetically engineered molecular motor
39	c3m9bK	Alignment	not modelled	10.2	24	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
40	c2wt7B	Alignment	not modelled	10.2	14	PDB header: transcription Chain: B: PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
41	d1vmaa1	Alignment	not modelled	9.9	21	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
42	c2z2qF	Alignment	not modelled	9.8	18	PDB header: virus/rna Chain: F: PDB Molecule: coat protein gamma; PDBTitle: crystal structure of flock house virus
43	c1degD	Alignment	not modelled	9.5	13	PDB header: PDB COMPND:
44	d1kbha	Alignment	not modelled	9.5	24	Fold: Nuclear receptor coactivator interlocking domain Superfamily: Nuclear receptor coactivator interlocking domain Family: Nuclear receptor coactivator interlocking domain
45	c1fosE	Alignment	not modelled	9.3	12	PDB header: transcription/dna Chain: E: PDB Molecule: p55-c-fos proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
46	c3hnwB	Alignment	not modelled	9.3	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
47	d1xvha1	Alignment	not modelled	9.3	16	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: GA module, an albumin-binding domain
48	c1fosF	Alignment	not modelled	9.1	15	PDB header: transcription/dna Chain: F: PDB Molecule: c-jun proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
49	c2xdjF	Alignment	not modelled	9.0	7	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
50	d1z0kb1	Alignment	not modelled	8.8	31	Fold: Long alpha-hairpin Superfamily: Rabenosyn-5 Rab-binding domain-like Family: Rabenosyn-5 Rab-binding domain-like
51	c2oevA	Alignment	not modelled	8.8	13	PDB header: protein transport Chain: A: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: crystal structure of alix/aiP1
52	c2v1yB	Alignment	not modelled	8.6	9	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
53	c2k10A	Alignment	not modelled	8.5	26	PDB header: antimicrobial protein Chain: A: PDB Molecule: ranatuerin-2csa; PDBTitle: conformational analysis of the broad-spectrum antibacterial2 peptide, ranatuerin-2csa: identification of a full length3 helix-turn-helix motif
54	d1yzma1	Alignment	not modelled	8.4	31	Fold: Long alpha-hairpin Superfamily: Rabenosyn-5 Rab-binding domain-like

					Family: Rabenosyn-5 Rab-binding domain-like
55	c2x7aB	Alignment	not modelled	8.4	11 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
56	c3n4xB	Alignment	not modelled	8.4	14 PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
57	c2dohC	Alignment	not modelled	8.3	40 PDB header: hydrolase Chain: C: PDB Molecule: plasminogen-binding group a streptococcal m-like protein PDBTitle: the x-ray crystallographic structure of the angiogenesis inhibitor,2 angiostatin, bound a to a peptide from the group a streptococcal3 surface protein pam
58	c1t2kD	Alignment	not modelled	8.3	15 PDB header: transcription/dna Chain: D: PDB Molecule: cyclic-amp-dependent transcription factor atf-2; PDBTitle: structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
59	d2c52b1	Alignment	not modelled	8.2	15 Fold: Nuclear receptor coactivator interlocking domain Superfamily: Nuclear receptor coactivator interlocking domain Family: Nuclear receptor coactivator interlocking domain
60	c2doiB	Alignment	not modelled	8.2	40 PDB header: hydrolase Chain: B: PDB Molecule: plasminogen-binding group a streptococcal m-like protein PDBTitle: the x-ray crystallographic structure of the angiogenesis inhibitor,2 angiostatin, bound to a peptide from the group a streptococcus3 protein pam
61	c2doiC	Alignment	not modelled	8.2	40 PDB header: hydrolase Chain: C: PDB Molecule: plasminogen-binding group a streptococcal m-like protein PDBTitle: the x-ray crystallographic structure of the angiogenesis inhibitor,2 angiostatin, bound to a peptide from the group a streptococcus3 protein pam
62	c1i5kD	Alignment	not modelled	8.1	40 PDB header: blood clotting Chain: D: PDB Molecule: m protein; PDBTitle: structure and binding determinants of the recombinant kringle-2 domain2 of human plasminogen to an internal peptide from a group a3 streptococcal surface protein
63	c1i5kC	Alignment	not modelled	8.1	40 PDB header: blood clotting Chain: C: PDB Molecule: m protein; PDBTitle: structure and binding determinants of the recombinant kringle-2 domain2 of human plasminogen to an internal peptide from a group a3 streptococcal surface protein
64	c1bg1A	Alignment	not modelled	8.1	15 PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
65	d1k8ib2	Alignment	not modelled	8.0	19 Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
66	c1ci6A	Alignment	not modelled	7.9	6 PDB header: transcription Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
67	c2kj4B	Alignment	not modelled	7.5	40 PDB header: blood clotting Chain: B: PDB Molecule: vek-30; PDBTitle: solution structure of the complex of vek-30 and plasminogen2 kringle 2
68	c1junB	Alignment	not modelled	7.4	24 PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
69	d2gqba1	Alignment	not modelled	7.4	18 Fold: RPA2825-like Superfamily: RPA2825-like Family: RPA2825-like
70	c1uo3B	Alignment	not modelled	7.4	36 PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
71	c1u9fC	Alignment	not modelled	7.3	36 PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
72	c1u9fB	Alignment	not modelled	7.3	36 PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
73	c1vmaA	Alignment	not modelled	7.3	13 PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
74	c1o8tA	Alignment	not modelled	7.3	19 PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein c-ii; PDBTitle: global structure and dynamics of human apolipoprotein ci2 in complex with micelles: evidence for increased mobility3 of the helix involved in the activation of lipoprotein4 lipase.
75	c1unuA	Alignment	not modelled	7.3	36 PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
76	c1unuB	Alignment	not modelled	7.3	36 PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
77	c1uo5A	Alignment	not modelled	7.2	36 PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
78	c1uo5B	Alignment	not modelled	7.2	36 PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4;

78	c1u0JB	Alignment	not modelled	7.2	30	PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles PDB header: cell cycle Chain: A: PDB Molecule: cell division topological specificity factor;
79	c2kxoA	Alignment	not modelled	7.2	38	PDBTitle: solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae PDB header: transcription Chain: D: PDB Molecule: general control protein gcn4;
80	c1u9fD	Alignment	not modelled	7.1	36	PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16) PDB header: apoptosis Chain: A: PDB Molecule: programmed cell death protein 5;
81	c1yybA	Alignment	not modelled	7.1	50	PDBTitle: solution structure of 1-26 fragment of human programmed2 cell death 5 protein PDB header: transcription/dna Chain: G: PDB Molecule: transcription factor pap1;
82	c1gd2G	Alignment	not modelled	7.1	13	PDBTitle: crystal structure of bzfp transcription factor pap1 bound2 to dna PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4;
83	c1untA	Alignment	not modelled	7.0	36	PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles PDB header: protein binding Chain: A: PDB Molecule: synphilin-1;
84	c2kesA	Alignment	not modelled	7.0	16	PDBTitle: solution structure of the coiled-coil domain of synphilin-1 PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit;
85	c1m1jA	Alignment	not modelled	7.0	10	PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4;
86	c1untB	Alignment	not modelled	6.9	36	PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
87	d1fxkc	Alignment	not modelled	6.8	9	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg16
88	c3a7pB	Alignment	not modelled	6.7	15	PDB header: sugar binding protein Chain: A: PDB Molecule: c-type lectin domain family 4 member m;
89	c3jqhA	Alignment	not modelled	6.7	45	PDBTitle: structure of the neck region of the glycan-binding receptor2 dc-signr PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4;
90	c2cceB	Alignment	not modelled	6.5	36	PDBTitle: parallel configuration of pli e20s PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4;
91	c2cceA	Alignment	not modelled	6.5	36	PDBTitle: parallel configuration of pli e20s PDB header: vimentin Chain: A: PDB Molecule: vimentin;
92	c1gk4A	Alignment	not modelled	6.5	18	PDBTitle: human vimentin coil 2b fragment (cys2) PDB header: structural protein Chain: B: PDB Molecule: vimentin;
93	c3kltB	Alignment	not modelled	6.5	11	PDBTitle: crystal structure of a vimentin fragment Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
94	d2auwa1	Alignment	not modelled	6.4	25	PDB header: endocytosis/exocytosis Chain: C: PDB Molecule: rab guanine nucleotide exchange factor sec2;
95	c2eqbC	Alignment	not modelled	6.4	17	PDBTitle: crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
96	d1fxka	Alignment	not modelled	6.4	11	PDB header: structural protein Chain: A: PDB Molecule: liprin-beta-2;
97	c3qh9A	Alignment	not modelled	6.1	13	PDBTitle: human liprin-beta2 coiled-coil PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4;
98	c1unvA	Alignment	not modelled	6.1	38	PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles PDB header: endocytosis/exocytosis Chain: M: PDB Molecule: rab guanine nucleotide exchange factor sec2;
99	c2e7sM	Alignment	not modelled	6.1	15	PDBTitle: crystal structure of the yeast sec2p gef domain