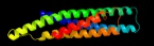
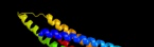
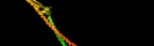
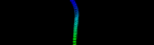
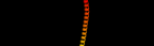
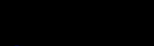
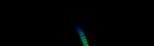
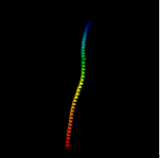
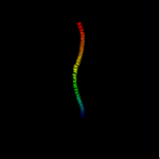
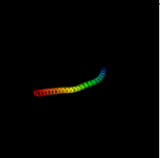
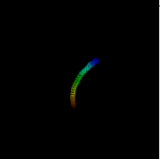
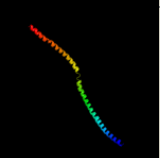
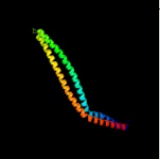
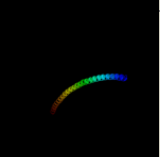
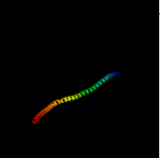
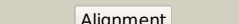
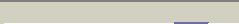
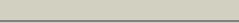
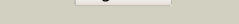
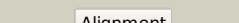
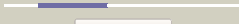
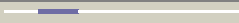
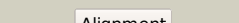
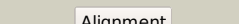
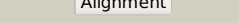
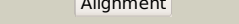
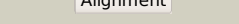
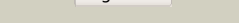


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1bf5A_	 Alignment		96.5	9	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: tyrosine phosphorylated stat-1/dna complex
2	c3cwgA_	 Alignment		96.2	12	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
3	c1bg1A_	 Alignment		94.7	6	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
4	c1ciiA_	 Alignment		90.0	9	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
5	c2efrB_	 Alignment		87.6	12	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	c1yvlB_	 Alignment		86.4	8	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
7	c3o0zD_	 Alignment		86.4	8	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
8	c2d3eD_	 Alignment		85.5	10	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
9	c3ojaB_	 Alignment		81.9	10	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
10	c1deqF_	 Alignment		80.2	10	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
11	c3ol1A_	 Alignment		80.2	15	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

12	c2v71A_	Alignment		79.9	11	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
13	c4gkwB_	Alignment		77.5	11	PDB header: structural protein Chain: B: PDB Molecule: spindle assembly abnormal protein 6; PDBTitle: crystal structure of the coiled-coil domain of c. elegans sas-6
14	c3ghgK_	Alignment		70.9	14	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
15	c3q8tB_	Alignment		70.0	9	PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
16	c2fxmB_	Alignment		61.0	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
17	c1ei3C_	Alignment		60.7	11	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
18	c3na7A_	Alignment		53.4	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
19	c3tnuB_	Alignment		49.1	14	PDB header: cytosolic protein Chain: B: PDB Molecule: keratin, type ii cytoskeletal 5; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
20	c1ei3E_	Alignment		46.8	11	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
21	c2v66C_	Alignment	not modelled	44.4	10	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.258 to 169)c
22	c2gl2B_	Alignment	not modelled	43.6	14	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,2y69g) of bacterial adhesin fada
23	c3u59C_	Alignment	not modelled	41.1	12	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
24	c1jchC_	Alignment	not modelled	35.5	6	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
25	c4a7fB_	Alignment	not modelled	35.3	11	PDB header: structural protein/hydrolase Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
26	c3ghgI_	Alignment	not modelled	31.1	11	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
27	c3dtpA_	Alignment	not modelled	26.3	12	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
28	c3tnuA_	Alignment	not modelled	22.7	15	PDB header: cytosolic protein Chain: A: PDB Molecule: keratin, type i cytoskeletal 14; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)

29	c1degO_	 Alignment	not modelled	21.9	9	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
30	c2b9cA_	 Alignment	not modelled	21.1	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
31	c2xcsD_	 Alignment	not modelled	19.4	38	PDB header: isomerase Chain: D: PDB Molecule: dna gyrase subunit b, dna gyrase subunit a; PDBTitle: the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
32	c3hizB_	 Alignment	not modelled	19.4	11	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
33	c4a55B_	 Alignment	not modelled	18.4	12	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
34	c1degD_	 Alignment	not modelled	17.1	9	PDB header: blood clotting Chain: D: PDB Molecule: fibrinogen (alpha chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
35	c2ocyB_	 Alignment	not modelled	16.8	11	PDB header: endocytosis/exocytosis Chain: B: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: complex of the guanine exchange factor sec2p and the rab2 gtpase sec4p
36	c2xkjE_	 Alignment	not modelled	15.7	31	PDB header: isomerase Chain: E: PDB Molecule: topoisomerase iv; PDBTitle: crystal structure of catalytic core of a. baumannii topo iv2 (pare-parc fusion truncate)
37	c3swkB_	 Alignment	not modelled	15.5	11	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
38	c3vkgA_	 Alignment	not modelled	14.7	9	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
39	c3hnbB_	 Alignment	not modelled	13.9	12	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
40	d2axtc1	 Alignment	not modelled	13.6	38	Fold: Photosystem II antenna protein-like Superfamily: Photosystem II antenna protein-like Family: Photosystem II antenna protein-like
41	c2axtc_	 Alignment	not modelled	13.6	38	PDB header: electron transport Chain: C: PDB Molecule: photosystem ii cp43 protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
42	c1bjtA_	 Alignment	not modelled	12.5	40	PDB header: topoisomerase Chain: A: PDB Molecule: topoisomerase ii; PDBTitle: topoisomerase ii residues 409-1201
43	d1bjta_	 Alignment	not modelled	12.5	40	Fold: Type II DNA topoisomerase Superfamily: Type II DNA topoisomerase Family: Type II DNA topoisomerase
44	c3ipkA_	 Alignment	not modelled	12.3	7	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
45	c2wpqA_	 Alignment	not modelled	12.3	16	PDB header: membrane protein Chain: A: PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
46	c2v1yB_	 Alignment	not modelled	12.1	11	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
47	c3qx3B_	 Alignment	not modelled	12.0	40	PDB header: isomerase/dna/isomerase inhibitor Chain: B: PDB Molecule: dna topoisomerase 2-beta; PDBTitle: human topoisomerase iibeta in complex with dna and etoposide
48	c2rd0B_	 Alignment	not modelled	11.6	13	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a human p110alpha/p85alpha complex
49	c4fm9A_	 Alignment	not modelled	10.5	40	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2-alpha; PDBTitle: human topoisomerase ii alpha bound to dna
50	d1unca_	 Alignment	not modelled	10.0	57	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
51	d1yu8x1	 Alignment	not modelled	9.8	43	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
52	c2xcqA_	 Alignment	not modelled	9.7	50	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit b, dna gyrase subunit a; PDBTitle: the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
		 Alignment				Fold: Glucocorticoid receptor-like (DNA-binding domain)

53	d1y0ja1	Alignment	not modelled	9.6	50	Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
54	c1c1gA	Alignment	not modelled	9.5	8	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
55	d1unda	Alignment	not modelled	9.4	57	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
56	c3j21f	Alignment	not modelled	9.3	50	PDB header: ribosome Chain: F: PDB Molecule: 50s ribosomal protein l6p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
57	c2i1kA	Alignment	not modelled	9.3	13	PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: moesin; PDBTitle: moesin from spodoptera frugiperda reveals the coiled-coil domain at2 3.0 angstrom resolution
58	d2vuti1	Alignment	not modelled	9.0	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
59	c4dylA	Alignment	not modelled	8.8	6	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase fes/fps; PDBTitle: f-bar domain of human fes tyrosine kinase
60	c4gfhA	Alignment	not modelled	8.8	40	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: topoisomerase ii-dna-ampnp complex
61	c2ww90	Alignment	not modelled	8.4	50	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l39; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
62	c2y3aB	Alignment	not modelled	8.2	12	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
63	d1gnfa	Alignment	not modelled	8.0	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
64	c3mstA	Alignment	not modelled	7.9	50	PDB header: transport protein Chain: A: PDB Molecule: putative nitrate transport protein; PDBTitle: crystal structure of a putative nitrate transport protein (tnv0104)2 from thermoplasma volcanium at 1.35 a resolution
65	c3ojaA	Alignment	not modelled	7.8	8	PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/apl1c complex
66	c2p03A	Alignment	not modelled	7.6	7	PDB header: cell adhesion Chain: A: PDB Molecule: alpha-2-macroglobulin receptor-associated PDBTitle: the structure of receptor-associated protein(rap)
67	c1fosF	Alignment	not modelled	7.5	10	PDB header: transcription/dna Chain: F: PDB Molecule: c-jun proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
68	c4a1bB	Alignment	not modelled	7.4	50	PDB header: ribosome Chain: B: PDB Molecule: rpl39; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rna and3 proteins of molecule 3.
69	c1izlL	Alignment	not modelled	7.3	71	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii: subunit psbb; PDBTitle: crystal structure of photosystem ii
70	c1izlB	Alignment	not modelled	7.2	71	PDB header: photosynthesis Chain: B: PDB Molecule: photosystem ii: subunit psbb; PDBTitle: crystal structure of photosystem ii
71	c2pmsD	Alignment	not modelled	7.0	15	PDB header: metal transport, hydrolase Chain: D: PDB Molecule: pneumococcal surface protein a (pspa); PDBTitle: crystal structure of the complex of human lactoferrin n-lobe and2 lactoferrin-binding domain of pneumococcal surface protein a
72	c2qa7C	Alignment	not modelled	6.8	9	PDB header: actin binding Chain: C: PDB Molecule: huntingtin-interacting protein 1; PDBTitle: crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable3 for hip-protein interactor (hippi)
73	c2zkr3	Alignment	not modelled	6.8	67	PDB header: ribosomal protein/rna Chain: 3: PDB Molecule: 60s ribosomal protein l39e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
74	c3cvfA	Alignment	not modelled	6.7	9	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
75	c1ci6A	Alignment	not modelled	6.6	10	PDB header: transcription Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
76	c3izso	Alignment	not modelled	6.5	50	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein rpl28 (l15p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
77	c2kaeA	Alignment	not modelled	6.4	33	PDB header: transcription/dna Chain: A: PDB Molecule: gata-type transcription factor; PDBTitle: data-driven model of med1:dna complex
						PDB header: structural protein

78	c2k6nA_	Alignment	not modelled	6.4	57	Chain: A: PDB Molecule: supervillin; PDBTitle: solution structure of human supervillin headpiece, minimized2 average
79	c2no2A_	Alignment	not modelled	6.4	9	PDB header: cell adhesion Chain: A: PDB Molecule: huntingtin-interacting protein 1; PDBTitle: crystal structure of the dllrkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
80	c2k2iB_	Alignment	not modelled	6.3	40	PDB header: cell cycle Chain: B: PDB Molecule: sfi1 peptide; PDBTitle: nmr solution structure of the c-terminal domain (t94-y172)2 of the human centrin 2 in complex with a repeat sequence of3 human sfi1 (r641-t660)
81	c3nicA_	Alignment	not modelled	6.2	50	PDB header: hydrolase/dna Chain: A: PDB Molecule: eco29kir; PDBTitle: dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
82	d2ap3a1	Alignment	not modelled	6.2	4	Fold: Four-helical up-and-down bundle Superfamily: MW0975(SA0943)-like Family: MW0975(SA0943)-like
83	c2l3xA_	Alignment	not modelled	6.2	14	PDB header: protein binding Chain: A: PDB Molecule: ablim2 protein; PDBTitle: villin head piece domain of human ablim2
84	c3zf7q_	Alignment	not modelled	6.1	50	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein l15; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
85	c1xr0A_	Alignment	not modelled	5.9	50	PDB header: signaling protein/growth factor receptor Chain: A: PDB Molecule: basic fibroblast growth factor receptor 1; PDBTitle: structural basis of snt ptb domain interactions with2 distinct neurotrophic receptors
86	d1qzpa_	Alignment	not modelled	5.7	14	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
87	c2o3oD_	Alignment	not modelled	5.6	60	PDB header: signaling protein Chain: D: PDB Molecule: yyci protein; PDBTitle: crystal structure of the sensor histidine kinase regulator yyci from2 bacillus subtilis
88	c2oexB_	Alignment	not modelled	5.6	11	PDB header: protein transport Chain: B: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: structure of alix/aip1 v domain
89	c3tnfB_	Alignment	not modelled	5.5	11	PDB header: protein transport Chain: B: PDB Molecule: lida; PDBTitle: lida from legionella in complex with active rab8a
90	d1yu5x1	Alignment	not modelled	5.5	43	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
91	c1t2kD_	Alignment	not modelled	5.4	13	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
92	c2wt7B_	Alignment	not modelled	5.4	15	PDB header: transcription Chain: B: PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
93	d1jcb2	Alignment	not modelled	5.4	25	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
94	c3s4rB_	Alignment	not modelled	5.2	10	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
95	d1ujsa_	Alignment	not modelled	5.2	14	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain