




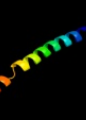

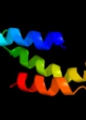

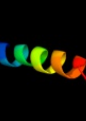


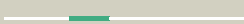


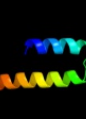








#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lf0A_	 Alignment		100.0	98	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yibI; PDBTitle: solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr, 3 residual dipolar couplings and small-angle x-ray scattering, nesg4 target sfr339/ocsp target sf3636
2	c1gk7A_	 Alignment		91.4	36	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
3	c1t3jA_	 Alignment		78.5	33	PDB header: membrane protein Chain: A: PDB Molecule: mitofusin 1; PDBTitle: mitofusin domain hr2 v686m/i708m mutant
4	c2a3dA_	 Alignment		68.3	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)
5	c1u0iA_	 Alignment		65.6	67	PDB header: de novo protein Chain: A: PDB Molecule: iaal-e3; PDBTitle: iaal-e3/k3 heterodimer
6	c2c5iT_	 Alignment		60.3	14	PDB header: protein transport Chain: T: PDB Molecule: t-snare affecting a late golgi compartment PDBTitle: n-terminal domain of tlg1 complexed with n-terminus of2 vps51 in distorted conformation
7	c1ce0B_	 Alignment		40.4	41	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 gc4 leucine zipper model
8	c1g6uB_	 Alignment		30.8	26	PDB header: de novo protein Chain: B: PDB Molecule: domain swapped dimer; PDBTitle: crystal structure of a domain swapped dimer
9	c2xzfA_	 Alignment		29.2	27	PDB header: cell adhesion Chain: A: PDB Molecule: immunoglobulin-binding protein eibd; PDBTitle: escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gc4 adaptors
10	c1u2uA_	 Alignment		24.3	61	PDB header: transcription Chain: A: PDB Molecule: general control protein gc4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
11	c1gp8A_	 Alignment		23.4	32	PDB header: viral protein Chain: A: PDB Molecule: protein (scaffolding protein); PDBTitle: nmr solution structure of the coat protein-binding domain2 of bacteriophage p22 scaffolding protein

12	clij2C_	Alignment		23.0	45	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvt coiled-coil trimer with threonine at the a(16)2 position
13	clztaA_	Alignment		21.7	45	PDB header: dna-binding motif Chain: A: PDB Molecule: leucine zipper monomer; PDBTitle: the solution structure of a leucine-zipper motif peptide
14	clij2B_	Alignment		21.1	45	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvt coiled-coil trimer with threonine at the a(16)2 position
15	c3u1aC_	Alignment		20.7	23	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
16	cllc2B_	Alignment		19.3	24	PDB header: contractile protein Chain: B: PDB Molecule: tropomyosin alpha chain, skeletal muscle; PDBTitle: deciphering the design of the tropomyosin molecule
17	cljldF_	Alignment		19.2	24	PDB header: contractile protein Chain: F: PDB Molecule: troponin i; PDBTitle: crystal structure of the 46kda domain of human cardiac2 troponin in the ca2+ saturated form
18	clrb6C_	Alignment		18.7	45	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
19	clrb1A_	Alignment		18.7	45	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
20	c3k7zB_	Alignment		18.7	45	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
21	clrb1B_	Alignment	not modelled	18.7	45	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
22	clswiA_	Alignment	not modelled	18.7	45	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4p1; PDBTitle: gcn4-leucine zipper core mutant as n16a complexed with2 benzene
23	c3k7zA_	Alignment	not modelled	18.7	45	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
24	clij3B_	Alignment	not modelled	18.7	45	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
25	clij3C_	Alignment	not modelled	18.7	45	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
26	c2ekkA_	Alignment	not modelled	17.9	55	PDB header: protein binding Chain: A: PDB Molecule: uba domain from e3 ubiquitin-protein ligase PDBTitle: solution structure of ruh-074, a human uba domain
27	dlwe3a2	Alignment	not modelled	16.0	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
28	dlkida_	Alignment	not modelled	16.0	26	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
						PDB header: transferase

29	c1wt6B_	Alignment	not modelled	14.8	30	Chain: B: PDB Molecule: myotonin-protein kinase; PDBTitle: coiled-coil domain of dmpk
30	d1sjpa2	Alignment	not modelled	14.5	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
31	c3he4A_	Alignment	not modelled	14.5	59	PDB header: de novo protein Chain: A: PDB Molecule: synzip6; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
32	c2dq3A_	Alignment	not modelled	13.9	23	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
33	c1yv0I_	Alignment	not modelled	13.8	22	PDB header: contractile protein Chain: I: PDB Molecule: troponin i, fast skeletal muscle; PDBTitle: crystal structure of skeletal muscle troponin in the ca2+-2 free state
34	c3m6cA_	Alignment	not modelled	13.8	17	PDB header: chaperone Chain: A: PDB Molecule: 60 kda chaperonin 1; PDBTitle: crystal structure of mycobacterium tuberculosis groel1 apical domain
35	c2o7hF_	Alignment	not modelled	13.5	41	PDB header: transcription Chain: F: PDB Molecule: general control protein gcn4; PDBTitle: crystal structure of trimeric coiled coil gcn4 leucine zipper
36	d1dl5a2	Alignment	not modelled	13.4	35	Fold: Protein-L-isoaspartyl O-methyltransferase, C-terminal domain Superfamily: Protein-L-isoaspartyl O-methyltransferase, C-terminal domain Family: Protein-L-isoaspartyl O-methyltransferase, C-terminal domain
37	d1rq2a1	Alignment	not modelled	13.2	32	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
38	c3ni0A_	Alignment	not modelled	12.8	32	PDB header: immune system Chain: A: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: crystal structure of mouse bst-2/tetherin ectodomain
39	d2c0sa1	Alignment	not modelled	12.5	18	Fold: ROP-like Superfamily: BAS1536-like Family: BAS1536-like
40	c3nmdA_	Alignment	not modelled	12.3	42	PDB header: transferase Chain: A: PDB Molecule: cgmp dependent protein kinase; PDBTitle: crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta
41	c2w9kA_	Alignment	not modelled	11.4	25	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crithidia fasciculata cytochrome c
42	c2etnA_	Alignment	not modelled	11.3	21	PDB header: transcription Chain: A: PDB Molecule: anti-cleavage anti-grea transcription factor PDBTitle: crystal structure of thermus aquaticus gfh1
43	c3oa7A_	Alignment	not modelled	10.9	16	PDB header: structural protein Chain: A: PDB Molecule: head morphogenesis protein, chaotic nuclear migration PDBTitle: structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
44	c4a19Q_	Alignment	not modelled	10.7	44	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l36; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rna and3 proteins of molecule 2.
45	c1ytzl_	Alignment	not modelled	10.5	22	PDB header: contractile protein Chain: I: PDB Molecule: troponin i; PDBTitle: crystal structure of skeletal muscle troponin in the ca2+-2 activated state
46	c1gk4A_	Alignment	not modelled	10.4	20	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)
47	d2nzca1	Alignment	not modelled	10.3	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: TM1266-like
48	c3lpeF_	Alignment	not modelled	10.3	17	PDB header: transferase Chain: F: PDB Molecule: dna-directed rna polymerase subunit e''; PDBTitle: crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
49	d2g3qa1	Alignment	not modelled	9.7	27	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
50	c3fgaD_	Alignment	not modelled	9.2	20	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: shugoshin-like 1; PDBTitle: structural basis of pp2a and sgo interaction
51	c2kswA_	Alignment	not modelled	9.1	50	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: oryctin; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for oryctin
52	d1ivsa1	Alignment	not modelled	9.0	13	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
53	d5csma_	Alignment	not modelled	8.8	17	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Allosteric chorismate mutase
54	c3izck_	Alignment	not modelled	8.7	33	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein rpl16 (l13p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome

55	c2rklB	Alignment	not modelled	8.6	24	PDB header: lipid transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein vta1; PDBTitle: crystal structure of s.cerevisiae vta1 c-terminal domain
56	d1uklc	Alignment	not modelled	8.6	9	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
57	c2l5gB	Alignment	not modelled	8.5	24	PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
58	d1gqea	Alignment	not modelled	8.1	15	Fold: Release factor Superfamily: Release factor Family: Release factor
59	c1gcmA	Alignment	not modelled	7.9	38	PDB header: transcription regulation Chain: A: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
60	c2zkrv	Alignment	not modelled	7.9	17	PDB header: ribosomal protein/rna Chain: V: PDB Molecule: rna expansion segment es9 part2; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
61	c1r48A	Alignment	not modelled	7.6	37	PDB header: transport protein Chain: A: PDB Molecule: proline/betaine transporter; PDBTitle: solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop
62	c3a5tB	Alignment	not modelled	7.5	26	PDB header: transcription regulator/dna Chain: B: PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
63	c2wukD	Alignment	not modelled	7.5	29	PDB header: cell cycle Chain: D: PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant
64	c1kddC	Alignment	not modelled	7.5	56	PDB header: de novo protein Chain: C: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
65	c1kddF	Alignment	not modelled	7.3	56	PDB header: de novo protein Chain: F: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
66	c1kddA	Alignment	not modelled	7.3	56	PDB header: de novo protein Chain: A: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
67	c3ol1A	Alignment	not modelled	7.2	22	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
68	d1oqya1	Alignment	not modelled	7.2	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
69	c1gcmB	Alignment	not modelled	7.1	38	PDB header: transcription regulation Chain: B: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
70	c3tqmD	Alignment	not modelled	7.1	18	PDB header: protein binding Chain: D: PDB Molecule: ribosome-associated factor y; PDBTitle: structure of an ribosomal subunit interface protein from coxiella2 burnetii
71	c2hx6A	Alignment	not modelled	7.0	13	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
72	c2a45J	Alignment	not modelled	6.9	7	PDB header: hydrolase/hydrolase inhibitor Chain: J: PDB Molecule: fibrinogen alpha chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin
73	c2z9fC	Alignment	not modelled	6.8	17	PDB header: biosynthetic protein Chain: C: PDB Molecule: cellulose synthase operon protein d; PDBTitle: crystal structure of accesd protein from acetobacter xylinum
74	c1gcmC	Alignment	not modelled	6.8	38	PDB header: transcription regulation Chain: C: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
75	c1sryB	Alignment	not modelled	6.7	12	PDB header: ligase(synthetase) Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
76	c3lt7D	Alignment	not modelled	6.5	29	PDB header: cell adhesion Chain: D: PDB Molecule: adhesin yada; PDBTitle: a transition from strong right-handed to canonical left-handed2 supercoiling in a conserved coiled coil segment of trimeric3 autotransporter adhesins - the m3 mutant structure
77	d1gpja1	Alignment	not modelled	6.4	20	Fold: Glutamyl tRNA-reductase dimerization domain Superfamily: Glutamyl tRNA-reductase dimerization domain Family: Glutamyl tRNA-reductase dimerization domain
78	c2xu6B	Alignment	not modelled	6.3	22	PDB header: protein binding Chain: B: PDB Molecule: mdv1 coiled coil; PDBTitle: mdv1 coiled coil domain
79	c3h5fC	Alignment	not modelled	6.3	29	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.

80	c3h5gC_	Alignment	not modelled	6.3	29	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.
81	c3h5fA_	Alignment	not modelled	6.3	29	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.
82	c3h5gA_	Alignment	not modelled	6.3	29	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.
83	c3h5fB_	Alignment	not modelled	6.3	29	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.
84	c3h5gB_	Alignment	not modelled	6.3	29	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.
85	c2e43A_	Alignment	not modelled	6.2	26	PDB header: transcription/dna Chain: A: PDB Molecule: ccaat/enhancer-binding protein beta; PDBTitle: crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
86	d1dp7p_	Alignment	not modelled	6.2	55	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: P4 origin-binding domain-like
87	c2ergA_	Alignment	not modelled	6.1	22	PDB header: transcription activator/dna Chain: A: PDB Molecule: regulatory protein leu3; PDBTitle: crystal structure of leu3 dna-binding domain with a single2 h50c mutation complexed with a 15mer dna duplex
88	c2wt7B_	Alignment	not modelled	6.1	19	PDB header: transcription Chain: B: PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
89	c1grjA_	Alignment	not modelled	5.9	7	PDB header: transcription regulation Chain: A: PDB Molecule: greA protein; PDBTitle: greA transcript cleavage factor from escherichia coli
90	d1mska_	Alignment	not modelled	5.9	45	Fold: Methionine synthase activation domain-like Superfamily: Methionine synthase activation domain-like Family: Methionine synthase SAM-binding domain
91	c1ij2A_	Alignment	not modelled	5.6	48	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
92	c1ofuB_	Alignment	not modelled	5.5	32	PDB header: bacterial cell division inhibitor Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of sula:ftsZ from pseudomonas aeruginosa
93	c2vawA_	Alignment	not modelled	5.4	32	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz pseudomonas aeruginosa gdp
94	c1u7mB_	Alignment	not modelled	5.3	40	PDB header: de novo protein Chain: B: PDB Molecule: four-helix bundle model; PDBTitle: solution structure of a diiron protein model: due ferri(ii)2 turn mutant
95	c3he5A_	Alignment	not modelled	5.3	32	PDB header: de novo protein Chain: A: PDB Molecule: synzip1; PDBTitle: heterospecific coiled-coil pair synzip2:synzip1