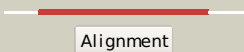
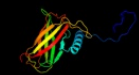
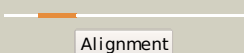

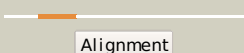

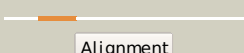
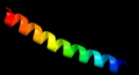
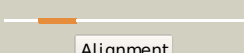
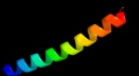
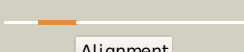
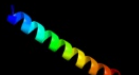
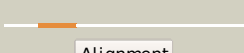
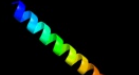
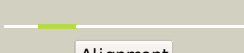


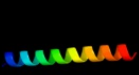



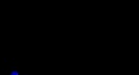
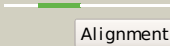
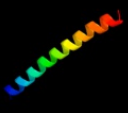
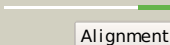

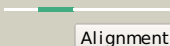

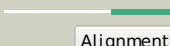

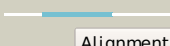

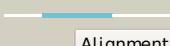







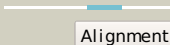
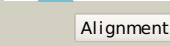
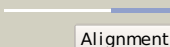


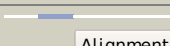
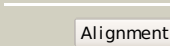



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jwyA_	 Alignment		100.0	100	PDB header: lipoprotein Chain: A: PDB Molecule: uncharacterized lipoprotein yaji; PDBTitle: solution nmr structure of uncharacterized lipoprotein yaji from2 escherichia coli. northeast structural genomics target er540
2	c1kddC_	 Alignment		83.8	29	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-d12la16l
3	c1kddF_	 Alignment		83.6	29	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-d12la16l
4	c1kddA_	 Alignment		83.6	29	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-d12la16l
5	c1kd9A_	 Alignment		83.3	29	PDB header: de novo protein Chain: A: PDB Molecule: gcn4 acid base heterodimer acid-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
6	c1kd9C_	 Alignment		83.3	29	PDB header: de novo protein Chain: C: PDB Molecule: gcn4 acid base heterodimer acid-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
7	c1kd9F_	 Alignment		83.3	29	PDB header: de novo protein Chain: F: PDB Molecule: gcn4 acid base heterodimer acid-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
8	c1kd8F_	 Alignment		69.2	26	PDB header: de novo protein Chain: F: PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
9	c1kd8C_	 Alignment		69.2	26	PDB header: de novo protein Chain: C: PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
10	c1kd8A_	 Alignment		67.8	26	PDB header: de novo protein Chain: A: PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
11	c2x7aB_	 Alignment		66.1	20	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

12	c3mkxC_		Alignment		56.6	20	PDB header: antiviral protein Chain: C: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: crystal structure of bst2/tetherin
13	c2zzjA_		Alignment		52.2	19	PDB header: lyase Chain: A: PDB Molecule: glucuronan lyase a; PDBTitle: crystal structure of endo-beta-1,4-glucuronan lyase from2 fungus trichoderma reesei
14	c1dipA_		Alignment		42.9	24	PDB header: acetylation Chain: A: PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
15	c1yyCA_		Alignment		40.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative late embryogenesis abundant protein; PDBTitle: solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
16	c2gr7C_		Alignment		38.0	19	PDB header: membrane protein Chain: C: PDB Molecule: adhesin; PDBTitle: hia 992-1098
17	d2gr7a1		Alignment		38.0	19	Fold: Pili subunits Superfamily: Pili subunits Family: YadA C-terminal domain-like
18	c1u2uA_		Alignment		37.8	37	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
19	c1kd8E_		Alignment		37.1	23	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
20	c3bvhC_		Alignment		34.5	20	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
21	c3bkpA_		Alignment	not modelled	33.3	21	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin; PDBTitle: crystal structure of the toxoplasma gondii cyclophilin, 49.m03261
22	c2yy0D_		Alignment	not modelled	32.7	21	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
23	d1xo8a_		Alignment	not modelled	29.4	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: LEA14-like Family: LEA14-like
24	c2hpcF_		Alignment	not modelled	26.0	19	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.
25	d1r8ia_		Alignment	not modelled	25.6	11	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Typo IV secretion system protein TraC Family: Typo IV secretion system protein TraC
26	c1r8iA_		Alignment	not modelled	25.6	11	PDB header: structural protein Chain: A: PDB Molecule: trac; PDBTitle: crystal structure of trac
27	c2vefB_		Alignment	not modelled	24.9	33	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
28	c1aq5C_		Alignment	not modelled	24.6	11	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

29	d1o75a2	Alignment	not modelled	24.5	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Tp47 lipoprotein, middle and C-terminal domains Family: Tp47 lipoprotein, middle and C-terminal domains
30	c3t97A	Alignment	not modelled	22.9	3	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore glycoprotein p62; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54
31	d1afwa2	Alignment	not modelled	22.6	21	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
32	c2xzaA	Alignment	not modelled	22.5	15	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
33	c3iynR	Alignment	not modelled	20.1	10	PDB header: virus Chain: R: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
34	d1smao	Alignment	not modelled	20.1	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
35	d1an2a	Alignment	not modelled	19.7	9	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
36	c1xnaA	Alignment	not modelled	19.6	15	PDB header: dna binding protein Chain: A: PDB Molecule: protein (dna-repair protein xrcc1); PDBTitle: nmr solution structure of the single-strand break repair2 protein xrcc1-n-terminal domain
37	d1eqwa	Alignment	not modelled	19.2	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
38	c2dzaA	Alignment	not modelled	19.1	25	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
39	d1eyea	Alignment	not modelled	19.0	33	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
40	c1cz7C	Alignment	not modelled	18.4	19	PDB header: contractile protein Chain: C: PDB Molecule: microtubule motor protein ncd; PDBTitle: the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
41	c3aqqD	Alignment	not modelled	18.0	18	PDB header: dna binding protein Chain: D: PDB Molecule: calcium-regulated heat stable protein 1; PDBTitle: crystal structure of human crhsp-24
42	c1kzaA	Alignment	not modelled	17.7	7	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	c2y5aA	Alignment	not modelled	17.5	33	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
44	c2e43A	Alignment	not modelled	17.1	15	PDB header: transcription/dna Chain: A: PDB Molecule: ccat/enhancer-binding protein beta; PDBTitle: crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
45	d1wu9a1	Alignment	not modelled	16.9	14	Fold: EB1 dimerisation domain-like Superfamily: EB1 dimerisation domain-like Family: EB1 dimerisation domain-like
46	c2ibyD	Alignment	not modelled	16.9	5	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystallographic and kinetic studies of human mitochondrial2 acetoacetyl-coa thiolase (t2): the importance of potassium and3 chloride for its structure and function
47	c2bmbA	Alignment	not modelled	16.8	33	PDB header: transferase Chain: A: PDB Molecule: folic acid synthesis protein fol1; PDBTitle: x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
48	c1coiA	Alignment	not modelled	16.2	19	PDB header: alpha-helical bundle Chain: A: PDB Molecule: coil-vald; PDBTitle: designed trimeric coiled coil-vald
49	c2xv5A	Alignment	not modelled	16.1	7	PDB header: structural protein Chain: A: PDB Molecule: lamin-a/c; PDBTitle: human lamin a coil 2b fragment
50	c1n73C	Alignment	not modelled	15.9	13	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
51	c1degF	Alignment	not modelled	15.5	16	PDB header: PDB COMPND:
52	d1e5ma2	Alignment	not modelled	15.5	14	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
53	c2vp8A	Alignment	not modelled	15.4	22	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
54	c3n4xB	Alignment	not modelled	15.3	14	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length

55	c1deqO_	Alignment	not modelled	14.9	13	PDB header: PDB COMPND:
56	dlesoa_	Alignment	not modelled	14.7	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like
57	clu0iA_	Alignment	not modelled	14.5	20	PDB header: de novo protein Chain: A: PDB Molecule: iaal-e3; PDBTitle: iaal-e3/k3 heterodimer
58	d1v5ja_	Alignment	not modelled	14.4	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
59	d1ajza_	Alignment	not modelled	14.4	25	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
60	d1ad1a_	Alignment	not modelled	14.4	25	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
61	c3pp5A_	Alignment	not modelled	14.1	21	PDB header: structural protein Chain: A: PDB Molecule: brk1; PDBTitle: high-resolution structure of the trimeric scar/wave complex precursor2 brk1
62	d1m3ka2	Alignment	not modelled	13.9	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
63	c3mcnA_	Alignment	not modelled	13.7	43	PDB header: transferase Chain: A: PDB Molecule: 2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine PDBTitle: crystal structure of the 6-hydroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
64	c3ghgK_	Alignment	not modelled	13.6	3	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
65	d2ix4a2	Alignment	not modelled	13.6	29	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
66	c1txqB_	Alignment	not modelled	13.5	14	PDB header: structural protein/protein binding Chain: B: PDB Molecule: microtubule-associated protein rp/eb family PDBTitle: crystal structure of the eb1 c-terminal domain complexed2 with the cap-gly domain of p150glued
67	d1txqb1	Alignment	not modelled	13.5	14	Fold: EB1 dimerisation domain-like Superfamily: EB1 dimerisation domain-like Family: EB1 dimerisation domain-like
68	c3lssA_	Alignment	not modelled	13.4	18	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: trypanosoma brucei seryl-trna synthetase in complex with atp
69	d2gfva2	Alignment	not modelled	13.3	43	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
70	c1r48A_	Alignment	not modelled	13.2	16	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
71	d1ulqa2	Alignment	not modelled	13.0	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
72	d1k32a4	Alignment	not modelled	12.9	31	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Tail specific protease, catalytic domain
73	c3p8cE_	Alignment	not modelled	12.9	25	PDB header: protein binding Chain: E: PDB Molecule: probable protein brick1; PDBTitle: structure and control of the actin regulatory wave complex
74	c3cm9J_	Alignment	not modelled	12.9	25	PDB header: immune system Chain: J: PDB Molecule: secretory component; PDBTitle: solution structure of human siga2
75	c3chnJ_	Alignment	not modelled	12.9	25	PDB header: immune system Chain: J: PDB Molecule: secretory component; PDBTitle: solution structure of human secretory iga1
76	c3rbgB_	Alignment	not modelled	12.7	17	PDB header: immune system Chain: B: PDB Molecule: cytotoxic and regulatory t-cell molecule; PDBTitle: crystal structure analysis of class-i mhc restricted t-cell associated2 molecule
77	c1bx2A_	Alignment	not modelled	12.7	42	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
78	d1bx2a_	Alignment	not modelled	12.7	42	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
79	d1wdkc2	Alignment	not modelled	12.6	13	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
80	d2ijra1	Alignment	not modelled	12.4	11	Fold: Api92-like Superfamily: Api92-like Family: Api92-like
81	d1ox0a2	Alignment	not modelled	12.3	36	Fold: Thiolase-like Superfamily: Thiolase-like

					Family: Thiolase-related
82	c3ni0A_	Alignment	not modelled	12.2	32 PDB header: immune system Chain: A: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: crystal structure of mouse bst-2/tetherin ectodomain
83	c3tr9A_	Alignment	not modelled	12.2	25 PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroi c2 acid from coxiella burnetii
84	d1hkfa_	Alignment	not modelled	12.1	8 Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
85	c2xdjF_	Alignment	not modelled	12.1	6 PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
86	c1ci6A_	Alignment	not modelled	12.0	9 PDB header: transcription Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
87	c1ca9D_	Alignment	not modelled	11.9	23 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
88	c1ei3E_	Alignment	not modelled	11.8	3 PDB header: PDB COMPND:
89	c1fmhA_	Alignment	not modelled	11.7	31 PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
90	c1t2kD_	Alignment	not modelled	11.7	16 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
91	d1nldl1	Alignment	not modelled	11.5	7 Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
92	c3m9bK_	Alignment	not modelled	11.5	15 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
93	c1fosF_	Alignment	not modelled	11.3	16 PDB header: transcription/dna Chain: F: PDB Molecule: c-jun proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
94	d1ub5a1	Alignment	not modelled	11.1	4 Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
95	c1jccC_	Alignment	not modelled	10.8	3 PDB header: membrane protein Chain: C: PDB Molecule: major outer membrane lipoprotein; PDBTitle: crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,l16a,v20a,l23a,v27a,m30a,v34a mutations
96	d1dpta_	Alignment	not modelled	10.6	13 Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
97	c1fosE_	Alignment	not modelled	10.6	12 PDB header: transcription/dna Chain: E: PDB Molecule: p55-c-fos proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
98	d1h3pl1	Alignment	not modelled	10.6	2 Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
99	c2q7cC_	Alignment	not modelled	10.3	11 PDB header: viral protein Chain: C: PDB Molecule: fusion protein between yeast variant gcn4 and PDBTitle: crystal structure of iqn17