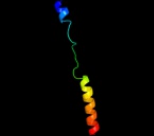
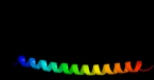
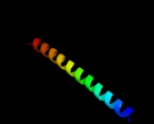
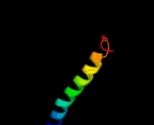
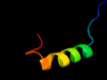


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1bgfa_	 Alignment		89.0	16	Fold: Transcription factor STAT-4 N-domain Superfamily: Transcription factor STAT-4 N-domain Family: Transcription factor STAT-4 N-domain
2	c3e98B_	 Alignment		43.6	14	PDB header: unknown function Chain: B: PDB Molecule: gaf domain of unknown function; PDBTitle: crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
3	c1ci6B_	 Alignment		39.1	22	PDB header: transcription Chain: B: PDB Molecule: transcription factor c/ebp beta; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
4	c3m9bK_	 Alignment		25.5	18	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
5	c3movB_	 Alignment		19.3	17	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of human lamin-b1 coil 2 segment
6	c3dmqA_	 Alignment		18.7	19	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase-associated protein rapa; PDBTitle: crystal structure of rapa, a swi2/snf2 protein that2 recycles rna polymerase during transcription
7	c3mudA_	 Alignment		18.2	15	PDB header: contractile protein Chain: A: PDB Molecule: dna repair protein xrcc4, tropomyosin alpha-1 chain; PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle
8	d1ivs1	 Alignment		16.9	17	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
9	c1debA_	 Alignment		16.2	26	PDB header: structural protein Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: crystal structure of the n-terminal coiled coil domain from2 apc
10	c3jrtA_	 Alignment		15.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron cassette protein vpc_cass2; PDBTitle: structure from the mobile metagenome of v. paracholerae:2 integron cassette protein vpc_cass2
11	c1yvlB_	 Alignment		15.4	14	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1

12	c3hnwB_	Alignment		13.6	17	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
13	c3dbyN_	Alignment		13.5	17	PDB header: structural genomics, unknown function Chain: N: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from bacillus cereus2 g9241 (csap target)
14	d1c8sa_	Alignment		13.3	32	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
15	d3dbya2	Alignment		13.1	25	Fold: Bromodomain-like Superfamily: Bacillus cereus metalloprotein-like Family: Bacillus cereus metalloprotein-like
16	c2ql7C_	Alignment		12.8	52	PDB header: transcription Chain: C: PDB Molecule: b-cell lymphoma 9 protein; PDBTitle: crystal structure of a beta-catenin/bcl9/tcf4 complex
17	c3lphD_	Alignment		11.5	31	PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer
18	d2cx1a2	Alignment		11.2	35	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Hypothetical protein APE0525, N-terminal domain
19	c2xdjF_	Alignment		11.1	15	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
20	d1rsoa_	Alignment		10.7	32	Fold: L27 domain Superfamily: L27 domain Family: L27 domain
21	d2i5nl1	Alignment	not modelled	9.7	18	Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits
22	c2x7lP_	Alignment	not modelled	9.5	31	PDB header: immune system Chain: P: PDB Molecule: hiv rev; PDBTitle: implications of the hiv-1 rev dimer structure at 3.2a2 resolution for multimeric binding to the rev response3 element
23	d2axta1	Alignment	not modelled	8.8	21	Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits
24	c2odxA_	Alignment	not modelled	8.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase polypeptide iv; PDBTitle: solution structure of zn(ii)cox4
25	d1jixa_	Alignment	not modelled	8.4	55	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: beta-Glycosyltransferase (DNA-modifying)
26	c1x8yA_	Alignment	not modelled	8.3	15	PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b
27	d3d19a2	Alignment	not modelled	8.3	43	Fold: Bromodomain-like Superfamily: Bacillus cereus metalloprotein-like Family: Bacillus cereus metalloprotein-like
28	c1q68A_	Alignment	not modelled	8.0	41	PDB header: membrane protein/transferase Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: solution structure of t-cell surface glycoprotein cd4 and2 proto-oncogene tyrosine-protein kinase lck fragments
						PDB header: vimentin

29	c1gk4A_	Alignment	not modelled	8.0	13	Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)
30	c2xusA_	Alignment	not modelled	7.7	34	PDB header: protein binding Chain: A: PDB Molecule: breast cancer metastasis-suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region
31	d1e3oc2	Alignment	not modelled	7.6	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
32	d3d19a1	Alignment	not modelled	7.6	21	Fold: Bromodomain-like Superfamily: Bacillus cereus metalloprotein-like Family: Bacillus cereus metalloprotein-like
33	d1m0ka_	Alignment	not modelled	7.5	32	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
34	c1m0ka_	Alignment	not modelled	7.5	32	PDB header: ion transport Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: bacteriorhodopsin k intermediate at 1.43 a resolution
35	d2ef1a1	Alignment	not modelled	6.8	17	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: ADP ribosyl cyclase-like
36	d2b3aa1	Alignment	not modelled	6.8	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
37	d1au7a2	Alignment	not modelled	6.7	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
38	c2jrrA_	Alignment	not modelled	6.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of q5lls5 from silicibacter2 pomeroyi. northeast structural genomics consortium target3 sir90
39	c3t97A_	Alignment	not modelled	6.4	19	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
40	d3dbya1	Alignment	not modelled	6.2	17	Fold: Bromodomain-like Superfamily: Bacillus cereus metalloprotein-like Family: Bacillus cereus metalloprotein-like
41	d1s35a2	Alignment	not modelled	6.0	15	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
42	c1zxaB_	Alignment	not modelled	5.9	33	PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 1, alpha isozyme; PDBTitle: solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
43	d1lfda_	Alignment	not modelled	5.7	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
44	c3ectA_	Alignment	not modelled	5.6	24	PDB header: transferase Chain: A: PDB Molecule: hexapeptide-repeat containing-acetyltransferase; PDBTitle: crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
45	c2rmgA_	Alignment	not modelled	5.6	26	PDB header: hormone Chain: A: PDB Molecule: urocortin-2; PDBTitle: human urocortin 2
46	c3fliH_	Alignment	not modelled	5.5	34	PDB header: protein binding Chain: H: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: human escrt-0 core complex
47	d1uaza_	Alignment	not modelled	5.5	23	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
48	d1nxca_	Alignment	not modelled	5.5	21	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
49	c2zdiC_	Alignment	not modelled	5.4	9	PDB header: chaperone Chain: C: PDB Molecule: prefoldin subunit alpha; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3