
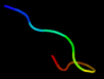









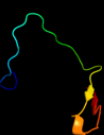

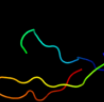







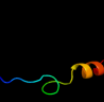


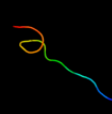








#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b24a1	 Alignment		26.8	45	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
2	d2piaa3	 Alignment		26.3	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
3	d1cwea_	 Alignment		22.8	30	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
4	d2afja1	 Alignment		15.1	21	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: SPRY domain
5	c2z4dA_	 Alignment		14.4	13	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn13; PDBTitle: nmr structures of yeast proteasome component rpn13
6	c3ts3D_	 Alignment		10.1	13	PDB header: viral protein Chain: D: PDB Molecule: capsid polypeptide; PDBTitle: crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
7	c3uatA_	 Alignment		9.8	28	PDB header: peptide binding protein Chain: A: PDB Molecule: disks large homolog 1; PDBTitle: guanylate kinase domains of the maguk family scaffold proteins as2 specific phospho-protein binding modules
8	c2w9vA_	 Alignment		9.3	38	PDB header: toxin Chain: A: PDB Molecule: short disintegrin jerdostatin; PDBTitle: solution structure of jerdostatin from trimeresurus2 jerdonii with end c-terminal residues n45g46 deleted
9	c2i46A_	 Alignment		8.9	11	PDB header: protein binding Chain: A: PDB Molecule: adrenocortical dysplasia protein homolog; PDBTitle: crystal structure of human tpp1
10	d1eg3a2	 Alignment		8.6	26	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
11	d1rkua_	 Alignment		8.5	13	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH

12	d2b6ca1	Alignment		7.9	26	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: BC3264-like
13	d1y0ja1	Alignment		7.3	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
14	c2p11A	Alignment		7.2	38	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bx_e_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
15	c3u7za	Alignment		7.1	11	PDB header: metal binding protein Chain: A: PDB Molecule: putative metal binding protein rumgna_00854; PDBTitle: crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
16	d1a3qa1	Alignment		7.1	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
17	d2f69a1	Alignment		7.1	60	Fold: open-sided beta-meander Superfamily: Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain Family: Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain
18	d2nn6g3	Alignment		7.0	27	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
19	c3m9bK	Alignment		6.9	10	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
20	c1q90R	Alignment		6.9	33	PDB header: photosynthesis Chain: R: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
21	d1q90r	Alignment	not modelled	6.9	33	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
22	c3pgeA	Alignment	not modelled	6.9	12	PDB header: dna binding protein Chain: A: PDB Molecule: sumo-modified proliferating cell nuclear antigen; PDBTitle: structure of sumoylated pcna
23	d2uubc1	Alignment	not modelled	6.9	31	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
24	d1twfc1	Alignment	not modelled	6.9	29	Fold: DCoH-like Superfamily: RBP11-like subunits of RNA polymerase Family: RNA polymerase alpha subunit dimerisation domain
25	d1whya	Alignment	not modelled	6.8	22	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
26	d1ji8a	Alignment	not modelled	6.8	26	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
27	c2kaeA	Alignment	not modelled	6.3	25	PDB header: transcription/dna Chain: A: PDB Molecule: gata-type transcription factor; PDBTitle: data-driven model of med1:dna complex
28	c2l25A	Alignment	not modelled	5.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: np_888769.1
29	c1a3qa	Alignment	not modelled	5.7	19	PDB header: transcription/dna Chain: A: PDB Molecule: protein (nuclear factor kappa-b p52);

					PDBTitle: human nf-kappa-b p52 bound to dna
30	c3s2xB	Alignment	not modelled	5.7	37 PDB header: transferase Chain: B: PDB Molecule: acetyl-coa synthase subunit alpha; PDBTitle: structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
31	d2fug31	Alignment	not modelled	5.4	16 Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
32	c2l1qA	Alignment	not modelled	5.4	58 PDB header: antimicrobial protein Chain: A: PDB Molecule: liver-expressed antimicrobial peptide 2; PDBTitle: solution structure of human liver expressed antimicrobial peptide 2
33	d2vuti1	Alignment	not modelled	5.3	43 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
34	d2ieca1	Alignment	not modelled	5.3	24 Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
35	d1gjiwa1	Alignment	not modelled	5.2	28 Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
36	d1f2fa	Alignment	not modelled	5.2	50 Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
37	c2kvoA	Alignment	not modelled	5.0	17 PDB header: photosynthesis Chain: A: PDB Molecule: photosystem ii reaction center psb28 protein; PDBTitle: solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171
38	c2de4B	Alignment	not modelled	5.0	20 PDB header: hydrolase Chain: B: PDB Molecule: dibenzothiophene desulfurization enzyme b; PDBTitle: crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid