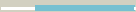
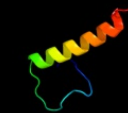
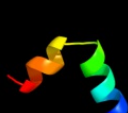
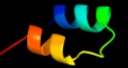


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hrkb1	 Alignment		39.4	22	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Arc1p N-terminal domain-like
2	c3hdfA_	 Alignment		24.4	16	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of truncated endolysin r21 from phage 21
3	c2elkA_	 Alignment		17.8	22	PDB header: transcription Chain: A: PDB Molecule: spcc24b10.08c protein; PDBTitle: solution structure of the sant domain of fission yeast2 spcc24b10.08c protein
4	c2diiA_	 Alignment		15.4	30	PDB header: transcription Chain: A: PDB Molecule: tfiih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
5	d2diiA1	 Alignment		15.0	30	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
6	c3e2sA_	 Alignment		15.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure reduced puta86-630 mutant y540s complexed with l-2 proline
7	d1nh1a_	 Alignment		14.7	16	Fold: Antivirulence factor Superfamily: Antivirulence factor Family: Antivirulence factor
8	c1nh1A_	 Alignment		14.7	16	PDB header: avirulence protein Chain: A: PDB Molecule: avirulence b protein; PDBTitle: crystal structure of the type iii effector avrb from2 pseudomonas syringae.
9	c2l9bA_	 Alignment		14.1	24	PDB header: transcription Chain: A: PDB Molecule: mrna 3'-end-processing protein rna15; PDBTitle: heterodimer between rna14p monkeytail domain and rna15p hinge domain2 of the yeast cf ia complex
10	d1gvda_	 Alignment		13.9	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
11	d1x41a1	 Alignment		13.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain

12	c1h88C	Alignment		13.0	20	PDB header: transcription/dna Chain: C: PDB Molecule: myb proto-oncogene protein; PDBTitle: crystal structure of ternary protein-dna complex1
13	d2okua1	Alignment		11.5	22	Fold: N-cbl like Superfamily: PG0775 C-terminal domain-like Family: PG0775 C-terminal domain-like
14	c2dimA	Alignment		11.4	15	PDB header: dna binding protein Chain: A: PDB Molecule: cell division cycle 5-like protein; PDBTitle: solution structure of the myb_dna-binding domain of human2 cell division cycle 5-like protein
15	c1wxpA	Alignment		11.0	22	PDB header: transport protein Chain: A: PDB Molecule: tho complex subunit 1; PDBTitle: solution structure of the death domain of nuclear matrix2 protein p84
16	d1a5ja1	Alignment		10.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
17	c2elpA	Alignment		10.1	43	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
18	c4a69C	Alignment		10.0	8	PDB header: transcription Chain: C: PDB Molecule: nuclear receptor corepressor 2; PDBTitle: structure of hdac3 bound to corepressor and inositol tetraphosphate
19	c2yusA	Alignment		9.9	33	PDB header: transcription Chain: A: PDB Molecule: swi/snf-related matrix-associated actin- PDBTitle: solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1
20	c1x41A	Alignment		9.8	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional adaptor 2-like, isoform b; PDBTitle: solution structure of the myb-like dna binding domain of2 human transcriptional adaptor 2-like, isoform b
21	c1x9dA	Alignment	not modelled	9.6	19	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum mannosyl-oligosaccharide 1, PDBTitle: crystal structure of human class i alpha-1,2-mannosidase in2 complex with thio-disaccharide substrate analogue
22	d1x9da1	Alignment	not modelled	9.6	19	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
23	d2f5va1	Alignment	not modelled	9.5	10	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
24	c2d9aA	Alignment	not modelled	9.4	20	PDB header: transcription Chain: A: PDB Molecule: myb-related protein b; PDBTitle: solution structure of rsgi ruh-050, a myb dna-binding2 domain in mouse cdna
25	c1guuA	Alignment	not modelled	9.3	20	PDB header: transcription Chain: A: PDB Molecule: myb proto-oncogene protein; PDBTitle: crystal structure of c-myb r1
26	d1guua	Alignment	not modelled	9.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
27	c2yqfA	Alignment	not modelled	9.3	9	PDB header: protein binding Chain: A: PDB Molecule: ankyrin-1; PDBTitle: solution structure of the death domain of ankyrin-1
28	d1h8ac1	Alignment	not modelled	8.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain

29	c2kxaA_	Alignment	not modelled	8.0	32	PDB header: viral protein, immune system Chain: A: PDB Molecule: haemagglutinin ha2 chain peptide; PDBTitle: the hemagglutinin fusion peptide (h1 subtype) at ph 7.4
30	c2egrA_	Alignment	not modelled	7.7	11	PDB header: transcription Chain: A: PDB Molecule: nuclear receptor corepressor 1; PDBTitle: solution structure of the first sant domain from human2 nuclear receptor corepressor 1
31	c1x3wB_	Alignment	not modelled	7.6	32	PDB header: hydrolase Chain: B: PDB Molecule: uv excision repair protein rad23; PDBTitle: structure of a peptide:n-glycanase-rad23 complex
32	c2anxB_	Alignment	not modelled	7.5	24	PDB header: hydrolase Chain: B: PDB Molecule: lysozyme; PDBTitle: crystal structure of bacteriophage p22 lysozyme mutant l87m
33	c1p8cD_	Alignment	not modelled	7.5	16	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
34	c1iboA_	Alignment	not modelled	7.0	32	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin ha2 chain peptide; PDBTitle: nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 7.4
35	c1ibnA_	Alignment	not modelled	7.0	32	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin ha2 chain peptide; PDBTitle: nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 5
36	d1tj1a2	Alignment	not modelled	7.0	16	Fold: TIM beta/alpha-barrel Superfamily: FAD-linked oxidoreductase Family: Proline dehydrogenase domain of bifunctional PutA protein
37	c1xopA_	Alignment	not modelled	6.8	30	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: nmr structure of g1v mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
38	d2cu7a1	Alignment	not modelled	6.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
39	d1nxca_	Alignment	not modelled	6.5	23	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
40	d1eo0a_	Alignment	not modelled	6.5	23	Fold: N-cbl like Superfamily: Conserved domain common to transcription factors TFIIIS, elongin A, CRSP70 Family: Conserved domain common to transcription factors TFIIIS, elongin A, CRSP70
41	c3g36D_	Alignment	not modelled	5.9	14	PDB header: nuclear protein Chain: D: PDB Molecule: protein dpy-30 homolog; PDBTitle: crystal structure of the human dpy-30-like c-terminal domain
42	c2l4gA_	Alignment	not modelled	5.5	32	PDB header: viral protein Chain: A: PDB Molecule: haemagglutinin; PDBTitle: influenza haemagglutinin fusion peptide mutant g13a
43	c2of5K_	Alignment	not modelled	5.4	23	PDB header: apoptosis Chain: K: PDB Molecule: leucine-rich repeat and death domain-containing PDBTitle: oligomeric death domain complex
44	d1e50b_	Alignment	not modelled	5.3	35	Fold: Core binding factor beta, CBF Superfamily: Core binding factor beta, CBF Family: Core binding factor beta, CBF
45	d1z0xa2	Alignment	not modelled	5.3	23	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
46	d1c6vx_	Alignment	not modelled	5.2	60	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
47	c1c6vX_	Alignment	not modelled	5.2	60	PDB header: dna binding protein Chain: X: PDB Molecule: protein (siu89134); PDBTitle: siv integrase (catalytic domain + dna biding domain2 comprising residues 50-293) mutant with phe 185 replaced3 by his (f185h)
48	d2gs4a1	Alignment	not modelled	5.2	17	Fold: Ferritin-like Superfamily: Ferritin-like Family: YciF-like
49	c3hdeA_	Alignment	not modelled	5.2	16	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of full-length endolysin r21 from phage 21