
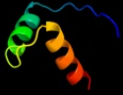



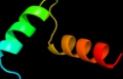





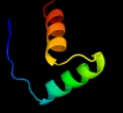



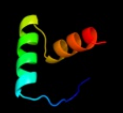



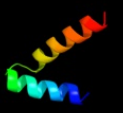

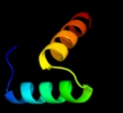











#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1q5vB_	 Alignment		95.3	35	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
2	c2bj3D_	 Alignment		95.2	20	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
3	d2bj7a1	 Alignment		95.2	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
4	c2ca9B_	 Alignment		94.6	23	PDB header: transcriptional regulation Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
5	d2hzaa1	 Alignment		93.1	36	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
6	d2hzab1	 Alignment		92.8	36	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
7	c2k5jB_	 Alignment		89.9	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
8	d2cpga_	 Alignment		72.3	26	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
9	d1y9ba1	 Alignment		29.3	14	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
10	c2kwpA_	 Alignment		25.7	14	PDB header: transcription Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: solution structure of the aminoterminal domain of e. coli nusa
11	c3kk4B_	 Alignment		22.3	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i

12	c2kkmA_	Alignment		18.9	37	PDB header: translation Chain: A: PDB Molecule: translation machinery-associated protein 16; PDBTitle: solution nmr structure of yeast protein yor252w [residues2 38-178]: northeast structural genomics consortium target3 yt654
13	d1svma_	Alignment		17.5	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
14	c2k29A_	Alignment		15.4	18	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
15	c1l2fA_	Alignment		14.7	31	PDB header: transcription Chain: A: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
16	c2k9lB_	Alignment		12.9	21	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid prn1, complete sequence; PDBTitle: nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
17	d1t6sa2	Alignment		12.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ScpB/YpuH-like
18	d1qx8a_	Alignment		11.8	55	Fold: ROP-like Superfamily: ROP protein Family: ROP protein
19	c2kebA_	Alignment		11.6	17	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase subunit alpha b; PDBTitle: nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
20	c2rbfB_	Alignment		10.8	19	PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
21	c2jvdA_	Alignment	not modelled	10.6	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein yncz; PDBTitle: solution nmr structure of the folded n-terminal fragment of2 upf0291 protein yncz from bacillus subtilis. northeast3 structural genomics target sr384-1-46
22	c2x7lP_	Alignment	not modelled	9.1	33	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	d1myla_	Alignment	not modelled	8.7	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
24	d1mnta_	Alignment	not modelled	8.3	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
25	c3h87D_	Alignment	not modelled	8.1	27	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
26	c2hepA_	Alignment	not modelled	7.4	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein yncz; PDBTitle: solution nmr structure of the upf0291 protein yncz from2 bacillus subtilis. northeast structural genomics target3 sr384.
27	d2hepa1	Alignment	not modelled	7.4	29	Fold: Long alpha-hairpin Superfamily: YncC-like Family: YncC-like
28	c3lphD_	Alignment	not modelled	6.8	33	PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer

29	d1b28a_	Alignment	not modelled	6.5	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
30	c2a8vA_	Alignment	not modelled	6.1	24	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
31	d2cz4a1	Alignment	not modelled	5.4	19	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
32	c2r0vB_	Alignment	not modelled	5.1	31	PDB header: transcription Chain: B: PDB Molecule: chromatin structure-remodeling complex protein PDBTitle: structure of the rsc4 tandem bromodomain acetylated at k25