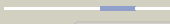
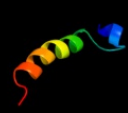
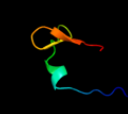
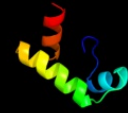
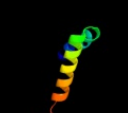
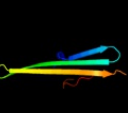
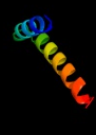
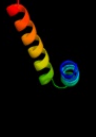
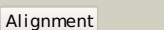
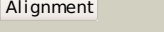
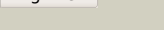
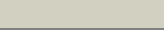
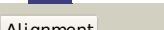
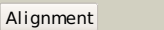
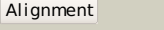
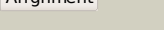
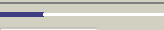
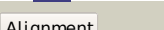
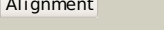
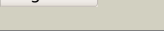
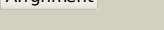
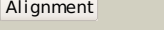


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l0kA_	 Alignment		25.5	34	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiiiid in complex2 with dna
2	dlug2a_	 Alignment		23.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
3	d2cc3a1	 Alignment		21.2	8	Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like
4	c3rggD_	 Alignment		18.8	10	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
5	d2ix0a3	 Alignment		16.9	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
6	dlu11a_	 Alignment		15.8	10	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
7	dl13la1	 Alignment		15.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
8	d2hsqa1	 Alignment		15.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
9	c2fw9A_	 Alignment		14.5	10	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
10	c3mzyA_	 Alignment		14.4	21	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
11	c3l1eA_	 Alignment		13.9	22	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin a chain; PDBTitle: bovine alphaa crystallin zinc bound

12	dlyioa1	Alignment		12.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
13	c2krfB	Alignment		11.8	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
14	c2wj7D	Alignment		11.5	12	PDB header: chaperone Chain: D: PDB Molecule: alpha-crystallin b chain; PDBTitle: human alphab crystallin
15	c1dgrW	Alignment		11.4	14	PDB header: plant protein Chain: W: PDB Molecule: canavalin; PDBTitle: refined crystal structure of canavalin from jack bean
16	d1p4wa	Alignment		11.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
17	d1qcza	Alignment		11.3	3	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
18	d3eipa	Alignment		11.1	10	Fold: FKBP-like Superfamily: Colicin E3 immunity protein Family: Colicin E3 immunity protein
19	c2jpcA	Alignment		11.1	16	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
20	c2ywxA	Alignment		11.1	8	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
21	c3lp6D	Alignment	not modelled	10.2	8	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
22	d1fsea	Alignment	not modelled	10.2	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
23	c3glaA	Alignment	not modelled	10.0	18	PDB header: chaperone Chain: A: PDB Molecule: low molecular weight heat shock protein; PDBTitle: crystal structure of the hspa from xanthomonas axonopodis
24	d1dgwa	Alignment	not modelled	9.6	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
25	c3trhl	Alignment	not modelled	9.3	3	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
26	d1qpza1	Alignment	not modelled	9.3	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
27	d1uija1	Alignment	not modelled	9.2	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
28	d2phla1	Alignment	not modelled	9.2	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein

29	c3orsD_	 Alignment	not modelled	8.9	5	PDB header: isomerase, biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
30	c3q9qB_	 Alignment	not modelled	8.0	35	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein beta-1; PDBTitle: hspb1 fragment second crystal form
31	c2jtwA_	 Alignment	not modelled	7.9	50	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
32	d1t3ua_	 Alignment	not modelled	7.5	7	Fold: Cell division protein ZapA-like Superfamily: Cell division protein ZapA-like Family: Cell division protein ZapA-like
33	d1a04a1	 Alignment	not modelled	7.5	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
34	d2bjca1	 Alignment	not modelled	7.3	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
35	c2nviA_	 Alignment	not modelled	7.3	42	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
36	c2bolA_	 Alignment	not modelled	6.6	15	PDB header: heat shock protein Chain: A: PDB Molecule: small heat shock protein; PDBTitle: crystal structure and assembly of tsp36, a metazoan small2 heat shock protein
37	d1fpoa1	 Alignment	not modelled	6.4	11	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
38	d1efaa1	 Alignment	not modelled	6.3	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
39	c2rnjA_	 Alignment	not modelled	6.3	16	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrra; PDBTitle: nmr structure of the s. aureus vrra dna binding domain
40	c1zljE_	 Alignment	not modelled	6.0	26	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
41	c2l8nA_	 Alignment	not modelled	6.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
42	c2bhmE_	 Alignment	not modelled	5.9	15	PDB header: bacterial protein Chain: E: PDB Molecule: type iv secretion system protein virb8; PDBTitle: crystal structure of virb8 from brucella suis
43	d1lcda_	 Alignment	not modelled	5.8	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
44	d1luxda_	 Alignment	not modelled	5.7	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
45	d1uika1	 Alignment	not modelled	5.7	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
46	d1ik9a1	 Alignment	not modelled	5.6	13	Fold: XRCC4, N-terminal domain Superfamily: XRCC4, N-terminal domain Family: XRCC4, N-terminal domain
47	c3o0lB_	 Alignment	not modelled	5.6	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
48	d2p81a1	 Alignment	not modelled	5.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
49	c3bw8B_	 Alignment	not modelled	5.6	20	PDB header: transferase Chain: B: PDB Molecule: mono-adp-ribosyltransferase c3; PDBTitle: crystal structure of the clostridium limosum c3 exoenzyme
50	d1xsva_	 Alignment	not modelled	5.5	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
51	c3hugA_	 Alignment	not modelled	5.5	21	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigl
52	d1o4va_	 Alignment	not modelled	5.4	8	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
53	c3guzB_	 Alignment	not modelled	5.3	19	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: structural and substrate-binding studies of pantothenate2 synthetase (ps) provide insights into homotropic inhibition3 by pantoate in ps's
		Alignment				Fold: SAM domain-like

54	d1go3f_	Alignment	not modelled	5.1	10	Superfamily: HRDC-like Family: RNA polymerase II subunit RBP4 (RpoF)
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