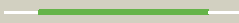
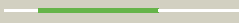
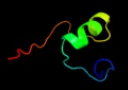
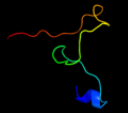
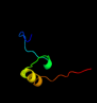
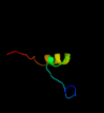
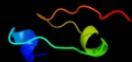
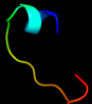


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h9qC_	 Alignment		53.2	19	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h)
2	c3fd3A_	 Alignment		52.6	23	PDB header: transcription regulator Chain: A: PDB Molecule: chromosome replication initiation inhibitor protein; PDBTitle: structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
3	c2hxrA_	 Alignment		45.6	20	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator cynr; PDBTitle: structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
4	c3jv9B_	 Alignment		39.1	22	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis
5	c2f7cA_	 Alignment		39.0	19	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate
6	c2h9bB_	 Alignment		33.2	21	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
7	d1koha2	 Alignment		30.5	26	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Non-canonical RBD domain
8	dlixca2	 Alignment		28.6	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
9	c2f78A_	 Alignment		20.2	23	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate
10	d1al3a_	 Alignment		18.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
11	c1al3A_	 Alignment		18.7	13	PDB header: transcription regulation Chain: A: PDB Molecule: cys regulon transcriptional activator cysb; PDBTitle: cofactor binding fragment of cysb from klebsiella aerogenes

12	cliz1B_	Alignment		18.5	6	PDB header: dna binding protein Chain: B: PDB Molecule: lysr-type regulatory protein; PDBTitle: crystal structure of cbnr, a lysr family transcriptional2 regulator
13	c3onmB_	Alignment		18.4	29	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator lrrha; PDBTitle: effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
14	c3tlbB_	Alignment		16.9	32	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: crystal structure of the full-length aphb n100e variant
15	d1ft8a2	Alignment		16.4	30	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Non-canonical RBD domain
16	c3fzjC_	Alignment		12.4	19	PDB header: transcription regulator Chain: C: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: tsar low resolution crystal structure, tetragonal form
17	c3kk4B_	Alignment		11.8	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
18	c3kosA_	Alignment		10.5	9	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator ampr; PDBTitle: structure of the ampr effector binding domain from citrobacter2 freundii
19	d2esna2	Alignment		10.1	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
20	c3a5dB_	Alignment		9.4	32	PDB header: hydrolase Chain: B: PDB Molecule: v-type atp synthase alpha chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
21	c3ispA_	Alignment	not modelled	8.5	28	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis
22	d1dwka2	Alignment	not modelled	8.0	56	Fold: Cyanase C-terminal domain Superfamily: Cyanase C-terminal domain Family: Cyanase C-terminal domain
23	d2b0ja1	Alignment	not modelled	6.4	35	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HMD dimerization domain-like
24	c2esnC_	Alignment	not modelled	6.1	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
25	c2iv1J_	Alignment	not modelled	5.9	40	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
26	c1w0jB_	Alignment	not modelled	5.8	32	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase alpha chain heart isoform, PDBTitle: beryllium fluoride inhibited bovine f1-atpase
27	c3ho7A_	Alignment	not modelled	5.7	23	PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
28	d1f6fa_	Alignment	not modelled	5.6	33	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines