




















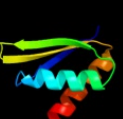








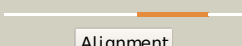

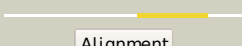

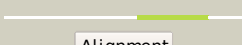

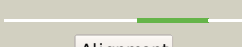






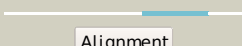
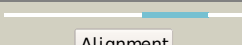





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3i6pF_</a>	 Alignment		100.0	46	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> ethanolamine utilization protein eutm; <b>PDBTitle:</b> ethanolamine utilization microcompartment shell subunit, eutm
2	<a href="#">c3ngkA_</a>	 Alignment		100.0	45	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> propanediol utilization protein pdua; <b>PDBTitle:</b> pdua from salmonella enterica typhimurium
3	<a href="#">d2a10a1</a>	 Alignment		100.0	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> CcmK-like <b>Family:</b> CcmK-like
4	<a href="#">d2a1ba1</a>	 Alignment		100.0	34	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> CcmK-like <b>Family:</b> CcmK-like
5	<a href="#">d2ewha1</a>	 Alignment		100.0	37	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> CcmK-like <b>Family:</b> CcmK-like
6	<a href="#">c3nwgA_</a>	 Alignment		100.0	29	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> microcompartments protein; <b>PDBTitle:</b> the crystal structure of a microcompartments protein from2 desulfitobacterium hafniense dcb
7	<a href="#">c3n79A_</a>	 Alignment		100.0	28	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> pdut; <b>PDBTitle:</b> pdut c38s mutant from salmonella enterica typhimurium
8	<a href="#">c3i71B_</a>	 Alignment		99.9	100	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ethanolamine utilization protein eutk; <b>PDBTitle:</b> ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain
9	<a href="#">c3io0A_</a>	 Alignment		99.8	22	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> etub protein; <b>PDBTitle:</b> crystal structure of etub from clostridium kluyveri
10	<a href="#">c3i82A_</a>	 Alignment		99.6	23	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> ethanolamine utilization protein eutl; <b>PDBTitle:</b> ethanolamine utilization microcompartment shell subunit, eutl closed2 form
11	<a href="#">c3cqiD_</a>	 Alignment		98.2	24	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> propanediol utilization protein pduu; <b>PDBTitle:</b> crystal structure of the pduu shell protein from the pdu2 microcompartment

12	<a href="#">c3ia0c_</a>		Alignment		98.1	28	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> ethanolamine utilization protein euts; <b>PDBTitle:</b> ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
13	<a href="#">c3f56F_</a>		Alignment		96.2	23	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> csos1d; <b>PDBTitle:</b> the structure of a previously undetected carboxysome shell2 protein: csos1d from prochlorococcus marinus med4
14	<a href="#">d1mka1</a>		Alignment		83.9	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator IclR, N-terminal domain
15	<a href="#">c2g7uB_</a>		Alignment		82.7	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
16	<a href="#">c3r4kD_</a>		Alignment		81.3	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
17	<a href="#">c2o0yB_</a>		Alignment		74.3	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
18	<a href="#">c2xroE_</a>		Alignment		64.9	19	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgv; <b>PDBTitle:</b> crystal structure of ttgv in complex with its dna operator
19	<a href="#">d1j5ya1</a>		Alignment		58.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
20	<a href="#">c1mkmA_</a>		Alignment		56.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> iclr transcriptional regulator; <b>PDBTitle:</b> crystal structure of the thermotoga maritima iclr
21	<a href="#">c3lstB_</a>		Alignment	not modelled	41.2	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calo1 methyltransferase; <b>PDBTitle:</b> crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
22	<a href="#">c2zmeA_</a>		Alignment	not modelled	37.2	35	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar-sorting protein snf8; <b>PDBTitle:</b> integrated structural and functional model of the human escrt-ii2 complex
23	<a href="#">c3cuqA_</a>		Alignment	not modelled	37.0	35	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar-sorting protein snf8; <b>PDBTitle:</b> integrated structural and functional model of the human escrt-ii2 complex
24	<a href="#">c3eqxB_</a>		Alignment	not modelled	36.0	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fic domain containing transcriptional regulator; <b>PDBTitle:</b> crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
25	<a href="#">c1f5tA_</a>		Alignment	not modelled	34.1	8	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
26	<a href="#">c2ia2D_</a>		Alignment	not modelled	33.9	21	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
27	<a href="#">d1jhfa1</a>		Alignment	not modelled	32.6	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
28	<a href="#">c3mq0A_</a>		Alignment	not modelled	32.4	22	<b>PDB header:</b> transcription repressor <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor of the blcabc operon; <b>PDBTitle:</b> crystal structure of agobacterium tumefaciens repressor

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29	<a href="#">c1w7pD_</a>	Alignment	not modelled	29.5	16	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> vps36p, ylr417w; <b>PDBTitle:</b> the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
30	<a href="#">c2v9vA_</a>	Alignment	not modelled	26.9	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> crystal structure of moorella thermoacetica selb(377-511)
31	<a href="#">c1u5tB_</a>	Alignment	not modelled	25.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> defective in vacuolar protein sorting; vps36p; <b>PDBTitle:</b> structure of the escrt-ii endosomal trafficking complex
32	<a href="#">c2v79B_</a>	Alignment	not modelled	25.0	23	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna replication protein dnad; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
33	<a href="#">c3cuoB_</a>	Alignment	not modelled	24.8	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
34	<a href="#">c2vn2B_</a>	Alignment	not modelled	24.7	18	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome replication initiation protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
35	<a href="#">c2x4hA_</a>	Alignment	not modelled	24.7	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
36	<a href="#">c1u5tA_</a>	Alignment	not modelled	23.9	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> appears to be functionally related to snf7; <b>PDBTitle:</b> structure of the escrt-ii endosomal trafficking complex
37	<a href="#">c2oqgA_</a>	Alignment	not modelled	21.6	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
38	<a href="#">c2zmeB_</a>	Alignment	not modelled	21.6	26	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein-sorting-associated protein 36; <b>PDBTitle:</b> integrated structural and functional model of the human escrt-ii2 complex
39	<a href="#">d2b0la1</a>	Alignment	not modelled	21.6	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Cody HTH domain
40	<a href="#">d1biaa1</a>	Alignment	not modelled	18.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
41	<a href="#">c3f6vA_</a>	Alignment	not modelled	17.7	39	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for2 arsenical resistance
42	<a href="#">c3f6oB_</a>	Alignment	not modelled	17.2	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of arsr family transcriptional regulator,2 rha00566
43	<a href="#">c3dp7B_</a>	Alignment	not modelled	16.8	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
44	<a href="#">c3mczB_</a>	Alignment	not modelled	16.4	37	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
45	<a href="#">c1j5yA_</a>	Alignment	not modelled	16.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, biotin repressor family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
46	<a href="#">d1u2wa1</a>	Alignment	not modelled	15.8	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
47	<a href="#">d1tw3a1</a>	Alignment	not modelled	15.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
48	<a href="#">d1u5ta2</a>	Alignment	not modelled	15.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
49	<a href="#">c2h09A_</a>	Alignment	not modelled	14.5	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from e. coli
50	<a href="#">d1wi9a_</a>	Alignment	not modelled	13.9	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PCI domain (PINT motif)
51	<a href="#">d1sfxa_</a>	Alignment	not modelled	12.9	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
52	<a href="#">c3hruA_</a>	Alignment	not modelled	11.6	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metalloregulator scar; <b>PDBTitle:</b> crystal structure of scar with bound zn2+

53	<a href="#">d2htja1</a>	Alignment	not modelled	10.9	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FaeA-like
54	<a href="#">c1r22B_</a>	Alignment	not modelled	10.8	25	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
55	<a href="#">c1x1aA_</a>	Alignment	not modelled	10.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> crtf-related protein; <b>PDBTitle:</b> crystal structure of bchu complexed with s-adenosyl-l-methionine
56	<a href="#">c2it0A_</a>	Alignment	not modelled	10.0	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
57	<a href="#">c1fx7C_</a>	Alignment	not modelled	9.6	9	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
58	<a href="#">d1ku9a_</a>	Alignment	not modelled	8.7	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
59	<a href="#">c3boqB_</a>	Alignment	not modelled	7.8	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
60	<a href="#">c2eo4A_</a>	Alignment	not modelled	7.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical histidine triad nucleotide-binding <b>PDBTitle:</b> crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfolobus tokodaii strain7
61	<a href="#">c3r0aB_</a>	Alignment	not modelled	7.3	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina maezi go1 (gi2 21227196)
62	<a href="#">d2frha1</a>	Alignment	not modelled	6.7	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
63	<a href="#">c3jthA_</a>	Alignment	not modelled	6.6	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu; <b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
64	<a href="#">c1dpuA_</a>	Alignment	not modelled	6.1	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a (rpa32) c-terminal domain; <b>PDBTitle:</b> solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
65	<a href="#">d1dpua_</a>	Alignment	not modelled	6.1	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of RPA32
66	<a href="#">d2qn6b1</a>	Alignment	not modelled	6.1	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eIF-2-alpha, C-terminal domain <b>Family:</b> eIF-2-alpha, C-terminal domain
67	<a href="#">c3d5cX_</a>	Alignment	not modelled	6.1	16	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> peptide chain release factor 1; <b>PDBTitle:</b> structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
68	<a href="#">c3gwzB_</a>	Alignment	not modelled	5.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mmcr; <b>PDBTitle:</b> structure of the mitomycin 7-o-methyltransferase mmcr
69	<a href="#">d1stza1</a>	Alignment	not modelled	5.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
70	<a href="#">c3nzlA_</a>	Alignment	not modelled	5.7	43	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein satb1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b
71	<a href="#">d1qzza1</a>	Alignment	not modelled	5.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
72	<a href="#">c2ifoA_</a>	Alignment	not modelled	5.4	15	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> inovirus; <b>PDBTitle:</b> model-building studies of inovirus: genetic variations on a2 geometric theme
73	<a href="#">d2a61a1</a>	Alignment	not modelled	5.3	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators