



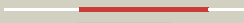



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3shoA_</a>	 Alignment		99.9	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rpir family; <b>PDBTitle:</b> crystal structure of rpir transcription factor from spharobacter2 thermophilus (sugar isomerase domain)
2	<a href="#">c3fxaA_</a>	 Alignment		99.9	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (Imof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
3	<a href="#">c2xhzC_</a>	 Alignment		99.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> arabinose 5-phosphate isomerase; <b>PDBTitle:</b> probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
4	<a href="#">c3etnD_</a>	 Alignment		99.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative phosphosugar isomerase involved in capsule <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
5	<a href="#">d1vima_</a>	 Alignment		99.9	19	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
6	<a href="#">d1m3sa_</a>	 Alignment		99.9	18	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
7	<a href="#">d1jeoa_</a>	 Alignment		99.9	22	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
8	<a href="#">c2puwA_</a>	 Alignment		99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isomerase domain of glutamine-fructose-6-phosphate <b>PDBTitle:</b> the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
9	<a href="#">c3trjC_</a>	 Alignment		99.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
10	<a href="#">c2zj3A_</a>	 Alignment		99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate <b>PDBTitle:</b> isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
11	<a href="#">d1x92a_</a>	 Alignment		99.8	20	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain

12	<a href="#">dlj5xa_</a>	<div><div></div><div>Alignment</div></div>		99.8	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
13	<a href="#">dltk9a_</a>	<div><div></div><div>Alignment</div></div>		99.8	19	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
14	<a href="#">c2yvab_</a>	<div><div></div><div>Alignment</div></div>		99.8	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dnaa initiator-associating protein diaa; <b>PDBTitle:</b> crystal structure of escherichia coli diaa
15	<a href="#">dlnria_</a>	<div><div></div><div>Alignment</div></div>		99.8	21	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
16	<a href="#">c1nriA_</a>	<div><div></div><div>Alignment</div></div>		99.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hi0754; <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
17	<a href="#">c2a3na_</a>	<div><div></div><div>Alignment</div></div>		99.8	19	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glucosamine-fructose-6-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
18	<a href="#">d1x94a_</a>	<div><div></div><div>Alignment</div></div>		99.8	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
19	<a href="#">c3fj1A_</a>	<div><div></div><div>Alignment</div></div>		99.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
20	<a href="#">c2x3ya_</a>	<div><div></div><div>Alignment</div></div>		99.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of gmha from burkholderia pseudomallei
21	<a href="#">c3euaD_</a>	<div><div></div><div>Alignment</div></div>	not modelled	99.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative fructose-aminoacid-6-phosphate deglycase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
22	<a href="#">c3hbaA_</a>	<div><div></div><div>Alignment</div></div>	not modelled	99.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
23	<a href="#">c3cvjB_</a>	<div><div></div><div>Alignment</div></div>	not modelled	99.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
24	<a href="#">c3iwfA_</a>	<div><div></div><div>Alignment</div></div>		99.7	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
25	<a href="#">c3g68A_</a>	<div><div></div><div>Alignment</div></div>	not modelled	99.7	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
26	<a href="#">c3tbfA_</a>	<div><div></div><div>Alignment</div></div>	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate aminotransferase <b>PDBTitle:</b> c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
						<b>Fold:</b> SIS domain

27	<a href="#">d1moqa_</a>	Alignment	not modelled	99.7	19	<b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
28	<a href="#">c2amlB_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
29	<a href="#">c3knzA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar binding protein; <b>PDBTitle:</b> crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
30	<a href="#">c3fkjA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerases; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
31	<a href="#">c2decA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 325aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
32	<a href="#">c1jxaA_</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine 6-phosphate synthase; <b>PDBTitle:</b> glucosamine 6-phosphate synthase with glucose 6-phosphate
33	<a href="#">c3odpA_</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase; <b>PDBTitle:</b> crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
34	<a href="#">d1x9ia_</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
35	<a href="#">c2o3fC_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybbh; <b>PDBTitle:</b> structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
36	<a href="#">d2o3fa1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> RpiR-like
37	<a href="#">c3i0zB_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase; <b>PDBTitle:</b> crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
38	<a href="#">c3c3jA_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase; <b>PDBTitle:</b> crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
39	<a href="#">c2q8nB_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of glucose-6-phosphate isomerase (ec2_5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
40	<a href="#">c1zzgB_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
41	<a href="#">c3ff1B_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structure of glucose 6-phosphate isomerase from staphylococcus aureus
42	<a href="#">d1c7qa_</a>	Alignment	not modelled	97.8	22	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
43	<a href="#">d1gzda_</a>	Alignment	not modelled	97.2	23	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
44	<a href="#">c3hjbA_</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
45	<a href="#">c3jx9B_</a>	Alignment	not modelled	97.1	10	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exigubacterium sp. 255-15 at 1.95 a resolution
46	<a href="#">d1iata_</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
47	<a href="#">d1lnwa_</a>	Alignment	not modelled	97.0	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
48	<a href="#">c3nqoB_</a>	Alignment	not modelled	97.0	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
49	<a href="#">c3ljkA_</a>	Alignment	not modelled	97.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> glucose-6-phosphate isomerase from francisella tularensis.
50	<a href="#">c2wu8A_</a>	Alignment	not modelled	97.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv

51	<a href="#">d1hm5a_</a>	Alignment	not modelled	96.9	20	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
52	<a href="#">c3ujhB_</a>	Alignment	not modelled	96.9	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
53	<a href="#">d1u0fa_</a>	Alignment	not modelled	96.9	24	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
54	<a href="#">d1q50a_</a>	Alignment	not modelled	96.8	24	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
55	<a href="#">c3bj6B_</a>	Alignment	not modelled	96.6	15	<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 transcription regulator sp03579
56	<a href="#">c3nbuC_</a>	Alignment	not modelled	96.5	22	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of pgi glucosephosphate isomerase
57	<a href="#">d3broa1</a>	Alignment	not modelled	96.5	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
58	<a href="#">c2o2cB_</a>	Alignment	not modelled	96.5	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase, glycosomal; <b>PDBTitle:</b> crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
59	<a href="#">c1t10A_</a>	Alignment	not modelled	96.4	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
60	<a href="#">c3pr3B_</a>	Alignment	not modelled	96.4	28	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
61	<a href="#">c3kp3B_</a>	Alignment	not modelled	96.3	10	<b>PDB header:</b> transcription regulator/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator tcar; <b>PDBTitle:</b> staphylococcus epidermidis in complex with ampicillin
62	<a href="#">c2nnnB_</a>	Alignment	not modelled	96.2	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
63	<a href="#">c3g3zA_</a>	Alignment	not modelled	96.1	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
64	<a href="#">d2a61a1</a>	Alignment	not modelled	96.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
65	<a href="#">d2etha1</a>	Alignment	not modelled	96.1	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
66	<a href="#">c2fa5B_</a>	Alignment	not modelled	96.1	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator marr/emrr family; <b>PDBTitle:</b> the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
67	<a href="#">c2rdpA_</a>	Alignment	not modelled	96.1	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearotheophilus
68	<a href="#">d2fbha1</a>	Alignment	not modelled	96.0	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
69	<a href="#">c2gxgA_</a>	Alignment	not modelled	96.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
70	<a href="#">d1yioa1</a>	Alignment	not modelled	96.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
71	<a href="#">c2zkbq_</a>	Alignment	not modelled	96.0	9	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rna expansion segment es3; <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
72	<a href="#">c3frwF_</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trpr protein from ruminococcus obeum
73	<a href="#">d1a04a1</a>	Alignment	not modelled	95.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
74	<a href="#">c3k0lA_</a>	Alignment	not modelled	95.8	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
75	<a href="#">d1s3ja_</a>	Alignment	not modelled	95.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
						<b>PDB header:</b> transcription regulator

76	<a href="#">c3r0aB_</a>	Alignment	not modelled	95.8	10	<b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
77	<a href="#">c3bpxB_</a>	Alignment	not modelled	95.7	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
78	<a href="#">d3deua1</a>	Alignment	not modelled	95.7	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
79	<a href="#">c3oopA_</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
80	<a href="#">c3tgnA_</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
81	<a href="#">c1x3uA_</a>	Alignment	not modelled	95.6	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein fixj; <b>PDBTitle:</b> solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
82	<a href="#">c3gbgA_</a>	Alignment	not modelled	95.6	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tcp pilus virulence regulatory protein; <b>PDBTitle:</b> crystal structure of txtt from vibrio cholerae o395
83	<a href="#">d1lj9a_</a>	Alignment	not modelled	95.5	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
84	<a href="#">c3deuB_</a>	Alignment	not modelled	95.5	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator slya; <b>PDBTitle:</b> crystal structure of transcription regulatory protein slya2 from salmonella typhimurium in complex with salicylate3 ligands
85	<a href="#">c3cjnA_</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
86	<a href="#">c3korD_</a>	Alignment	not modelled	95.4	21	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
87	<a href="#">c3iz6A_</a>	Alignment	not modelled	95.3	10	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa (s2p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of tritium aestivum translating 80s ribosome
88	<a href="#">d1fsea_</a>	Alignment	not modelled	95.3	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
89	<a href="#">c3bjaa_</a>	Alignment	not modelled	95.3	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
90	<a href="#">c2rnjA_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> nmr structure of the s. aureus vvar dna binding domain
91	<a href="#">c3bchA_</a>	Alignment	not modelled	95.1	9	<b>PDB header:</b> cell adhesion, ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa; <b>PDBTitle:</b> crystal structure of the human laminin receptor precursor
92	<a href="#">c1s1hB_</a>	Alignment	not modelled	95.1	12	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 40s ribosomal protein s0-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
93	<a href="#">c3ooaA_</a>	Alignment	not modelled	95.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2118 protein; <b>PDBTitle:</b> the structure of a protein with unkown function from listeria innocua
94	<a href="#">c3kxD_</a>	Alignment	not modelled	95.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
95	<a href="#">c3mklB_</a>	Alignment	not modelled	95.0	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator gadx; <b>PDBTitle:</b> crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
96	<a href="#">d1jhfa1</a>	Alignment	not modelled	95.0	20	<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
97	<a href="#">c3boqB_</a>	Alignment	not modelled	95.0	8	<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
98	<a href="#">c2k9sA_</a>	Alignment	not modelled	94.9	6	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose operon regulatory protein; <b>PDBTitle:</b> solution structure of dna binding domain of e. coli arac
99	<a href="#">c3nrvC_</a>	Alignment	not modelled	94.9	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> putative transcriptional regulator (marr/emrr family); <b>PDBTitle:</b> crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
100	<a href="#">c2krfB_</a>	Alignment	not modelled	94.9	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a
						<b>PDB header:</b> dna binding protein



101	<a href="#">c2l4aA_</a>	Alignment	not modelled	94.8	19	<b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
102	<a href="#">c3e6mD_</a>	Alignment	not modelled	94.8	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
103	<a href="#">d2fbia1</a>	Alignment	not modelled	94.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
104	<a href="#">d1p4wa_</a>	Alignment	not modelled	94.8	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
105	<a href="#">d1l3la1</a>	Alignment	not modelled	94.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
106	<a href="#">d1jhga_</a>	Alignment	not modelled	94.8	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
107	<a href="#">c1zljE_</a>	Alignment	not modelled	94.8	19	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
108	<a href="#">c3mn2B_</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable arac family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
109	<a href="#">d2cg4a1</a>	Alignment	not modelled	94.7	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
110	<a href="#">c1bdhA_</a>	Alignment	not modelled	94.6	31	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
111	<a href="#">d1jgsa_</a>	Alignment	not modelled	94.6	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
112	<a href="#">c2qwwB_</a>	Alignment	not modelled	94.6	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
113	<a href="#">d2jioa2</a>	Alignment	not modelled	94.6	14	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
114	<a href="#">d1stza1</a>	Alignment	not modelled	94.5	20	<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
115	<a href="#">d2cfxa1</a>	Alignment	not modelled	94.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
116	<a href="#">c3lsgD_</a>	Alignment	not modelled	94.5	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> two-component response regulator yesn; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
117	<a href="#">c3k2zA_</a>	Alignment	not modelled	94.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> crystal structure of a lexa protein from thermotoga maritima
118	<a href="#">c1bl0A_</a>	Alignment	not modelled	94.5	12	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (multiple antibiotic resistance protein); <b>PDBTitle:</b> multiple antibiotic resistance protein (mara)/dna complex
119	<a href="#">d1trra_</a>	Alignment	not modelled	94.5	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
120	<a href="#">c3ecoB_</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mepr; <b>PDBTitle:</b> crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa