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Description	P37014
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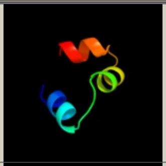
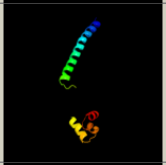
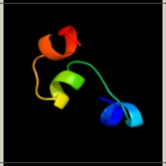
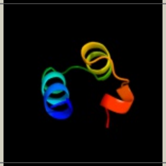
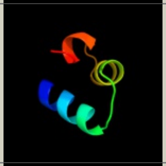
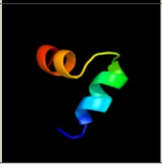
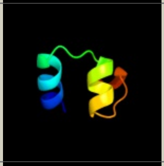
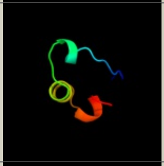
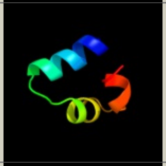
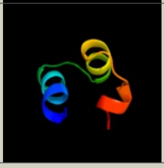
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a9xa1	Alignment		84.8	13	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
2	c2x48B_	Alignment		82.3	7	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
3	c2gm4B_	Alignment		67.0	13	**PDB header:**recombination, dna **Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase; **PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
4	d1s6la1	Alignment		65.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
5	d1p4wa_	Alignment		64.5	16	**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)
6	d1vola2	Alignment		60.9	12	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
7	c2jpcA_	Alignment		60.7	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
8	c1x3uA_	Alignment		60.1	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
9	d1a04a1	Alignment		55.7	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)
10	d1yioa1	Alignment		54.3	6	**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)
11	c2phcB_	Alignment		53.1	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii

12	c2krfB_	Alignment		53.0	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
13	c1zljE_	Alignment		52.6	16	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
14	d1vz0a1	Alignment		52.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
15	d1fsea_	Alignment		52.4	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)
16	c2rnjA_	Alignment		52.0	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
17	c3mmlD_	Alignment		47.0	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
18	c1h0mD_	Alignment		46.1	13	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
19	c1r71B_	Alignment		43.1	15	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
20	d1l3la1	Alignment		42.3	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)
21	c3oepA_	Alignment	not modelled	41.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988; **PDBTitle:** crystal structure of ttha0988 in space group p43212
22	c3cloC_	Alignment	not modelled	40.0	19	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
23	c1u78A_	Alignment	not modelled	39.3	6	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
24	d1r71a_	Alignment	not modelled	38.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
25	c2q0oA_	Alignment	not modelled	37.4	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
26	d1aisb2	Alignment	not modelled	35.8	15	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
27	c3mzyA_	Alignment	not modelled	34.5	19	**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
28	d2p7vb1	Alignment	not modelled	33.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors

						Family: Sigma4 domain
29	d1trra_	Alignment	not modelled	33.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
30	d1q08a_	Alignment	not modelled	32.9	20	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
31	c3sztB_	Alignment	not modelled	32.6	6	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
32	c3trbA_	Alignment	not modelled	32.6	3	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence-associated protein i; **PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
33	c1m6vE_	Alignment	not modelled	32.4	13	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
34	c3qp5C_	Alignment	not modelled	32.3	6	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
35	c2k9lA_	Alignment	not modelled	31.8	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
36	d1ijwc_	Alignment	not modelled	31.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
37	d1rp3a1	Alignment	not modelled	31.3	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
38	c3fymA_	Alignment	not modelled	31.3	8	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
39	d1ku2a1	Alignment	not modelled	30.9	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
40	d1jhga_	Alignment	not modelled	30.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
41	c3t72o_	Alignment	not modelled	30.4	11	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
42	d1hcra_	Alignment	not modelled	30.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
43	d1z6ra1	Alignment	not modelled	29.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
44	d1bl0a2	Alignment	not modelled	29.4	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
45	d2a6ca1	Alignment	not modelled	28.0	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
46	c2o8xA_	Alignment	not modelled	27.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
47	c3t76A_	Alignment	not modelled	27.5	3	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
48	d2et1a1	Alignment	not modelled	27.4	0	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
49	c3korD_	Alignment	not modelled	27.3	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
50	c3c3wB_	Alignment	not modelled	26.8	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
51	d1d5ya1	Alignment	not modelled	26.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
52	c2jvlA_	Alignment	not modelled	24.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
53	d1smyf2	Alignment	not modelled	24.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
54	d1fxza2	Alignment	not modelled	24.0	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein

55	c1vz0B_	Alignment	not modelled	23.2	19	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**chromosome partitioning protein parb; **PDBTitle:** chromosome segregation protein spo0j from thermus2 thermophilus
56	d1ic8a2	Alignment	not modelled	23.2	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
57	d1ku7a_	Alignment	not modelled	23.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
58	d1or7a1	Alignment	not modelled	22.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
59	c1aisB_	Alignment	not modelled	22.0	18	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**protein (transcription initiation factor iib); **PDBTitle:** tata-binding protein/transcription factor (ii)b/tata-box2 complex from pyrococcus woesei
60	d2iv2x2	Alignment	not modelled	21.7	23	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
61	d1vola1	Alignment	not modelled	21.6	11	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
62	d1r8ea1	Alignment	not modelled	21.1	9	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
63	d1s7oa_	Alignment	not modelled	20.9	0	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
64	d1ku3a_	Alignment	not modelled	20.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
65	d5crxb2	Alignment	not modelled	20.6	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
66	d2ga1a1	Alignment	not modelled	20.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
67	d1xsva_	Alignment	not modelled	20.3	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
68	c3b7hA_	Alignment	not modelled	20.1	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
69	c1c9bI_	Alignment	not modelled	19.8	13	**PDB header:**transcription/dna **Chain:** I: **PDB Molecule:**general transcription factor iib; **PDBTitle:** crystal structure of a human tbp core domain-human tfiib2 core domain complex bound to an extended, modified3 adenoviral major late promoter (admlp)
70	d1od5a1	Alignment	not modelled	19.7	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
71	d1fxza1	Alignment	not modelled	19.5	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
72	d1y9qa1	Alignment	not modelled	19.4	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
73	c1l0oC_	Alignment	not modelled	18.8	6	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
74	d1l0oc_	Alignment	not modelled	18.8	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
75	d1ufma_	Alignment	not modelled	18.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
76	c2wusR_	Alignment	not modelled	18.4	6	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
77	d1ttya_	Alignment	not modelled	18.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
78	d2cg4a1	Alignment	not modelled	18.0	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
79	d1dpua_	Alignment	not modelled	17.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
80	c1dpuA_	Alignment	not modelled	17.9	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human

						rpa322 complexed with ung2(73-88)
81	d1k61a_	Alignment	not modelled	17.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
82	d1f44a2	Alignment	not modelled	17.6	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
83	d2r5yb1	Alignment	not modelled	17.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
84	d1x2na1	Alignment	not modelled	17.4	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
85	d1b0na2	Alignment	not modelled	17.4	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
86	d2cyya1	Alignment	not modelled	17.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
87	d3bula1	Alignment	not modelled	17.2	11	**Fold:**Methionine synthase domain-like **Superfamily:**Methionine synthase domain **Family:**Methionine synthase domain
88	c2kpjA_	Alignment	not modelled	17.1	0	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
89	d1uija1	Alignment	not modelled	16.9	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
90	d1uika2	Alignment	not modelled	16.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
91	c2q1zA_	Alignment	not modelled	16.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rpoe, ecf sige; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
92	d1h0ha2	Alignment	not modelled	16.3	9	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
93	c1rnlA_	Alignment	not modelled	16.1	13	**PDB header:**signal transduction protein **Chain:** A: **PDB Molecule:**nitrate/nitrite response regulator protein narl; **PDBTitle:** the nitrate/nitrite response regulator protein narl from narl
94	c2elhA_	Alignment	not modelled	16.1	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
95	d1bl0a1	Alignment	not modelled	16.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
96	d1od5a2	Alignment	not modelled	15.9	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
97	d1g8ma1	Alignment	not modelled	15.7	17	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
98	d1q1ha_	Alignment	not modelled	15.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcription factor E/IIe-alpha, N-terminal domain
99	c1q1hA_	Alignment	not modelled	15.7	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor e; **PDBTitle:** an extended winged helix domain in general transcription2 factor e/iie alpha