Phyre^2

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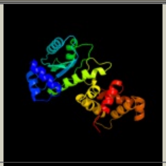
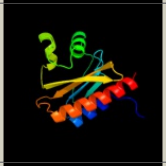
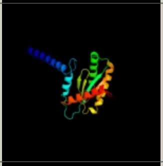
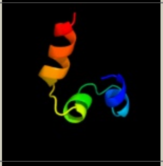
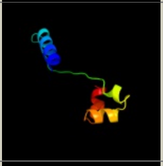
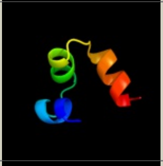
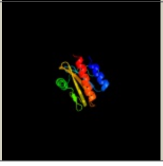
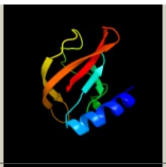
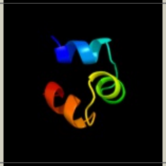
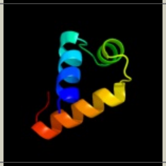
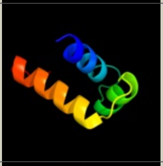
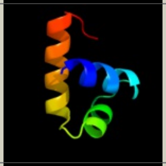
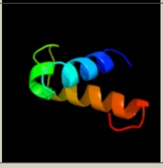
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3onqB_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**regulator of polyketide synthase expression; **PDBTitle:** crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
2	c2gx5B_	Alignment		98.8	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**gtp-sensing transcriptional pleiotropic repressor cody; **PDBTitle:** n-terminal gaf domain of transcriptional pleiotropic repressor cody
3	c2w1rA_	Alignment		97.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of the c-terminal domain of b. subtilis2 spovt
4	c3ezuA_	Alignment		97.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
5	d1fipa_	Alignment		97.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
6	d1ntca_	Alignment		97.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
7	d1etob_	Alignment		97.1	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
8	d1umqa_	Alignment		97.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
9	c1umqA_	Alignment		97.1	19	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
10	d1etxa_	Alignment		97.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
11	c2w1tB_	Alignment		97.0	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt

12	d1p0za_	Alignment		96.8	18	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
13	d1g2ha_	Alignment		96.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	c2esnC_	Alignment		96.6	20	**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
15	c1iz1B_	Alignment		96.4	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**lysr-type regulatory protein; **PDBTitle:** crystal structure of cbnr, a lysr family transcriptional2 regulator
16	c3m1eA_	Alignment		96.4	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of benm_dbd
17	d2esna1	Alignment		96.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LysR-like transcriptional regulators
18	c3e7lD_	Alignment		96.2	10	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
19	c3t1bB_	Alignment		96.2	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** crystal structure of the full-length aphb n100e variant
20	c3ispA_	Alignment		96.2	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator **PDBTitle:** crystal structure of argp from mycobacterium tuberculosis
21	c3breA_	Alignment	not modelled	96.1	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
22	c3fzjC_	Alignment	not modelled	95.9	11	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** tsar low resolution crystal structure, tetragonal form
23	c3hhgF_	Alignment	not modelled	95.8	13	**PDB header:**transcription regulator **Chain:** F: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
24	c2vjwA_	Alignment	not modelled	95.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gaf family protein; **PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
25	d1b9ma1	Alignment	not modelled	95.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of molybdate-dependent transcriptional regulator ModE
26	d1ixca1	Alignment	not modelled	95.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LysR-like transcriptional regulators
27	c3fzvC_	Alignment	not modelled	95.6	14	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
28	c1w25B_	Alignment	not modelled	95.6	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
						Fold: Profilin-like

29	d3by8a1	Alignment	not modelled	95.2	20	**Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
30	c1b9nA_	Alignment	not modelled	94.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein (mode); **PDBTitle:** regulator from escherichia coli
31	c3fpvC_	Alignment	not modelled	93.9	16	**PDB header:**heme binding protein **Chain:** C: **PDB Molecule:**extracellular haem-binding protein; **PDBTitle:** crystal structure of hbps
32	c1zljE_	Alignment	not modelled	93.4	10	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
33	c3eeaB_	Alignment	not modelled	93.3	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**gaf domain/hd domain protein; **PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
34	c3mmhA_	Alignment	not modelled	93.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
35	d1a04a1	Alignment	not modelled	92.3	11	**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)
36	c2ijlB_	Alignment	not modelled	92.3	4	**PDB header:**transcription **Chain:** B: **PDB Molecule:**molybdenum-binding transcriptional repressor; **PDBTitle:** the structure of a putative mode from agrobacterium tumefaciens.
37	d2veaa1	Alignment	not modelled	92.2	16	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
38	c2rnjA_	Alignment	not modelled	91.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
39	d1rp3a2	Alignment	not modelled	91.6	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
40	c3hugA_	Alignment	not modelled	91.3	17	**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
41	d1p4wa_	Alignment	not modelled	91.2	14	**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)
42	c3e0yA_	Alignment	not modelled	91.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca
43	c3ibjB_	Alignment	not modelled	91.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
44	d1l3la1	Alignment	not modelled	91.0	8	**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)
45	d1yioa1	Alignment	not modelled	90.9	10	**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)
46	c3qp5C_	Alignment	not modelled	90.7	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
47	c3hcyB_	Alignment	not modelled	90.1	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative two-component sensor histidine kinase protein; **PDBTitle:** the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
48	d1fsea_	Alignment	not modelled	90.0	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)
49	d1or7a1	Alignment	not modelled	89.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
50	c2krfB_	Alignment	not modelled	89.5	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
51	c3sztB_	Alignment	not modelled	89.4	11	**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
52	c3iclA_	Alignment	not modelled	89.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**eal/ggdef domain protein; **PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
53	c3mtkA_	Alignment	not modelled	88.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase/phosphodiesterase; **PDBTitle:** x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target

						clr27c
54	d2coba1	Alignment	not modelled	88.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
55	c3c2wB_	Alignment	not modelled	88.5	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state
56	c3i5aA_	Alignment	not modelled	88.2	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
57	c3ksiA_	Alignment	not modelled	88.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
58	d2cg4a1	Alignment	not modelled	88.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
59	c1h0mD_	Alignment	not modelled	87.5	8	**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
60	c2q0oA_	Alignment	not modelled	87.4	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
61	c3p01C_	Alignment	not modelled	87.4	15	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
62	c3ignA_	Alignment	not modelled	87.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase; **PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
63	c3o5yA_	Alignment	not modelled	87.2	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
64	c1x3uA_	Alignment	not modelled	87.0	11	**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
65	c3cloC_	Alignment	not modelled	86.4	17	**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
66	c2jpcA_	Alignment	not modelled	85.9	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
67	d2cfxa1	Alignment	not modelled	85.8	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
68	d2a2la1	Alignment	not modelled	85.6	18	**Fold:**Profilin-like **Superfamily:**GlcG-like **Family:**GlcG-like
69	c3fosA_	Alignment	not modelled	85.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
70	c2cfxD_	Alignment	not modelled	85.1	3	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
71	c2vbzA_	Alignment	not modelled	84.7	7	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
72	d1xsva_	Alignment	not modelled	84.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
73	d1i1ga1	Alignment	not modelled	84.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
74	c2p6tH_	Alignment	not modelled	83.9	12	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
75	d2cyya1	Alignment	not modelled	83.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
76	c2o8xA_	Alignment	not modelled	83.3	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
77	c2cg4B_	Alignment	not modelled	83.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
78	c2l4aA_	Alignment	not modelled	83.2	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein;

						PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
79	d1s7oa_	Alignment	not modelled	83.2	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
80	c3i5bA_	Alignment	not modelled	83.2	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
81	c3trcA_	Alignment	not modelled	82.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
82	d1ulya_	Alignment	not modelled	82.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein PH1932
83	c2e7xA_	Alignment	not modelled	81.9	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
84	d1w25a3	Alignment	not modelled	81.4	13	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
85	c3i4pA_	Alignment	not modelled	81.3	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
86	c1bl0A_	Alignment	not modelled	81.1	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
87	c3hyiA_	Alignment	not modelled	79.9	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein duf199/whia; **PDBTitle:** crystal structure of full-length duf199/whia from thermatoga maritima
88	d2jn6a1	Alignment	not modelled	79.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
89	c2dbbA_	Alignment	not modelled	78.6	10	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
90	d1i3ja_	Alignment	not modelled	78.0	14	**Fold:**DNA-binding domain of intron-encoded endonucleases **Superfamily:**DNA-binding domain of intron-encoded endonucleases **Family:**DNA-binding domain of intron-encoded endonucleases
91	c3klnC_	Alignment	not modelled	77.8	11	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
92	c1rp3G_	Alignment	not modelled	77.6	9	**PDB header:**transcription **Chain:** G: **PDB Molecule:**rna polymerase sigma factor sigma-28 (flia); **PDBTitle:** cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
93	c2k9sA_	Alignment	not modelled	77.4	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
94	c3mzyA_	Alignment	not modelled	76.6	7	**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
95	c2e1cA_	Alignment	not modelled	76.0	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
96	c1i1gA_	Alignment	not modelled	75.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
97	c3i5cA_	Alignment	not modelled	75.5	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response **PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
98	c1or7A_	Alignment	not modelled	75.1	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
99	d1mc0a1	Alignment	not modelled	74.6	9	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
100	c3cuoB_	Alignment	not modelled	73.9	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
101	c2gqqB_	Alignment	not modelled	73.8	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**leucine-responsive regulatory protein; **PDBTitle:** crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
102	c3ci6B_	Alignment	not modelled	72.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase;

						PDBTitle: crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
103	c2ia0A_	Alignment	not modelled	72.7	17	**PDB header:** structural genomics, unknown function **Chain:** A: **PDB Molecule:** putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
104	c1u78A_	Alignment	not modelled	72.2	19	**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
105	c3pjwA_	Alignment	not modelled	72.2	11	**PDB header:** lyase **Chain:** A: **PDB Molecule:** cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
106	c2q1zA_	Alignment	not modelled	71.3	16	**PDB header:** transcription **Chain:** A: **PDB Molecule:** rpoe, ecf sige; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
107	d1jhfa1	Alignment	not modelled	70.5	10	**Fold:** DNA/RNA-binding 3-helical bundle **Superfamily:** "Winged helix" DNA-binding domain **Family:** LexA repressor, N-terminal DNA-binding domain
108	d1vhma_	Alignment	not modelled	70.5	16	**Fold:** Profilin-like **Superfamily:** GAF domain-like **Family:** GAF domain
109	c1vhmB_	Alignment	not modelled	70.2	17	**PDB header:** structural genomics, unknown function **Chain:** B: **PDB Molecule:** protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
110	d2p4wa1	Alignment	not modelled	70.1	19	**Fold:** DNA/RNA-binding 3-helical bundle **Superfamily:** "Winged helix" DNA-binding domain **Family:** PF1790-like
111	c1rnlA_	Alignment	not modelled	70.0	11	**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
112	c1zn2A_	Alignment	not modelled	68.6	9	**PDB header:** transcription regulator **Chain:** A: **PDB Molecule:** response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
113	c3c3wB_	Alignment	not modelled	68.2	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
114	c3e98B_	Alignment	not modelled	67.5	8	**PDB header:** unknown function **Chain:** B: **PDB Molecule:** gaf domain of unknown function; **PDBTitle:** crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
115	c2jscB_	Alignment	not modelled	67.5	19	**PDB header:** transcription **Chain:** B: **PDB Molecule:** transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
116	d2oola1	Alignment	not modelled	67.0	15	**Fold:** Profilin-like **Superfamily:** GAF domain-like **Family:** GAF domain
117	c2o9bA_	Alignment	not modelled	66.4	18	**PDB header:** transferase **Chain:** A: **PDB Molecule:** bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
118	c3hvwA_	Alignment	not modelled	66.1	10	**PDB header:** lyase **Chain:** A: **PDB Molecule:** diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
119	d2o9ca1	Alignment	not modelled	66.0	16	**Fold:** Profilin-like **Superfamily:** GAF domain-like **Family:** GAF domain
120	c3p01A_	Alignment	not modelled	65.5	15	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120