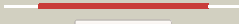


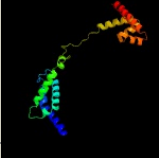

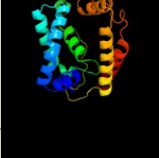
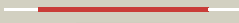

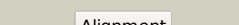
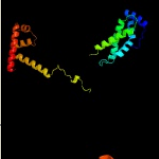
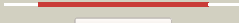






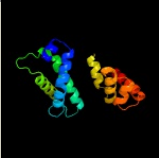






# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3414c\_(sigD)\_3833218\_3833856  
 Date Fri Aug 9 18:20:08 BST 2019  
 Unique Job ID 4fcb47adba324add

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6in7B_</a>	 Alignment		99.9	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> crystal structure of alga in complex with muca(cyto)
2	<a href="#">c6dvdF_</a>	 Alignment		99.9	22	<b>PDB header:</b> transferase/dna <b>Chain:</b> F: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigl; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
3	<a href="#">c2q1zA_</a>	 Alignment		99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rpoe, ecf sige; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
4	<a href="#">c1or7A_</a>	 Alignment		99.9	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-e factor; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
5	<a href="#">c5ipmF_</a>	 Alignment		99.9	27	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpos; <b>PDBTitle:</b> sigmas-transcription initiation complex with 4-nt nascent rna
6	<a href="#">c4cxfA_</a>	 Alignment		99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor cnrh; <b>PDBTitle:</b> structure of cnrh in complex with the cytosolic domain of cnry
7	<a href="#">c3vdoA_</a>	 Alignment		99.9	24	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor sigk; <b>PDBTitle:</b> structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
8	<a href="#">c5wurB_</a>	 Alignment		99.9	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigw; <b>PDBTitle:</b> crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
9	<a href="#">c6c03A_</a>	 Alignment		99.9	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative rna polymerase ecf-subfamily sigma factor; <b>PDBTitle:</b> the crystal structure streptomyces venezuelae rsbn-bldn complex
10	<a href="#">c5uxxC_</a>	 Alignment		99.8	20	<b>PDB header:</b> dna binding protein/unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> co-crystal structure of the sigma factor rpoe in complex with the2 anti-sigma factor nepr from bartonella quintana
11	<a href="#">c5zx3F_</a>	 Alignment		99.8	18	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigh; <b>PDBTitle:</b> mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h

12	<a href="#">c1rp3G_</a>	Alignment		99.8	13	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> rna polymerase sigma factor sigma-28 (fliA); <b>PDBTitle:</b> cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm
13	<a href="#">c5tw1F_</a>	Alignment		99.8	17	<b>PDB header:</b> transcription activator/transferase/dna <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor sigma; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
14	<a href="#">c3t0yA_</a>	Alignment		99.8	22	<b>PDB header:</b> transcription regulator/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
15	<a href="#">c5xe7A_</a>	Alignment		99.7	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigj; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
16	<a href="#">c6c05F_</a>	Alignment		99.7	19	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor sigma; <b>PDBTitle:</b> mycobacterium tuberculosis rnap holo/rbpA in relaxed state
17	<a href="#">c2lfwA_</a>	Alignment		99.7	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> phyr sigma-like domain; <b>PDBTitle:</b> nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
18	<a href="#">c3wodF_</a>	Alignment		99.6	19	<b>PDB header:</b> transferase/transcription <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> rna polymerase-gp39 complex
19	<a href="#">c3mzyA_</a>	Alignment		99.6	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
20	<a href="#">c2a6eF_</a>	Alignment		99.5	22	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> crystal structure of the t. thermophilus rna polymerase2 holoenzyme
21	<a href="#">c1l9uH_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> sigma factor sigma; <b>PDBTitle:</b> thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
22	<a href="#">c3hugA_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
23	<a href="#">c3vepA_</a>	Alignment	not modelled	99.4	98	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-d factor; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
24	<a href="#">c4iqcX_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> transcription, transferase <b>Chain:</b> X: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> x-ray crystal structure of escherichia coli sigma70 holoenzyme
25	<a href="#">d1rp3a2</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
26	<a href="#">d1or7a1</a>	Alignment	not modelled	99.2	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
27	<a href="#">c3iydF_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
28	<a href="#">d1or7a2</a>	Alignment	not modelled	99.1	23	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
						<b>PDB header:</b> hydrolase

29	<a href="#">c5fgmA_</a>	Alignment	not modelled	99.1	25	<b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigr; <b>PDBTitle:</b> streptomyces coelicolor sigr region 4
30	<a href="#">c2o8xA_</a>	Alignment	not modelled	99.1	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
31	<a href="#">c2o7gA_</a>	Alignment	not modelled	99.1	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the pribnow box recognition region of sigc from2 mycobacterium tuberculosis
32	<a href="#">d1xsva_</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
33	<a href="#">d1smyf2</a>	Alignment	not modelled	99.0	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
34	<a href="#">d1or7b2</a>	Alignment	not modelled	99.0	26	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
35	<a href="#">d1s7oa_</a>	Alignment	not modelled	99.0	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
36	<a href="#">d1ku7a_</a>	Alignment	not modelled	98.8	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
37	<a href="#">d1ttya_</a>	Alignment	not modelled	98.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
38	<a href="#">d1ku3a_</a>	Alignment	not modelled	98.6	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
39	<a href="#">c3n0rA_</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr stress response regulator at 1.25 angstrom2 resolution
40	<a href="#">c3t72o_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> O: <b>PDB Molecule:</b> pho box dna (strand 1); <b>PDBTitle:</b> phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
41	<a href="#">d1h3la_</a>	Alignment	not modelled	98.4	19	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
42	<a href="#">d2p7vb1</a>	Alignment	not modelled	98.4	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
43	<a href="#">d1yioa1</a>	Alignment	not modelled	98.3	24	<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)
44	<a href="#">c1x3uA_</a>	Alignment	not modelled	98.1	21	<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
45	<a href="#">c4lfuA_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> crystal structure of escherichia coli sdia in the space group c2
46	<a href="#">c3qp5C_</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> cvir transcriptional regulator; <b>PDBTitle:</b> crystal structure of cvir bound to antagonist chlorolactone (cl)
47	<a href="#">c3sztB_</a>	Alignment	not modelled	98.0	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
48	<a href="#">c2q0oA_</a>	Alignment	not modelled	98.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
49	<a href="#">c1h0mD_</a>	Alignment	not modelled	98.0	33	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional activator protein trar; <b>PDBTitle:</b> three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
50	<a href="#">d1rp3a3</a>	Alignment	not modelled	97.9	12	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
51	<a href="#">d1a04a1</a>	Alignment	not modelled	97.9	26	<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)
52	<a href="#">c1zljE_</a>	Alignment	not modelled	97.9	26	<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
53	<a href="#">c6jqsA_</a>	Alignment	not modelled	97.8	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> structure of transcription factor, gere
54	<a href="#">c5d4dP_</a>	Alignment	not modelled	97.7	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> P: <b>PDB Molecule:</b> rna polymerase sigma factor siga; <b>PDBTitle:</b> crystal structure of thermus thermophilus product complex for2 transcription initiation with nad and ctp <b>PDB header:</b> transcription

55	<a href="#">c2krfB</a>	Alignment	not modelled	97.7	21	<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
56	<a href="#">d1p4wa</a>	Alignment	not modelled	97.7	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)
57	<a href="#">d1l3la1</a>	Alignment	not modelled	97.7	33	<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)
58	<a href="#">c2rnjA</a>	Alignment	not modelled	97.7	33	<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
59	<a href="#">d1fsea</a>	Alignment	not modelled	97.7	28	<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)
60	<a href="#">c1ku2A</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> sigma factor siga; <b>PDBTitle:</b> crystal structure of thermus aquaticus rna polymerase sigma2 subunit fragment containing regions 1.2 to 3.1
61	<a href="#">c5f64C</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> C; <b>PDB Molecule:</b> positive transcription regulator evga; <b>PDBTitle:</b> putative positive transcription regulator (sensor evgs) from shigella2 flexneri
62	<a href="#">c3c3wB</a>	Alignment	not modelled	97.6	25	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> two component transcriptional regulatory protein devr; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
63	<a href="#">c5o8yG</a>	Alignment	not modelled	97.6	23	<b>PDB header:</b> transcription <b>Chain:</b> G; <b>PDB Molecule:</b> transcriptional regulatory protein rcsb; <b>PDBTitle:</b> conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
64	<a href="#">c3cloC</a>	Alignment	not modelled	97.6	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> C; <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 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
65	<a href="#">c4yn8A</a>	Alignment	not modelled	97.5	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> response regulator chra; <b>PDBTitle:</b> crystal structure of response regulator chra in heme-sensing two2 component system
66	<a href="#">c4qicC</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> signaling protein/dna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> sensory transduction regulatory protein, anti-anti-sigma <b>PDBTitle:</b> co-crystal structure of anti-anti-sigma factor phyr complexed with2 anti-sigma factor nepr from bartonella quintana
67	<a href="#">c3klnC</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
68	<a href="#">c1zn2A</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styf
69	<a href="#">c4hyeB</a>	Alignment	not modelled	97.4	26	<b>PDB header:</b> transcription activator <b>Chain:</b> B; <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
70	<a href="#">c4if4A</a>	Alignment	not modelled	97.4	32	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus
71	<a href="#">c5hevC</a>	Alignment	not modelled	97.4	30	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
72	<a href="#">c1rn1A</a>	Alignment	not modelled	97.4	28	<b>PDB header:</b> signal transduction protein <b>Chain:</b> A; <b>PDB Molecule:</b> nitrate/nitrite response regulator protein narl; <b>PDBTitle:</b> the nitrate/nitrite response regulator protein narl from narl
73	<a href="#">c2jpcA</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
74	<a href="#">c4go1A</a>	Alignment	not modelled	97.3	22	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator lsrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrr from e.2 coli.
75	<a href="#">c5xt2C</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> response regulator fixj; <b>PDBTitle:</b> crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
76	<a href="#">c4x8kA</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> transcription activator <b>Chain:</b> A; <b>PDB Molecule:</b> rna polymerase sigma factor siga; <b>PDBTitle:</b> mycobacterium tuberculosis rbpA-sid in complex with sigmaa domain 2
77	<a href="#">c6ideA</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator luxr family; <b>PDBTitle:</b> crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
78	<a href="#">c1u78A</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A; <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
79	<a href="#">c6paxA</a>	Alignment	not modelled	96.2	17	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A; <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions

80	<a href="#">d1pdnc_</a>	Alignment	not modelled	96.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
81	<a href="#">c2vzA_</a>	Alignment	not modelled	96.1	21	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
82	<a href="#">d2cg4a1</a>	Alignment	not modelled	96.0	19	<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
83	<a href="#">c2dbbA_</a>	Alignment	not modelled	96.0	11	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
84	<a href="#">d1smyf3</a>	Alignment	not modelled	96.0	20	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
85	<a href="#">d2cfxa1</a>	Alignment	not modelled	95.9	14	<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
86	<a href="#">c2cg4B_</a>	Alignment	not modelled	95.8	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
87	<a href="#">c2ia0A_</a>	Alignment	not modelled	95.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
88	<a href="#">d1ku2a2</a>	Alignment	not modelled	95.8	21	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
89	<a href="#">c2cfxD_</a>	Alignment	not modelled	95.7	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpC; <b>PDBTitle:</b> structure of b.subtilis lrpC
90	<a href="#">d1ilga1</a>	Alignment	not modelled	95.6	19	<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
91	<a href="#">c2p6tH_</a>	Alignment	not modelled	95.5	16	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
92	<a href="#">c2l4aA_</a>	Alignment	not modelled	95.4	23	<b>PDB header:</b> dna binding protein <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
93	<a href="#">d2cyya1</a>	Alignment	not modelled	95.4	12	<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
94	<a href="#">c2e1cA_</a>	Alignment	not modelled	95.4	12	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
95	<a href="#">c2e7xA_</a>	Alignment	not modelled	95.3	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
96	<a href="#">c1ilgA_</a>	Alignment	not modelled	95.3	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
97	<a href="#">c4pcqC_</a>	Alignment	not modelled	95.2	21	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> possible transcriptional regulatory protein (probably <b>PDBTitle:</b> crystal structure of mtbaldr (rv2779c)
98	<a href="#">d1siga_</a>	Alignment	not modelled	95.1	11	<b>Fold:</b> Sigma2 domain of RNA polymerase sigma factors <b>Superfamily:</b> Sigma2 domain of RNA polymerase sigma factors <b>Family:</b> Sigma2 domain of RNA polymerase sigma factors
99	<a href="#">d1k78a1</a>	Alignment	not modelled	95.0	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
100	<a href="#">c3i4pA_</a>	Alignment	not modelled	94.7	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
101	<a href="#">c4czdA_</a>	Alignment	not modelled	94.7	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
102	<a href="#">c4czdD_</a>	Alignment	not modelled	94.5	16	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
103	<a href="#">d2jn6a1</a>	Alignment	not modelled	94.4	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
104	<a href="#">d6paxa1</a>	Alignment	not modelled	94.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
						<b>PDB header:</b> transcription/dna



105	<a href="#">c2w7nA_</a>	Alignment	not modelled	94.1	26	<b>Chain:</b> A; <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
106	<a href="#">c5yixA_</a>	Alignment	not modelled	94.1	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> caulobacter crescentus gcra sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
107	<a href="#">c2elhA_</a>	Alignment	not modelled	93.9	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
108	<a href="#">d2d1ha1</a>	Alignment	not modelled	93.9	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
109	<a href="#">c5z7iC_</a>	Alignment	not modelled	93.8	31	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C; <b>PDB Molecule:</b> cell cycle regulatory protein gcra; <b>PDBTitle:</b> caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
110	<a href="#">d1r1ua_</a>	Alignment	not modelled	93.7	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
111	<a href="#">c6cmvA_</a>	Alignment	not modelled	93.6	13	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator lrs14-like protein; <b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2) from2 sulfobolus acidocaldarius
112	<a href="#">c4omzG_</a>	Alignment	not modelled	93.6	16	<b>PDB header:</b> transcription <b>Chain:</b> G; <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
113	<a href="#">c2r0qF_</a>	Alignment	not modelled	93.5	21	<b>PDB header:</b> recombination/dna <b>Chain:</b> F; <b>PDB Molecule:</b> putative transposon tn552 dna-invertase bin3; <b>PDBTitle:</b> crystal structure of a serine recombinase- dna regulatory2 complex
114	<a href="#">c1r22B_</a>	Alignment	not modelled	93.5	20	<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
115	<a href="#">c2gqqB_</a>	Alignment	not modelled	93.1	23	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
116	<a href="#">c4nb5D_</a>	Alignment	not modelled	93.1	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
117	<a href="#">c2lkpB_</a>	Alignment	not modelled	93.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator, arsr family; <b>PDBTitle:</b> solution structure of apo-nmtr
118	<a href="#">c2oqqA_</a>	Alignment	not modelled	92.7	15	<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
119	<a href="#">c3pqqD_</a>	Alignment	not modelled	92.6	15	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> biofilm growth-associated repressor; <b>PDBTitle:</b> crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
120	<a href="#">d1r1ta_</a>	Alignment	not modelled	92.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators