





















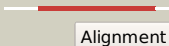
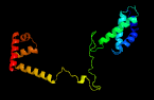
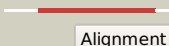







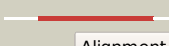
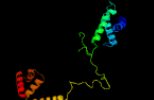






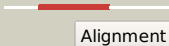
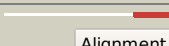
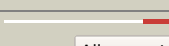
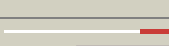

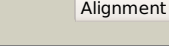
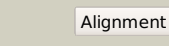
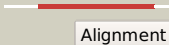


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0182c_(sigG)_213026_214138
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	564d0f37da8fa525

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xe7A_	 Alignment		100.0	29	PDB header: dna binding protein Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigj; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
2	c5uxxC_	 Alignment		100.0	26	PDB header: dna binding protein/unknown function Chain: C: PDB Molecule: rna polymerase sigma factor; PDBTitle: co-crystal structure of the sigma factor rpoe in complex with the2 anti-sigma factor nepr from bartonella quintana
3	c3t0yA_	 Alignment		100.0	22	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
4	c2lfwA_	 Alignment		100.0	22	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
5	c4cxF_	 Alignment		99.9	28	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
6	c5wurB_	 Alignment		99.9	27	PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
7	c6dvdF_	 Alignment		99.9	29	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigl; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor l) with 6 nt spacer and bromine3 labelled in position "-11
8	c5zx3F_	 Alignment		99.9	27	PDB header: transcription Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
9	c6c03A_	 Alignment		99.9	29	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
10	c1or7A_	 Alignment		99.9	25	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
11	c3vdoA_	 Alignment		99.9	19	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis

12	c5ipmF_	 Alignment		99.9	17	PDB header: transcription, transferase/dna/rna Chain: F; PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
13	c2q1zA_	 Alignment		99.9	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
14	c1rp3G_	 Alignment		99.9	18	PDB header: transcription Chain: G; PDB Molecule: rna polymerase sigma factor sigma-28 (flia); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm
15	c5tw1F_	 Alignment		99.8	19	PDB header: transcription activator/transferase/dna Chain: F; PDB Molecule: rna polymerase sigma factor siga; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
16	c3mzyA_	 Alignment		99.8	21	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
17	c6c05F_	 Alignment		99.8	18	PDB header: transcription Chain: F; PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpa in relaxed state
18	c3wodF_	 Alignment		99.8	19	PDB header: transferase/transcription Chain: F; PDB Molecule: rna polymerase sigma factor; PDBTitle: rna polymerase-gp39 complex
19	d1h3la_	 Alignment		99.7	35	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
20	d1or7b2	 Alignment		99.7	29	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
21	d1or7a2	 Alignment	not modelled	99.7	27	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
22	d1nwwa_	 Alignment	not modelled	99.7	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
23	d3en8a1	 Alignment	not modelled	99.6	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
24	c3wmdA_	 Alignment	not modelled	99.6	15	PDB header: isomerase Chain: A; PDB Molecule: probable monensin biosynthesis isomerase; PDBTitle: crystal structure of epoxide hydrolase monbi
25	c3msoA_	 Alignment	not modelled	99.6	13	PDB header: isomerase Chain: A; PDB Molecule: steroid delta-isomerase; PDBTitle: crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
26	c3n0rA_	 Alignment	not modelled	99.6	21	PDB header: signaling protein Chain: A; PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
27	c2a6eF_	 Alignment	not modelled	99.6	19	PDB header: transferase Chain: F; PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: crystal structure of the t. thermophilus rna polymerase2 holoenzyme
28	c5cxoA_	 Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: intriguing role of epoxide hydrolase/cyclase-like enzyme salbiii in2 pyran ring formation in polyether salinomycin PDB header: isomerase

29	c3f8xD	Alignment	not modelled	99.6	11	Chain: D: PDB Molecule: putative delta-5-3-ketosteroid isomerase; PDBTitle: crystal structure of a putative delta-5-3-ketosteroid isomerase2 (eca2236) from pectobacterium atrosepticum scri1043 at 1.55 a3 resolution
30	c2o7gA	Alignment	not modelled	99.6	28	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the pribnow box recognition region of sigc from2 mycobacterium tuberculosis
31	c1l9uH	Alignment	not modelled	99.6	20	PDB header: transcription Chain: H: PDB Molecule: sigma factor siga; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
32	c4h3uB	Alignment	not modelled	99.6	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein with ketosteroid isomerase-2 like protein fold from catenulispora acidiphila dsm 44928
33	c3f40A	Alignment	not modelled	99.6	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at 1.27 a3 resolution
34	d2bnga1	Alignment	not modelled	99.6	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
35	c4lmiA	Alignment	not modelled	99.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative ketosteroid isomerase from kribbella2 flavida dsm 17836
36	d2k54a1	Alignment	not modelled	99.5	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0742-like
37	c3b4oB	Alignment	not modelled	99.5	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: phenazine biosynthesis protein a/b; PDBTitle: crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
38	c3h3hA	Alignment	not modelled	99.5	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_ii0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
39	d1ohpa1	Alignment	not modelled	99.5	19	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
40	c3fh1A	Alignment	not modelled	99.5	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (mll8193)2 from mesorhizobium loti at 1.60 a resolution
41	d1oh0a	Alignment	not modelled	99.5	21	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
42	c5evhA	Alignment	not modelled	99.5	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of known function protein from kribbella flavida dsm2 17836
43	d3dm8a1	Alignment	not modelled	99.5	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
44	d3dmca1	Alignment	not modelled	99.5	9	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
45	c3ff2A	Alignment	not modelled	99.5	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized cystatin fold protein (yp_497570.1) from PDBTitle: crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution
46	c3ff0A	Alignment	not modelled	99.5	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: phenazine biosynthesis protein phzb 2; PDBTitle: crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
47	d2a15a1	Alignment	not modelled	99.4	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
48	c3k0zB	Alignment	not modelled	99.4	13	PDB header: lyase Chain: B: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of putative polyketide cyclase (np_977253.1) from2 bacillus cereus atcc 10987 at 1.91 a resolution
49	c6d34B	Alignment	not modelled	99.4	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: terc; PDBTitle: apo crystal structure of terc, a terfestatin biosynthesis enzyme
50	c3fijA	Alignment	not modelled	99.4	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein conserved in bacteria with a PDBTitle: crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
51	d3ebta1	Alignment	not modelled	99.4	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
52	c3rgaA	Alignment	not modelled	99.4	13	PDB header: isomerase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of epoxide hydrolase for polyether lasalocid a2 biosynthesis
53	d3ec9a1	Alignment	not modelled	99.4	18	Fold: Cystatin-like Superfamily: NTF2-like

						Family: PhzA/PhzB-like
54	c4kvhA	Alignment	not modelled	99.4	10	PDB header: unknown function Chain: A: PDB Molecule: ketosteroid isomerase fold protein hmuk_0747; PDBTitle: crystal structure of ketosteroid isomerase fold protein hmuk_0747
55	c1z1sA	Alignment	not modelled	99.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa3332; PDBTitle: crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
56	d1tuha	Alignment	not modelled	99.4	20	Fold: Cystatin-like Superfamily: NTF2-like Family: Hypothetical protein egc068 from a soil-derived mobile gene cassette
57	c1tuhA	Alignment	not modelled	99.4	20	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein egc068; PDBTitle: structure of bal32a from a soil-derived mobile gene cassette
58	c3f14A	Alignment	not modelled	99.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of ntf2-like protein of unknown function2 (yp_680363.1) from cytophaga hutchinsonii atcc 33406 at 1.45 a3 resolution
59	c5aigA	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: limonene-1,2-epoxide hydrolase; PDBTitle: discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries. tomsk-sample-3 valpromide complex
60	d1s5aa	Alignment	not modelled	99.4	16	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
61	c4igcX	Alignment	not modelled	99.4	18	PDB header: transcription, transferase Chain: X: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: x-ray crystal structure of escherichia coli sigma70 holoenzyme
62	d1z1sa1	Alignment	not modelled	99.4	17	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
63	c3hk4B	Alignment	not modelled	99.4	8	PDB header: lyase Chain: B: PDB Molecule: mlr7391 protein; PDBTitle: crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
64	c3hugA	Alignment	not modelled	99.4	24	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
65	c4u13B	Alignment	not modelled	99.4	19	PDB header: transferase Chain: B: PDB Molecule: putative polyketide cyclase sma1630; PDBTitle: crystal structure of putative polyketide cyclase (protein sma1630)2 from sinorhizobium meliloti at 2.3 a resolution
66	c3fgyB	Alignment	not modelled	99.3	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein (bx_e_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution
67	d3dxa1	Alignment	not modelled	99.3	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0744-like
68	d2f99a1	Alignment	not modelled	99.3	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
69	c5aiiP	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: P: PDB Molecule: limonene-1,2-epoxide hydrolase; PDBTitle: discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries.3 ch55-sample-peg complex
70	c3vepA	Alignment	not modelled	99.3	32	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
71	d1rp3a2	Alignment	not modelled	99.3	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
72	c3f8hA	Alignment	not modelled	99.3	17	PDB header: unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
73	d1or7a1	Alignment	not modelled	99.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
74	d2gexa1	Alignment	not modelled	99.3	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
75	c2o8xA	Alignment	not modelled	99.3	26	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
76	d1sjwa	Alignment	not modelled	99.3	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
77	c6a5hB	Alignment	not modelled	99.3	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: 101015d; PDBTitle: the structure of [4+2] and [6+4] cyclase in the biosynthetic pathway2 of unidentified natural product PDB header: isomerase

78	c3i0yC_	Alignment	not modelled	99.3	11	Chain: C; PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution
79	c3f7xA_	Alignment	not modelled	99.2	14	PDB header: unknown function Chain: A; PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
80	c3g8zA_	Alignment	not modelled	99.2	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein of unknown function with cystatin-like fold; PDBTitle: crystal structure of protein of unknown function with cystatin-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
81	d1s7oa_	Alignment	not modelled	99.2	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
82	d2geya1	Alignment	not modelled	99.2	12	Fold: Cystatin-like Superfamily: NTF2-like Family: SnoaL-like polyketide cyclase
83	c3g0kA_	Alignment	not modelled	99.2	6	PDB header: ca-binding protein Chain: A; PDB Molecule: putative membrane protein; PDBTitle: crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
84	c3grdA_	Alignment	not modelled	99.2	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized ntf2-superfamily protein; PDBTitle: crystal structure of ntf2-superfamily protein with unknown function2 (np_977240.1) from bacillus cereus atcc 10987 at 1.25 a resolution
85	c3iydF_	Alignment	not modelled	99.2	18	PDB header: transcription/dna Chain: F; PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
86	d1xsva_	Alignment	not modelled	99.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
87	c3kkqA_	Alignment	not modelled	99.2	10	PDB header: lyase Chain: A; PDB Molecule: putative snoa-like polyketide cyclase; PDBTitle: crystal structure of putative snoa-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution
88	c5fgmA_	Alignment	not modelled	99.2	34	PDB header: hydrolase Chain: A; PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
89	c5x9jB_	Alignment	not modelled	99.2	13	PDB header: isomerase Chain: B; PDB Molecule: prhc; PDBTitle: structre of prhc from penicillium brasilianum nbrc 6234
90	c3f9sB_	Alignment	not modelled	99.1	12	PDB header: lyase Chain: B; PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
91	c4lqqA_	Alignment	not modelled	99.1	12	PDB header: lyase Chain: A; PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (cv_0247) from2 chromobacterium violaceum atcc 12472 at 2.72 a resolution
92	c3ehcA_	Alignment	not modelled	99.1	13	PDB header: unknown function Chain: A; PDB Molecule: snoa-like polyketide cyclase; PDBTitle: crystal structure of a snoa-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
93	c5x7lA_	Alignment	not modelled	99.1	17	PDB header: isomerase Chain: A; PDB Molecule: tsrd; PDBTitle: structure of tsrd from streptomyces laurentii
94	d1smyf2	Alignment	not modelled	99.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
95	c4qicC_	Alignment	not modelled	99.1	19	PDB header: signaling protein/dna binding protein Chain: C; PDB Molecule: sensory transduction regulatory protein, anti-anti-sigma PDBTitle: co-crystal structure of anti-anti-sigma factor phyr complexed with2 anti-sigma factor nepr from bartonella quintana
96	d1m98a2	Alignment	not modelled	99.1	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Orange carotenoid protein, C-terminal domain
97	d1ttya_	Alignment	not modelled	98.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
98	d1rp3a3	Alignment	not modelled	98.9	11	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
99	c6fejA_	Alignment	not modelled	98.9	13	PDB header: photosynthesis Chain: A; PDB Molecule: all4940 protein; PDBTitle: anabaena apo-c-terminal domain homolog protein
100	c5x9kA_	Alignment	not modelled	98.9	9	PDB header: isomerase Chain: A; PDB Molecule: austinol synthesis protein h; PDBTitle: strucutre of aush from aspergillus nidulans
101	c3ke7A_	Alignment	not modelled	98.9	12	PDB header: isomerase Chain: A; PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution

102	c5wqhE	Alignment	not modelled	98.9	11	PDB header: isomerase Chain: E; PDB Molecule: isomerase trt14; PDBTitle: structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d
103	d1ku7a	Alignment	not modelled	98.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
104	d1ku3a	Alignment	not modelled	98.8	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
105	c3t72o	Alignment	not modelled	98.7	23	PDB header: transcription/dna Chain: O; PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
106	d2p7vb1	Alignment	not modelled	98.6	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
107	c3h51A	Alignment	not modelled	98.5	8	PDB header: protein binding Chain: A; PDB Molecule: putative calcium/calmodulin dependent protein kinase ii PDBTitle: crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution
108	d2rcda1	Alignment	not modelled	98.5	17	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
109	d2qxfa1	Alignment	not modelled	98.4	14	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
110	c3gwrA	Alignment	not modelled	98.3	16	PDB header: protein binding Chain: A; PDB Molecule: putative calcium/calmodulin-dependent protein kinase type PDBTitle: crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
111	d1vioa1	Alignment	not modelled	98.3	18	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)
112	c3f7sA	Alignment	not modelled	98.2	13	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
113	c3robC	Alignment	not modelled	98.2	10	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
114	c3qp5C	Alignment	not modelled	98.2	14	PDB header: transcription Chain: C; PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
115	d3cnxa1	Alignment	not modelled	98.2	16	Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like
116	c4lfuA	Alignment	not modelled	98.1	23	PDB header: dna binding protein Chain: A; PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
117	c3sztB	Alignment	not modelled	98.1	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
118	d3b7ca1	Alignment	not modelled	98.1	13	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
119	c4ovmE	Alignment	not modelled	98.1	14	PDB header: unknown function Chain: E; PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
120	c2q0oA	Alignment	not modelled	98.1	28	PDB header: transcription Chain: A; PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing