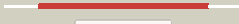


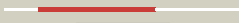






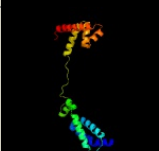

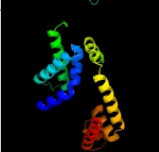



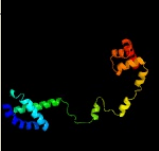

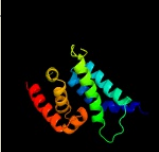





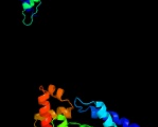


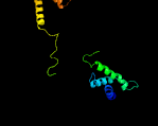




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1189_(sigl)_1332098_1332970
 Date Wed Jul 31 22:05:27 BST 2019
 Unique Job ID 06da4bff67781a21

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xe7A_	 Alignment		100.0	30	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	c3t0yA_	 Alignment		99.9	23	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
3	c5uxxC_	 Alignment		99.9	16	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
4	c2lfwA_	 Alignment		99.9	18	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	21	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	c6dvdF_	 Alignment		99.9	26	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 I) with 6 nt spacer and bromine3 labelled in position "-11
7	c6in7B_	 Alignment		99.9	24	PDB header: transcription Chain: B; PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
8	c1or7A_	 Alignment		99.9	22	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
9	c5zx3F_	 Alignment		99.9	19	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
10	c5wurB_	 Alignment		99.9	23	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
11	c6c03A_	 Alignment		99.9	25	PDB header: transcription Chain: A; PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex

12	c3vdoA	Alignment		99.9	22	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
13	c2q1zA	Alignment		99.9	11	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	c5jpmF	Alignment		99.9	16	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
15	c1rp3G	Alignment		99.8	14	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
16	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
17	c6c05F	Alignment		99.7	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		99.7	14	PDB header: transferase/transcription Chain: F: PDB Molecule: rna polymerase sigma factor; PDBTitle: rna polymerase-gp39 complex
19	c3mzyA	Alignment		99.7	24	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
20	d1or7a2	Alignment		99.6	18	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	c3n0rA	Alignment	not modelled	99.5	21	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
22	d1or7b2	Alignment	not modelled	99.5	19	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
23	d1h3la	Alignment	not modelled	99.5	16	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
24	c2a6eF	Alignment	not modelled	99.5	14	PDB header: transferase Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: crystal structure of the t. thermophilus rna polymerase2 holoenzyme
25	c2o7gA	Alignment	not modelled	99.4	25	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
26	c1l9uH	Alignment	not modelled	99.4	17	PDB header: transcription Chain: H: PDB Molecule: sigma factor siga; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
27	c3hugA	Alignment	not modelled	99.3	22	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
28	c3vepA	Alignment	not modelled	99.2	24	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 Fold: DNA/RNA-binding 3-helical bundle

29	d1or7a1	Alignment	not modelled	99.2	28	Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
30	c4iqcX	Alignment	not modelled	99.2	14	PDB header: transcription, transferase Chain: X: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: x-ray crystal structure of escherichia coli sigma70 holoenzyme
31	c2o8xA	Alignment	not modelled	99.2	25	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
32	d1rp3a2	Alignment	not modelled	99.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
33	d1s7oa	Alignment	not modelled	99.2	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
34	d1xsva	Alignment	not modelled	99.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
35	c5fgmA	Alignment	not modelled	99.1	22	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
36	d1smyf2	Alignment	not modelled	99.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
37	c4qicC	Alignment	not modelled	99.0	18	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
38	c3f8xD	Alignment	not modelled	99.0	20	PDB header: isomerase 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
39	c3f40A	Alignment	not modelled	99.0	20	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
40	d3en8a1	Alignment	not modelled	99.0	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
41	c3msoA	Alignment	not modelled	98.9	23	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
42	c3iydF	Alignment	not modelled	98.9	16	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
43	c5cxoA	Alignment	not modelled	98.9	16	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
44	d1ohpa1	Alignment	not modelled	98.9	18	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
45	d1ttya	Alignment	not modelled	98.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
46	c3fh1A	Alignment	not modelled	98.9	17	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
47	c3fjA	Alignment	not modelled	98.9	19	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
48	c5evhA	Alignment	not modelled	98.8	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of known function protein from kribbella flavida dsm2 17836
49	c4lmiA	Alignment	not modelled	98.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative ketosteroid isomerase from kribbella2 flavida dsm 17836
50	d1oh0a	Alignment	not modelled	98.8	11	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
51	d2k54a1	Alignment	not modelled	98.8	12	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0742-like
52	d1ku7a	Alignment	not modelled	98.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
53	c3wmdA	Alignment	not modelled	98.8	16	PDB header: isomerase Chain: A: PDB Molecule: probable monensin biosynthesis isomerase; PDBTitle: crystal structure of epoxide hydrolase monbi

54	d3dmca1	Alignment	not modelled	98.7	12	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
55	d1ku3a_	Alignment	not modelled	98.7	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
56	c3h3hA_	Alignment	not modelled	98.7	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_i0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
57	d3dm8a1	Alignment	not modelled	98.7	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
58	c4u13B_	Alignment	not modelled	98.7	17	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
59	d1nwwa_	Alignment	not modelled	98.7	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
60	d1rp3a3	Alignment	not modelled	98.6	10	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
61	c3t72o_	Alignment	not modelled	98.6	17	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
62	d1s5aa_	Alignment	not modelled	98.6	15	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
63	d2bnga1	Alignment	not modelled	98.6	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
64	d1z1sa1	Alignment	not modelled	98.6	15	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
65	c1z1sA_	Alignment	not modelled	98.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa3332; PDBTitle: crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
66	c4kvhA_	Alignment	not modelled	98.6	18	PDB header: unknown function Chain: A: PDB Molecule: ketosteroid isomerase fold protein hmuk_0747; PDBTitle: crystal structure of ketosteroid isomerase fold protein hmuk_0747
67	c3ff2A_	Alignment	not modelled	98.6	15	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
68	c1tuhA_	Alignment	not modelled	98.5	17	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein egc068; PDBTitle: structure of bal32a from a soil-derived mobile gene cassette
69	d1tuha_	Alignment	not modelled	98.5	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Hypothetical protein egc068 from a soil-derived mobile gene cassette
70	c4h3uB_	Alignment	not modelled	98.5	15	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
71	d3ec9a1	Alignment	not modelled	98.5	15	Fold: Cystatin-like Superfamily: NTF2-like Family: PhzA/PhzB-like
72	d2p7vb1	Alignment	not modelled	98.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
73	d3ebta1	Alignment	not modelled	98.5	21	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
74	d2a15a1	Alignment	not modelled	98.5	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
75	c6fejA_	Alignment	not modelled	98.5	11	PDB header: photosynthesis Chain: A: PDB Molecule: all4940 protein; PDBTitle: anabaena apo-c-terminal domain homolog protein
76	c5aigA_	Alignment	not modelled	98.5	13	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
77	c6d34B_	Alignment	not modelled	98.5	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: terc; PDBTitle: apo crystal structure of terc, a terfestatin biosynthesis enzyme
78	c5aiiP_	Alignment	not modelled	98.5	18	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

79	c3fgyB	Alignment	not modelled	98.4	16	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
80	c6a5hB	Alignment	not modelled	98.4	15	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
81	c3rgaA	Alignment	not modelled	98.4	14	PDB header: isomerase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of epoxide hydrolase for polyether lasalocid a2 biosynthesis
82	d1m98a2	Alignment	not modelled	98.3	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Orange carotenoid protein, C-terminal domain
83	c3g8zA	Alignment	not modelled	98.3	23	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
84	c3f14A	Alignment	not modelled	98.3	14	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
85	c3k0zB	Alignment	not modelled	98.3	11	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
86	c3f8hA	Alignment	not modelled	98.3	16	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
87	c3b4oB	Alignment	not modelled	98.2	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
88	c3i0yC	Alignment	not modelled	98.2	20	PDB header: isomerase 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
89	c3h51A	Alignment	not modelled	98.2	13	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
90	d1vioa1	Alignment	not modelled	98.1	29	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)
91	c3hk4B	Alignment	not modelled	98.1	17	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
92	c3ke7A	Alignment	not modelled	98.1	14	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
93	c3f7xA	Alignment	not modelled	98.1	17	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
94	d3dxa1	Alignment	not modelled	98.1	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0744-like
95	d2f99a1	Alignment	not modelled	98.0	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
96	d2gexa1	Alignment	not modelled	98.0	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
97	c4ifuA	Alignment	not modelled	98.0	16	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
98	c3grdA	Alignment	not modelled	98.0	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
99	c3sztB	Alignment	not modelled	98.0	23	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
100	c4lqaA	Alignment	not modelled	97.9	20	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
101	c5x7IA	Alignment	not modelled	97.9	22	PDB header: isomerase Chain: A: PDB Molecule: tsrd; PDBTitle: structure of tsrd from streptomyces laurentii
102	c3qp5C	Alignment	not modelled	97.9	20	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone

					(cl)
103	c1x3uA_	Alignment	not modelled	97.9	23 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
104	c5x9jB_	Alignment	not modelled	97.9	10 PDB header: isomerase Chain: B: PDB Molecule: prhc; PDBTitle: strucutre of prhc from penicillium brasilianum nbrc 6234
105	c2q0aA_	Alignment	not modelled	97.9	27 PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
106	c3f9sB_	Alignment	not modelled	97.9	9 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
107	c1h0mD_	Alignment	not modelled	97.9	20 PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
108	c3ff0A_	Alignment	not modelled	97.9	13 PDB header: biosynthetic protein Chain: A: PDB Molecule: phenazine biosynthesis protein phzb2; PDBTitle: crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
109	c3ehcA_	Alignment	not modelled	97.8	12 PDB header: unknown function Chain: A: PDB Molecule: snoal-like polyketide cyclase; PDBTitle: crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
110	d2geya1	Alignment	not modelled	97.8	14 Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
111	d1a04a1	Alignment	not modelled	97.8	28 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	c5wqhE_	Alignment	not modelled	97.7	10 PDB header: isomerase Chain: E: PDB Molecule: isomerase trt14; PDBTitle: structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d
113	c1zljE_	Alignment	not modelled	97.7	26 PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
114	d1sjwa_	Alignment	not modelled	97.7	20 Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
115	c3gwrA_	Alignment	not modelled	97.6	13 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
116	c2krfB_	Alignment	not modelled	97.6	18 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
117	c3f7sA_	Alignment	not modelled	97.6	10 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
118	c3g0kA_	Alignment	not modelled	97.6	15 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
119	c6jqsA_	Alignment	not modelled	97.5	19 PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
120	c2rnjA_	Alignment	not modelled	97.5	21 PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: nmr structure of the s. aureus vrar dna binding domain