



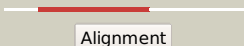







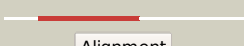


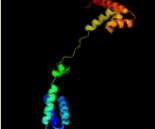








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3328c_(sig)_3713565_3714503
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	17d68dc4c9c6266d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xe7A_</a>	 Alignment		100.0	97	<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
2	<a href="#">c3t0yA_</a>	 Alignment		99.9	30	<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
3	<a href="#">c2lfwA_</a>	 Alignment		99.9	16	<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
4	<a href="#">c5uxxC_</a>	 Alignment		99.9	19	<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
5	<a href="#">c5zx3F_</a>	 Alignment		99.9	21	<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
6	<a href="#">c6in7B_</a>	 Alignment		99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> crystal structure of algu in complex with muca(cyto)
7	<a href="#">c4cxA_</a>	 Alignment		99.9	25	<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
8	<a href="#">c6dvdF_</a>	 Alignment		99.9	26	<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 l) with 6 nt spacer and bromine3 labelled in position "-11
9	<a href="#">c1or7A_</a>	 Alignment		99.9	19	<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
10	<a href="#">c5wurB_</a>	 Alignment		99.9	23	<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
11	<a href="#">c6c03A_</a>	 Alignment		99.9	27	<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

12	<a href="#">c5ipmF_</a>	Alignment		99.9	15	<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
13	<a href="#">c2q1zA_</a>	Alignment		99.9	17	<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
14	<a href="#">c3vdoA_</a>	Alignment		99.9	16	<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
15	<a href="#">c1rp3G_</a>	Alignment		99.8	16	<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
16	<a href="#">c5tw1F_</a>	Alignment		99.7	19	<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
17	<a href="#">c3mzyA_</a>	Alignment		99.7	17	<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
18	<a href="#">c6c05F_</a>	Alignment		99.7	18	<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
19	<a href="#">c3wodF_</a>	Alignment		99.7	13	<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
20	<a href="#">c3n0rA_</a>	Alignment		99.6	23	<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
21	<a href="#">c1l9uH_</a>	Alignment	not modelled	99.4	14	<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="#">d1or7a2</a>	Alignment	not modelled	99.4	15	<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
23	<a href="#">c2a6eF_</a>	Alignment	not modelled	99.4	17	<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
24	<a href="#">d1h3la_</a>	Alignment	not modelled	99.4	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
25	<a href="#">d1or7b2</a>	Alignment	not modelled	99.4	17	<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
26	<a href="#">d3en8a1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
27	<a href="#">d1nwwa_</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
28	<a href="#">c2o7gA_</a>	Alignment	not modelled	99.3	26	<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
29	<a href="#">c5cvaA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> epoxide hydrolase;

29	<a href="#">c3cxaA</a>	Alignment	not modelled	99.3	13	<b>PDBTitle:</b> intriguing role of epoxide hydrolase/cyclase-like enzyme salbiii in 2 pyran ring formation in polyether salinomycin <b>PDB header:</b> isomerase
30	<a href="#">c3f8xD</a>	Alignment	not modelled	99.3	15	<b>Chain:</b> D: <b>PDB Molecule:</b> putative delta-5-3-ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of a putative delta-5-3-ketosteroid isomerase2 (eca2236) from pectobacterium atrosepticum scri1043 at 1.55 a3 resolution
31	<a href="#">c3hugA</a>	Alignment	not modelled	99.3	20	<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
32	<a href="#">d3dmca1</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
33	<a href="#">c3wmdA</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable monensin biosynthesis isomerase; <b>PDBTitle:</b> crystal structure of epoxide hydrolase monbi
34	<a href="#">c3vepA</a>	Alignment	not modelled	99.2	24	<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
35	<a href="#">d1ohpa1</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
36	<a href="#">c3f40A</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at 1.27 a3 resolution
37	<a href="#">d3dm8a1</a>	Alignment	not modelled	99.2	7	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
38	<a href="#">c3fh1A</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function (mll8193)2 from mesorhizobium loti at 1.60 a resolution
39	<a href="#">c1tuhA</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein egc068; <b>PDBTitle:</b> structure of bal32a from a soil-derived mobile gene cassette
40	<a href="#">d1tuha</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Hypothetical protein egc068 from a soil-derived mobile gene cassette
41	<a href="#">c2o8xA</a>	Alignment	not modelled	99.2	28	<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 of 2 mycobacterium tuberculosis sigc
42	<a href="#">d1or7a1</a>	Alignment	not modelled	99.2	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
43	<a href="#">d1rp3a2</a>	Alignment	not modelled	99.2	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> Sigma4 domain
44	<a href="#">d1s7oa</a>	Alignment	not modelled	99.2	16	<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
45	<a href="#">d2k54a1</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0742-like
46	<a href="#">c4igcX</a>	Alignment	not modelled	99.2	15	<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
47	<a href="#">c5evhA</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of known function protein from kribbella flavida dsm2 17836
48	<a href="#">d1oh0a</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
49	<a href="#">c3ff2A</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized cystatin fold protein (yp_497570.1) from <b>PDBTitle:</b> crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution
50	<a href="#">c1z1sA</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa3332; <b>PDBTitle:</b> crystal structure of putative isomerase pa3332 from 2 pseudomonas aeruginosa
51	<a href="#">d1z1sa1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
52	<a href="#">d3ebta1</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
53	<a href="#">c3msoA</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> steroid delta-isomerase; <b>PDBTitle:</b> crystal structure of a steroid delta-isomerase (np_250810.1) from 2 pseudomonas aeruginosa at 2.57 a resolution
						<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized snoal-like protein;

54	<a href="#">c3h3hA_</a>	Alignment	not modelled	99.1	12	<b>PDBTitle:</b> crystal structure of a snoal-like protein of unknown function2 (bth_ii0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
55	<a href="#">d3ec9a1</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
56	<a href="#">c4lmiA_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase from kribbella2 flavida dsm 17836
57	<a href="#">d1xsva_</a>	Alignment	not modelled	99.1	17	<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
58	<a href="#">c6d34B_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> terc; <b>PDBTitle:</b> apo crystal structure of terc, a terfestatin biosynthesis enzyme
59	<a href="#">c4h3uB_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of hypothetical protein with ketosteroid isomerase-2 like protein fold from catenulispora acidiphila dsm 44928
60	<a href="#">d2a15a1</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
61	<a href="#">c5fgmA_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigr; <b>PDBTitle:</b> streptomyces coelicolor sigr region 4
62	<a href="#">d2bnga1</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
63	<a href="#">d1s5aa_</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
64	<a href="#">c6a5hB_</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> 101015d; <b>PDBTitle:</b> the structure of [4+2] and [6+4] cyclase in the biosynthetic pathway2 of unidentified natural product
65	<a href="#">c4u13B_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide cyclase sma1630; <b>PDBTitle:</b> crystal structure of putative polyketide cyclase (protein sma1630)2 from sinorhizobium meliloti at 2.3 a resolution
66	<a href="#">c4kvhA_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ketosteroid isomerase fold protein hmuk_0747; <b>PDBTitle:</b> crystal structure of ketosteroid isomerase fold protein hmuk_0747
67	<a href="#">c3fgyB_</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein (bx_e_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution
68	<a href="#">c3fijA_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein conserved in bacteria with a <b>PDBTitle:</b> 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
69	<a href="#">d1smyf2</a>	Alignment	not modelled	99.0	10	<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
70	<a href="#">c3f14A_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function2 (yp_680363.1) from cytophaga hutchinsonii atcc 33406 at 1.45 a3 resolution
71	<a href="#">c4qicC_</a>	Alignment	not modelled	99.0	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
72	<a href="#">c3k0zB_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of putative polyketide cyclase (np_977253.1) from2 bacillus cereus atcc 10987 at 1.91 a resolution
73	<a href="#">c3b4oB_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> phenazine biosynthesis protein a/b; <b>PDBTitle:</b> crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
74	<a href="#">c3f8hA_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
75	<a href="#">c3iydF_</a>	Alignment	not modelled	98.9	14	<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
76	<a href="#">d1ttya_</a>	Alignment	not modelled	98.9	18	<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
77	<a href="#">c3g8zA_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function with cystatin-like fold; <b>PDBTitle:</b> crystal structure of protein of unknown function with cystatin-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
						<b>PDB header:</b> hydrolase

78	<a href="#">c5aiiP_</a>	Alignment	not modelled	98.9	24	<b>Chain:</b> P; <b>PDB Molecule:</b> limonene-1,2-epoxide hydrolase; <b>PDBTitle:</b> discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries.3 ch55-sample-peg complex
79	<a href="#">d2f99a1</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
80	<a href="#">c3hk4B_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> mlr7391 protein; <b>PDBTitle:</b> crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
81	<a href="#">d1sjwa_</a>	Alignment	not modelled	98.8	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
82	<a href="#">c3i0yC_</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution
83	<a href="#">c5aigA_</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> limonene-1,2-epoxide hydrolase; <b>PDBTitle:</b> discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries. tomsk-sample-3 valpromide complex
84	<a href="#">d3dxa01</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0744-like
85	<a href="#">d1m98a2</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Orange carotenoid protein, C-terminal domain
86	<a href="#">c3rgaA_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of epoxide hydrolase for polyether lasalocid a2 biosynthesis
87	<a href="#">c3ff0A_</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> phenazine biosynthesis protein phzb 2; <b>PDBTitle:</b> crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
88	<a href="#">c4lqgA_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (cv_0247) from2 chromobacterium violaceum atcc 12472 at 2.72 a resolution
89	<a href="#">d1ku7a_</a>	Alignment	not modelled	98.7	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> Sigma4 domain
90	<a href="#">c3f7xA_</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
91	<a href="#">d2geva1</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
92	<a href="#">c3f9sB_</a>	Alignment	not modelled	98.7	11	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
93	<a href="#">c6fejA_</a>	Alignment	not modelled	98.7	10	<b>PDB header:</b> photosynthesis <b>Chain:</b> A; <b>PDB Molecule:</b> all4940 protein; <b>PDBTitle:</b> anabaena apo-c-terminal domain homolog protein
94	<a href="#">d1ku3a_</a>	Alignment	not modelled	98.7	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
95	<a href="#">c3grdA_</a>	Alignment	not modelled	98.7	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized ntf2-superfamily protein; <b>PDBTitle:</b> crystal structure of ntf2-superfamily protein with unknown function2 (np_977240.1) from bacillus cereus atcc 10987 at 1.25 a resolution
96	<a href="#">d2gexa1</a>	Alignment	not modelled	98.6	23	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
97	<a href="#">c3g0kA_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> ca-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> 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
98	<a href="#">c3t72o_</a>	Alignment	not modelled	98.6	19	<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
99	<a href="#">c5x9jB_</a>	Alignment	not modelled	98.6	10	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> prhc; <b>PDBTitle:</b> strucutre of prhc from penicillium brasilianum nbrc 6234
100	<a href="#">c3h51A_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> putative calcium/calmodulin dependent protein kinase ii <b>PDBTitle:</b> crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution
101	<a href="#">c3ke7A_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> putative ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at

					1.45 a resolution
102	<a href="#">d2p7vb1</a>	Alignment	not modelled	98.5	18 <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
103	<a href="#">c3ehcA</a>	Alignment	not modelled	98.5	10 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> snoal-like polyketide cyclase; <b>PDBTitle:</b> crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
104	<a href="#">d1rp3a3</a>	Alignment	not modelled	98.5	13 <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
105	<a href="#">c5x7IA</a>	Alignment	not modelled	98.4	20 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> tsrd; <b>PDBTitle:</b> structure of tsrd from streptomyces laurentii
106	<a href="#">c3kkqA</a>	Alignment	not modelled	98.3	22 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative snoal-like polyketide cyclase; <b>PDBTitle:</b> crystal structure of putative snoal-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution
107	<a href="#">d1yioa1</a>	Alignment	not modelled	98.2	11 <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)
108	<a href="#">c5x9kA</a>	Alignment	not modelled	98.1	11 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> austinol synthesis protein h; <b>PDBTitle:</b> strucutre of aush from aspergillus nidulans
109	<a href="#">c5wqhE</a>	Alignment	not modelled	98.1	8 <b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> isomerase trt14; <b>PDBTitle:</b> structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretinin d
110	<a href="#">c3qp5C</a>	Alignment	not modelled	98.1	18 <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)
111	<a href="#">c3f7sA</a>	Alignment	not modelled	98.1	9 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
112	<a href="#">c3sztB</a>	Alignment	not modelled	98.0	11 <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
113	<a href="#">c3robC</a>	Alignment	not modelled	98.0	17 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
114	<a href="#">c4lfuA</a>	Alignment	not modelled	98.0	16 <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
115	<a href="#">c3hx8A</a>	Alignment	not modelled	98.0	15 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution
116	<a href="#">d2rcda1</a>	Alignment	not modelled	98.0	14 <b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
117	<a href="#">c3gwrA</a>	Alignment	not modelled	98.0	12 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative calcium/calmodulin-dependent protein kinase type <b>PDBTitle:</b> 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
118	<a href="#">c1x3uA</a>	Alignment	not modelled	97.9	13 <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
119	<a href="#">c2q0oA</a>	Alignment	not modelled	97.9	15 <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
120	<a href="#">d3cu3a1</a>	Alignment	not modelled	97.9	12 <b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like