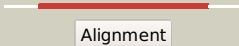



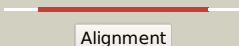

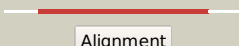

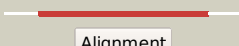

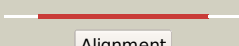

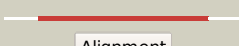




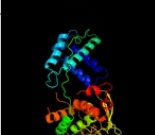




















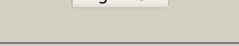
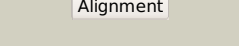




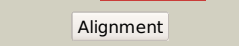
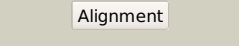
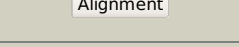
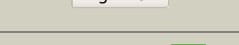
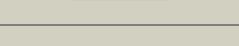
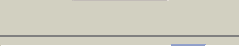

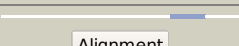
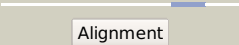
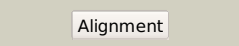

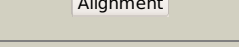
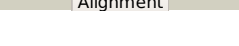
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1701_(xerD)_1926209_1927144
Date	Fri Aug 2 13:30:30 BST 2019
Unique Job ID	9b9d3715e1090991

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5hxyE_	 Alignment		100.0	27	PDB header: recombination Chain: E; PDB Molecule: tyrosine recombinase xera; PDBTitle: crystal structure of xera recombinase
2	c5vfzA_	 Alignment		100.0	24	PDB header: dna binding protein Chain: A; PDB Molecule: gp33; PDBTitle: integrase from mycobacterium phage brujita
3	c5jjvA_	 Alignment		100.0	22	PDB header: recombination Chain: A; PDB Molecule: tyrosine recombinase xerh; PDBTitle: crystal structure of xerh site-specific recombinase bound to 2 palindromic difh substrate: post-cleavage complex
4	c1a0pA_	 Alignment		100.0	40	PDB header: dna recombination Chain: A; PDB Molecule: site-specific recombinase xerd; PDBTitle: site-specific recombinase, xerd
5	c1ma7A_	 Alignment		100.0	14	PDB header: hydrolase, ligase/dna Chain: A; PDB Molecule: cre recombinase; PDBTitle: crystal structure of cre site-specific recombinase 2 complexed with a mutant dna substrate, loxp-a8/t27
6	c1crxA_	 Alignment		100.0	14	PDB header: replication/dna Chain: A; PDB Molecule: cre recombinase; PDBTitle: cre recombinase/dna complex reaction intermediate i
7	c6en2A_	 Alignment		100.0	16	PDB header: recombination Chain: A; PDB Molecule: int protein; PDBTitle: structure of the tn1549 transposon integrase (aa 82-397, r225k) in 2 complex with a circular intermediate dna (ci6b-dna)
8	c2a3vA_	 Alignment		100.0	28	PDB header: recombination Chain: A; PDB Molecule: site-specific recombinase inti4; PDBTitle: structural basis for broad dna-specificity in integron recombination
9	c1z1bA_	 Alignment		100.0	21	PDB header: dna binding protein/dna Chain: A; PDB Molecule: integrase; PDBTitle: crystal structure of a lambda integrase dimer bound to a 2 coc' core site
10	d1p7da_	 Alignment		100.0	20	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
11	c4a8eA_	 Alignment		100.0	27	PDB header: cell cycle Chain: A; PDB Molecule: probable tyrosine recombinase xerc-like; PDBTitle: the structure of a dimeric xer recombinase from archaea

12	c5dcfA	Alignment		99.9	43	PDB header: recombination Chain: A: PDB Molecule: tyrosine recombinase xerd,dna translocase ftsk; PDBTitle: c-terminal domain of xerd recombinase in complex with gamma domain of2 ftsk
13	c3nkhB	Alignment		99.9	20	PDB header: recombination Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of integrase from mrsa strain staphylococcus aureus
14	d1aiha	Alignment		99.8	20	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
15	c5c6kB	Alignment		99.8	25	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: bacteriophage p2 integrase catalytic domain
16	d1a0pa2	Alignment		99.8	41	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
17	d1f44a2	Alignment		99.8	13	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
18	c3uxuA	Alignment		99.7	16	PDB header: recombination Chain: A: PDB Molecule: probable integrase; PDBTitle: the structure of the catalytic domain of the sulfobolus spindle-shaped2 viral integrase reveals an evolutionarily conserved catalytic core3 and supports a mechanism of dna cleavage in trans
19	d1ae9a	Alignment		99.7	19	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
20	d5crxb2	Alignment		99.4	16	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
21	c3nrwA	Alignment	not modelled	99.4	21	PDB header: recombination Chain: A: PDB Molecule: phage integrase/site-specific recombinase; PDBTitle: crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
22	d1f44a1	Alignment	not modelled	99.2	13	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
23	d1a0pa1	Alignment	not modelled	99.1	38	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
24	c2khaA	Alignment	not modelled	99.1	15	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
25	c2oxoA	Alignment	not modelled	99.1	24	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
26	c2keyA	Alignment	not modelled	99.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative phage integrase; PDBTitle: solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
27	c2kd1A	Alignment	not modelled	99.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dna integration/recombination/inversion protein; PDBTitle: solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f

28	c2kiwA	 Alignment	not modelled	98.9	11	PDB header: dna binding protein Chain: A: PDB Molecule: int protein; PDBTitle: solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
29	c2kkpA	 Alignment	not modelled	98.9	19	PDB header: dna binding protein Chain: A: PDB Molecule: phage integrase; PDBTitle: solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
30	c3lysC	 Alignment	not modelled	98.9	10	PDB header: recombination Chain: C: PDB Molecule: prophage pi2 protein 01, integrase; PDBTitle: crystal structure of the n-terminal domain of the prophage pi2 protein2 01 (integrase) from lactococcus lactis, northeast structural genomics3 consortium target kr124f
31	c2kj8A	 Alignment	not modelled	98.9	11	PDB header: dna binding protein Chain: A: PDB Molecule: putative prophage cps-53 integrase; PDBTitle: nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
32	c2kobA	 Alignment	not modelled	98.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a
33	c2kj9A	 Alignment	not modelled	98.8	13	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
34	c2kkvA	 Alignment	not modelled	98.8	13	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of an integrase domain from protein spa42882 from salmonella enterica, northeast structural genomics consortium3 target slr105h
35	c2khvA	 Alignment	not modelled	98.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phage integrase; PDBTitle: solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
36	c2kj5A	 Alignment	not modelled	98.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phage integrase; PDBTitle: solution nmr structure of a domain from a putative phage integrase2 protein nmul_a0064 from nitrosospira multiformis, northeast3 structural genomics consortium target nmr46c
37	c2v6eB	 Alignment	not modelled	96.3	11	PDB header: hydrolase Chain: B: PDB Molecule: protelemorase; PDBTitle: protelomerase telk complexed with substrate dna
38	c4f43A	 Alignment	not modelled	93.1	13	PDB header: recombination/dna Chain: A: PDB Molecule: protelemorase; PDBTitle: protelomerase telb mutant r255a complexed with caag hairpin dna
39	c3sqiA	 Alignment	not modelled	58.1	19	PDB header: dna binding protein/dna Chain: A: PDB Molecule: kla0e03807p; PDBTitle: dna binding domain of ndc10
40	c3t79A	 Alignment	not modelled	58.1	19	PDB header: dna binding protein/dna Chain: A: PDB Molecule: kla0e03807p; PDBTitle: ndc10: a platform for inner kinetochore assembly in budding yeast
41	d1s7oa	 Alignment	not modelled	52.6	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
42	c3mzyA	 Alignment	not modelled	50.5	11	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
43	c3vdoA	 Alignment	not modelled	47.2	18	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
44	c5fgmA	 Alignment	not modelled	22.6	11	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
45	c3sohB	 Alignment	not modelled	20.5	8	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
46	d1trra	 Alignment	not modelled	20.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
47	c4cxfA	 Alignment	not modelled	20.0	13	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
48	c6b7qA	 Alignment	not modelled	15.9	17	PDB header: cell invasion Chain: A: PDB Molecule: sdea; PDBTitle: crystal structure of legionella effector protein sdea (lpg2157) aa.2 211-910
49	d1vz0a1	 Alignment	not modelled	15.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
50	c3vepA	 Alignment	not modelled	15.4	7	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
51	c3hugA	 Alignment	not modelled	15.0	18	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 sigI
52	d2auwa1	Alignment	not modelled	14.9	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
53	d1jhga_	Alignment	not modelled	13.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
54	c1r71B_	Alignment	not modelled	13.2	12	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in complex with2 the operator dna
55	c2x48B_	Alignment	not modelled	12.7	28	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
56	c1umqA_	Alignment	not modelled	12.1	15	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
57	d1umqa_	Alignment	not modelled	12.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
58	d1v2za_	Alignment	not modelled	11.8	28	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
59	d1r8ja1	Alignment	not modelled	11.8	28	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
60	c6dvdF_	Alignment	not modelled	11.7	18	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigI; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
61	c5jwrE_	Alignment	not modelled	11.5	28	PDB header: transcription regulator Chain: E: PDB Molecule: circadian clock protein kaia; PDBTitle: crystal structure of foldswitch-stabilized kaib in complex with the n-2 terminal ci domain of kaic and a dimer of kaia c-terminal domains3 from thermosynechococcus elongatus
62	d1sv1a_	Alignment	not modelled	11.1	28	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
63	c6in7B_	Alignment	not modelled	10.6	11	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
64	c2e8mA_	Alignment	not modelled	10.5	16	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
65	c5wurB_	Alignment	not modelled	10.5	16	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
66	d1or7a1	Alignment	not modelled	10.4	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
67	d1xsva_	Alignment	not modelled	10.1	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
68	d1fsea_	Alignment	not modelled	9.9	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)
69	d1hcra_	Alignment	not modelled	9.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
70	d1ijwc_	Alignment	not modelled	9.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
71	c2kq6A_	Alignment	not modelled	9.3	20	PDB header: transport protein Chain: A: PDB Molecule: polycystin-2; PDBTitle: the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity
72	c2f4qA_	Alignment	not modelled	9.2	21	PDB header: isomerase Chain: A: PDB Molecule: type i topoisomerase, putative; PDBTitle: crystal structure of deinococcus radiodurans topoisomerase ib
73	c2mhhA_	Alignment	not modelled	9.1	20	PDB header: metal binding protein Chain: A: PDB Molecule: polycystic kidney disease protein 2; PDBTitle: solution structure of a ef-hand domain from sea urchin polycystin-2
74	c2mqkA_	Alignment	not modelled	8.0	9	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the nub aaa+ atpase
75	d1r71a_	Alignment	not modelled	7.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
76	c2q1zA_	Alignment	not modelled	7.6	14	PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sigI; PDBTitle: crystal structure of rhodobacter sphaeroides sigI in

						complex with the2 anti-sigma chrr
77	c3t0yA	Alignment	not modelled	7.5	5	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
78	d1ujoa	Alignment	not modelled	7.5	17	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
79	c3frwF	Alignment	not modelled	7.5	12	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
80	c2rniA	Alignment	not modelled	6.9	14	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
81	c5of3E	Alignment	not modelled	6.8	9	PDB header: replication Chain: E: PDB Molecule: dna primase large subunit pril; PDBTitle: crystal structure of the heterotrimeric prislx primase from s.2 solfataricus.
82	c2kleA	Alignment	not modelled	6.6	24	PDB header: membrane protein Chain: A: PDB Molecule: polycystin-2; PDBTitle: isic refined solution structure of the calcium binding2 domain of the c-terminal cytosolic domain of polycystin-2
83	c1u78A	Alignment	not modelled	6.5	6	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
84	c2auvA	Alignment	not modelled	6.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: potential nad-reducing hydrogenase subunit; PDBTitle: solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
85	d1rp3a2	Alignment	not modelled	6.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
86	c5uxxC	Alignment	not modelled	6.4	11	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
87	c5zx3F	Alignment	not modelled	6.3	14	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
88	c1wwuA	Alignment	not modelled	6.1	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein flj21935; PDBTitle: solution structure of the sam_pnt domain of human protein2 flj21935
89	c1x3uA	Alignment	not modelled	6.0	14	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
90	c3i6xC	Alignment	not modelled	6.0	10	PDB header: calmodulin-binding, membrane protein Chain: C: PDB Molecule: ras gtpase-activating-like protein iqgap1; PDBTitle: crystal structure of the calponin homology domain of iqgap1
91	c2lfwA	Alignment	not modelled	6.0	6	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
92	d1smyf2	Alignment	not modelled	5.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
93	c4r0gA	Alignment	not modelled	5.9	22	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of lpg0393 from legionella pneumophila
94	c2jpcA	Alignment	not modelled	5.9	26	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
95	d1a04a1	Alignment	not modelled	5.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
96	d2g7la1	Alignment	not modelled	5.8	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
97	d1q08a	Alignment	not modelled	5.5	32	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
98	d1h67a	Alignment	not modelled	5.5	8	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
99	c2o8xA	Alignment	not modelled	5.5	15	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