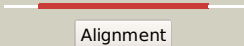

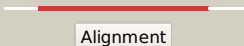

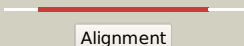







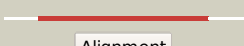











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2894c_xerC_3203404_3204300
Date	Thu Aug 8 16:20:04 BST 2019
Unique Job ID	7645b087cfc84ebd

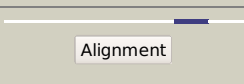
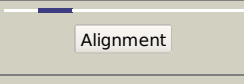
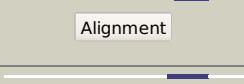
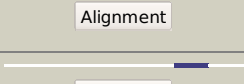
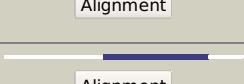
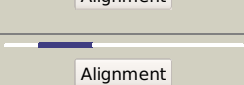
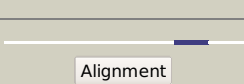
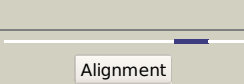
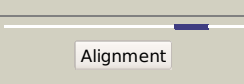
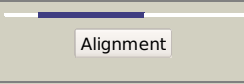

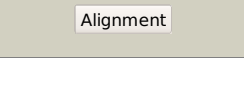

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5hxyE_	 Alignment		100.0	26	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	c5ijvA_	 Alignment		100.0	19	PDB header: recombination Chain: A; PDB Molecule: tyrosine recombinase xerh; PDBTitle: crystal structure of xerh site-specific recombinase bound to2 palindromic difh substrate: post-cleavage complex
4	c1ma7A_	 Alignment		100.0	12	PDB header: hydrolase, ligase/dna Chain: A; PDB Molecule: cre recombinase; PDBTitle: crystal structure of cre site-specific recombinase2 complexed with a mutant dna substrate, loxp-a8/t27
5	c1crxA_	 Alignment		100.0	11	PDB header: replication/dna Chain: A; PDB Molecule: cre recombinase; PDBTitle: cre recombinase/dna complex reaction intermediate i
6	c1a0pA_	 Alignment		100.0	39	PDB header: dna recombination Chain: A; PDB Molecule: site-specific recombinase xerd; PDBTitle: site-specific recombinase, xerd
7	c6en2A_	 Alignment		100.0	20	PDB header: recombination Chain: A; PDB Molecule: int protein; PDBTitle: structure of the tn1549 transposon integrase (aa 82-397, r225k) in2 complex with a circular intermediate dna (ci6b-dna)
8	c2a3vA_	 Alignment		100.0	24	PDB header: recombination Chain: A; PDB Molecule: site-specific recombinase inti4; PDBTitle: structural basis for broad dna-specificity in integron recombination
9	c4a8eA_	 Alignment		100.0	26	PDB header: cell cycle Chain: A; PDB Molecule: probable tyrosine recombinase xerc-like; PDBTitle: the structure of a dimeric xer recombinase from archaea
10	d1p7da_	 Alignment		100.0	19	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
11	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 a2 coc' core site

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	18	PDB header: recombination Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of integrase from mrsa strain staphylococcus aureus
14	d1a0pa2	Alignment		99.9	42	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
15	d1aiha_	Alignment		99.9	23	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
16	d1f44a2	Alignment		99.9	11	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
17	c5c6kB_	Alignment		99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: bacteriophage p2 integrase catalytic domain
18	d1ae9a_	Alignment		99.7	17	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
19	c3uxuA_	Alignment		99.7	11	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
20	d5crxb2	Alignment		99.6	13	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
21	c3nrwA_	Alignment	not modelled	99.5	15	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	99.4	13	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
23	d1a0pa1	Alignment	not modelled	99.4	30	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
24	c2oxoA_	Alignment	not modelled	99.2	19	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
25	c2khqA_	Alignment	not modelled	99.1	13	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
26	c2keyA_	Alignment	not modelled	99.1	19	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	c2kiwA_	Alignment	not modelled	99.0	9	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). PDB header: structural genomics, unknown function

28	c2kd1A	Alignment	not modelled	99.0	17	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
29	c3lysC	Alignment	not modelled	99.0	19	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
30	c2kkpA	Alignment	not modelled	99.0	16	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).
31	c2kobA	Alignment	not modelled	98.9	19	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
32	c2kj8A	Alignment	not modelled	98.8	16	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
33	c2kj9A	Alignment	not modelled	98.8	17	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	98.7	17	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	c2kj5A	Alignment	not modelled	98.4	19	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
36	c2khvA	Alignment	not modelled	98.4	10	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.
37	c2v6eB	Alignment	not modelled	96.8	16	PDB header: hydrolase Chain: B: PDB Molecule: protelemorase; PDBTitle: protelomerase telk complexed with substrate dna
38	c4f43A	Alignment	not modelled	95.1	18	PDB header: recombination/dna Chain: A: PDB Molecule: protelemorase; PDBTitle: protelomerase tela mutant r255a complexed with caag hairpin dna
39	c3vdoA	Alignment	not modelled	45.2	20	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic rfn(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
40	c3t79A	Alignment	not modelled	43.9	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: klla0e03807p; PDBTitle: ndc10: a platform for inner kinetochore assembly in budding yeast
41	c3sqiA	Alignment	not modelled	43.9	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: klla0e03807p; PDBTitle: dna binding domain of ndc10
42	c3mzyA	Alignment	not modelled	39.1	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	d1s7oa	Alignment	not modelled	34.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
44	c2f4qA	Alignment	not modelled	22.2	16	PDB header: isomerase Chain: A: PDB Molecule: type i topoisomerase, putative; PDBTitle: crystal structure of deinococcus radiodurans topoisomerase ib
45	d1trra	Alignment	not modelled	21.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
46	c5lnfA	Alignment	not modelled	20.7	10	PDB header: chaperone Chain: A: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: solution nmr structure of farnesylated pex19, c-terminal domain
47	c4cxfA	Alignment	not modelled	20.5	18	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	d1vz0a1	Alignment	not modelled	19.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
49	c5fgmA	Alignment	not modelled	19.1	17	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
50	c5jwrE	Alignment	not modelled	18.5	31	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
						Fold: KaiA/RbsU domain

51	d1r8ja1	Alignment	not modelled	18.0	31	Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
52	d1v2za	Alignment	not modelled	17.1	31	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
53	d1sv1a	Alignment	not modelled	17.0	31	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
54	c6b7qA	Alignment	not modelled	16.8	19	PDB header: cell invasion Chain: A: PDB Molecule: sdea; PDBTitle: crystal structure of legionella effector protein sdea (lpg2157) aa.2 211-910
55	d1jhga	Alignment	not modelled	16.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
56	c3sohB	Alignment	not modelled	16.3	8	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
57	c2wi8D	Alignment	not modelled	13.3	9	PDB header: protein transport Chain: D: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: x-ray crystal structure of pex19p
58	c1r71B	Alignment	not modelled	12.3	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
59	d1umqa	Alignment	not modelled	12.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
60	c1umqA	Alignment	not modelled	12.0	10	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
61	d2auwa1	Alignment	not modelled	11.5	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
62	c3hugA	Alignment	not modelled	11.2	20	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
63	c3vepA	Alignment	not modelled	10.8	16	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
64	c2lfwA	Alignment	not modelled	10.7	15	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
65	c6in7B	Alignment	not modelled	10.2	11	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
66	c5of3E	Alignment	not modelled	10.2	12	PDB header: replication Chain: E: PDB Molecule: dna primase large subunit pril; PDBTitle: crystal structure of the heterotrimeric prilx primase from s.2 solfataricus.
67	c5wurB	Alignment	not modelled	9.7	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
68	c6c03A	Alignment	not modelled	9.6	15	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
69	d1xsva	Alignment	not modelled	8.8	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
70	d1or7a1	Alignment	not modelled	8.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
71	c6dvdF	Alignment	not modelled	8.2	20	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
72	d1iufa1	Alignment	not modelled	8.1	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
73	c2o8xA	Alignment	not modelled	8.0	16	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
74	c4r0gA	Alignment	not modelled	7.8	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of lpg0393 from legionella pneumophila
75	d1r71a	Alignment	not modelled	7.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
76	d2f2ab1	Alignment	not modelled	7.5	14	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like

77	d1fsea_	 Alignment	not modelled	6.9	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)
78	d1dda_	 Alignment	not modelled	6.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: SCF ubiquitin ligase complex WHB domain
79	c3t0yA_	 Alignment	not modelled	6.7	15	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
80	c5zq2C_	 Alignment	not modelled	6.5	21	PDB header: cell invasion Chain: C: PDB Molecule: side; PDBTitle: side apo form
81	c3frwF_	 Alignment	not modelled	6.3	14	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
82	c2h7fx_	 Alignment	not modelled	6.1	18	PDB header: isomerase/dna Chain: X: PDB Molecule: dna topoisomerase 1; PDBTitle: structure of variola topoisomerase covalently bound to dna
83	d2o4ta1	 Alignment	not modelled	5.9	16	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
84	c2kq6A_	 Alignment	not modelled	5.6	17	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
85	d1ijwc_	 Alignment	not modelled	5.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
86	d1hcra_	 Alignment	not modelled	5.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
87	c5zx3F_	 Alignment	not modelled	5.5	10	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	c2x48B_	 Alignment	not modelled	5.3	25	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfobolus islandicus rudivirus 1
89	c2kp7A_	 Alignment	not modelled	5.3	27	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a