



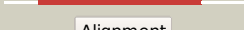
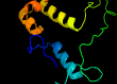
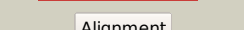


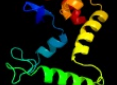
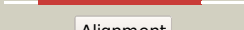

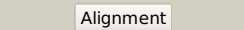

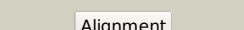
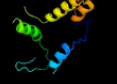
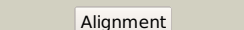
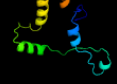
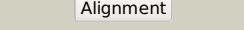
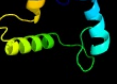
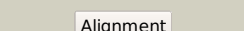








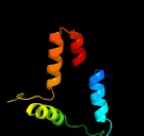


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2309c (-)_2581853_2582308
Date	Mon Aug 5 13:25:45 BST 2019
Unique Job ID	7ce9d05832f36273

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nkhB_	 Alignment		99.9	23	PDB header: recombination Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of integrase from mrsa strain staphylococcus aureus
2	c5jivA_	 Alignment		99.9	23	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
3	c6en2A_	 Alignment		99.9	25	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)
4	c5dcfA_	 Alignment		99.9	29	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
5	c5vfvA_	 Alignment		99.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: gp33; PDBTitle: integrase from mycobacterium phage brujita
6	c2a3vA_	 Alignment		99.8	26	PDB header: recombination Chain: A: PDB Molecule: site-specific recombinase inti4; PDBTitle: structural basis for broad dna-specificity in integron recombination
7	c5hxyE_	 Alignment		99.8	26	PDB header: recombination Chain: E: PDB Molecule: tyrosine recombinase xera; PDBTitle: crystal structure of xera recombinase
8	c1ma7A_	 Alignment		99.8	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
9	d1aiha_	 Alignment		99.8	24	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
10	c1z1bA_	 Alignment		99.7	23	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
11	c1crxA_	 Alignment		99.7	13	PDB header: replication/dna Chain: A: PDB Molecule: cre recombinase; PDBTitle: cre recombinase/dna complex reaction intermediate i

12	c5c6kB	Alignment		99.7	24	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: bacteriophage p2 integrase catalytic domain
13	c1a0pA	Alignment		99.7	23	PDB header: dna recombination Chain: A: PDB Molecule: site-specific recombinase xerd; PDBTitle: site-specific recombinase, xerd
14	c4a8eA	Alignment		99.6	21	PDB header: cell cycle Chain: A: PDB Molecule: probable tyrosine recombinase xerc-like; PDBTitle: the structure of a dimeric xer recombinase from archaea
15	d1p7da	Alignment		99.6	21	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
16	c3uxuA	Alignment		99.6	13	PDB header: recombination Chain: A: PDB Molecule: probable integrase; PDBTitle: the structure of the catalytic domain of the sulfolobus spindle-shaped2 viral integrase reveals an evolutionarily conserved catalytic core3 and supports a mechanism of dna cleavage in trans
17	d1f44a2	Alignment		99.5	15	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
18	d1a0pa2	Alignment		99.5	28	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
19	d1ae9a	Alignment		99.4	20	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
20	d5crxb2	Alignment		99.0	13	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
21	c2f4qA	Alignment	not modelled	92.4	17	PDB header: isomerase Chain: A: PDB Molecule: type i topoisomerase, putative; PDBTitle: crystal structure of deinococcus radiodurans topoisomerase ib
22	c2v6eB	Alignment	not modelled	89.0	13	PDB header: hydrolase Chain: B: PDB Molecule: protelemorase; PDBTitle: protelomerase telk complexed with substrate dna
23	c4f43A	Alignment	not modelled	88.9	17	PDB header: recombination/dna Chain: A: PDB Molecule: protelomerase; PDBTitle: protelomerase tela mutant r255a complexed with caag hairpin dna
24	c2h7fx	Alignment	not modelled	87.3	14	PDB header: isomerase/dna Chain: X: PDB Molecule: dna topoisomerase 1; PDBTitle: structure of variola topoisomerase covalently bound to dna
25	c2b9sA	Alignment	not modelled	76.4	18	PDB header: isomerase/dna Chain: A: PDB Molecule: topoisomerase i-like protein; PDBTitle: crystal structure of heterodimeric I. donovani topoisomerase i-2 vanadate-dna complex
26	d1a41a	Alignment	not modelled	75.3	14	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
27	d1k4ta2	Alignment	not modelled	74.8	20	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
28	d1rr8c1	Alignment	not modelled	63.4	20	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
						PDB header: isomerase/dna

29	c1rrjA	Alignment	not modelled	58.7	20	Chain: A: PDB Molecule: dna topoisomerase i; PDBTitle: structural mechanisms of camptothecin resistance by2 mutations in human topoisomerase i
30	c1a31A	Alignment	not modelled	53.6	20	PDB header: isomerase/dna Chain: A: PDB Molecule: protein (topoisomerase i); PDBTitle: human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
31	d1l8qa1	Alignment	not modelled	39.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
32	d6paxa1	Alignment	not modelled	22.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
33	d1j1va	Alignment	not modelled	20.0	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
34	c2mqkA	Alignment	not modelled	18.7	13	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
35	c3sohB	Alignment	not modelled	16.5	14	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
36	c1p4eB	Alignment	not modelled	15.3	18	PDB header: dna binding protein/recombination/dna Chain: B: PDB Molecule: recombinase flp protein; PDBTitle: flpe w330f mutant-dna holliday junction complex
37	c1nh3A	Alignment	not modelled	14.3	20	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase i; PDBTitle: human topoisomerase i ara-c complex
38	d1k78a1	Alignment	not modelled	13.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
39	c2uwqA	Alignment	not modelled	13.1	15	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis-stimulating of p53 protein 2; PDBTitle: solution structure of aspp2 n-terminus
40	c5zktA	Alignment	not modelled	12.2	17	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
41	c3oouA	Alignment	not modelled	10.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
42	c5zktB	Alignment	not modelled	9.9	17	PDB header: transcription Chain: B: PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
43	d1g99a1	Alignment	not modelled	8.3	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
44	c4m70E	Alignment	not modelled	8.0	16	PDB header: plant protein Chain: E: PDB Molecule: ran gtpase activating protein 2; PDBTitle: crystal structure of potato rx-cc domain in complex with rangap2-wpp2 domain
45	c3pvpA	Alignment	not modelled	8.0	11	PDB header: dna binding protein/dna Chain: A: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
46	d2vlqa1	Alignment	not modelled	7.7	11	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
47	d1gxha	Alignment	not modelled	7.2	11	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
48	d1ayia	Alignment	not modelled	6.3	11	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
49	d1xc5a1	Alignment	not modelled	6.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
50	c2v1IA	Alignment	not modelled	6.3	16	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
51	c4qkoA	Alignment	not modelled	5.7	5	PDB header: antimicrobial protein Chain: A: PDB Molecule: pyocin-s2 immunity protein; PDBTitle: the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
52	c3lsgD	Alignment	not modelled	5.7	9	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
53	d2e1za1	Alignment	not modelled	5.4	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
54	c3pkrA	Alignment	not modelled	5.4	7	PDB header: motor protein Chain: A: PDB Molecule: flagellar motor switch protein; PDBTitle: crystal structure of flig (residue 86-343) from h. pylori
						PDB header: transcription

55	c2eqrA_	Alignment	not modelled	5.4	10	Chain: A; PDB Molecule: nuclear receptor corepressor 1; PDBTitle: solution structure of the first sant domain from human2 nuclear receptor corepressor 1
56	c2jwB_	Alignment	not modelled	5.3	22	PDB header: membrane protein Chain: B; PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxs data
57	d2auwa1	Alignment	not modelled	5.2	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
58	c6ioyD_	Alignment	not modelled	5.2	25	PDB header: transferase Chain: D; PDB Molecule: acetate kinase; PDBTitle: crystal structure of porphyromonas gingivalis acetate kinase
59	c4a69C_	Alignment	not modelled	5.1	13	PDB header: transcription Chain: C; PDB Molecule: nuclear receptor corepressor 2; PDBTitle: structure of hdac3 bound to corepressor and inositol tetraphosphate
60	c2no8A_	Alignment	not modelled	5.1	12	PDB header: immune system Chain: A; PDB Molecule: colicin-e2 immunity protein; PDBTitle: nmr structure analysis of the colicin immuntiy protein im2