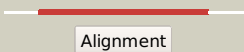
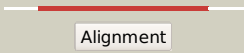
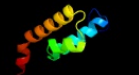


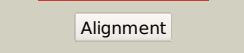



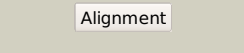

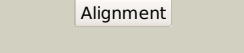


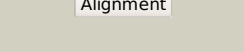

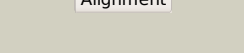




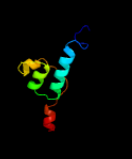



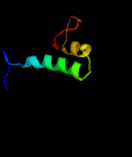




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3751_(-)_4199052_4199267
Date	Fri Aug 9 18:20:45 BST 2019
Unique Job ID	bd0996976df40376

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6en2A_	 Alignment		99.8	35	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)
2	c3nkhB_	 Alignment		99.7	25	PDB header: recombination Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of integrase from mrsa strain staphylococcus aureus
3	c5jivA_	 Alignment		99.7	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
4	c5hxyE_	 Alignment		99.7	34	PDB header: recombination Chain: E: PDB Molecule: tyrosine recombinase xera; PDBTitle: crystal structure of xera recombinase
5	c5vfa_	 Alignment		99.7	20	PDB header: dna binding protein Chain: A: PDB Molecule: gp33; PDBTitle: integrase from mycobacterium phage brujita
6	c2a3vA_	 Alignment		99.6	30	PDB header: recombination Chain: A: PDB Molecule: site-specific recombinase inti4; PDBTitle: structural basis for broad dna-specificity in integron recombination
7	c5dcfA_	 Alignment		99.6	25	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
8	c1a0pA_	 Alignment		99.6	23	PDB header: dna recombination Chain: A: PDB Molecule: site-specific recombinase xerd; PDBTitle: site-specific recombinase, xerd
9	c1ma7A_	 Alignment		99.6	19	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
10	c3uxuA_	 Alignment		99.5	21	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
11	c1crxA_	 Alignment		99.5	19	PDB header: replication/dna Chain: A: PDB Molecule: cre recombinase; PDBTitle: cre recombinase/dna complex reaction intermediate i

12	c5c6kB	Alignment		99.5	31	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: bacteriophage p2 integrase catalytic domain
13	d1aiha	Alignment		99.5	31	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
14	d1f44a2	Alignment		99.5	17	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
15	c4a8eA	Alignment		99.5	29	PDB header: cell cycle Chain: A: PDB Molecule: probable tyrosine recombinase xerc-like; PDBTitle: the structure of a dimeric xer recombinase from archaea
16	c1z1bA	Alignment		99.3	24	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
17	d1a0pa2	Alignment		99.2	23	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
18	d1p7da	Alignment		99.1	24	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
19	d1ae9a	Alignment		98.9	16	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
20	d5crxb2	Alignment		98.7	22	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
21	c2v6eB	Alignment	not modelled	87.7	24	PDB header: hydrolase Chain: B: PDB Molecule: protelemorase; PDBTitle: protelomerase telc complexed with substrate dna
22	c4f43A	Alignment	not modelled	68.6	25	PDB header: recombination/dna Chain: A: PDB Molecule: protelomerase; PDBTitle: protelomerase tela mutant r255a complexed with caag hairpin dna
23	c2f4qA	Alignment	not modelled	48.8	23	PDB header: isomerase Chain: A: PDB Molecule: type i topoisomerase, putative; PDBTitle: crystal structure of deinococcus radiodurans topoisomerase ib
24	c2h7fx	Alignment	not modelled	46.2	19	PDB header: isomerase/dna Chain: X: PDB Molecule: dna topoisomerase 1; PDBTitle: structure of variola topoisomerase covalently bound to dna
25	d1a41a	Alignment	not modelled	42.1	19	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
26	c2mqkA	Alignment	not modelled	34.7	15	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
27	d2auwa1	Alignment	not modelled	30.3	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
28	d1l8qa1	Alignment	not modelled	29.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
						PDB header: motor protein

29	c3sohB	Alignment	not modelled	28.1	11	Chain: B; PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
30	c3pvpA	Alignment	not modelled	18.5	13	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
31	d2aq0a1	Alignment	not modelled	16.7	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
32	c5of3E	Alignment	not modelled	13.4	12	PDB header: replication Chain: E; PDB Molecule: dna primase large subunit pril; PDBTitle: crystal structure of the heterotrimeric prislx primase from s.2 solfataricus.
33	c2vz4A	Alignment	not modelled	12.5	12	PDB header: transcription Chain: A; PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
34	c4ua2B	Alignment	not modelled	12.4	11	PDB header: dna binding protein Chain: B; PDB Molecule: regulatory protein; PDBTitle: crystal structure of dual function transcriptional regulator merr from2 bacillus megaterium mb1
35	d1xc5a1	Alignment	not modelled	10.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
36	c2auwB	Alignment	not modelled	10.7	14	PDB header: unknown function Chain: B; PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
37	c4r4eA	Alignment	not modelled	10.4	21	PDB header: transcription regulator/dna Chain: A; PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
38	c3vdoA	Alignment	not modelled	9.9	14	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
39	c2yqkA	Alignment	not modelled	9.5	15	PDB header: transcription/apoptosis Chain: A; PDB Molecule: arginine-glutamic acid dipeptide repeats protein; PDBTitle: solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats
40	c3hh0C	Alignment	not modelled	8.4	16	PDB header: transcription regulator Chain: C; PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
41	c2eqrA	Alignment	not modelled	8.3	16	PDB header: transcription Chain: A; PDB Molecule: nuclear receptor corepressor 1; PDBTitle: solution structure of the first sant domain from human2 nuclear receptor corepressor 1
42	c3pkrA	Alignment	not modelled	8.0	4	PDB header: motor protein Chain: A; PDB Molecule: flagellar motor switch protein; PDBTitle: crystal structure of flig (residue 86-343) from h. pylori
43	d2iw5b1	Alignment	not modelled	7.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
44	c2x0lB	Alignment	not modelled	7.3	18	PDB header: transcription Chain: B; PDB Molecule: rest corepressor 1; PDBTitle: crystal structure of a neuro-specific splicing variant of2 human histone lysine demethylase lsd1.
45	c2iw5B	Alignment	not modelled	7.3	18	PDB header: oxidoreductase/transcription regulator Chain: B; PDB Molecule: rest corepressor 1; PDBTitle: structural basis for corest-dependent demethylation of nucleosomes by2 the human lsd1 histone demethylase
46	c2xajB	Alignment	not modelled	7.3	18	PDB header: transcription Chain: B; PDB Molecule: rest corepressor 1; PDBTitle: crystal structure of lsd1-corest in complex with (-)-trans-2 2-phenylcyclopropyl-1-amine
47	c2v1dB	Alignment	not modelled	7.3	18	PDB header: oxidoreductase/repressor Chain: B; PDB Molecule: rest corepressor 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
48	c4a69C	Alignment	not modelled	6.7	13	PDB header: transcription Chain: C; PDB Molecule: nuclear receptor corepressor 2; PDBTitle: structure of hdac3 bound to corepressor and inositol tetraphosphate
49	c3gpvA	Alignment	not modelled	6.6	8	PDB header: transcription regulator Chain: A; PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
50	c3skqA	Alignment	not modelled	6.0	18	PDB header: metal transport Chain: A; PDB Molecule: mitochondrial distribution and morphology protein 38; PDBTitle: mdm38 is a 14-3-3-like receptor and associates with the protein2 synthesis machinery at the inner mitochondrial membrane
51	d1bl0a2	Alignment	not modelled	5.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
52	d1d5ya2	Alignment	not modelled	5.8	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
53	d2crga1	Alignment	not modelled	5.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain