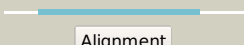

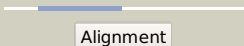
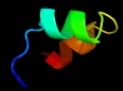
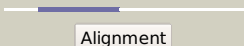



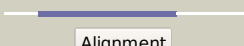

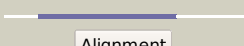

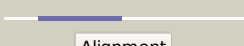


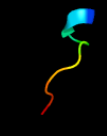

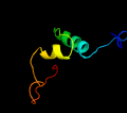










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3643 (-) _4081339_4081530
Date	Fri Aug 9 18:20:33 BST 2019
Unique Job ID	9bdb3a0f2c5de2fc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3uxuA_	 Alignment		30.6	20	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
2	c3nkhB_	 Alignment		26.9	27	PDB header: recombination Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of integrase from mrsa strain staphylococcus aureus
3	c1z1bA_	 Alignment		14.7	20	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
4	c6en2A_	 Alignment		14.2	23	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)
5	d2cpga_	 Alignment		10.5	36	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
6	c1ea4K_	 Alignment		10.5	36	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
7	d1aiha_	 Alignment		10.2	24	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
8	c4xaiP_	 Alignment		9.1	64	PDB header: transcription Chain: P: PDB Molecule: grunge, isoform j; PDBTitle: crystal structure of red flour beetle nr2e1/tlx
9	c3gt2A_	 Alignment		7.5	21	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
10	c1rxrD_	 Alignment		7.3	46	PDB header: replication inhibitor Chain: D: PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
11	d1rxra1	 Alignment		7.3	46	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like

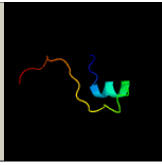
12	d3bl2a1	Alignment		6.4	48	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
13	c4tskA	Alignment		5.7	36	PDB header: oxidoreductase, isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
14	c5hxyE	Alignment		5.7	20	PDB header: recombination Chain: E: PDB Molecule: tyrosine recombinase xera; PDBTitle: crystal structure of xera recombinase
15	c5c6kB	Alignment		5.4	19	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: bacteriophage p2 integrase catalytic domain

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[c2a3vA](#)



Alignment



5.2

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PDB header: recombination
Chain: A: **PDB Molecule:** site-specific recombinase inti4;
PDB title: structural basis for broad dna-specificity in integron recombination