


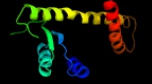


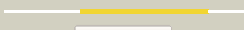

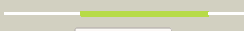


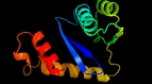





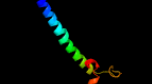

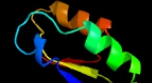









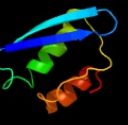



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3387_(-)_3800966_3801643
Date	Fri Aug 9 18:20:05 BST 2019
Unique Job ID	35d504a13e0efff6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	 Alignment		98.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	 Alignment		97.2	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
3	d1asua_	 Alignment		91.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
4	d1cxqa_	 Alignment		78.3	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	c5cz1B_	 Alignment		64.5	12	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmv integrase
6	c3nf9A_	 Alignment		62.3	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
7	c1c0mA_	 Alignment		50.3	20	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
8	c4mq3A_	 Alignment		49.2	14	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
9	c5j9wB_	 Alignment		43.5	14	PDB header: transferase Chain: B: PDB Molecule: chromatin modification-related protein eaf6; PDBTitle: crystal structure of the nua4 core complex
10	d1h5ya_	 Alignment		31.3	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
11	c3kksB_	 Alignment		29.4	13	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii

12	c3j6vl	Alignment		28.1	20	PDB header: ribosome Chain: I: PDB Molecule: 28s ribosomal protein s9, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
13	d1exqa	Alignment		25.6	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
14	c3jcaE	Alignment		23.5	12	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
15	c3tsmB	Alignment		21.3	16	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 bruceella melitensis
16	c5u1cD	Alignment		19.5	24	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
17	c3qjaA	Alignment		18.4	18	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
18	c3hpgC	Alignment		15.4	12	PDB header: transferase Chain: C: PDB Molecule: integrase; PDBTitle: visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
19	c5ejkG	Alignment		15.4	18	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
20	c3f9kv	Alignment		15.3	13	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
21	d1ka9f	Alignment	not modelled	15.1	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
22	c5u1cA	Alignment	not modelled	14.5	17	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
23	d2h1ta1	Alignment	not modelled	14.3	24	Fold: Spiral beta-roll Superfamily: PA1994-like Family: PA1994-like
24	c6orjA	Alignment	not modelled	14.3	20	PDB header: viral protein Chain: A: PDB Molecule: phikz164; PDBTitle: central spike of phikz phage tail
25	c2etjA	Alignment	not modelled	13.7	16	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hii; PDBTitle: crystal structure of ribonuclease hii (ec 3.1.26.4) (rnase hii)2 (tm0915) from thermotoga maritima at 1.74 a resolution
26	d2etja1	Alignment	not modelled	13.7	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
27	c1k6yB	Alignment	not modelled	13.6	21	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
28	d1c0ma2	Alignment	not modelled	13.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
29	c6hnaA	Alignment	not modelled	13.6	18	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase;

29	c6v1aA_	Alignment	not modelled	13.8	18	PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> nctc 11168
30	d1c6va_	Alignment	not modelled	13.2	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
31	d1bcoa2	Alignment	not modelled	13.1	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
32	d1a53a_	Alignment	not modelled	11.1	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
33	c5uncB_	Alignment	not modelled	8.8	14	PDB header: isomerase Chain: B; PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from <i>Streptomyces platensis</i> subsp. <i>rosaceus</i>
34	c4v1af_	Alignment	not modelled	8.2	17	PDB header: ribosome Chain: F; PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
35	c2wcvl_	Alignment	not modelled	7.5	12	PDB header: isomerase Chain: I; PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
36	c5mlpA_	Alignment	not modelled	7.3	21	PDB header: ligase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: structure of cdps from <i>Rickettsiella grylli</i>
37	c5ooma_	Alignment	not modelled	7.2	14	PDB header: ribosome Chain: A; PDB Molecule: 16s ribosomal rna; PDBTitle: structure of a native assembly intermediate of the human mitochondrial 2 ribosome with unfolded interfacial rna
38	c3mvaA_	Alignment	not modelled	7.0	20	PDB header: isomerase Chain: A; PDB Molecule: protein fucu; PDBTitle: the crystal structure of fucu from <i>Bifidobacterium longum</i> to 1.65a
39	d1zuna1	Alignment	not modelled	6.8	8	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
40	c1bcoA_	Alignment	not modelled	6.7	14	PDB header: transposase Chain: A; PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
41	c3e7nB_	Alignment	not modelled	6.4	28	PDB header: transport protein Chain: B; PDB Molecule: d-ribose high-affinity transport system; PDBTitle: crystal structure of d-ribose high-affinity transport system from <i>Salmonella typhimurium</i> lt2
42	c5vliC_	Alignment	not modelled	6.2	25	PDB header: viral protein/de novo protein Chain: C; PDB Molecule: computationally designed peptide hb1.6928.2.3; PDBTitle: computationally designed inhibitor peptide hb1.6928.2.3 in complex 2 with influenza hemagglutinin (a/puertorico/8/1934)
43	c3p13B_	Alignment	not modelled	6.2	20	PDB header: isomerase Chain: B; PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
44	c1zunA_	Alignment	not modelled	6.2	8	PDB header: transferase Chain: A; PDB Molecule: sulfate adenylyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase 2 heterodimer from <i>Pseudomonas syringae</i>
45	c4a34L_	Alignment	not modelled	6.1	20	PDB header: isomerase Chain: L; PDB Molecule: rbsd/fucu transport protein family protein; PDBTitle: crystal structure of the fucose mutarotase in complex with 2 l-fucose from <i>Streptococcus pneumoniae</i>
46	c2oq2B_	Alignment	not modelled	5.9	6	PDB header: oxidoreductase Chain: B; PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
47	d1ogda_	Alignment	not modelled	5.5	28	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
48	d2ob5a1	Alignment	not modelled	5.4	20	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
49	c3hosA_	Alignment	not modelled	5.4	14	PDB header: transferase, dna binding protein/dna cds; Chain: A; PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
50	c6hlwB_	Alignment	not modelled	5.1	15	PDB header: viral protein Chain: B; PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)