



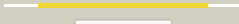

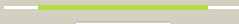

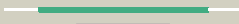











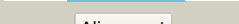

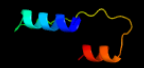






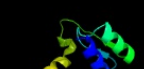



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2961 (-)_3313293_3313682
Date	Thu Aug 8 16:20:12 BST 2019
Unique Job ID	04f72b9a9d6eecd7

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	 Alignment		97.6	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	 Alignment		97.5	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
3	d1asua_	 Alignment		79.4	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
4	d1cxqa_	 Alignment		66.6	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	c3nf9A_	 Alignment		47.2	17	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
6	c5cz1B_	 Alignment		41.0	10	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmvtv integrase
7	c2oq2B_	 Alignment		38.2	5	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
8	c1c0mA_	 Alignment		33.3	18	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
9	d1zuna1	 Alignment		32.9	8	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
10	c2etjA_	 Alignment		32.6	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
11	d2etja1	 Alignment		32.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H

12	c1zunA_	Alignment		32.5	8	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
13	c3e0dA_	Alignment		26.2	17	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
14	c4mq3A_	Alignment		25.1	17	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
15	c5u1cD_	Alignment		21.8	22	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
16	c2o8vA_	Alignment		19.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: paps reductase in a covalent complex with thioredoxin c35a
17	c5ejkG_	Alignment		18.6	11	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
18	c3jcaE_	Alignment		17.6	13	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
19	c5u1cA_	Alignment		16.5	14	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
20	d1exqa_	Alignment		16.3	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
21	c4zyaA_	Alignment	not modelled	15.9	17	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase, cytoplasmic; PDBTitle: the n-terminal extension domain of human asparaginyl-trna synthetase
22	c2hnhA_	Alignment	not modelled	15.5	22	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
23	d1c6va_	Alignment	not modelled	14.7	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
24	c4bvvB_	Alignment	not modelled	14.0	10	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine-phosphosulphate reductase; PDBTitle: structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
25	c1k6yB_	Alignment	not modelled	13.1	22	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
26	c6hlwB_	Alignment	not modelled	12.7	14	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)
27	c4v0hC_	Alignment	not modelled	12.2	24	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase domain-containing protein 1 1; PDBTitle: human metallo beta lactamase domain containing protein 1 (hmb1ac1)
28	c5lewA_	Alianment	not modelled	11.6	17	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit alpha;

						PDBTitle: dna polymerase
29	c2ejsA_	Alignment	not modelled	10.8	14	PDB header: ligase Chain: A: PDB Molecule: autocrine motility factor receptor, isoform 2; PDBTitle: solution structure of ruh-076, a human cue domain
30	c6hmvB_	Alignment	not modelled	10.7	14	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-d68 (fusion protein, lvvy mutant)
31	c2qsrA_	Alignment	not modelled	10.6	19	PDB header: transcription Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of c-terminal domain of transcription-repair2 coupling factor
32	c5fkvA_	Alignment	not modelled	9.7	22	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
33	c3tsmB_	Alignment	not modelled	9.6	16	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
34	c6f45D_	Alignment	not modelled	9.6	14	PDB header: viral protein Chain: D: PDB Molecule: receptor recognition protein; PDBTitle: crystal structure of the gp37-gp38 adhesin tip complex of the2 bacteriophage s16 long tail fiber
35	c3noyA_	Alignment	not modelled	9.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
36	d1vp8a_	Alignment	not modelled	8.9	20	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
37	d1c0ma2	Alignment	not modelled	8.6	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
38	d2fm8c1	Alignment	not modelled	8.5	10	Fold: SipA N-terminal domain-like Superfamily: SipA N-terminal domain-like Family: SipA N-terminal domain-like
39	c3qjaA_	Alignment	not modelled	8.4	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
40	c6nkeA_	Alignment	not modelled	7.9	13	PDB header: transferase Chain: A: PDB Molecule: geranylgeranylgeranyl phosphate synthase; PDBTitle: wild-type gggps from thermoplasma volcanium
41	d2eyqa6	Alignment	not modelled	7.6	15	Fold: TRCF domain-like Superfamily: TRCF domain-like Family: TRCF domain
42	d1xi3a_	Alignment	not modelled	7.2	17	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
43	d1a6qa1	Alignment	not modelled	7.0	20	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain
44	d1sura_	Alignment	not modelled	7.0	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
45	c3ih1A_	Alignment	not modelled	7.0	20	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
46	c6bmaA_	Alignment	not modelled	7.0	20	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc. 11168
47	c6hltD_	Alignment	not modelled	6.7	0	PDB header: viral protein Chain: D: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)
48	c3f9kv_	Alignment	not modelled	6.3	13	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
49	d1ni5a1	Alignment	not modelled	6.2	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
50	c5my5A_	Alignment	not modelled	6.2	12	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic substrate-binding protein; PDBTitle: tungstate binding protein - tupa - from desulfovibrio alaskensis g20
51	d1ng7a_	Alignment	not modelled	6.1	21	Fold: Soluble domain of poliovirus core protein 3a Superfamily: Soluble domain of poliovirus core protein 3a Family: Soluble domain of poliovirus core protein 3a
52	c1ng7A_	Alignment	not modelled	6.1	21	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein [core protein p3a]; PDBTitle: the solution structure of the soluble domain of poliovirus2 3a protein
53	d1xria_	Alignment	not modelled	6.0	24	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
54	c3hngC_	Alignment	not modelled	6.0	13	PDB header: transferase Chain: C: PDB Molecule: integrase;

54	c3npqc_	Alignment	not modelled	5.9	15	PDBTitle: visna virus integrase (residues 1-219) in complex with ledgf2 lbd: examples of open integrase dimer-dimer interfaces
55	d1wj7a1	Alignment	not modelled	5.9	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
56	c2b5dX_	Alignment	not modelled	5.8	11	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
57	c2f46A_	Alignment	not modelled	5.8	19	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
58	c2wcvl_	Alignment	not modelled	5.5	12	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
59	c3ff4A_	Alignment	not modelled	5.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412