
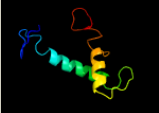
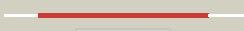






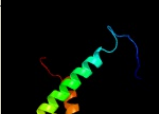





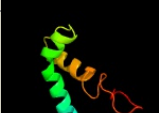






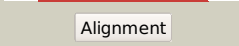






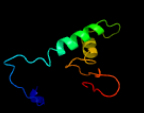
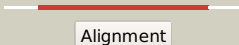

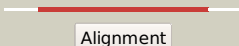

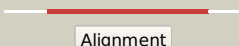


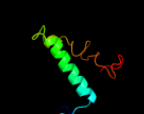
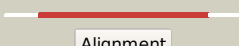
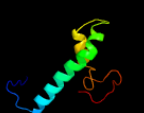
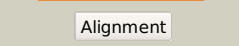
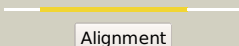
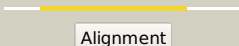
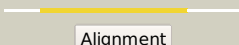
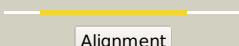
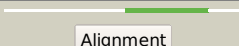
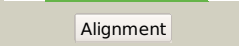



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2087_(-)_2344002_2344232
Date	Mon Aug 5 13:25:20 BST 2019
Unique Job ID	5d3be358a7d5f1ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f9kV_	 Alignment		98.0	11	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
2	d1bcoa2	 Alignment		98.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
3	c5cz1B_	 Alignment		97.7	11	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
4	c3nf9A_	 Alignment		96.9	8	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
5	d1asua_	 Alignment		96.4	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
6	c4mq3A_	 Alignment		96.2	19	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
7	d1c0ma2	 Alignment		96.1	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
8	c3kksB_	 Alignment		95.9	14	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
9	c1bcoA_	 Alignment		95.6	14	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
10	c5u1cA_	 Alignment		95.4	8	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
11	d1hyva_	 Alignment		95.4	9	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain

12	d1exqa_	 Alignment		95.0	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
13	c1k6yB_	 Alignment		94.5	10	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
14	c3jcaE_	 Alignment		94.4	19	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
15	c1ex4A_	 Alignment		94.2	8	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
16	c1c0mA_	 Alignment		94.1	14	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
17	c5m0rF_	 Alignment		94.0	16	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
18	d1c6va_	 Alignment		93.3	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
19	c3l2tB_	 Alignment		92.5	9	PDB header: recombination/dna Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
20	c3hpgC_	 Alignment		90.1	18	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
21	d1cxqa_	 Alignment	not modelled	83.8	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
22	c2f7tA_	 Alignment	not modelled	79.9	10	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
23	c3f2kB_	 Alignment	not modelled	76.1	17	PDB header: transferase Chain: B: PDB Molecule: histone-lysine n-methyltransferase setmar; PDBTitle: structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
24	c5cr4B_	 Alignment	not modelled	71.7	12	PDB header: hydrolase Chain: B: PDB Molecule: sleeping beauty transposase, sb100x; PDBTitle: crystal structure of the sleeping beauty transposase catalytic domain
25	c3hosA_	 Alignment	not modelled	70.4	10	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
26	c4fcyA_	 Alignment	not modelled	53.4	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
27	c3dlrA_	 Alignment	not modelled	52.0	8	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv integrase
28	c6n1cB_	 Alignment	not modelled	50.8	5	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from

						legionella2 pneumophila philadelphia 1
29	c4lugA_	Alignment	not modelled	44.9	0	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase ppa1 from arabidopsis2 thaliana
30	c3fq3H_	Alignment	not modelled	44.0	8	PDB header: hydrolase Chain: H: PDB Molecule: inorganic pyrophosphatase:bacterial/archaeal inorganic PDBTitle: crystal structure of inorganic phosphatase from brucella melitensis
31	c3g0tA_	Alignment	not modelled	37.7	20	PDB header: transferase Chain: A: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
32	d2prda_	Alignment	not modelled	37.1	5	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
33	d1i40a_	Alignment	not modelled	36.3	8	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
34	d1twla_	Alignment	not modelled	30.5	8	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
35	d1udea_	Alignment	not modelled	29.9	8	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
36	c2mzyA_	Alignment	not modelled	29.5	14	PDB header: iron binding protein Chain: A: PDB Molecule: probable fe(2+)-trafficking protein; PDBTitle: 1h, 13c, and 15n chemical shift assignments and structure of probable2 fe(2+)-trafficking protein from burkholderia pseudomallei 1710b.
37	c6cfzD_	Alignment	not modelled	27.4	17	PDB header: nuclear protein Chain: D: PDB Molecule: duo1; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
38	d1w0ba_	Alignment	not modelled	27.3	8	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
39	c3ld3A_	Alignment	not modelled	27.3	8	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic phosphatase from anaplasma2 phagocytophilum at 1.75a resolution
40	c3d63B_	Alignment	not modelled	26.4	5	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from burkholderia2 pseudomallei
41	d1z8ua1	Alignment	not modelled	24.7	8	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
42	c2uxsA_	Alignment	not modelled	24.1	13	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: 2.7a crystal structure of inorganic pyrophosphatase (rv3628)2 from mycobacterium tuberculosis at ph 7.5
43	c1ygzC_	Alignment	not modelled	18.0	0	PDB header: hydrolase Chain: C: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from helicobacter2 pylori
44	c3tr4C_	Alignment	not modelled	17.4	3	PDB header: hydrolase Chain: C: PDB Molecule: inorganic pyrophosphatase; PDBTitle: structure of an inorganic pyrophosphatase (ppa) from coxiella burnetii
45	d1b7ea_	Alignment	not modelled	16.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
46	c5tj5P_	Alignment	not modelled	15.6	23	PDB header: motor protein Chain: P: PDB Molecule: v-type proton atpase subunit d; PDBTitle: atomic model for the membrane-embedded motor of a eukaryotic v-atpase
47	d2gtaa1	Alignment	not modelled	14.6	25	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
48	c5teaF_	Alignment	not modelled	13.1	5	PDB header: hydrolase Chain: F: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of an inorganic pyrophosphatase from neisseria2 gonorrhoeae
49	c1xb4C_	Alignment	not modelled	11.9	19	PDB header: unknown function Chain: C: PDB Molecule: hypothetical 23.6 kda protein in yuh1-ura8 intergenic PDBTitle: crystal structure of subunit vps25 of the endosomal trafficking2 complex escrt-ii
50	d1xs8a_	Alignment	not modelled	11.5	13	Fold: YggX-like Superfamily: YggX-like Family: YggX-like
51	c3u21B_	Alignment	not modelled	11.5	17	PDB header: transcription regulation, dna binding Chain: B: PDB Molecule: nuclear factor related to kappa-b-binding protein; PDBTitle: crystal structure of a fragment of nuclear factor related to kappa-b-2 binding protein (residues 370-495) (nfrkb) from homo sapiens at 2.183 a resolution
52	c2kdtA_	Alignment	not modelled	11.3	27	PDB header: protein transport Chain: A: PDB Molecule: neuroendocrine convertase 1; PDBTitle: pc1/3 dcsG sorting domain structure in dpc
53	c2ke3A_	Alignment	not modelled	11.2	27	PDB header: hydrolase Chain: A: PDB Molecule: neuroendocrine convertase 1; PDBTitle: pc1/3 dcsG sorting domain in chaps

54	c5wrtB_	Alignment	not modelled	10.8	13	PDB header: hydrolase Chain: B: PDB Molecule: soluble inorganic pyrophosphatase; PDBTitle: crystal structure of type i inorganic pyrophosphatase from toxoplasma2 gondii.
55	c2f42A_	Alignment	not modelled	10.2	15	PDB header: chaperone Chain: A: PDB Molecule: stip1 homology and u-box containing protein 1; PDBTitle: dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
56	d2bcqa2	Alignment	not modelled	9.8	25	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
57	c3h3hA_	Alignment	not modelled	9.7	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_ii0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
58	c2cj0A_	Alignment	not modelled	9.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: chloroperoxidase; PDBTitle: chloroperoxidase complexed with nitrate
59	d1qeza_	Alignment	not modelled	9.3	5	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
60	c3emjL_	Alignment	not modelled	9.0	5	PDB header: hydrolase Chain: L: PDB Molecule: inorganic pyrophosphatase; PDBTitle: 2.2 a crystal structure of inorganic pyrophosphatase from2 rickettsia prowazekii (p21 form)
61	c6nmcC_	Alignment	not modelled	8.1	23	PDB header: unknown function/rna Chain: C: PDB Molecule: acrva1; PDBTitle: cryoem structure of the lbcas12a-crrna-2xacrva1 complex
62	d1jmsa3	Alignment	not modelled	7.7	25	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
63	c3lo0A_	Alignment	not modelled	7.5	4	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis
64	d2gtad1	Alignment	not modelled	7.3	12	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
65	c3k6qB_	Alignment	not modelled	7.3	5	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
66	c5ejkG_	Alignment	not modelled	7.2	7	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
67	d2vana1	Alignment	not modelled	7.0	33	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
68	d3b77a1	Alignment	not modelled	6.9	17	Fold: PH domain-like barrel Superfamily: PH domain-like Family: BPHL domain
69	c4wz1B_	Alignment	not modelled	6.5	11	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase lubx; PDBTitle: crystal structure of u-box 2 of lubx / legu2 / lpp2887 from legionella2 pneumophila str. paris, wild-type
70	c5yrqE_	Alignment	not modelled	6.4	13	PDB header: dna binding protein Chain: E: PDB Molecule: dna repair protein rad5,dna repair protein rev1; PDBTitle: crystal structure of rad5 and rev1
71	c1bmxA_	Alignment	not modelled	6.2	13	PDB header: viral protein Chain: A: PDB Molecule: human immunodeficiency virus type 1 capsid; PDBTitle: hiv-1 capsid protein major homology region peptide analog,2 nmr, 8 structures
72	d2fmpa2	Alignment	not modelled	5.9	45	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
73	c3cuqC_	Alignment	not modelled	5.9	19	PDB header: protein transport Chain: C: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
74	c2kkmA_	Alignment	not modelled	5.8	13	PDB header: translation Chain: A: PDB Molecule: translation machinery-associated protein 16; PDBTitle: solution nmr structure of yeast protein yor252w [residues2 38-178]; northeast structural genomics consortium target3 yt654
75	c4rnxA_	Alignment	not modelled	5.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase 1; PDBTitle: k154 circular permutation of old yellow enzyme