
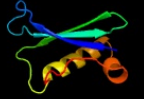

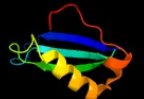




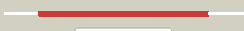






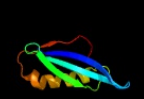





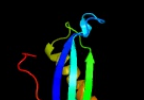


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1765A (-) _1999149_1999364
Date	Fri Aug 2 13:30:37 BST 2019
Unique Job ID	2e0359d54271509a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1c0mA_</a>	 Alignment		99.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (integrase); <b>PDBTitle:</b> crystal structure of rsv two-domain integrase
2	<a href="#">d1asua_</a>	 Alignment		99.0	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
3	<a href="#">d1cxqa_</a>	 Alignment		99.0	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
4	<a href="#">d1c0ma2</a>	 Alignment		99.0	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
5	<a href="#">c5ejkG_</a>	 Alignment		98.9	20	<b>PDB header:</b> transferase/dna <b>Chain:</b> G: <b>PDB Molecule:</b> gag-pro-pol polyprotein; <b>PDBTitle:</b> crystal structure of the rous sarcoma virus intasome
6	<a href="#">d1bcoa2</a>	 Alignment		98.9	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> mu transposase, core domain
7	<a href="#">c5cz1B_</a>	 Alignment		98.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the catalytic core domain of mmtv integrase
8	<a href="#">c4mq3A_</a>	 Alignment		98.7	21	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> the 1.1 angstrom structure of catalytic core domain of fiv integrase
9	<a href="#">c3nf9A_</a>	 Alignment		98.6	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
10	<a href="#">c4fcyA_</a>	 Alignment		98.5	24	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposase; <b>PDBTitle:</b> crystal structure of the bacteriophage mu transposome
11	<a href="#">c3jcaE_</a>	 Alignment		98.5	17	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> core model of the mouse mammary tumor virus intasome

12	<a href="#">dlc6va_</a>	Alignment		98.4	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
13	<a href="#">c5u1cD_</a>	Alignment		98.3	18	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> hiv-1 integrase, sso7d chimera; <b>PDBTitle:</b> structure of tetrameric hiv-1 strand transfer complex intasome
14	<a href="#">dlxqa_</a>	Alignment		98.3	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
15	<a href="#">c3kksB_</a>	Alignment		98.3	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of catalytic core domain of biv integrase in crystal2 form ii
16	<a href="#">clx4A_</a>	Alignment		98.3	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> hiv-1 integrase catalytic core and c-terminal domain
17	<a href="#">c1bcoA_</a>	Alignment		98.1	23	<b>PDB header:</b> transposase <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage mu transposase; <b>PDBTitle:</b> bacteriophage mu transposase core domain
18	<a href="#">c3f9kV_</a>	Alignment		98.1	13	<b>PDB header:</b> viral protein, recombination <b>Chain:</b> V: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> two domain fragment of hiv-2 integrase in complex with ledgf ibd
19	<a href="#">dlhyva_</a>	Alignment		97.9	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
20	<a href="#">c5u1cA_</a>	Alignment		97.9	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hiv-1 integrase, sso7d chimera; <b>PDBTitle:</b> structure of tetrameric hiv-1 strand transfer complex intasome
21	<a href="#">c3dlrA_</a>	Alignment	not modelled	97.5	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the catalytic core domain from pfv integrase
22	<a href="#">c1k6yB_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of a two-domain fragment of hiv-1 integrase
23	<a href="#">c3hpgC_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
24	<a href="#">c5m0rF_</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
25	<a href="#">c3l2tB_</a>	Alignment	not modelled	96.2	23	<b>PDB header:</b> recombination/dna <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
26	<a href="#">c5xnwA_</a>	Alignment	not modelled	27.2	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate cyclase exoy; <b>PDBTitle:</b> crystal structure of exoy, a unique nucleotidyl cyclase toxin from2 pseudomonas aeruginosa
27	<a href="#">dlS99a_</a>	Alignment	not modelled	22.5	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> Putative thiamin/HMP-binding protein YkoF
28	<a href="#">c2xk0A_</a>	Alignment	not modelled	21.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> polycomb protein pcl; <b>PDBTitle:</b> solution structure of the tudor domain from drosophila2 polycomblike (pcl) <b>PDB header:</b> hydrolase

29	<a href="#">c3ks7D_</a>	Alignment	not modelled	18.7	29	<b>Chain:</b> D; <b>PDB Molecule:</b> putative putative pngase f; <b>PDBTitle:</b> crystal structure of putative peptide:n-glycosidase f (pngase f)2 (yp_210507.1) from bacteroides fragilis nctc 9343 at 2.30 a3 resolution
30	<a href="#">d1d6za3</a>	Alignment	not modelled	17.9	28	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
31	<a href="#">c4f48A_</a>	Alignment	not modelled	15.5	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the x-ray structural of fimxeal-c-di-gmp-pilz complexes from2 xanthomonas campestris
32	<a href="#">c2e4jA_</a>	Alignment	not modelled	15.2	13	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> prostaglandin-h2 d-isomerase; <b>PDBTitle:</b> solution structure of mouse lipocalin-type prostaglandin d2 synthase
33	<a href="#">c5ho0A_</a>	Alignment	not modelled	13.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> extracellular arabinanase; <b>PDBTitle:</b> crystal structure of abna (closed conformation), a gh43 extracellular2 arabinanase from geobacillus stearothermophilus
34	<a href="#">c3pz8A_</a>	Alignment	not modelled	13.2	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> segment polarity protein dishevelled homolog dvl-1; <b>PDBTitle:</b> crystal structure of dvl1-dix(y17d) mutant
35	<a href="#">d2oqea3</a>	Alignment	not modelled	13.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
36	<a href="#">c3cqrB_</a>	Alignment	not modelled	12.1	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> violaxanthin de-epoxidase, chloroplast; <b>PDBTitle:</b> crystal structure of the lipocalin domain of violaxanthin de-epoxidase2 (vde) at ph5
37	<a href="#">c4b6a_</a>	Alignment	not modelled	11.8	14	<b>PDB header:</b> ribosome <b>Chain:</b> I; <b>PDB Molecule:</b> 60s ribosomal protein I10; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
38	<a href="#">c3kzpA_</a>	Alignment	not modelled	11.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative diguanylate cyclase/phosphodiesterase; <b>PDBTitle:</b> crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes
39	<a href="#">d1w6ga3</a>	Alignment	not modelled	10.9	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
40	<a href="#">c3lv4B_</a>	Alignment	not modelled	10.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glycoside hydrolase yxia; <b>PDBTitle:</b> crystal structure of the glycoside hydrolase, family 43 yxia protein2 from bacillus licheniformis. northeast structural genomics consortium3 target bir14.
41	<a href="#">d2c9aa1</a>	Alignment	not modelled	10.5	6	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
42	<a href="#">c4bvvB_</a>	Alignment	not modelled	9.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoadenosine-phosphosulphate reductase; <b>PDBTitle:</b> structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
43	<a href="#">d2basa1</a>	Alignment	not modelled	8.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> EAL domain-like <b>Family:</b> EAL domain
44	<a href="#">c2m0oA_</a>	Alignment	not modelled	8.6	21	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> phd finger protein 1; <b>PDBTitle:</b> the solution structure of human phf1 in complex with h3k36me3
45	<a href="#">c3hvbB_</a>	Alignment	not modelled	8.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> protein fimx; <b>PDBTitle:</b> crystal structure of the dual-domain ggdef-eal module of fimx from2 pseudomonas aeruginosa
46	<a href="#">c1h2iG_</a>	Alignment	not modelled	8.3	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> G; <b>PDB Molecule:</b> dna repair protein rad52 homolog; <b>PDBTitle:</b> human rad52 protein, n-terminal domain
47	<a href="#">c4p37A_</a>	Alignment	not modelled	8.1	42	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative poly(a) polymerase catalytic subunit; <b>PDBTitle:</b> crystal structure of the megavirus polyadenylate synthase
48	<a href="#">c4q6jB_</a>	Alignment	not modelled	7.9	22	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> lmo0131 protein; <b>PDBTitle:</b> crystal structure of eal domain protein from listeria monocytogenes2 egd-e
49	<a href="#">d1d6za2</a>	Alignment	not modelled	7.8	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
50	<a href="#">c4a1aH_</a>	Alignment	not modelled	7.6	11	<b>PDB header:</b> ribosome <b>Chain:</b> H; <b>PDB Molecule:</b> 60s ribosomal protein I10; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
51	<a href="#">c6n2oB_</a>	Alignment	not modelled	7.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> pyruvate ferredoxin/ferredoxin oxidoreductase, beta <b>PDBTitle:</b> 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
52	<a href="#">d1ebda3</a>	Alignment	not modelled	7.2	10	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
53	<a href="#">d1kn0a_</a>	Aliament	not modelled	7.1	14	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like

						<b>Family:</b> The homologous-pairing domain of Rad52 recombinase
54	<a href="#">c3s83A_</a>	Alignment	not modelled	6.3	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ggdef family protein; <b>PDBTitle:</b> eal domain of phosphodiesterase pdea
55	<a href="#">c2k23A_</a>	Alignment	not modelled	5.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipocalin 2; <b>PDBTitle:</b> solution structure analysis of the rlcn2
56	<a href="#">c3pz7A_</a>	Alignment	not modelled	5.8	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dixin; <b>PDBTitle:</b> crystal structure of ccd1-dix domain
57	<a href="#">d1gesa3</a>	Alignment	not modelled	5.6	19	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
58	<a href="#">c3zf7K_</a>	Alignment	not modelled	5.5	6	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 60s ribosomal protein l10, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
59	<a href="#">c3l2uA_</a>	Alignment	not modelled	5.4	22	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitegravir)
60	<a href="#">c4lykB_</a>	Alignment	not modelled	5.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic di-gmp phosphodiesterase yaha; <b>PDBTitle:</b> crystal structure of the eal domain of c-di-gmp specific2 phosphodiesterase yaha in complex with activating cofactor mg++
61	<a href="#">c5swcE_</a>	Alignment	not modelled	5.4	11	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> the structure of the beta-carbonic anhydrase ccaa
62	<a href="#">d3grsa3</a>	Alignment	not modelled	5.3	19	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
63	<a href="#">d1dsla3</a>	Alignment	not modelled	5.2	14	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
64	<a href="#">d1w2za3</a>	Alignment	not modelled	5.2	31	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
65	<a href="#">c3qkgA_</a>	Alignment	not modelled	5.2	11	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> protein ambp; <b>PDBTitle:</b> crystal structure of alpha-1-microglobulin at 2.3 a resolution
66	<a href="#">c2r6oB_</a>	Alignment	not modelled	5.2	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative diguanylate cyclase/phosphodiesterase (ggdef & eal <b>PDBTitle:</b> crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
67	<a href="#">c4wseA_</a>	Alignment	not modelled	5.1	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative poly(a) polymerase catalytic subunit; <b>PDBTitle:</b> crystal structure of the mimivirus polyadenylate synthase