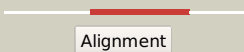

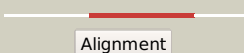

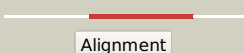

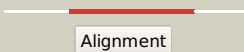
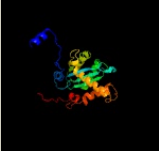
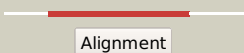

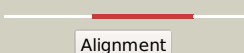

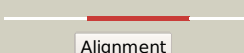





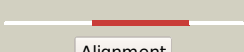

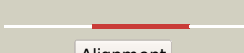



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2807 (-)_3113668_3114822
Date	Wed Aug 7 12:50:47 BST 2019
Unique Job ID	a917be80650ba451

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f9kV_	 Alignment		100.0	18	PDB header: viral protein, recombination Chain: V; PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf1b
2	c1c0mA_	 Alignment		100.0	11	PDB header: transferase Chain: A; PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
3	c3l2tB_	 Alignment		100.0	19	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)
4	c3jcaE_	 Alignment		100.0	13	PDB header: viral protein Chain: E; PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
5	c5m0rF_	 Alignment		100.0	11	PDB header: hydrolase Chain: F; PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
6	c1ex4A_	 Alignment		100.0	19	PDB header: viral protein Chain: A; PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
7	d1c0mA2	 Alignment		100.0	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
8	c3hpgC_	 Alignment		100.0	12	PDB header: transferase Chain: C; PDB Molecule: integrase; PDBTitle: visna virus integrase (residues 1-219) in complex with ledgf21b: examples of open integrase dimer-dimer interfaces
9	c5u1cA_	 Alignment		100.0	15	PDB header: viral protein Chain: A; PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
10	c3nf9A_	 Alignment		100.0	21	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
11	c5cz1B_	 Alignment		100.0	13	PDB header: hydrolase Chain: B; PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase

12	d1asua_	Alignment		100.0	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
13	c4mq3A_	Alignment		100.0	18	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
14	c3kksB_	Alignment		99.9	19	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
15	d1hyva_	Alignment		99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
16	d1exqa_	Alignment		99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
17	c1k6yB_	Alignment		99.9	18	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
18	c3dlrA_	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv integrase
19	d1cxqa_	Alignment		99.9	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
20	c5ejkG_	Alignment		99.9	7	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
21	d1c6va_	Alignment	not modelled	99.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
22	c5u1cD_	Alignment	not modelled	99.9	15	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
23	c3l2uA_	Alignment	not modelled	99.8	14	PDB header: recombination/dna Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitegravir)
24	c4fcyA_	Alignment	not modelled	99.7	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
25	d1bcoa2	Alignment	not modelled	99.7	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
26	c1bcoA_	Alignment	not modelled	99.6	11	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
27	c3hosA_	Alignment	not modelled	99.1	13	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
28	c5cr4B_	Alignment	not modelled	97.4	10	PDB header: hydrolase Chain: B: PDB Molecule: sleeping beauty transposase, sb100x; PDBTitle: crystal structure of the sleeping beauty transposase catalytic domain

29	c3f2kB	Alignment	not modelled	95.6	8	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
30	c6paxA	Alignment	not modelled	94.2	12	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
31	d1pdnc	Alignment	not modelled	92.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
32	c1u78A	Alignment	not modelled	92.6	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
33	c2f7tA	Alignment	not modelled	89.0	9	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
34	c1z4hA	Alignment	not modelled	76.8	21	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of 2 atypical excisionase
35	c4yo3G	Alignment	not modelled	74.2	25	PDB header: transport protein Chain: G: PDB Molecule: tssa; PDBTitle: enteroaggregative escherichia coli tssa n-terminal fragment
36	c2k27A	Alignment	not modelled	72.4	9	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
37	d1zuna1	Alignment	not modelled	56.8	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
38	c1zunA	Alignment	not modelled	53.4	9	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
39	c4j2nB	Alignment	not modelled	46.8	16	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
40	c6dk4A	Alignment	not modelled	45.9	15	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni peroxide stress regulator
41	c3k32D	Alignment	not modelled	43.3	4	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein mj0690; PDBTitle: the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm
42	c6g7cF	Alignment	not modelled	42.8	26	PDB header: transport protein Chain: F: PDB Molecule: impa-related domain protein; PDBTitle: nt2-ctd domains of the tssa component from the type vi secretion2 system of aeromonas hydrophila.
43	c4j2nA	Alignment	not modelled	38.7	18	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
44	c2yopB	Alignment	not modelled	37.3	11	PDB header: apoptosis Chain: B: PDB Molecule: protein fam3b; PDBTitle: long wavelength s-sad structure of fam3b pander
45	c2kpiA	Alignment	not modelled	35.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
46	c6amaO	Alignment	not modelled	34.7	24	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
47	c5byhM	Alignment	not modelled	34.7	22	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
48	c3eyyA	Alignment	not modelled	32.5	16	PDB header: transport Chain: A: PDB Molecule: putative iron uptake regulatory protein; PDBTitle: structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
49	c6fkqC	Alignment	not modelled	32.5	15	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
50	c5lc4A	Alignment	not modelled	32.1	10	PDB header: signaling protein Chain: A: PDB Molecule: protein fam3c; PDBTitle: xray structure of mouse fam3c ilei dimer
51	d1ni5a1	Alignment	not modelled	30.7	7	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
52	c3hefB	Alignment	not modelled	29.7	37	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
53	c1umqA	Alignment	not modelled	28.0	26	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity

54	d1umqa	Alignment	not modelled	28.0	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
55	c3ckvA	Alignment	not modelled	27.1	12	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
56	d1adra	Alignment	not modelled	23.6	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
57	c2xcjB	Alignment	not modelled	22.8	22	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
58	c3omtA	Alignment	not modelled	21.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
59	c3h5tA	Alignment	not modelled	21.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
60	c5l33A	Alignment	not modelled	20.7	22	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
61	c2lcvA	Alignment	not modelled	20.2	24	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
62	c2l8nA	Alignment	not modelled	19.8	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
63	c1bdhA	Alignment	not modelled	19.6	8	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
64	c3trbA	Alignment	not modelled	19.5	9	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addition module antidote protein of a higa (higa)2 family from coxiella burnetii
65	d1efaa1	Alignment	not modelled	19.3	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
66	c5yszA	Alignment	not modelled	19.2	33	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
67	c3edpB	Alignment	not modelled	18.9	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
68	c3clcC	Alignment	not modelled	18.7	4	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
69	d2bjca1	Alignment	not modelled	18.3	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
70	c1efaA	Alignment	not modelled	18.2	15	PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
71	d1qpza1	Alignment	not modelled	18.1	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
72	c2owlA	Alignment	not modelled	18.0	18	PDB header: recombination Chain: A: PDB Molecule: recombination-associated protein rdgc; PDBTitle: crystal structure of e. coli rdgc
73	c2ebyA	Alignment	not modelled	17.6	4	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
74	d1g2ha	Alignment	not modelled	17.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
75	c1g2hA	Alignment	not modelled	17.2	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
76	d1lutxa	Alignment	not modelled	17.2	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
77	c6sbsB	Alignment	not modelled	16.9	18	PDB header: transcription Chain: B: PDB Molecule: regulatory protein; PDBTitle: ytra from sulfolobus acidocaldarius, a gntR-family transcription2 factor
78	c4l5eA	Alignment	not modelled	16.6	21	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
79	c3f8mA	Alignment	not modelled	16.5	24	PDB header: transcription Chain: A: PDB Molecule: gntR-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis PDB header: transcription regulator

80	c3bwgA	Alignment	not modelled	16.1	18	Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
81	c6iwqE	Alignment	not modelled	16.1	8	PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
82	c6gsil	Alignment	not modelled	15.6	18	PDB header: virus Chain: I: PDB Molecule: vp2; PDBTitle: feline calicivirus strain f9 bound to a soluble ectodomain fragment of f2 feline junctional adhesion molecule a - leading to assembly of a3 portal structure at a unique three-fold axis.
83	c6gsiK	Alignment	not modelled	15.6	18	PDB header: virus Chain: K: PDB Molecule: vp2; PDBTitle: feline calicivirus strain f9 bound to a soluble ectodomain fragment of f2 feline junctional adhesion molecule a - leading to assembly of a3 portal structure at a unique three-fold axis.
84	d2jn6a1	Alignment	not modelled	15.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
85	d2icta1	Alignment	not modelled	15.3	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
86	d1y9qa1	Alignment	not modelled	14.9	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
87	d1lcda	Alignment	not modelled	14.6	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
88	c3neuA	Alignment	not modelled	14.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
89	c2w57A	Alignment	not modelled	14.5	14	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
90	c2vpiA	Alignment	not modelled	13.9	8	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
91	c3eetA	Alignment	not modelled	13.9	12	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator
92	d1omza	Alignment	not modelled	13.8	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
93	d1uxda	Alignment	not modelled	13.8	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
94	c4i7hA	Alignment	not modelled	13.7	14	PDB header: transcription Chain: A: PDB Molecule: peroxide stress sensing regulator; PDBTitle: structural basis for peroxide sensing and gene regulation by perr from2 streptococcus pyogenes
95	c2m8gX	Alignment	not modelled	13.6	11	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
96	c5mm1A	Alignment	not modelled	13.5	5	PDB header: membrane protein Chain: A: PDB Molecule: dolichol monophosphate mannose synthase; PDBTitle: dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose
97	c3vk0B	Alignment	not modelled	13.3	9	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 neisseria
98	c3cecA	Alignment	not modelled	13.2	13	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
99	c2z86D	Alignment	not modelled	13.2	14	PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from escherichia coli2 strain k4 (k4cp) complexed with udp-glcua and udp