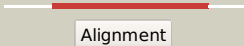

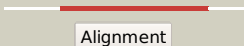
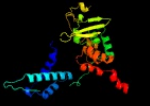
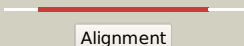







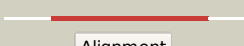




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2646 (-) _2970561_2971559
Date	Wed Aug 7 12:50:29 BST 2019
Unique Job ID	c20083e1e87f4094

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5vfzA_</a>	 Alignment		100.0	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> gp33; <b>PDBTitle:</b> integrase from mycobacterium phage brujita
2	<a href="#">c5jivA_</a>	 Alignment		100.0	23	<b>PDB header:</b> recombination <b>Chain:</b> A; <b>PDB Molecule:</b> tyrosine recombinase xerh; <b>PDBTitle:</b> crystal structure of xerh site-specific recombinase bound to 2 palindromic difh substrate: post-cleavage complex
3	<a href="#">c1z1bA_</a>	 Alignment		100.0	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A; <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of a lambda integrase dimer bound to a 2 coc' core site
4	<a href="#">c5hxyE_</a>	 Alignment		100.0	18	<b>PDB header:</b> recombination <b>Chain:</b> E; <b>PDB Molecule:</b> tyrosine recombinase xera; <b>PDBTitle:</b> crystal structure of xera recombinase
5	<a href="#">d1p7da_</a>	 Alignment		100.0	21	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
6	<a href="#">c1ma7A_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase, ligase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> cre recombinase; <b>PDBTitle:</b> crystal structure of cre site-specific recombinase 2 complexed with a mutant dna substrate, loxp-a8/t27
7	<a href="#">c1crxA_</a>	 Alignment		100.0	14	<b>PDB header:</b> replication/dna <b>Chain:</b> A; <b>PDB Molecule:</b> cre recombinase; <b>PDBTitle:</b> cre recombinase/dna complex reaction intermediate i
8	<a href="#">c6en2A_</a>	 Alignment		100.0	21	<b>PDB header:</b> recombination <b>Chain:</b> A; <b>PDB Molecule:</b> int protein; <b>PDBTitle:</b> structure of the tn1549 transposon integrase (aa 82-397, r225k) in 2 complex with a circular intermediate dna (ci6b-dna)
9	<a href="#">c2a3vA_</a>	 Alignment		100.0	20	<b>PDB header:</b> recombination <b>Chain:</b> A; <b>PDB Molecule:</b> site-specific recombinase inti4; <b>PDBTitle:</b> structural basis for broad dna-specificity in integron recombination
10	<a href="#">c4a8eA_</a>	 Alignment		100.0	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> probable tyrosine recombinase xerc-like; <b>PDBTitle:</b> the structure of a dimeric xer recombinase from archaea
11	<a href="#">c1a0pA_</a>	 Alignment		100.0	21	<b>PDB header:</b> dna recombination <b>Chain:</b> A; <b>PDB Molecule:</b> site-specific recombinase xerd; <b>PDBTitle:</b> site-specific recombinase, xerd

12	<a href="#">c5c6kB</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> bacteriophage p2 integrase catalytic domain
13	<a href="#">c5dcfA</a>	Alignment		100.0	24	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine recombinase xerd,dna translocase ftsk; <b>PDBTitle:</b> c-terminal domain of xerd recombinase in complex with gamma domain of f2 ftsk
14	<a href="#">d1aiha</a>	Alignment		100.0	24	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
15	<a href="#">c3nkhB</a>	Alignment		99.9	16	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of integrase from mrsa strain staphylococcus aureus
16	<a href="#">d1a0pa2</a>	Alignment		99.9	23	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
17	<a href="#">d1ae9a</a>	Alignment		99.9	22	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
18	<a href="#">d1f44a2</a>	Alignment		99.9	15	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
19	<a href="#">c3uxuA</a>	Alignment		99.9	13	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> probable integrase; <b>PDBTitle:</b> the structure of the catalytic domain of the sulfobolus spindle-shaped2 viral integrase reveals an evolutionarily conserved catalytic core3 and supports a mechanism of dna cleavage in trans
20	<a href="#">d5crxb2</a>	Alignment		99.7	17	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
21	<a href="#">c2khqA</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
22	<a href="#">c2kiwA</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> int protein; <b>PDBTitle:</b> solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
23	<a href="#">c2oxoA</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
24	<a href="#">c3lysC</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> prophage pi2 protein 01, integrase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the prophage pi2 protein2 01 (integrase) from lactococcus lactis, northeast structural genomics3 consortium target kr124f
25	<a href="#">c2kobA</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a
26	<a href="#">c2kkaA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase; <b>PDBTitle:</b> solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
27	<a href="#">c2kd1A</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dna integration/recombination/inversion protein;

27	<a href="#">c2ku1A</a>	Alignment	not modelled	99.4	14	<b>PDBTitle:</b> solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f <b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase/site-specific recombinase;
28	<a href="#">c3nrwA</a>	Alignment	not modelled	99.4	16	<b>PDBTitle:</b> crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase;
29	<a href="#">c2khvA</a>	Alignment	not modelled	99.4	12	<b>PDBTitle:</b> solution nmr structure of protein nmul_a0922 from2 nitrospira multiformis. northeast structural genomics3 consortium target nmr38b. <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrator;
30	<a href="#">c2kj9A</a>	Alignment	not modelled	99.4	12	<b>PDBTitle:</b> nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative phage integrase;
31	<a href="#">c2keyA</a>	Alignment	not modelled	99.4	13	<b>PDBTitle:</b> solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative prophage cps-53 integrase;
32	<a href="#">c2kj8A</a>	Alignment	not modelled	99.4	12	<b>PDBTitle:</b> nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrator;
33	<a href="#">c2kkvA</a>	Alignment	not modelled	99.3	7	<b>PDBTitle:</b> solution nmr structure of an integrase domain from protein spa42882 from salmonella enterica, northeast structural genomics consortium3 target slr105h <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase;
34	<a href="#">c2kj5A</a>	Alignment	not modelled	99.3	15	<b>PDBTitle:</b> solution nmr structure of a domain from a putative phage integrase2 protein nmul_a0064 from nitrospira multiformis, northeast3 structural genomics consortium target nmr46c <b>Fold:</b> SAM domain-like <b>Superfamily:</b> lambda integrase-like, N-terminal domain <b>Family:</b> lambda integrase-like, N-terminal domain
35	<a href="#">d1a0pa1</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> lambda integrase-like, N-terminal domain <b>Family:</b> lambda integrase-like, N-terminal domain
36	<a href="#">d1f44a1</a>	Alignment	not modelled	98.2	15	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> lambda integrase-like, N-terminal domain <b>Family:</b> lambda integrase-like, N-terminal domain
37	<a href="#">c2v6eB</a>	Alignment	not modelled	97.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proteomerase; <b>PDBTitle:</b> protelomerase telk complexed with substrate dna
38	<a href="#">c4f43A</a>	Alignment	not modelled	95.2	17	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> proteomerase; <b>PDBTitle:</b> protelomerase tela mutant r255a complexed with caag hairpin dna <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> type i topoisomerase, putative; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans topoisomerase ib
39	<a href="#">c2f4qA</a>	Alignment	not modelled	62.9	20	<b>PDB header:</b> isomerase/dna <b>Chain:</b> X: <b>PDB Molecule:</b> dna topoisomerase 1; <b>PDBTitle:</b> structure of variola topoisomerase covalently bound to dna
40	<a href="#">c2h7fx</a>	Alignment	not modelled	48.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigr; <b>PDBTitle:</b> streptomyces coelicolor sigr region 4
41	<a href="#">c5fgmA</a>	Alignment	not modelled	43.7	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrator; <b>PDBTitle:</b> structure of the arm-type binding domain of hpi integrase
42	<a href="#">c3jtzA</a>	Alignment	not modelled	14.9	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
43	<a href="#">c2o8xA</a>	Alignment	not modelled	13.7	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iswi protein; <b>PDBTitle:</b> sant domain structure of xenopus remodeling factor iswi
44	<a href="#">c2nogA</a>	Alignment	not modelled	11.1	4	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
45	<a href="#">d2hh6a1</a>	Alignment	not modelled	10.3	17	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-d factor; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
46	<a href="#">c3vepA</a>	Alignment	not modelled	9.9	18	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
47	<a href="#">d1zsc1</a>	Alignment	not modelled	9.3	31	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
48	<a href="#">d1ou8a</a>	Alignment	not modelled	9.0	19	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
49	<a href="#">c5ow2A</a>	Alignment	not modelled	8.4	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> japanese encephalitis virus capsid protein
50	<a href="#">d1ou9a</a>	Alignment	not modelled	8.2	19	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
51	<a href="#">d1sfka</a>	Alignment	not modelled	7.8	4	<b>Fold:</b> Flavivirus capsid protein C <b>Superfamily:</b> Flavivirus capsid protein C <b>Family:</b> Flavivirus capsid protein C

52	<a href="#">d2aq0a1</a>	Alignment	not modelled	7.7	13	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
53	<a href="#">c6b7qA</a>	Alignment	not modelled	7.6	17	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> sdea; <b>PDBTitle:</b> crystal structure of legionella effector protein sdea (lpg2157) aa.2 211-910
54	<a href="#">d1yfna1</a>	Alignment	not modelled	7.3	25	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
55	<a href="#">d1ofcx1</a>	Alignment	not modelled	7.0	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
56	<a href="#">d1dzfa2</a>	Alignment	not modelled	6.8	20	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
57	<a href="#">c5of3E</a>	Alignment	not modelled	6.7	8	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> dna primase large subunit pril; <b>PDBTitle:</b> crystal structure of the heterotrimeric prislx primase from s.2 solfataricus.
58	<a href="#">c2lvsA</a>	Alignment	not modelled	6.7	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of a crispr repeat binding protein
59	<a href="#">c3h0gE</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc1; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
60	<a href="#">d1khda1</a>	Alignment	not modelled	6.5	17	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
61	<a href="#">c30ouA</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2118 protein; <b>PDBTitle:</b> the structure of a protein with unknwn function from listeria innocua
62	<a href="#">d1hmja</a>	Alignment	not modelled	6.2	9	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
63	<a href="#">d1a41a</a>	Alignment	not modelled	5.8	12	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Eukaryotic DNA topoisomerase I, catalytic core
64	<a href="#">d1r6ra</a>	Alignment	not modelled	5.8	4	<b>Fold:</b> Flavivirus capsid protein C <b>Superfamily:</b> Flavivirus capsid protein C <b>Family:</b> Flavivirus capsid protein C
65	<a href="#">c1r6rA</a>	Alignment	not modelled	5.8	4	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> solution structure of dengue virus capsid protein reveals a2 new fold
66	<a href="#">d1luxca</a>	Alignment	not modelled	5.8	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
67	<a href="#">d2o3la1</a>	Alignment	not modelled	5.7	19	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
68	<a href="#">c4qiwH</a>	Alignment	not modelled	5.6	11	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> dna-directed rna polymerase subunit h; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
69	<a href="#">d2auwa1</a>	Alignment	not modelled	5.6	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NEO471 C-terminal domain-like
70	<a href="#">d1mzga</a>	Alignment	not modelled	5.5	21	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
71	<a href="#">c2y9zA</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> imitation switch protein 1 (del_atpase); <b>PDBTitle:</b> chromatin remodeling factor isw1a(del_atpase) in dna complex
72	<a href="#">c2l8nA</a>	Alignment	not modelled	5.5	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor cytr; <b>PDBTitle:</b> nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
73	<a href="#">c5chhA</a>	Alignment	not modelled	5.4	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arac family transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
74	<a href="#">c3hugA</a>	Alignment	not modelled	5.2	21	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigI
75	<a href="#">d1ijwc</a>	Alignment	not modelled	5.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
76	<a href="#">d1hcra</a>	Alignment	not modelled	5.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
77	<a href="#">d1eika</a>	Alignment	not modelled	5.1	13	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
						<b>PDB header:</b> structural genomics, unknown function

78	<a href="#">c2kpgA_</a>	Alignment	not modelled	5.1	17	<b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of agrobacterium tumefaciens protein atu1219:2 northeast structural genomics consortium target att14
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