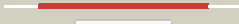
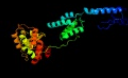


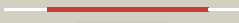

















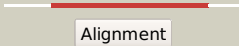









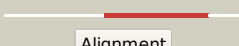

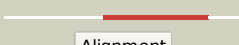






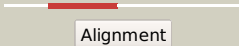

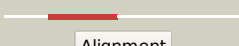




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2659c (- )_2979701_2980828
Date	Wed Aug 7 12:50:31 BST 2019
Unique Job ID	1b2e7bbaedc25c67

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1z1bA_</a>	 Alignment		100.0	17	<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 a2 coc' core site
2	<a href="#">c5jivA_</a>	 Alignment		100.0	16	<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 to2 palindromic difh substrate: post-cleavage complex
3	<a href="#">c5vfvA_</a>	 Alignment		100.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp33; <b>PDBTitle:</b> integrase from mycobacterium phage brujita
4	<a href="#">c6en2A_</a>	 Alignment		100.0	16	<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) in2 complex with a circular intermediate dna (ci6b-dna)
5	<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
6	<a href="#">d1p7da_</a>	 Alignment		100.0	18	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
7	<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 recombinase2 complexed with a mutant dna substrate, loxp-a8/t27
8	<a href="#">c2a3vA_</a>	 Alignment		100.0	17	<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
9	<a href="#">c1crxA_</a>	 Alignment		100.0	13	<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
10	<a href="#">c1a0pA_</a>	 Alignment		100.0	19	<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
11	<a href="#">c3nkhB_</a>	 Alignment		99.9	21	<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

12	<a href="#">c4a8eA</a>	 Alignment		99.9	16	<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
13	<a href="#">c5dcfA</a>	 Alignment		99.9	23	<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 ftsk
14	<a href="#">c5c6kB</a>	 Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> bacteriophage p2 integrase catalytic domain
15	<a href="#">d1aiha</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
16	<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
17	<a href="#">d1a0pa2</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="#">c3uxuA</a>	 Alignment		99.8	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
19	<a href="#">d1ae9a</a>	 Alignment		99.8	18	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
20	<a href="#">d5crxb2</a>	 Alignment		99.6	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="#">c2kj9A</a>	 Alignment	not modelled	99.2	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <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
22	<a href="#">c2kkvA</a>	 Alignment	not modelled	99.2	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution nmr structure of an integrase domain from protein spa42882 from salmonella enterica, northeast structural genomics consortium3 target slr105h
23	<a href="#">c2kkpA</a>	 Alignment	not modelled	99.2	21	<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).
24	<a href="#">c2kd1A</a>	 Alignment	not modelled	99.2	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dna integration/recombination/inversion protein; <b>PDBTitle:</b> solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
25	<a href="#">c2kiwA</a>	 Alignment	not modelled	99.2	17	<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).
26	<a href="#">c2kj8A</a>	 Alignment	not modelled	99.1	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative prophage cps-53 integrase; <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> structural genomics, unknown function

27	<a href="#">c2khvA</a>	Alignment	not modelled	99.1	8	<b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase; <b>PDBTitle:</b> solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
28	<a href="#">c2khqA</a>	Alignment	not modelled	99.1	19	<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
29	<a href="#">c2kobA</a>	Alignment	not modelled	99.1	21	<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
30	<a href="#">c2kj5A</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase; <b>PDBTitle:</b> solution nmr structure of a domain from a putative phage integrase2 protein nmul_a0064 from nitrosospira multiformis, northeast3 structural genomics consortium target nmr46c
31	<a href="#">c2oxoA</a>	Alignment	not modelled	99.1	22	<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
32	<a href="#">c3lysC</a>	Alignment	not modelled	99.0	14	<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
33	<a href="#">c3nrwA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase/site-specific recombinase; <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
34	<a href="#">c2keyA</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative phage integrase; <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
35	<a href="#">c3ju0A</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase; <b>PDBTitle:</b> structure of the arm-type binding domain of hai7 integrase
36	<a href="#">d1a0pa1</a>	Alignment	not modelled	97.5	12	<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="#">c3jtzA</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> structure of the arm-type binding domain of hpi integrase
38	<a href="#">c2v6eB</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protelemorase; <b>PDBTitle:</b> protelomerase telk complexed with substrate dna
39	<a href="#">d1gccA</a>	Alignment	not modelled	95.9	20	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> GCC-box binding domain
40	<a href="#">d1f44a1</a>	Alignment	not modelled	94.6	12	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> lambda integrase-like, N-terminal domain <b>Family:</b> lambda integrase-like, N-terminal domain
41	<a href="#">c5wx9A</a>	Alignment	not modelled	94.6	15	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ethylene-responsive transcription factor erf096; <b>PDBTitle:</b> crystal structure of aterf96 with gcc-box
42	<a href="#">c4f43A</a>	Alignment	not modelled	94.1	12	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protelomerase; <b>PDBTitle:</b> protelomerase tela mutant r255a complexed with caag hairpin dna
43	<a href="#">c2k49A</a>	Alignment	not modelled	92.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0339 protein so_3888; <b>PDBTitle:</b> solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
44	<a href="#">c2k8eA</a>	Alignment	not modelled	90.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0339 protein yegp; <b>PDBTitle:</b> solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102.
45	<a href="#">d3bida1</a>	Alignment	not modelled	90.8	7	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
46	<a href="#">d2k8ea1</a>	Alignment	not modelled	90.7	12	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
47	<a href="#">d2k49a2</a>	Alignment	not modelled	90.0	10	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
48	<a href="#">d2k7ia1</a>	Alignment	not modelled	89.3	19	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
49	<a href="#">c2k7iB</a>	Alignment	not modelled	89.3	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0339 protein atu0232; <b>PDBTitle:</b> solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
50	<a href="#">c6a27B</a>	Alignment	not modelled	89.0	7	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0339 family protein;

50	<a href="#">c0qzcb_</a>	Alignment	not modelled	85.0	7	<b>PDBTitle:</b> nmr solution structure of the hvo_2922 protein from haloferax volcanii <b>PDB header:</b> isomerase
51	<a href="#">c2f4qA_</a>	Alignment	not modelled	84.3	15	<b>Chain:</b> A: <b>PDB Molecule:</b> type i topoisomerase, putative; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans topoisomerase ib
52	<a href="#">d1bb8a_</a>	Alignment	not modelled	83.4	25	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> DNA-binding domain from tn916 integrase
53	<a href="#">d2k8ea2</a>	Alignment	not modelled	77.6	5	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
54	<a href="#">d2k49a1</a>	Alignment	not modelled	76.6	0	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
55	<a href="#">c2mqkA_</a>	Alignment	not modelled	63.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent target dna activator b; <b>PDBTitle:</b> solution structure of n terminal domain of the mub aaa+ atpase
56	<a href="#">d1z1ba1</a>	Alignment	not modelled	48.7	14	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> lambda integrase N-terminal domain
57	<a href="#">c1kjkA_</a>	Alignment	not modelled	48.7	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution structure of the lambda integrase amino-terminal2 domain
58	<a href="#">c6b7qA_</a>	Alignment	not modelled	36.3	14	<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
59	<a href="#">d1zj8a1</a>	Alignment	not modelled	33.7	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
60	<a href="#">c2h7fx_</a>	Alignment	not modelled	30.7	24	<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
61	<a href="#">d1aopa2</a>	Alignment	not modelled	29.3	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
62	<a href="#">c3igmA_</a>	Alignment	not modelled	28.6	9	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> pf14_0633 protein; <b>PDBTitle:</b> a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna
63	<a href="#">c2n3qA_</a>	Alignment	not modelled	28.2	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> double-stranded rna-binding protein 4; <b>PDBTitle:</b> solution structure of drb4 dsrbd1 (viz. drb4(1-72))
64	<a href="#">d2auwa1</a>	Alignment	not modelled	27.9	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE0471 C-terminal domain-like
65	<a href="#">d2akja1</a>	Alignment	not modelled	27.5	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
66	<a href="#">d1t95a3</a>	Alignment	not modelled	16.6	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> Hypothetical protein AF0491, C-terminal domain
67	<a href="#">d1p9qc3</a>	Alignment	not modelled	16.1	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> Hypothetical protein AF0491, C-terminal domain
68	<a href="#">c3sohB_</a>	Alignment	not modelled	15.2	13	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar motor switch protein flig; <b>PDBTitle:</b> architecture of the flagellar rotor
69	<a href="#">c2l8nA_</a>	Alignment	not modelled	14.4	7	<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
70	<a href="#">d1nera_</a>	Alignment	not modelled	14.3	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
71	<a href="#">c5zq2C_</a>	Alignment	not modelled	12.5	13	<b>PDB header:</b> cell invasion <b>Chain:</b> C: <b>PDB Molecule:</b> side; <b>PDBTitle:</b> side apo form
72	<a href="#">c2l2nA_</a>	Alignment	not modelled	11.2	18	<b>PDB header:</b> rna binding protein, plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> hyponastic leave 1; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for the first2 dsrbd of protein hyl1
73	<a href="#">c1rk8C_</a>	Alignment	not modelled	11.0	24	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> within the bgcn gene intron protein; <b>PDBTitle:</b> structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
74	<a href="#">d1rk8c_</a>	Alignment	not modelled	11.0	24	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain <b>Family:</b> Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
75	<a href="#">c3adiC_</a>	Alignment	not modelled	10.8	19	<b>PDB header:</b> gene regulation/rna <b>Chain:</b> C: <b>PDB Molecule:</b> f21m12.9 protein; <b>PDBTitle:</b> structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
76	<a href="#">c5yimC_</a>	Alignment	not modelled	9.8	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sdea; <b>PDBTitle:</b> structure of a legionella effector

77	<a href="#">c2auwB</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ne0471; <b>PDBTitle:</b> crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
78	<a href="#">c3vdoA</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor sigk; <b>PDBTitle:</b> structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
79	<a href="#">c2ef8A</a>	Alignment	not modelled	7.8	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription factor; <b>PDBTitle:</b> crystal structure of c.ecot38is
80	<a href="#">c2lcvA</a>	Alignment	not modelled	7.3	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
81	<a href="#">d1lcda</a>	Alignment	not modelled	7.2	12	<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
82	<a href="#">d2aq0a1</a>	Alignment	not modelled	7.1	24	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
83	<a href="#">d1ijwc</a>	Alignment	not modelled	6.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
84	<a href="#">d1hcra</a>	Alignment	not modelled	6.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
85	<a href="#">c2ltsA</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein rde-4; <b>PDBTitle:</b> solution structure of rde-4(150-235)
86	<a href="#">d1qpza1</a>	Alignment	not modelled	6.7	12	<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
87	<a href="#">d1rkta1</a>	Alignment	not modelled	6.4	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
88	<a href="#">d1q08a</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
89	<a href="#">c6d0tA</a>	Alignment	not modelled	5.9	28	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> bb1; <b>PDBTitle:</b> de novo design of a fluorescence-activating beta barrel - bb1
90	<a href="#">d1dwka1</a>	Alignment	not modelled	5.8	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Cyanase N-terminal domain
91	<a href="#">c3bsuF</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> F: <b>PDB Molecule:</b> ribonuclease h1; <b>PDBTitle:</b> hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna
92	<a href="#">d2bjca1</a>	Alignment	not modelled	5.7	15	<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
93	<a href="#">c5xqlA</a>	Alignment	not modelled	5.7	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug-efflux transporter 1 regulator; <b>PDBTitle:</b> crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
94	<a href="#">d1s7oa</a>	Alignment	not modelled	5.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
95	<a href="#">d1x49a1</a>	Alignment	not modelled	5.5	14	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
96	<a href="#">c1f8aB</a>	Alignment	not modelled	5.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase nima-interacting 1; <b>PDBTitle:</b> structural basis for the phosphoserine-proline recognition by group iv2 ww domains
97	<a href="#">c4r4eA</a>	Alignment	not modelled	5.2	22	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator glnr; <b>PDBTitle:</b> structure of glnr-dna complex
98	<a href="#">d1z0xa1</a>	Alignment	not modelled	5.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
99	<a href="#">c2b9sA</a>	Alignment	not modelled	5.2	20	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase i-like protein; <b>PDBTitle:</b> crystal structure of heterodimeric l. donovani topoisomerase i-2 vanadate-dna complex