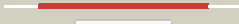



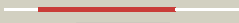

























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2943 (-) _3288474_3289715
Date	Thu Aug 8 16:20:10 BST 2019
Unique Job ID	896a444765a84451

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4fcyA_</a>	 Alignment		100.0	14	<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 transpososome
2	<a href="#">c1bcoA_</a>	 Alignment		99.9	15	<b>PDB header:</b> transposase <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriophage mu transposase; <b>PDBTitle:</b> bacteriophage mu transposase core domain
3	<a href="#">c3f9kV_</a>	 Alignment		99.8	19	<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
4	<a href="#">d1bcoa2</a>	 Alignment		99.8	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> mu transposase, core domain
5	<a href="#">c5u1cA_</a>	 Alignment		99.8	15	<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
6	<a href="#">c5cz1B_</a>	 Alignment		99.8	16	<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 mmv integrase
7	<a href="#">c5m0rF_</a>	 Alignment		99.8	21	<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
8	<a href="#">c1c0mA_</a>	 Alignment		99.7	17	<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
9	<a href="#">c3jcaE_</a>	 Alignment		99.7	14	<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
10	<a href="#">d1lasua_</a>	 Alignment		99.7	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
11	<a href="#">c3nf9A_</a>	 Alignment		99.7	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

12	<a href="#">d1c0ma2</a>	Alignment		99.7	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
13	<a href="#">c3hosA</a>	Alignment		99.7	16	<b>PDB header:</b> transferase, dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element mariner, complete cds; <b>PDBTitle:</b> crystal structure of the mariner mos1 paired end complex with mg
14	<a href="#">c3kksB</a>	Alignment		99.7	17	<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
15	<a href="#">c1ex4A</a>	Alignment		99.7	15	<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
16	<a href="#">c4mq3A</a>	Alignment		99.6	14	<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
17	<a href="#">d1hyva</a>	Alignment		99.6	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
18	<a href="#">c3hpgC</a>	Alignment		99.6	20	<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
19	<a href="#">d1exqa</a>	Alignment		99.6	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
20	<a href="#">c1k6yB</a>	Alignment		99.6	17	<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
21	<a href="#">d1c6va</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
22	<a href="#">d1cxqa</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
23	<a href="#">c5ejkG</a>	Alignment	not modelled	99.4	10	<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
24	<a href="#">c3l2tB</a>	Alignment	not modelled	99.4	14	<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)
25	<a href="#">c5u1cD</a>	Alignment	not modelled	99.2	14	<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
26	<a href="#">c1u78A</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
27	<a href="#">c3dlrA</a>	Alignment	not modelled	99.1	14	<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
28	<a href="#">c6paxA</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

29	<a href="#">d1pdnc_</a>	Alignment	not modelled	99.0	28	<b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
30	<a href="#">c3l2uA_</a>	Alignment	not modelled	98.7	12	<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)
31	<a href="#">c2k27A_</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
32	<a href="#">c5cr4B_</a>	Alignment	not modelled	98.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sleeping beauty transposase, sb100x; <b>PDBTitle:</b> crystal structure of the sleeping beauty transposase catalytic domain
33	<a href="#">d1k78a1</a>	Alignment	not modelled	97.9	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
34	<a href="#">d6paxa1</a>	Alignment	not modelled	97.7	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
35	<a href="#">d2jn6a1</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
36	<a href="#">c4go1A_</a>	Alignment	not modelled	97.5	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator Isrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor Isrr from e.2 coli.
37	<a href="#">c1hlvA_</a>	Alignment	not modelled	97.4	22	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
38	<a href="#">c2w48D_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
39	<a href="#">c2mqkA_</a>	Alignment	not modelled	97.2	25	<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
40	<a href="#">c2elhA_</a>	Alignment	not modelled	97.0	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
41	<a href="#">c3f2kB_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histone-lysine n-methyltransferase setmar; <b>PDBTitle:</b> structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
42	<a href="#">c2f7tA_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mos1 transposase; <b>PDBTitle:</b> crystal structure of the catalytic domain of mos1 mariner2 transposase
43	<a href="#">d1bcoa1</a>	Alignment	not modelled	96.8	20	<b>Fold:</b> mu transposase, C-terminal domain <b>Superfamily:</b> mu transposase, C-terminal domain <b>Family:</b> mu transposase, C-terminal domain
44	<a href="#">c1umqA_</a>	Alignment	not modelled	96.5	21	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
45	<a href="#">d1umqa_</a>	Alignment	not modelled	96.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
46	<a href="#">d1ntca_</a>	Alignment	not modelled	96.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
47	<a href="#">d1hlva1</a>	Alignment	not modelled	96.5	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
48	<a href="#">c2lvsA_</a>	Alignment	not modelled	96.5	41	<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
49	<a href="#">c3fmyA_</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
50	<a href="#">d1fipa_</a>	Alignment	not modelled	96.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
51	<a href="#">c1iufA_</a>	Alignment	not modelled	96.3	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> centromere abp1 protein; <b>PDBTitle:</b> low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
52	<a href="#">d1xsva_</a>	Alignment	not modelled	96.3	20	<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
53	<a href="#">c2rn7A_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
54	<a href="#">c2kpiA_</a>	Alignment	not modelled	96.3	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural

						genomics consortium target err9a
55	<a href="#">c3sztB_</a>	Alignment	not modelled	96.3	28	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
56	<a href="#">c5jaaB_</a>	Alignment	not modelled	96.2	21	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 toxin-antitoxin complex
57	<a href="#">d2ppxA1</a>	Alignment	not modelled	96.2	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
58	<a href="#">c2ppxA_</a>	Alignment	not modelled	96.2	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1735; <b>PDBTitle:</b> crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
59	<a href="#">c1g2hA_</a>	Alignment	not modelled	96.1	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein tyrr homolog; <b>PDBTitle:</b> solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
60	<a href="#">d1g2ha_</a>	Alignment	not modelled	96.1	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
61	<a href="#">c4ifuA_</a>	Alignment	not modelled	96.1	37	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> crystal structure of escherichia coli sdia in the space group c2
62	<a href="#">d1biaa1</a>	Alignment	not modelled	96.1	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
63	<a href="#">c5j9iH_</a>	Alignment	not modelled	96.1	21	<b>PDB header:</b> antitoxin <b>Chain:</b> H: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 antitoxin c-terminal domain
64	<a href="#">c2m8gX_</a>	Alignment	not modelled	96.1	11	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> structure, function, and tethering of dna-binding domains in 542 transcriptional activators
65	<a href="#">c3hefB_</a>	Alignment	not modelled	96.1	23	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small subunit
66	<a href="#">c3hugA_</a>	Alignment	not modelled	96.1	30	<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 sigl
67	<a href="#">c2q0oA_</a>	Alignment	not modelled	96.1	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
68	<a href="#">c1y9qA_</a>	Alignment	not modelled	96.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
69	<a href="#">d1etxa_</a>	Alignment	not modelled	96.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
70	<a href="#">c5byhM_</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor; <b>PDBTitle:</b> crystal structure of escherichia coli rna polymerase -sigma542 holoenzyme complex
71	<a href="#">c4l5eA_</a>	Alignment	not modelled	96.0	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of a. aeolicus ntrc1 dna binding domain
72	<a href="#">c3e7lD_</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
73	<a href="#">c5fgmA_</a>	Alignment	not modelled	96.0	32	<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
74	<a href="#">c2o8xA_</a>	Alignment	not modelled	95.9	27	<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
75	<a href="#">d1bw6a_</a>	Alignment	not modelled	95.9	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
76	<a href="#">d1rp3a2</a>	Alignment	not modelled	95.9	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
77	<a href="#">c3op9A_</a>	Alignment	not modelled	95.9	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from listeria innocua
78	<a href="#">c3bs3A_</a>	Alignment	not modelled	95.9	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
79	<a href="#">c2fjrB_</a>	Alignment	not modelled	95.8	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
80	<a href="#">d2b5aa1</a>	Alianment	not modelled	95.8	9	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains

						<b>Family:</b> SinR domain-like
81	<a href="#">d1s7oa</a>	Alignment	not modelled	95.8	19	<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
82	<a href="#">d1etob</a>	Alignment	not modelled	95.8	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
83	<a href="#">d1adra</a>	Alignment	not modelled	95.8	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
84	<a href="#">c3b7hA</a>	Alignment	not modelled	95.8	24	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
85	<a href="#">d1or7a1</a>	Alignment	not modelled	95.8	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
86	<a href="#">c5chhA</a>	Alignment	not modelled	95.8	17	<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
87	<a href="#">d1tc3c</a>	Alignment	not modelled	95.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
88	<a href="#">c4j2nB</a>	Alignment	not modelled	95.7	24	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
89	<a href="#">c3omtA</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
90	<a href="#">c2cg4B</a>	Alignment	not modelled	95.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
91	<a href="#">d1utxa</a>	Alignment	not modelled	95.7	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
92	<a href="#">c6gh5M</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor,rna polymerase sigma-54 <b>PDBTitle:</b> cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
93	<a href="#">c4ybaA</a>	Alignment	not modelled	95.6	26	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein c; <b>PDBTitle:</b> the structure of the c.kpn2i controller protein
94	<a href="#">c3vepA</a>	Alignment	not modelled	95.6	24	<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
95	<a href="#">d1y9qa1</a>	Alignment	not modelled	95.6	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Probable transcriptional regulator VC1968, N-terminal domain
96	<a href="#">d1a04a1</a>	Alignment	not modelled	95.6	42	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
97	<a href="#">c2xcjB</a>	Alignment	not modelled	95.5	18	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> c protein; <b>PDBTitle:</b> crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
98	<a href="#">c2bnoA</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
99	<a href="#">c3ivpD</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative transposon-related dna-binding protein; <b>PDBTitle:</b> the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
100	<a href="#">c5ui5I</a>	Alignment	not modelled	95.5	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> I: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> crystal structure of aquifex aeolicus sigman bound to promoter dna
101	<a href="#">c3vdoA</a>	Alignment	not modelled	95.5	22	<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
102	<a href="#">c5woqA</a>	Alignment	not modelled	95.5	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator clgr; <b>PDBTitle:</b> crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
103	<a href="#">c6fkqC</a>	Alignment	not modelled	95.5	12	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> rv1990c (mbca); <b>PDBTitle:</b> crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
104	<a href="#">c4j2nA</a>	Alignment	not modelled	95.5	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
105	<a href="#">c6jqsA</a>	Alignment	not modelled	95.4	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> structure of transcription factor, gere
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

106	<a href="#">d1j5ya1</a>	Alignment	not modelled	95.4	19	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
107	<a href="#">c1h0mD_</a>	Alignment	not modelled	95.4	29	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional activator protein trar; <b>PDBTitle:</b> three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
108	<a href="#">d1r69a_</a>	Alignment	not modelled	95.4	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
109	<a href="#">c3gn5B_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygit/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygit/b3021)
110	<a href="#">c3clcC_</a>	Alignment	not modelled	95.4	8	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
111	<a href="#">c3vk0B_</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of hypothetical transcription factor nhf from2 neisseria
112	<a href="#">c3f52A_</a>	Alignment	not modelled	95.3	13	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> clp gene regulator (clgr); <b>PDBTitle:</b> crystal structure of the clp gene regulator clgr from c. glutamicum
113	<a href="#">c1zljE_</a>	Alignment	not modelled	95.3	32	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
114	<a href="#">c5z7iC_</a>	Alignment	not modelled	95.3	34	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle regulatory protein gcrA; <b>PDBTitle:</b> caulobacter crescentus gcrA dna-binding domain(dbd)in complex with2 unmethylated dsdna
115	<a href="#">c2mezA_</a>	Alignment	not modelled	95.3	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multiprotein bridging factor (mbp-like); <b>PDBTitle:</b> flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor
116	<a href="#">d1y7ya1</a>	Alignment	not modelled	95.3	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
117	<a href="#">c2ef8A_</a>	Alignment	not modelled	95.3	15	<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
118	<a href="#">d1p4wa_</a>	Alignment	not modelled	95.3	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
119	<a href="#">d1x57a1</a>	Alignment	not modelled	95.2	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
120	<a href="#">d2croa_</a>	Alignment	not modelled	95.2	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors