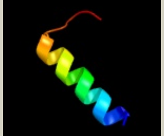
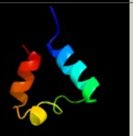
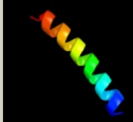
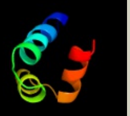
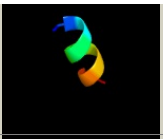
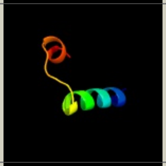
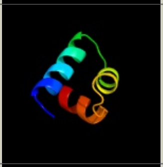
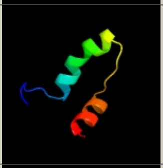
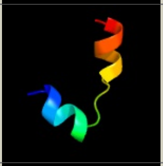
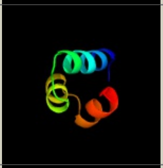
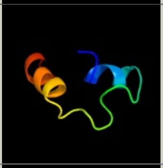
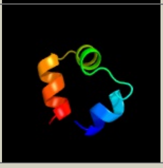
Email	mdejesus@rockefeller.edu
Description	RVBD3770B_(-)_4216256_4216447
Date	Fri Aug 9 18:20:47 BST 2019
Unique Job ID	e7212ca139bc72ee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fcyA_	Alignment		85.0	10	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposase; **PDBTitle:** crystal structure of the bacteriophage mu transpososome
2	c1u78A_	Alignment		61.4	23	**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
3	c5cajB_	Alignment		43.3	29	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0246 protein yaaa; **PDBTitle:** crystal structure of e. coli yaaa, a member of the duf328/upf02462 family
4	c2rn7A_	Alignment		29.7	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
5	c3hosA_	Alignment		25.0	26	**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
6	c2fjrB_	Alignment		22.9	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
7	c5j10A_	Alignment		22.0	42	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**peptide design 2l4hc2_24; **PDBTitle:** de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
8	d1pdnc_	Alignment		20.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
9	c5wzhA_	Alignment		19.0	18	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**pumilio homolog 23; **PDBTitle:** structure of apum23-ggaauugacgg
10	c2elhA_	Alignment		18.9	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
11	d2jn6a1	Alignment		18.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like

12	c2kvvA_	Alignment		17.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative excisionase; **PDBTitle:** solution nmr of putative excisionase from klebsiella pneumoniae,2 northeast structural genomics consortium target target kpr49
13	c5svdA_	Alignment		15.7	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolar protein 9; **PDBTitle:** nop9, a new puf-like protein, prevents premature pre-rrna cleavage to2 correctly process mature 18s rrna
14	c6paxA_	Alignment		15.7	13	**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
15	c3zhiA_	Alignment		12.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ci; **PDBTitle:** n-terminal domain of the ci repressor from bacteriophage tp901-1
16	c5tmxA_	Alignment		12.5	35	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein sini; **PDBTitle:** solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
17	d6paxa1	Alignment		11.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
18	c6amaO_	Alignment		10.5	22	**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
19	c5lgmA_	Alignment		9.5	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fusion protein 5.5/5.7; **PDBTitle:** gp5.7 mutant l42a
20	d2icta1	Alignment		9.5	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
21	c3hefB_	Alignment	not modelled	9.3	19	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small subunit
22	c4j2nB_	Alignment	not modelled	9.3	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gp37; **PDBTitle:** crystal structure of mycobacteriophage pukovnik xis
23	d1d1da1	Alignment	not modelled	9.1	27	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
24	d1eoqa_	Alignment	not modelled	9.0	27	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
25	d1wh7a_	Alignment	not modelled	8.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
26	c4rp3A_	Alignment	not modelled	8.4	23	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**disks large 1 tumor suppressor protein; **PDBTitle:** crystal structure of the l27 domain of discs large 1 (target id2 nysgrc-010766) from drosophila melanogaster bound to a potassium ion3 (space group p212121)
27	d1k78a1	Alignment	not modelled	8.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
28	c4j2nA_	Alignment	not modelled	7.9	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gp37; **PDBTitle:** crystal structure of mycobacteriophage pukovnik xis
29	c1hlvA_	Alignment	not modelled	7.7	15	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of cenp-b(1-129) complexed with the

						cenp-2 b box dna
30	c1y6uA_	Alignment	not modelled	6.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916; **PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
31	d1or7c_	Alignment	not modelled	5.9	44	**Fold:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Superfamily:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Family:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
32	c1or7C_	Alignment	not modelled	5.9	44	**PDB header:**transcription **Chain:** C: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
33	d1j9ia_	Alignment	not modelled	5.3	33	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
34	c3t76A_	Alignment	not modelled	5.2	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
35	c2zztA_	Alignment	not modelled	5.2	50	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein