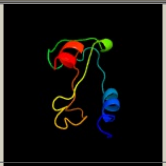
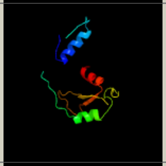
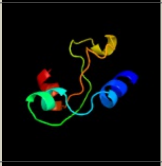
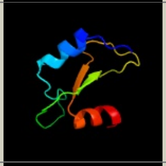
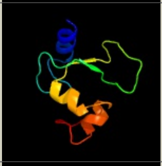
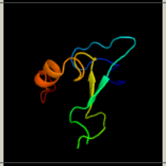
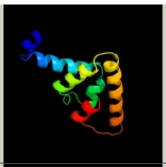
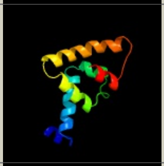
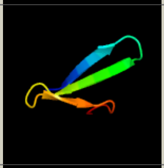
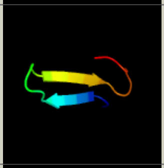
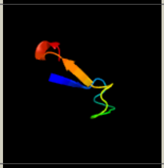
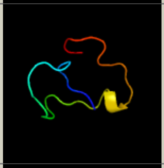
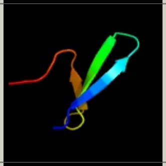
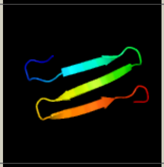
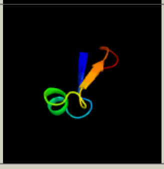
Email	mdejesus@rockefeller.edu
Description	RVBD2100_(-)_2358397_2360049
Date	Mon Aug 5 13:25:21 BST 2019
Unique Job ID	30db1af8979f11fc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	Alignment		98.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hnh endonuclease; **PDBTitle:** x-ray structure of the nhn endonuclease from geobacter2 metallireducens. northeast structural genomics consortium target3 gmr87.
2	c5mkwA_	Alignment		98.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna annealing helicase and endonuclease zranb3; **PDBTitle:** crystal structure of the human zranb3 hnh domain
3	c6ghcA_	Alignment		98.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5-methylcytosine-specific restriction enzyme a; **PDBTitle:** modification dependent ecokmcra restriction endonuclease
4	c5x1hS_	Alignment		97.9	24	**PDB header:**protein transport **Chain:** S: **PDB Molecule:**icmj (dotn); **PDBTitle:** structure of legionella pneumophila dotn
5	c5h0mA_	Alignment		97.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hnh endonuclease; **PDBTitle:** crystal structure of deep-sea thermophilic bacteriophage gve2 hnh2 endonuclease with zinc ion
6	c5vgbA_	Alignment		97.4	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**crispr-associated endonuclease cas9; **PDBTitle:** crystal structure of nmecas9 hnh domain bound to anti-crispr acriic1
7	c5zmmD_	Alignment		97.1	31	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**uncharacterized protein mcra; **PDBTitle:** structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra
8	c4ogeA_	Alignment		96.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hnh endonuclease domain protein; **PDBTitle:** crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii
9	c5axwA_	Alignment		95.8	11	**PDB header:**hydrolase/rna/dna **Chain:** A: **PDB Molecule:**crispr-associated endonuclease cas9; **PDBTitle:** crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)
10	c6ghsA_	Alignment		89.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tagi restriction endonuclease; **PDBTitle:** modification dependent tagi restriction endonuclease
11	d1vz0a1	Alignment		88.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like

12	c3mkyP_	Alignment		81.7	25	**PDB header:**dna binding protein/dna **Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
13	c3mkzU_	Alignment		76.6	25	**PDB header:**dna-binding protein/dna **Chain:** U: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-272)-18mer complex, p21 form
14	d2ho2a1	Alignment		75.7	43	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
15	d2ysca1	Alignment		69.0	41	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
16	d2jb0b1	Alignment		66.1	23	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
17	c4cmqB_	Alignment		60.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**crispr-associated endonuclease cas9/csn1; **PDBTitle:** crystal structure of mn-bound s.pyogenes cas9
18	d2e45a1	Alignment		56.0	41	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
19	c4ld3A_	Alignment		49.9	25	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structural analysis of the microcephaly protein cpap g-box domain2 suggests a role in centriole elongation.
20	d2gykb1	Alignment		45.8	23	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
21	c3plwA_	Alignment	not modelled	44.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**recombination enhancement function protein; **PDBTitle:** ref protein from p1 bacteriophage
22	c1r71B_	Alignment	not modelled	44.5	18	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in complex with2 the operator dna
23	d2dlka1	Alignment	not modelled	41.9	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
24	c3sztB_	Alignment	not modelled	39.5	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
25	c4go1A_	Alignment	not modelled	38.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lsrr; **PDBTitle:** crystal structure of full length transcription repressor lsrr from e.2 coli.
26	c4bxrB_	Alignment	not modelled	38.1	26	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cpap; **PDBTitle:** structure of the wild-type tcp10 domain of danio rerio cpap in complex2 with a peptide of danio rerio stil
27	c4by2C_	Alignment	not modelled	36.4	16	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**anastral spindle 2, sas 4; **PDBTitle:** sas-4 (dcpap) tcp domain in complex with a proline rich motif of ana22 (dstil) of drosophila melanogaster
28	c3t0yA_	Alignment	not modelled	35.4	22	**PDB header:**transcription regulator/protein binding **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
						PDB header:dna binding protein

29	c4lfuA_	Alignment	not modelled	34.8	20	**Chain:** A: **PDB Molecule:**regulatory protein sdia; **PDBTitle:** crystal structure of escherichia coli sdia in the space group c2
30	d2glia4	Alignment	not modelled	32.8	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
31	c4uhpA_	Alignment	not modelled	32.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**large component of pyocin ap41; **PDBTitle:** crystal structure of the pyocin ap41 dnase-immunity complex
32	c2w48D_	Alignment	not modelled	32.0	22	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
33	c1va1A_	Alignment	not modelled	30.4	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor sp1; **PDBTitle:** solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
34	c5g2xC_	Alignment	not modelled	29.9	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**group ii intron-encoded protein ltra; **PDBTitle:** structure a of group ii intron complexed with its reverse2 transcriptase
35	d1ncsa_	Alignment	not modelled	29.1	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
36	c7ceiB_	Alignment	not modelled	29.0	23	**PDB header:**immune system **Chain:** B: **PDB Molecule:**protein (colicin e7 immunity protein); **PDBTitle:** the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
37	c4qkoH_	Alignment	not modelled	29.0	27	**PDB header:**antimicrobial protein **Chain:** H: **PDB Molecule:**pyocin-s2; **PDBTitle:** the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
38	d1a1ia1	Alignment	not modelled	28.7	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
39	d1zfda_	Alignment	not modelled	28.2	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
40	c4umkA_	Alignment	not modelled	28.2	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**probable chromosome-partitioning protein parb; **PDBTitle:** the complex of spo0j and pars dna in chromosomal partition system
41	c1orxA_	Alignment	not modelled	27.9	56	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
42	c2b8tA_	Alignment	not modelled	26.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
43	c1k48A_	Alignment	not modelled	26.8	56	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** refined structure and disulfide pairing of the kalata b12 peptide
44	c1pxeA_	Alignment	not modelled	26.4	55	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**neural zinc finger transcription factor 1; **PDBTitle:** solution structure of a cchhc domain of neural zinc finger2 factor-1
45	c1jjzA_	Alignment	not modelled	26.3	56	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** refined structure and disulfide pairing of the kalata b12 peptide
46	c5ew5C_	Alignment	not modelled	26.3	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**colicin-e9; **PDBTitle:** crystal structure of colicin e9 in complex with its immunity protein2 im9
47	c5xe7A_	Alignment	not modelled	25.3	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ecf rna polymerase sigma factor sigj; **PDBTitle:** crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
48	c4ttnA_	Alignment	not modelled	25.0	56	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** quasi-racemic structure of [g6a]kalata b1
49	c4ttoA_	Alignment	not modelled	24.8	56	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** quasi-racemic structure of [v25a] kalata b1
50	c4ttmA_	Alignment	not modelled	24.7	56	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** racemic structure of kalata b1 (kb1)
51	d1pt4a_	Alignment	not modelled	24.7	56	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
52	c1n1uA_	Alignment	not modelled	24.6	44	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** nmr structure of [ala1,15]kalata b1
53	d1n1ua_	Alignment	not modelled	24.6	44	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
54	c2f2iA_	Alignment	not modelled	24.5	56	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of [p20d,v21k]-kalata b1
55	c2khbA_	Alignment	not modelled	24.4	56	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1;

						PDBTitle: solution structure of linear kalata b1 (loop 6)
56	c2o01N_	Alignment	not modelled	24.3	33	**PDB header:**photosynthesis **Chain:** N: **PDB Molecule:**photosystem i-n subunit; **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
57	c2mn1A_	Alignment	not modelled	24.3	56	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**kalata b1[w23ww]; **PDBTitle:** solution structure of kalata b1[w23ww]
58	d1a1ga1	Alignment	not modelled	24.2	21	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
59	c4dzoA_	Alignment	not modelled	23.8	31	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**mitotic spindle assembly checkpoint protein mad1; **PDBTitle:** structure of human mad1 c-terminal domain reveals its involvement in2 kinetochore targeting
60	d1a1ha1	Alignment	not modelled	23.7	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
61	d1nb1a_	Alignment	not modelled	23.5	56	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
62	c1nb1A_	Alignment	not modelled	23.5	56	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** high resolution solution structure of kalata b1
63	d1ejga_	Alignment	not modelled	23.4	40	**Fold:**Crambin-like **Superfamily:**Crambin-like **Family:**Crambin-like
64	d1u86a1	Alignment	not modelled	23.4	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
65	d1jmna_	Alignment	not modelled	23.0	40	**Fold:**Crambin-like **Superfamily:**Crambin-like **Family:**Crambin-like
66	c2jpcA_	Alignment	not modelled	22.8	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
67	d2glia5	Alignment	not modelled	22.5	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
68	c6dhrA_	Alignment	not modelled	22.4	44	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**rivi3; **PDBTitle:** nmr solution structure of rivi3
69	c2kerA_	Alignment	not modelled	22.3	28	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**alpha-amylase inhibitor z-2685; **PDBTitle:** alpha-amylase inhibitor parvulustat (z-2685) from2 streptomyces parvulus
70	c2f2jA_	Alignment	not modelled	22.1	40	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of [w19k, p20n, v21k]-kalata b1
71	c1kalA_	Alignment	not modelled	21.7	56	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** elucidation of the primary and three-dimensional structure2 of the uterotonic polypeptide kalata b1
72	c2lamA_	Alignment	not modelled	21.6	44	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**cyclotide cter m; **PDBTitle:** three-dimensional structure of the cyclotide cter m
73	d1r71a_	Alignment	not modelled	21.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
74	d1tf3a2	Alignment	not modelled	21.6	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
75	d1f2ig1	Alignment	not modelled	21.3	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
76	c3e4hA_	Alignment	not modelled	20.9	44	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**varv peptide f; **PDBTitle:** crystal structure of the cyclotide varv f
77	c2lurA_	Alignment	not modelled	20.9	56	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata; **PDBTitle:** nmr solution structure of kb1[ghrw;23-28]
78	d1ubdc3	Alignment	not modelled	20.8	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
79	d1aaya1	Alignment	not modelled	20.4	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
80	d1bhia_	Alignment	not modelled	20.4	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
81	d2glia3	Alignment	not modelled	20.2	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
82	c1h0mD_	Alignment	not modelled	19.7	8	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing

						protein trar bound2 to its autoinducer and to its target dna
83	d1s7oa_	Alignment	not modelled	19.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
84	c4omhA_	Alignment	not modelled	19.1	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**geranylgeranyl diphosphate cyclase; **PDBTitle:** crystal structure of the bacterial diterpene cyclase cotb2 variant2 f149l
85	d2b8ta2	Alignment	not modelled	19.0	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
86	c2k7gA_	Alignment	not modelled	18.8	44	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**varv peptide f; **PDBTitle:** solution structure of varv f
87	c5yixB_	Alignment	not modelled	18.6	20	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**cell cycle regulatory protein gcra; **PDBTitle:** caulobacter crescentus gcra sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
88	c2gj0A_	Alignment	not modelled	18.5	44	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cycloviolacin o14; **PDBTitle:** cycloviolacin o14
89	d2dlka2	Alignment	not modelled	18.5	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
90	d1sp2a_	Alignment	not modelled	18.0	25	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
91	d1xsva_	Alignment	not modelled	17.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
92	c2m9oA_	Alignment	not modelled	17.2	44	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b7; **PDBTitle:** solution structure of kalata b7
93	c3hslX_	Alignment	not modelled	17.2	40	**PDB header:**replication **Chain:** X: **PDB Molecule:**orf59; **PDBTitle:** the crystal structure of pf-8, the dna polymerase accessory subunit2 from kaposi's sarcoma-associated herpesvirus
94	c3vepA_	Alignment	not modelled	17.0	30	**PDB header:**membrane protein/transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-d factor; **PDBTitle:** crystal structure of sigd4 in complex with its negative regulator rsda
95	d1ubdc4	Alignment	not modelled	16.7	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
96	c5fgmA_	Alignment	not modelled	16.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ecf rna polymerase sigma factor sigr; **PDBTitle:** streptomyces coelicolor sigr region 4
97	c1vz0B_	Alignment	not modelled	16.5	18	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**chromosome-partitioning protein spo0j; **PDBTitle:** chromosome segregation protein spo0j from thermus thermophilus
98	d1nbla_	Alignment	not modelled	16.4	50	**Fold:**Crambin-like **Superfamily:**Crambin-like **Family:**Crambin-like
99	d1orla_	Alignment	not modelled	16.4	40	**Fold:**Crambin-like **Superfamily:**Crambin-like **Family:**Crambin-like