







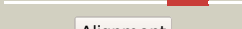
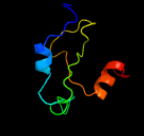
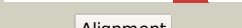

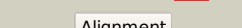

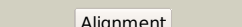

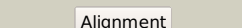

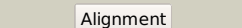


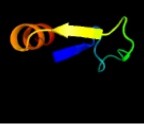


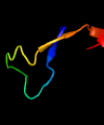

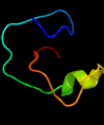



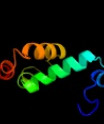


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1765c_(-)_1997425_1998522
Date	Fri Aug 2 13:30:37 BST 2019
Unique Job ID	9169e1d63c01b8ff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ghcA_	 Alignment		99.2	19	PDB header: hydrolase Chain: A; PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent ecokmcra restriction endonuclease
2	c2qgpA_	 Alignment		99.2	21	PDB header: hydrolase Chain: A; PDB Molecule: hnh endonuclease; PDBTitle: x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium target3 gmr87.
3	c5x1hS_	 Alignment		99.0	20	PDB header: protein transport Chain: S; PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
4	c5mkwA_	 Alignment		98.9	30	PDB header: hydrolase Chain: A; PDB Molecule: dna annealing helicase and endonuclease zranb3; PDBTitle: crystal structure of the human zranb3 hnh domain
5	c5zmmD_	 Alignment		98.6	25	PDB header: dna binding protein Chain: D; PDB Molecule: uncharacterized protein mcra; PDBTitle: structure of the type iv phosphorothioation-dependent restriction2 endonuclease scmcra
6	c5h0mA_	 Alignment		98.5	20	PDB header: hydrolase Chain: A; PDB Molecule: hnh endonuclease; PDBTitle: crystal structure of deep-sea thermophilic bacteriophage gve2 hnh2 endonuclease with zinc ion
7	c5vgbA_	 Alignment		98.1	21	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of nmecas9 hnh domain bound to anti-crispr acric1
8	c4ogeA_	 Alignment		97.3	28	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		96.7	13	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		96.3	19	PDB header: hydrolase Chain: A; PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	d2gykb1	 Alignment		92.6	30	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif

12	c4cmqB_	Alignment		86.9	13	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
13	d1vz0a1	Alignment		86.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
14	d2jb0b1	Alignment		86.0	31	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
15	c3mkyP_	Alignment		75.8	10	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
16	c5g2xC_	Alignment		70.9	23	PDB header: transferase Chain: C: PDB Molecule: group ii intron-encoded protein Itra; PDBTitle: structure a of group ii intron complexed with its reverse2 transcriptase
17	c5ew5C_	Alignment		69.9	25	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
18	c4qkoH_	Alignment		68.9	38	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
19	c4uhpA_	Alignment		68.6	32	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
20	c3mkzU_	Alignment		67.6	11	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
21	c7ceiB_	Alignment	not modelled	62.4	29	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
22	c3plwA_	Alignment	not modelled	52.7	20	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
23	d2dlka1	Alignment	not modelled	45.2	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
24	c1r71B_	Alignment	not modelled	42.2	20	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
25	d1zfdA_	Alignment	not modelled	40.3	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
26	d1a1ga1	Alignment	not modelled	38.8	24	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
27	d1a1a1	Alignment	not modelled	37.2	24	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
28	d1a1ha1	Alignment	not modelled	36.5	24	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
						Fold: Crambin-like

29	d1eiga_	Alignment	not modelled	35.4	25	Superfamily: Crambin-like Family: Crambin-like
30	d1u86a1	Alignment	not modelled	35.0	22	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	c1va1A_	Alignment	not modelled	34.0	50	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
32	d1r71a_	Alignment	not modelled	32.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
33	d2glia4	Alignment	not modelled	31.9	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
34	d1ncsa_	Alignment	not modelled	31.8	39	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
35	d1jmna_	Alignment	not modelled	28.7	25	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
36	d1aaya1	Alignment	not modelled	27.9	24	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
37	d2glia5	Alignment	not modelled	27.5	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
38	c1vz0B_	Alignment	not modelled	27.1	12	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome-partitioning protein spo0j; PDBTitle: chromosome segregation protein spo0j from thermus thermophilus
39	d1tf3a2	Alignment	not modelled	26.9	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
40	d1f2ig1	Alignment	not modelled	26.7	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
41	d2glia3	Alignment	not modelled	26.0	18	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	c1pxeA_	Alignment	not modelled	25.8	45	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
43	d1ubdc3	Alignment	not modelled	25.6	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
44	d1sp2a_	Alignment	not modelled	25.4	24	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
45	c3sztB_	Alignment	not modelled	24.4	14	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
46	c1orxA_	Alignment	not modelled	23.1	56	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
47	d1ubdc4	Alignment	not modelled	22.2	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
48	d1tf3a1	Alignment	not modelled	22.2	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
49	d1tf6a1	Alignment	not modelled	22.2	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
50	d1okha_	Alignment	not modelled	22.0	17	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
51	d1orla_	Alignment	not modelled	21.7	25	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
52	d1bhia_	Alignment	not modelled	21.6	47	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
53	d2dlka2	Alignment	not modelled	21.6	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
54	c1jzA_	Alignment	not modelled	21.3	56	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
55	c1k48A_	Alignment	not modelled	21.2	56	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
56	c3f0vA_	Alignment	not modelled	21.1	17	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator;

56	c3vya_	Alignment	not modelled	21.1	17	PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr PDB header: dna binding protein
57	c4ifuA_	Alignment	not modelled	20.5	8	Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
58	d1nbla_	Alignment	not modelled	20.4	18	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
59	c5yixB_	Alignment	not modelled	19.9	27	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
60	d1jmpa_	Alignment	not modelled	19.5	25	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
61	c4ttnA_	Alignment	not modelled	19.3	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
62	c4ttoA_	Alignment	not modelled	19.1	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
63	c4ttmA_	Alignment	not modelled	19.0	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
64	d1pt4a_	Alignment	not modelled	19.0	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
65	d1nlua_	Alignment	not modelled	18.9	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
66	c1n1uA_	Alignment	not modelled	18.9	44	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
67	c2f2iA_	Alignment	not modelled	18.8	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
68	c2khaA_	Alignment	not modelled	18.7	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
69	c4go1A_	Alignment	not modelled	18.5	4	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
70	d1nbia_	Alignment	not modelled	18.5	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
71	c1nb1A_	Alignment	not modelled	18.5	56	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
72	c1zw8A_	Alignment	not modelled	17.5	27	PDB header: transcription Chain: A: PDB Molecule: zinc-responsive transcriptional regulator zap1; PDBTitle: solution structure of a zap1 zinc-responsive domain2 provides insights into metalloregulatory transcriptional3 repression in saccharomyces cerevisiae
73	d2b8ta2	Alignment	not modelled	16.9	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
74	c6dhrA_	Alignment	not modelled	16.8	44	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
75	c1kalA_	Alignment	not modelled	16.8	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
76	c2f2jA_	Alignment	not modelled	16.3	36	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
77	c3e4hA_	Alignment	not modelled	15.6	44	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
78	c2lamA_	Alignment	not modelled	15.5	56	PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
79	c2w48D_	Alignment	not modelled	15.4	13	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
80	c2jydA_	Alignment	not modelled	15.3	50	PDB header: metal binding protein Chain: A: PDB Molecule: f5 domain of myelin transcription factor 1; PDBTitle: structure of the fifth zinc finger of myelin transcription2 factor 1
81	c3nctC_	Alignment	not modelled	14.6	8	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
82	c2lurA_	Alignment	not modelled	14.5	63	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]

83	d2cg4a1	Alignment	not modelled	14.4	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
84	c2k7gA	Alignment	not modelled	14.3	44	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f
85	c2lq6A	Alignment	not modelled	13.3	21	PDB header: metal binding protein Chain: A: PDB Molecule: bromodomain-containing protein 1; PDBTitle: solution structure of brd1 phd2 finger
86	d2glia2	Alignment	not modelled	13.3	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
87	c2m9oA	Alignment	not modelled	12.8	44	PDB header: plant protein Chain: A: PDB Molecule: kalata-b7; PDBTitle: solution structure of kalata b7
88	c2mn1A	Alignment	not modelled	12.8	38	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
89	d1w6ga1	Alignment	not modelled	12.3	16	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
90	c2o8xA	Alignment	not modelled	12.0	26	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
91	c2o01N	Alignment	not modelled	11.9	44	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
92	c3i4pA	Alignment	not modelled	11.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
93	c2wsfN	Alignment	not modelled	11.3	40	PDB header: photosynthesis Chain: N: PDB Molecule: photosystem i-n subunit; PDBTitle: improved model of plant photosystem i
94	d1biaa1	Alignment	not modelled	11.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
95	c4umkA	Alignment	not modelled	11.1	11	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
96	c3qi7A	Alignment	not modelled	10.7	25	PDB header: unknown function Chain: A: PDB Molecule: secreted protein of unknown function duf1311; PDBTitle: crystal structure of a duf1311 family protein (pp0307) from2 pseudomonas putida kt2440 at 1.85 a resolution
97	c5fgmA	Alignment	not modelled	10.7	22	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
98	d1j5ya1	Alignment	not modelled	10.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
99	d1xsva	Alignment	not modelled	10.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like