

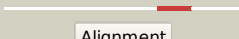
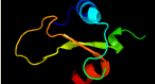
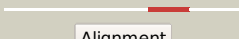
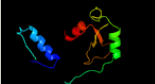









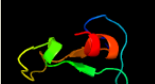



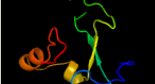


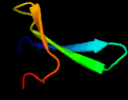






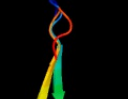



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3776 (-)_4221267_4222826
Date	Fri Aug 9 18:20:48 BST 2019
Unique Job ID	3c747906bd043d79

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		98.8	19	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.
2	c5mkwA_	 Alignment		98.5	26	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		98.2	15	PDB header: hydrolase Chain: A; PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eokmcra restriction endonuclease
4	c5x1hS_	 Alignment		98.2	22	PDB header: protein transport Chain: S; PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
5	c5h0mA_	 Alignment		97.7	23	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	19	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
7	c5zmmD_	 Alignment		97.2	34	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		96.3	24	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		95.9	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		91.9	24	PDB header: hydrolase Chain: A; PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	d1vz0a1	 Alignment		79.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like

12	d2ho2a1	Alignment		79.7	39	Fold: WW domain-like Superfamily: WW domain Family: WW domain
13	c3mkyP_	Alignment		79.5	22	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
14	d2jb0b1	Alignment		76.5	23	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
15	d2ysca1	Alignment		72.7	41	Fold: WW domain-like Superfamily: WW domain Family: WW domain
16	c3mkzU_	Alignment		69.5	24	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
17	c4cmqB_	Alignment		68.8	16	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
18	c4by2C_	Alignment		68.8	33	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
19	c3plwA_	Alignment		66.3	24	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
20	d2e45a1	Alignment		62.6	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
21	d2gykb1	Alignment	not modelled	62.5	23	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
22	c4ld3A_	Alignment	not modelled	60.0	28	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.
23	c4bxbB_	Alignment	not modelled	56.9	30	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
24	d2dlka1	Alignment	not modelled	46.9	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
25	c4uhpA_	Alignment	not modelled	43.6	27	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
26	c4qkoH_	Alignment	not modelled	41.8	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
27	c1r71B_	Alignment	not modelled	40.8	19	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
28	c7ceiB_	Alignment	not modelled	39.0	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 PDB header: hydrolase

29	c5ew5C_	Alignment	not modelled	37.5	19	Chain: C; PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
30	d1r71a_	Alignment	not modelled	36.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
31	c1va1A_	Alignment	not modelled	34.9	38	PDB header: transcription Chain: A; PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
32	c3sztB_	Alignment	not modelled	34.8	13	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
33	d1a1ia1	Alignment	not modelled	33.6	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
34	d2glia4	Alignment	not modelled	33.5	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
35	d1ncsa_	Alignment	not modelled	33.0	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
36	d1zfd_	Alignment	not modelled	32.9	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
37	c5g2xC_	Alignment	not modelled	29.5	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
38	d1a1ga1	Alignment	not modelled	28.8	21	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
39	d1a1ha1	Alignment	not modelled	27.6	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
40	d1u86a1	Alignment	not modelled	27.1	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
41	d1tf3a2	Alignment	not modelled	26.0	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	c1pxeA_	Alignment	not modelled	25.1	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
43	c1jzA_	Alignment	not modelled	24.8	56	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
44	c1k48A_	Alignment	not modelled	24.8	56	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
45	d1ubdc3	Alignment	not modelled	24.7	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
46	c4go1A_	Alignment	not modelled	24.7	17	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
47	d1f2ig1	Alignment	not modelled	24.6	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
48	d1aaya1	Alignment	not modelled	24.5	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
49	d2glia3	Alignment	not modelled	23.7	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
50	d2glia5	Alignment	not modelled	23.3	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
51	d1ejga_	Alignment	not modelled	23.2	40	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
52	d1jmna_	Alignment	not modelled	23.0	40	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
53	c4lfuA_	Alignment	not modelled	22.2	18	PDB header: dna binding protein Chain: A; PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
54	d1sp2a_	Alignment	not modelled	22.0	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
55	d2dlka2	Alignment	not modelled	22.0	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
						PDB header: plant protein

56	c4ttnA	Alignment	not modelled	21.8	56	Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
57	c4ttoA	Alignment	not modelled	21.6	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
58	c4ttmA	Alignment	not modelled	21.5	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
59	d1n1ua	Alignment	not modelled	21.5	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
60	c1n1uA	Alignment	not modelled	21.5	44	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
61	d1pt4a	Alignment	not modelled	21.5	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
62	c2f2iA	Alignment	not modelled	21.4	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
63	c2khaA	Alignment	not modelled	21.2	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
64	c2mn1A	Alignment	not modelled	21.1	56	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
65	c2w48D	Alignment	not modelled	20.3	17	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
66	c3t0yA	Alignment	not modelled	19.7	13	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
67	c1kalA	Alignment	not modelled	19.7	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
68	d1bhia	Alignment	not modelled	19.6	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
69	c6dhrA	Alignment	not modelled	19.0	44	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
70	d1ubdc4	Alignment	not modelled	19.0	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
71	c2z2sD	Alignment	not modelled	18.9	18	PDB header: transcription Chain: D: PDB Molecule: anti-sigma factor chrr, transcriptional activator chrr; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
72	d1nb1a	Alignment	not modelled	18.8	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
73	c1nb1A	Alignment	not modelled	18.8	56	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
74	c2lamA	Alignment	not modelled	18.5	44	PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
75	c2wsfN	Alignment	not modelled	18.3	50	PDB header: photosynthesis Chain: N: PDB Molecule: photosystem i-n subunit; PDBTitle: improved model of plant photosystem i
76	c2o01N	Alignment	not modelled	18.3	50	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
77	c3e4hA	Alignment	not modelled	18.0	44	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
78	c2f2jA	Alignment	not modelled	17.4	40	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
79	c5yixB	Alignment	not modelled	16.9	18	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
80	c2lurA	Alignment	not modelled	16.9	56	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
81	c2b8tA	Alignment	not modelled	16.8	20	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
82	c5xe7A	Alignment	not modelled	16.7	24	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
						Fold: Glucocorticoid receptor-like (DNA-binding domain)

83	d1wiga2	Alignment	not modelled	16.4	27	Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
84	c2kukA	Alignment	not modelled	16.3	31	PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
85	c2kerA	Alignment	not modelled	15.8	19	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-amylase inhibitor z-2685; PDBTitle: alpha-amylase inhibitor parvulostat (z-2685) from2 streptomyces parvulus
86	d1w6ga1	Alignment	not modelled	15.8	19	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
87	c1orxA	Alignment	not modelled	15.7	40	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
88	d1okha	Alignment	not modelled	15.5	50	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
89	d1nbla	Alignment	not modelled	15.4	70	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
90	d2b8ta2	Alignment	not modelled	15.4	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
91	d1orla	Alignment	not modelled	14.8	40	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
92	c2k7gA	Alignment	not modelled	14.6	44	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f
93	c2gj0A	Alignment	not modelled	14.5	44	PDB header: plant protein Chain: A: PDB Molecule: cycloviolacin o14; PDBTitle: cycloviolacin o14
94	c2jmbA	Alignment	not modelled	14.0	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu4866; PDBTitle: solution structure of the protein atu4866 from agrobacterium2 tumefaciens
95	d1jmpa	Alignment	not modelled	13.8	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
96	c2m9oA	Alignment	not modelled	13.6	44	PDB header: plant protein Chain: A: PDB Molecule: kalata-b7; PDBTitle: solution structure of kalata b7
97	d1s7oa	Alignment	not modelled	12.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
98	c4umkA	Alignment	not modelled	12.1	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
99	d1igqa	Alignment	not modelled	12.0	22	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Transcriptional repressor protein KorB