
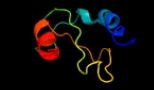
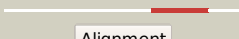
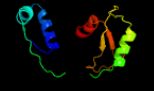
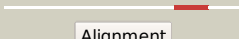

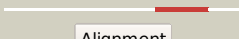

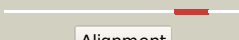

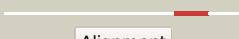




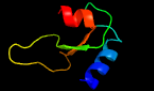



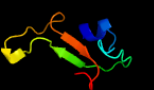





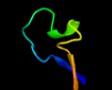
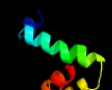
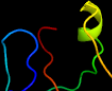

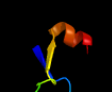
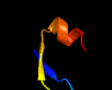


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3074 (-) _3436776_3438050
Date	Thu Aug 8 16:20:25 BST 2019
Unique Job ID	694535dabdfc4f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		98.9	24	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	c6ghcA_	 Alignment		98.8	17	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eokmcra restriction endonuclease
3	c5mkwA_	 Alignment		98.8	27	PDB header: hydrolase Chain: A: PDB Molecule: dna annealing helicase and endonuclease zranb3; PDBTitle: crystal structure of the human zranb3 hnh domain
4	c5x1hS_	 Alignment		98.4	15	PDB header: protein transport Chain: S: PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
5	c5h0mA_	 Alignment		98.1	18	PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease; PDBTitle: crystal structure of deep-sea thermophilic bacteriophage gve2 hnh2 endonuclease with zinc ion
6	c5vqbA_	 Alignment		97.9	24	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		97.8	28	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		96.7	33	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		95.4	15	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		93.0	23	PDB header: hydrolase Chain: A: PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	c4cmqB_	 Alignment		88.6	18	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9

12	d2gykb1	Alignment		85.4	18	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
13	c3mkyP_	Alignment		84.4	15	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
14	c3mkzU_	Alignment		84.0	15	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
15	d2jb0b1	Alignment		82.2	19	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
16	d1vz0a1	Alignment		76.3	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
17	c5g2xC_	Alignment		60.1	17	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
18	c4qkoH_	Alignment		59.0	19	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		57.6	16	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
20	c7ceiB_	Alignment		56.5	13	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
21	c5ew5C_	Alignment	not modelled	55.9	16	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
22	c3plwA_	Alignment	not modelled	45.4	18	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
23	d2dlka1	Alignment	not modelled	44.6	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
24	c1r71B_	Alignment	not modelled	42.8	15	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	d1ejga_	Alignment	not modelled	42.2	27	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
26	d1r71a_	Alignment	not modelled	41.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
27	d1a1ga1	Alignment	not modelled	40.1	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
28	d1jmna_	Alignment	not modelled	38.1	18	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
						Fold: beta-beta-alpha zinc fingers

29	d1zfda_	Alignment	not modelled	37.8	27	Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
30	d1alial	Alignment	not modelled	37.7	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	d1alha1	Alignment	not modelled	35.5	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
32	c1va1A_	Alignment	not modelled	34.7	20	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
33	d1u86a1	Alignment	not modelled	34.3	40	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
34	d2qlia4	Alignment	not modelled	34.2	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
35	c1orxA_	Alignment	not modelled	34.1	31	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
36	d1okha_	Alignment	not modelled	33.2	27	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
37	d1ncsa_	Alignment	not modelled	32.8	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
38	d1nbla_	Alignment	not modelled	32.6	27	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
39	c2kukA_	Alignment	not modelled	30.9	31	PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
40	d1bhia_	Alignment	not modelled	30.8	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
41	d1jmpa_	Alignment	not modelled	29.9	18	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
42	d1lorla_	Alignment	not modelled	29.8	18	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
43	c1k48A_	Alignment	not modelled	29.7	31	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
44	d1f2ig1	Alignment	not modelled	29.7	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
45	c1jzA_	Alignment	not modelled	29.6	31	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
46	d1n1ua_	Alignment	not modelled	29.1	23	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
47	c1n1uA_	Alignment	not modelled	29.1	23	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
48	d1tf3a2	Alignment	not modelled	29.0	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
49	c2mn1A_	Alignment	not modelled	28.8	31	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
50	d1aaya1	Alignment	not modelled	28.2	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
51	c2f2IA_	Alignment	not modelled	27.9	31	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
52	d1pt4a_	Alignment	not modelled	27.7	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
53	d1sp2a_	Alignment	not modelled	27.0	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
54	c4ttnA_	Alignment	not modelled	26.8	31	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
55	c2khaA_	Alignment	not modelled	26.7	31	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
56	c4ttoA_	Alignment	not modelled	26.6	31	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1

57	c4ttmA	Alignment	not modelled	26.6	31	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
58	c1nb1A	Alignment	not modelled	26.0	31	PDB header: antibiotic Chain: A; PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
59	d1nb1a	Alignment	not modelled	26.0	31	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
60	d2glia3	Alignment	not modelled	25.7	12	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
61	d2glia5	Alignment	not modelled	25.4	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
62	c2lurA	Alignment	not modelled	25.3	31	PDB header: plant protein Chain: A; PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
63	d1ubdc3	Alignment	not modelled	25.1	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
64	c2lamA	Alignment	not modelled	24.7	31	PDB header: antiviral protein Chain: A; PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
65	d2ysca1	Alignment	not modelled	24.4	36	Fold: WW domain-like Superfamily: WW domain Family: WW domain
66	c1pxeA	Alignment	not modelled	24.4	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
67	d1w6ga1	Alignment	not modelled	23.9	27	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
68	c3e4hA	Alignment	not modelled	23.8	23	PDB header: plant protein Chain: A; PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
69	c6dhrA	Alignment	not modelled	23.2	31	PDB header: plant protein Chain: A; PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
70	c2k7gA	Alignment	not modelled	22.4	23	PDB header: plant protein Chain: A; PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f
71	d2dlka2	Alignment	not modelled	21.4	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
72	d1ubdc4	Alignment	not modelled	20.7	19	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
73	c6et6A	Alignment	not modelled	20.6	18	PDB header: antimicrobial protein Chain: A; PDB Molecule: lysozyme; PDBTitle: crystal structure of muramidase from acinetobacter baumannii ab 5075uw2 prophage
74	d1tf6a1	Alignment	not modelled	20.2	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
75	c2m9oA	Alignment	not modelled	20.1	31	PDB header: plant protein Chain: A; PDB Molecule: kalata-b7; PDBTitle: solution structure of kalata b7
76	c3cwbQ	Alignment	not modelled	20.0	37	PDB header: oxidoreductase Chain: Q; PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
77	d2b8ta2	Alignment	not modelled	19.9	10	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
78	c2f2jA	Alignment	not modelled	19.3	31	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
79	d1ulea	Alignment	not modelled	19.1	17	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
80	d1tf3a1	Alignment	not modelled	18.4	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
81	d1mswd	Alignment	not modelled	16.9	33	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: T7 RNA polymerase
82	c4go1A	Alignment	not modelled	16.9	26	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator Isrr; PDBTitle: crystal structure of full length transcription repressor Isrr from e.2 coli.
83	c2lq6A	Alignment	not modelled	16.4	16	PDB header: metal binding protein Chain: A; PDB Molecule: bromodomain-containing protein 1; PDBTitle: solution structure of brd1 phd2 finger
						PDB header: plant protein

84	c2jwmA_	Alignment	not modelled	15.8	31	Chain: A: PDB Molecule: kalata-b7; PDBTitle: nmr spatial srcture of ternary complex kalata b7/mn2+/dpc2 micelle
85	c5yixB_	Alignment	not modelled	15.6	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
86	c2msoA_	Alignment	not modelled	14.1	38	PDB header: toxin Chain: A: PDB Molecule: conotoxin gm9.1; PDBTitle: solution study of cgm9a
87	c2w48D_	Alignment	not modelled	14.0	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
88	c1zw8A_	Alignment	not modelled	14.0	14	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
89	c1vz0B_	Alignment	not modelled	14.0	16	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome-partitioning protein spo0j; PDBTitle: chromosome segregation protein spo0j from thermus thermophilus
90	c3t0yA_	Alignment	not modelled	13.9	26	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
91	c2pncB_	Alignment	not modelled	13.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase, liver isozyme; PDBTitle: crystal structure of bovine plasma copper-containing amine oxidase in2 complex with clonidine
92	c2ajwA_	Alignment	not modelled	13.6	40	PDB header: toxin Chain: A: PDB Molecule: alpha-conotoxin mii; PDBTitle: structure of the cyclic conotoxin mii-6
93	d1w2za1	Alignment	not modelled	13.5	27	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
94	c2ak0A_	Alignment	not modelled	13.2	33	PDB header: toxin Chain: A: PDB Molecule: alpha-conotoxin mii; PDBTitle: structure of cyclic conotoxin mii-7
95	d2oqea1	Alignment	not modelled	13.0	23	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
96	c3sztB_	Alignment	not modelled	13.0	22	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
97	c1ixtA_	Alignment	not modelled	12.8	38	PDB header: toxin Chain: A: PDB Molecule: spasmodic protein tx9a-like protein; PDBTitle: structure of a novel p-superfamily spasmodic conotoxin2 reveals an inhibitory cystine knot motif
98	d1ixta_	Alignment	not modelled	12.8	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Conotoxin
99	c1kalA_	Alignment	not modelled	12.6	44	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