
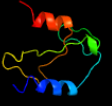
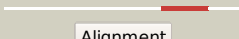

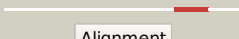




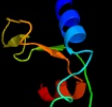












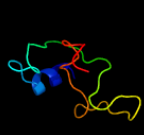




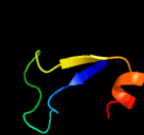
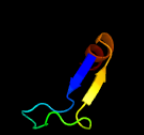

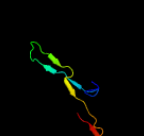


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1945 (-) _2195996_2197360
Date	Mon Aug 5 13:25:04 BST 2019
Unique Job ID	a50cc270a6ea8b1c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		99.1	18	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		98.9	21	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent ecomcra restriction endonuclease
3	c5mkwA_	 Alignment		98.7	13	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		98.6	15	PDB header: protein transport Chain: S: PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
5	c5h0mA_	 Alignment		98.1	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		98.0	23	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		97.7	20	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		97.1	17	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		96.8	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		95.1	12	PDB header: hydrolase Chain: A: PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	d2gykb1	 Alignment		89.7	18	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif

12	c4cmqB_	Alignment		88.6	22	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
13	d2jb0b1	Alignment		83.8	19	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
14	c4qkoH_	Alignment		64.5	16	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
15	c3plwA_	Alignment		62.2	21	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
16	c5ew5C_	Alignment		61.5	16	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
17	c7ceiB_	Alignment		59.6	16	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
18	c4uhpA_	Alignment		58.4	23	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
19	c5g2xC_	Alignment		50.9	25	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
20	c2pncB_	Alignment		43.7	14	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
21	d2dlka1	Alignment	not modelled	42.9	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
22	d1w6ga1	Alignment	not modelled	38.1	16	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
23	c1nbwA_	Alignment	not modelled	36.8	21	PDB header: hydrolase Chain: A: PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
24	d1vz0a1	Alignment	not modelled	36.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
25	d2ysca1	Alignment	not modelled	34.3	32	Fold: WW domain-like Superfamily: WW domain Family: WW domain
26	c3mkzU_	Alignment	not modelled	33.6	20	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
27	c3mkyP_	Alignment	not modelled	32.5	20	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
28	d1a1ga1	Alignment	not modelled	31.0	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
29	d1zfda_	Alignment	not modelled	30.9	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers

						Family: Classic zinc finger, C2H2
30	d1w2za1	Alignment	not modelled	29.1	9	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
31	c1va1A	Alignment	not modelled	29.0	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	d1ncsa	Alignment	not modelled	28.4	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
33	d1a1a1	Alignment	not modelled	28.2	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
34	d2ho2a1	Alignment	not modelled	27.3	23	Fold: WW domain-like Superfamily: WW domain Family: WW domain
35	d2glia4	Alignment	not modelled	27.0	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
36	c2b8tA	Alignment	not modelled	25.2	17	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
37	d2oqea1	Alignment	not modelled	24.9	9	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
38	d1d6za1	Alignment	not modelled	24.7	19	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
39	d1ejga	Alignment	not modelled	23.4	27	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
40	c3higB	Alignment	not modelled	23.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: amiloride-sensitive amine oxidase; PDBTitle: crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
41	c1pxeA	Alignment	not modelled	22.9	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
42	c1ui7A	Alignment	not modelled	22.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylethylamine oxidase; PDBTitle: site-directed mutagenesis of his433 involved in binding of2 copper ion in arthrobacter globiformis amine oxidase
43	c2c10D	Alignment	not modelled	22.8	19	PDB header: oxidoreductase Chain: D: PDB Molecule: membrane copper amine oxidase; PDBTitle: the structure of a truncated, soluble version of semicarbazide-2 sensitive amine oxidase
44	c1orxA	Alignment	not modelled	22.3	27	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
45	d1u86a1	Alignment	not modelled	22.1	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
46	d1a1ha1	Alignment	not modelled	21.9	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
47	c1d6uB	Alignment	not modelled	21.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
48	c1ekmC	Alignment	not modelled	21.1	9	PDB header: oxidoreductase Chain: C: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure at 2.5 a resolution of zinc-substituted2 copper amine oxidase of hansenula polymorpha expressed in3 escherichia coli
49	d1tf3a2	Alignment	not modelled	21.1	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
50	d1f2ig1	Alignment	not modelled	20.9	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
51	d1bhia	Alignment	not modelled	20.8	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
52	d1jmna	Alignment	not modelled	20.7	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
53	c3loyB	Alignment	not modelled	20.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of a copper-containing benzylamine oxidase from2 hansenula polymorpha
54	d1ubdc3	Alignment	not modelled	20.0	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
55	d2b8ta2	Alignment	not modelled	19.9	7	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
						Fold: beta-beta-alpha zinc fingers

56	d1aaya1	Alignment	not modelled	19.5	25	Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
57	d1sp2a	Alignment	not modelled	19.5	17	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
58	d2glia3	Alignment	not modelled	19.2	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
59	c3nbbC	Alignment	not modelled	18.5	9	PDB header: oxidoreductase Chain: C; PDB Molecule: peroxisomal primary amine oxidase; PDBTitle: crystal structure of mutant y305f expressed in e. coli in the copper2 amine oxidase from hansenula polymorpha
60	c1k48A	Alignment	not modelled	17.7	27	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
61	c1jzA	Alignment	not modelled	17.7	27	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
62	c5yixB	Alignment	not modelled	17.1	23	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
63	d2dlka2	Alignment	not modelled	16.6	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
64	c3pg6D	Alignment	not modelled	16.2	16	PDB header: ligase Chain: D; PDB Molecule: e3 ubiquitin-protein ligase dtx3l; PDBTitle: the carboxyl terminal domain of human deltex 3-like
65	d2glia5	Alignment	not modelled	15.4	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
66	c3ga3A	Alignment	not modelled	15.2	17	PDB header: hydrolase Chain: A; PDB Molecule: interferon-induced helicase c domain-containing PDBTitle: crystal structure of the c-terminal domain of human mda5
67	c1ksiA	Alignment	not modelled	14.8	9	PDB header: oxidoreductase Chain: A; PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of a eukaryotic (pea seedling) copper-containing2 amine oxidase at 2.2a resolution
68	d1tf6a1	Alignment	not modelled	14.8	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
69	d1zela1	Alignment	not modelled	14.7	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like
70	d1tf3a1	Alignment	not modelled	14.3	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
71	d1nbla	Alignment	not modelled	14.1	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
72	c2f2iA	Alignment	not modelled	14.0	27	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
73	c2w4rB	Alignment	not modelled	13.6	19	PDB header: hydrolase Chain: B; PDB Molecule: probable atp-dependent rna helicase dhx58; PDBTitle: crystal structure of the regulatory domain of human lgp2
74	c2mn1A	Alignment	not modelled	13.6	44	PDB header: unknown function Chain: A; PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
75	d1n1ua	Alignment	not modelled	13.6	20	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
76	c1n1uA	Alignment	not modelled	13.6	20	PDB header: antibiotic Chain: A; PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
77	d1okha	Alignment	not modelled	13.4	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
78	d1ubdc4	Alignment	not modelled	12.8	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
79	d1pt4a	Alignment	not modelled	12.7	27	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
80	d1oria	Alignment	not modelled	12.7	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
81	c4ttnA	Alignment	not modelled	12.6	27	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
82	c4ttoA	Alignment	not modelled	12.6	27	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
						PDB header: plant protein

83	c4ttmA_	Alignment	not modelled	12.5	27	Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
84	c2khaA_	Alignment	not modelled	12.3	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
85	d1jpa_	Alignment	not modelled	12.1	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
86	c2f2jA_	Alignment	not modelled	12.0	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
87	c2lurA_	Alignment	not modelled	11.8	27	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
88	d1nb1a_	Alignment	not modelled	11.6	27	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
89	c1nb1A_	Alignment	not modelled	11.6	27	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
90	c2lamA_	Alignment	not modelled	11.4	20	PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
91	d1nbwa3	Alignment	not modelled	11.2	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
92	c3e4hA_	Alignment	not modelled	11.0	20	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
93	c3cwbQ_	Alignment	not modelled	10.9	13	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
94	c2jydA_	Alignment	not modelled	10.9	60	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
95	c1ka1A_	Alignment	not modelled	10.8	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
96	c6dhrA_	Alignment	not modelled	10.4	27	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
97	c3epvB_	Alignment	not modelled	10.3	17	PDB header: metal binding protein Chain: B: PDB Molecule: nickel and cobalt resistance protein cnrr; PDBTitle: x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
98	d1xx6a2	Alignment	not modelled	9.6	17	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
99	c2k7gA_	Alignment	not modelled	9.4	20	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f