






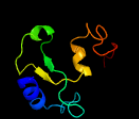






















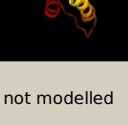


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1702c_(-)_1927218_1928582
Date	Fri Aug 2 13:30:30 BST 2019
Unique Job ID	fa34f5f4b2935643

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		99.1	12	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	16	PDB header: hydrolase Chain: A; PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eokmcra restriction endonuclease
3	c5mkwA_	 Alignment		98.7	23	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	c5vgbA_	 Alignment		98.2	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
6	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
7	c5zmmD_	 Alignment		97.8	24	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		97.2	13	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		96.9	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		94.8	12	PDB header: hydrolase Chain: A; PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	c4cmqB_	 Alignment		85.8	14	PDB header: hydrolase Chain: B; PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9

12	d2gykb1	Alignment		85.1	24	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
13	d2jb0b1	Alignment		77.6	19	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
14	c4qkoH	Alignment		56.1	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
15	c5g2xC	Alignment		54.7	22	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
16	c7ceiB	Alignment		52.2	19	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
17	c5ew5C	Alignment		51.7	22	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
18	c4uhpA	Alignment		51.1	23	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
19	d2dlka1	Alignment		47.7	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
20	c3mkzU	Alignment		47.7	24	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
21	c3mkyP	Alignment	not modelled	44.6	23	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
22	d1a1ga1	Alignment	not modelled	38.7	21	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
23	d1zfda	Alignment	not modelled	37.7	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
24	c1va1A	Alignment	not modelled	34.8	25	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
25	d1a1ia1	Alignment	not modelled	33.9	21	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
26	d1ncsa	Alignment	not modelled	33.4	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
27	c2b8tA	Alignment	not modelled	31.9	14	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
28	c3plwA	Alignment	not modelled	31.9	23	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
						Fold: beta-beta-alpha zinc fingers

29	d2glia4	Alignment	not modelled	31.2	22	Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
30	d1u86a1	Alignment	not modelled	28.3	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	d1vz0a1	Alignment	not modelled	28.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
32	d1a1ha1	Alignment	not modelled	27.2	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
33	d1tf3a2	Alignment	not modelled	27.1	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
34	d1ubdc3	Alignment	not modelled	26.0	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
35	d1f2ig1	Alignment	not modelled	25.6	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
36	d1aaya1	Alignment	not modelled	25.5	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
37	d1sp2a_	Alignment	not modelled	25.2	17	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
38	d2glia3	Alignment	not modelled	24.4	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
39	d1ejga_	Alignment	not modelled	23.1	18	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
40	d2b8ta2	Alignment	not modelled	23.0	21	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
41	d2dlka2	Alignment	not modelled	23.0	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	c1pxeA_	Alignment	not modelled	22.3	36	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	d1bhia_	Alignment	not modelled	21.9	21	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
44	d1jmna_	Alignment	not modelled	20.6	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
45	d1ubdc4	Alignment	not modelled	20.2	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
46	d1w6ga1	Alignment	not modelled	19.4	22	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
47	d2glia5	Alignment	not modelled	19.0	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
48	c3cwbQ_	Alignment	not modelled	18.0	16	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of 2 the polyketide crocacin-d
49	d2ysca1	Alignment	not modelled	17.9	29	Fold: WW domain-like Superfamily: WW domain Family: WW domain
50	d1tf6a1	Alignment	not modelled	17.2	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
51	c1nbwA_	Alignment	not modelled	17.1	21	PDB header: hydrolase Chain: A: PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
52	d1tf3a1	Alignment	not modelled	16.2	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
53	c4ttnA_	Alignment	not modelled	15.0	33	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
54	c4ttoA_	Alignment	not modelled	14.9	33	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
55	c4ttmA_	Alignment	not modelled	14.8	33	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
56	d1pt4a_	Alignment	not modelled	14.8	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides

						Family: Kalata B1
57	d1n1ua_	Alignment	not modelled	14.7	22	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
58	c1n1uA_	Alignment	not modelled	14.7	22	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
59	c2khaA_	Alignment	not modelled	14.6	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
60	c2f2iA_	Alignment	not modelled	14.5	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
61	c2mn1A_	Alignment	not modelled	14.4	33	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
62	d1nbla_	Alignment	not modelled	13.9	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
63	c5yixB_	Alignment	not modelled	13.8	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
64	d1orla_	Alignment	not modelled	13.5	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
65	d1w2za1	Alignment	not modelled	13.5	16	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
66	c6dhrA_	Alignment	not modelled	13.4	33	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
67	d1okha_	Alignment	not modelled	13.4	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
68	c1nb1A_	Alignment	not modelled	13.3	33	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
69	d1nbla_	Alignment	not modelled	13.3	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
70	d1xx6a2	Alignment	not modelled	13.2	17	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
71	c2pncB_	Alignment	not modelled	12.5	9	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
72	d1jmpa_	Alignment	not modelled	12.1	10	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
73	c1orxA_	Alignment	not modelled	12.1	20	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
74	c2lamA_	Alignment	not modelled	11.9	33	PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
75	c3e4hA_	Alignment	not modelled	11.8	22	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
76	d1d6za1	Alignment	not modelled	11.7	9	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
77	d2bvya1	Alignment	not modelled	11.5	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
78	d2ho2a1	Alignment	not modelled	11.3	25	Fold: WW domain-like Superfamily: WW domain Family: WW domain
79	c2o01N_	Alignment	not modelled	11.1	40	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
80	c2wsfN_	Alignment	not modelled	11.1	40	PDB header: photosynthesis Chain: N: PDB Molecule: photosystem i-n subunit; PDBTitle: improved model of plant photosystem i
81	c1ka1A_	Alignment	not modelled	10.9	33	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
82	d2oqea1	Alignment	not modelled	10.7	9	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
83	c2k7gA_	Alignment	not modelled	10.4	22	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f

84	d2cxha1	Alignment	not modelled	10.4	23	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Brix domain
85	c2cxhA	Alignment	not modelled	10.4	23	PDB header: rna binding protein Chain: A: PDB Molecule: probable brix-domain ribosomal biogenesis protein; PDBTitle: crystal structure of probable ribosomal biogenesis protein from <i>2 aeropyrum pernix k1</i>
86	c2jydA	Alignment	not modelled	10.3	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 transcription factor 1
87	c2c10D	Alignment	not modelled	10.1	16	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
88	c1ui7A	Alignment	not modelled	10.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylethylamine oxidase; PDBTitle: site-directed mutagenesis of his433 involved in binding of 2 copper ion in arthrobacter globiformis amine oxidase
89	c2lurA	Alignment	not modelled	10.0	38	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
90	c3higB	Alignment	not modelled	9.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: amiloride-sensitive amine oxidase; PDBTitle: crystal structure of human diamine oxidase in complex with the 2 inhibitor berenil
91	c2kukA	Alignment	not modelled	9.9	22	PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
92	c5sydA	Alignment	not modelled	9.8	60	PDB header: oxidoreductase Chain: A: PDB Molecule: azurin, chimeric construct; PDBTitle: circularly permuted azurin (cpaz) based on p. aeruginosa azurin 2 sequence
93	c1zw8A	Alignment	not modelled	9.8	27	PDB header: transcription Chain: A: PDB Molecule: zinc-responsive transcriptional regulator zap1; PDBTitle: solution structure of a zap1 zinc-responsive domain 2 provides insights into metalloregulatory transcriptional 3 repression in <i>saccharomyces cerevisiae</i>
94	c2qj0A	Alignment	not modelled	9.8	33	PDB header: plant protein Chain: A: PDB Molecule: cycloviolacin o14; PDBTitle: cycloviolacin o14
95	c2msoA	Alignment	not modelled	9.8	38	PDB header: toxin Chain: A: PDB Molecule: conotoxin gm9.1; PDBTitle: solution study of cgm9a
96	c1d6uB	Alignment	not modelled	9.2	9	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with 2 beta-phenylethylamine
97	c2m9oA	Alignment	not modelled	9.0	22	PDB header: plant protein Chain: A: PDB Molecule: kalata-b7; PDBTitle: solution structure of kalata b7
98	c2f2jA	Alignment	not modelled	9.0	20	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
99	c1ekmC	Alignment	not modelled	8.9	9	PDB header: oxidoreductase Chain: C: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure at 2.5 a resolution of zinc-substituted 2 copper amine oxidase of <i>hansenula polymorpha</i> expressed in <i>escherichia coli</i>