


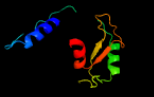
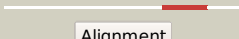

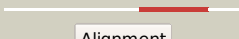

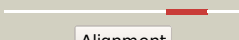

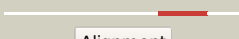











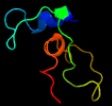

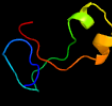
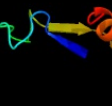



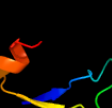



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0094c_(-)_103707_104660
Date	Tue Jul 23 14:50:13 BST 2019
Unique Job ID	828eb630249198e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		99.2	13	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		99.0	17	PDB header: hydrolase Chain: A; PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent ecomcra restriction endonuclease
3	c5mkwA_	 Alignment		98.8	15	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		98.8	14	PDB header: protein transport Chain: S; PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
5	c5h0mA_	 Alignment		98.3	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	c5zmmD_	 Alignment		98.2	21	PDB header: dna binding protein Chain: D; PDB Molecule: uncharacterized protein mcra; PDBTitle: structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra
7	c5vgaA_	 Alignment		98.0	17	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		97.2	19	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		96.5	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		95.6	13	PDB header: hydrolase Chain: A; PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	d2gykb1	 Alignment		87.0	15	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif

12	c4cmqB_	Alignment		84.1	15	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
13	d2jb0b1	Alignment		74.4	19	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
14	c5g2xC_	Alignment		70.0	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
15	c4qk0H_	Alignment		51.8	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
16	c3plwA_	Alignment		47.6	20	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
17	c4uhpA_	Alignment		46.0	23	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
18	c5ew5C_	Alignment		45.1	9	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
19	c7ceiB_	Alignment		44.9	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
20	d2dlka1	Alignment		34.6	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
21	c2b8tA_	Alignment	not modelled	29.5	16	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
22	d1w6ga1	Alignment	not modelled	28.1	16	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
23	d2glia4	Alignment	not modelled	26.7	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
24	d1zfdA_	Alignment	not modelled	23.6	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
25	c1va1A_	Alignment	not modelled	23.6	38	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
26	d1a1ia1	Alignment	not modelled	22.4	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
27	d1w2za1	Alignment	not modelled	21.4	9	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
28	d1a1ga1	Alignment	not modelled	21.4	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
						PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme

29	c3cwbQ_	Alignment	not modelled	21.0	12	protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
30	c2pncB_	Alignment	not modelled	20.0	13	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
31	d1ncsa_	Alignment	not modelled	19.8	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
32	d1a1ha1	Alignment	not modelled	18.8	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
33	c3e2iA_	Alignment	not modelled	18.4	10	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from s. aureus
34	d2ysca1	Alignment	not modelled	17.6	26	Fold: WW domain-like Superfamily: WW domain Family: WW domain
35	d1u86a1	Alignment	not modelled	17.6	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
36	c1orxA_	Alignment	not modelled	17.5	36	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
37	d1d6za1	Alignment	not modelled	17.3	19	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
38	d1bhia_	Alignment	not modelled	17.0	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
39	d2b8ta2	Alignment	not modelled	16.6	8	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
40	d2oqea1	Alignment	not modelled	16.5	9	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
41	c1k48A_	Alignment	not modelled	16.5	44	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
42	d1f2ig1	Alignment	not modelled	16.4	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
43	c1pxeA_	Alignment	not modelled	16.2	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
44	c1jizA_	Alignment	not modelled	16.1	44	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
45	c2c10D_	Alignment	not modelled	16.0	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
46	d1tf3a2	Alignment	not modelled	16.0	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
47	d1sp2a_	Alignment	not modelled	15.9	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
48	d1ejga_	Alignment	not modelled	15.9	27	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
49	d1ubdc3	Alignment	not modelled	15.9	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
50	c1ui7A_	Alignment	not modelled	15.7	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
51	d1aaya1	Alignment	not modelled	15.7	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
52	d2glia3	Alignment	not modelled	15.6	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
53	c3higB_	Alignment	not modelled	15.3	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
54	d1pt4a_	Alignment	not modelled	14.9	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
55	c2f2iA_	Alignment	not modelled	14.9	44	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
						PDB header: plant protein

56	c4ttnA	Alignment	not modelled	14.8	44	Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
57	d1n1ua	Alignment	not modelled	14.8	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
58	c1n1uA	Alignment	not modelled	14.8	33	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
59	c2khaA	Alignment	not modelled	14.7	44	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
60	c4ttoA	Alignment	not modelled	14.7	44	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
61	c1d6uB	Alignment	not modelled	14.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
62	c4ttmA	Alignment	not modelled	14.6	44	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
63	c2mn1A	Alignment	not modelled	14.6	44	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
64	c1ekmC	Alignment	not modelled	13.9	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 hanseula polymorpha expressed in3 escherichia coli
65	c5yixB	Alignment	not modelled	13.8	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
66	c3pgbA	Alignment	not modelled	13.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of aspergillus nidulans amine oxidase
67	d1nb1a	Alignment	not modelled	13.8	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
68	c1nb1A	Alignment	not modelled	13.8	44	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
69	c3loyB	Alignment	not modelled	13.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of a copper-containing benzylamine oxidase from2 hanseula polymorpha
70	d1jmna	Alignment	not modelled	13.4	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
71	c1ka1A	Alignment	not modelled	13.4	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
72	d1zela1	Alignment	not modelled	13.4	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like
73	d2qlia5	Alignment	not modelled	13.1	57	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
74	c2w4rB	Alignment	not modelled	13.0	14	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase dhx58; PDBTitle: crystal structure of the regulatory domain of human lgp2
75	d1tf6a1	Alignment	not modelled	12.7	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
76	c3ga3A	Alignment	not modelled	12.7	23	PDB header: hydrolase Chain: A: PDB Molecule: interferon-induced helicase c domain-containing PDBTitle: crystal structure of the c-terminal domain of human mda5
77	c2kukA	Alignment	not modelled	12.5	23	PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
78	c6dhrA	Alignment	not modelled	12.5	44	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
79	d2ho2a1	Alignment	not modelled	12.5	26	Fold: WW domain-like Superfamily: WW domain Family: WW domain
80	c2lurA	Alignment	not modelled	12.4	44	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
81	c2lamA	Alignment	not modelled	12.3	33	PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
82	d1tf3a1	Alignment	not modelled	12.3	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2

83	c3nbbC	Alignment	not modelled	12.3	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
84	d2dlka2	Alignment	not modelled	12.0	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
85	c2f2jA	Alignment	not modelled	11.8	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
86	c3e4hA	Alignment	not modelled	11.6	33	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
87	c1zw8A	Alignment	not modelled	11.1	38	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
88	c1zrtD	Alignment	not modelled	10.6	16	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
89	c2k7gA	Alignment	not modelled	10.4	33	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f
90	c2gj0A	Alignment	not modelled	10.2	44	PDB header: plant protein Chain: A: PDB Molecule: cycloviolacin o14; PDBTitle: cycloviolacin o14
91	d1wiga2	Alignment	not modelled	10.2	19	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
92	d1ubdc4	Alignment	not modelled	10.2	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
93	c1ksia	Alignment	not modelled	9.8	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
94	d1nbla	Alignment	not modelled	9.4	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
95	c2m9oA	Alignment	not modelled	9.3	33	PDB header: plant protein Chain: A: PDB Molecule: kalata-b7; PDBTitle: solution structure of kalata b7
96	d1okha	Alignment	not modelled	8.9	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
97	d1orla	Alignment	not modelled	8.5	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
98	d1jmpa	Alignment	not modelled	8.0	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
99	d1iura	Alignment	not modelled	7.4	18	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain