
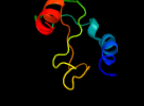
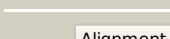
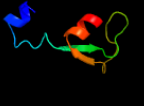
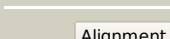

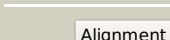

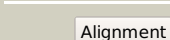

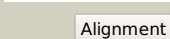

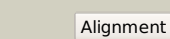

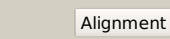


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1378c_(-)_1551234_1552661
Date	Wed Jul 31 22:05:48 BST 2019
Unique Job ID	1a55f11cccc9afe8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		98.6	25	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		98.1	22	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		98.0	21	PDB header: hydrolase Chain: A; PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eocmcrA restriction endonuclease
4	c5vgbA_	 Alignment		97.4	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
5	c5h0mA_	 Alignment		97.3	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	c5x1hS_	 Alignment		97.3	17	PDB header: protein transport Chain: S; PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
7	c5zmmD_	 Alignment		97.0	27	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		94.9	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	d1vz0a1	 Alignment		84.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
11	c6ghsA_	 Alignment		80.4	20	PDB header: hydrolase Chain: A; PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease

12	c4cmqB_	Alignment		76.0	23	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
13	c6et6A_	Alignment		59.7	20	PDB header: antimicrobial protein Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of muramidase from acinetobacter baumannii ab 5075uw2 prophage
14	c1r71B_	Alignment		49.8	16	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
15	d1ejga_	Alignment		48.2	25	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
16	d1jmna_	Alignment		46.7	17	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
17	d2dlka1	Alignment		46.5	30	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
18	d1r71a_	Alignment		44.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
19	c2qnfB_	Alignment		42.0	22	PDB header: hydrolase/dna Chain: B: PDB Molecule: recombination endonuclease vii; PDBTitle: crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
20	d1lokha_	Alignment		37.4	25	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
21	d1nbla_	Alignment	not modelled	36.7	25	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
22	d1jmpa_	Alignment	not modelled	34.5	17	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
23	d1lorla_	Alignment	not modelled	34.1	17	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
24	c3mkzU_	Alignment	not modelled	34.0	20	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
25	d1bhia_	Alignment	not modelled	32.8	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
26	d1a1ga1	Alignment	not modelled	31.4	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
27	d1ncsa_	Alignment	not modelled	31.2	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
28	c6dhrA_	Alignment	not modelled	30.4	31	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
29	d1zfda_	Alignment	not modelled	29.5	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers

						Family: Classic zinc finger, C2H2
30	d1u86a1	Alignment	not modelled	28.9	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	d1e7la2	Alignment	not modelled	28.4	22	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Recombination endonuclease VII, N-terminal domain
32	d2qlia4	Alignment	not modelled	27.8	22	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
33	d1a1ia1	Alignment	not modelled	27.8	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
34	c3mkyP_	Alignment	not modelled	27.5	22	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
35	c1orxA_	Alignment	not modelled	27.5	33	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
36	c1pxeA_	Alignment	not modelled	27.1	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
37	d2r4qa1	Alignment	not modelled	26.0	43	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
38	c1jzA_	Alignment	not modelled	25.5	33	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
39	c1k48A_	Alignment	not modelled	25.1	33	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
40	c1va1A_	Alignment	not modelled	25.1	20	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
41	c3cwbQ_	Alignment	not modelled	24.4	33	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
42	c2f2iA_	Alignment	not modelled	24.1	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
43	d1n1ua_	Alignment	not modelled	24.0	22	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
44	c1n1uA_	Alignment	not modelled	24.0	22	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
45	d1pt4a_	Alignment	not modelled	23.9	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
46	c4ttnA_	Alignment	not modelled	23.8	33	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
47	d1a1ha1	Alignment	not modelled	23.8	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
48	c2khaA_	Alignment	not modelled	23.6	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
49	c2mn1A_	Alignment	not modelled	23.6	33	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
50	c4ttoA_	Alignment	not modelled	23.6	33	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
51	c4ttmA_	Alignment	not modelled	23.5	33	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
52	c1ka1A_	Alignment	not modelled	22.8	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
53	d2jb0b1	Alignment	not modelled	22.8	19	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
54	d1aaya1	Alignment	not modelled	22.1	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
55	d1f2ig1	Alignment	not modelled	21.6	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
56	d1nblA_	Alignment	not modelled	21.5	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides

					Family:Kalata B1
57	c1nb1A_	Alignment	not modelled	21.5	33 PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
58	d2gykb1	Alignment	not modelled	21.4	15 Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNNH-motif
59	d1w6ga1	Alignment	not modelled	21.4	23 Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
60	c2f2jA_	Alignment	not modelled	21.1	33 PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
61	c2ak0A_	Alignment	not modelled	21.0	33 PDB header: toxin Chain: A: PDB Molecule: alpha-conotoxin mii; PDBTitle: structure of cyclic conotoxin mii-7
62	c2kukA_	Alignment	not modelled	20.6	22 PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
63	d2glia5	Alignment	not modelled	20.5	25 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
64	c2jydA_	Alignment	not modelled	20.3	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 transcription2 factor 1
65	c2lurA_	Alignment	not modelled	20.2	33 PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
66	d1tf3a2	Alignment	not modelled	19.8	19 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
67	c3e4hA_	Alignment	not modelled	19.7	22 PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
68	c2lamA_	Alignment	not modelled	19.1	33 PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
69	c4clvB_	Alignment	not modelled	19.1	21 PDB header: metal binding protein Chain: B: PDB Molecule: nickel-cobalt-cadmium resistance protein nccx; PDBTitle: crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
70	c2ajwA_	Alignment	not modelled	18.8	40 PDB header: toxin Chain: A: PDB Molecule: alpha-conotoxin mii; PDBTitle: structure of the cyclic conotoxin mii-6
71	d1sp2a_	Alignment	not modelled	18.6	27 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
72	d1ubdc4	Alignment	not modelled	18.3	21 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
73	c2yiuE_	Alignment	not modelled	18.2	16 PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
74	c2gj0A_	Alignment	not modelled	17.8	33 PDB header: plant protein Chain: A: PDB Molecule: cycloviolacin o14; PDBTitle: cycloviolacin o14
75	d2glia3	Alignment	not modelled	17.2	13 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
76	d2dlka2	Alignment	not modelled	17.2	33 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
77	d1ubdc3	Alignment	not modelled	17.2	13 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
78	c2k7gA_	Alignment	not modelled	17.0	22 PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f
79	c3goxB_	Alignment	not modelled	17.0	19 PDB header: hydrolase/dna Chain: B: PDB Molecule: restriction endonuclease hpy99i; PDBTitle: crystal structure of the beta-beta-alpha-me type ii restriction2 endonuclease hpy99i in the absence of edta
80	c2b8tA_	Alignment	not modelled	16.9	12 PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
81	d2b8ta2	Alignment	not modelled	16.8	21 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
82	c5yixB_	Alignment	not modelled	16.1	29 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
					PDB header: plant protein

83	c2m9oA_	Alignment	not modelled	16.0	22	Chain: A; PDB Molecule: kalata-b7; PDBTitle: solution structure of kalata b7
84	c4i1IA_	Alignment	not modelled	15.8	17	PDB header: transcription regulator Chain: A; PDB Molecule: forkhead box protein p3; PDBTitle: structural and biological features of foxp3 dimerization relevant to2 regulatory t cell function
85	d1rbli_	Alignment	not modelled	15.3	29	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
86	d2ysca1	Alignment	not modelled	15.0	41	Fold: WW domain-like Superfamily: WW domain Family: WW domain
87	c5xe7A_	Alignment	not modelled	14.6	28	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
88	c5g2xC_	Alignment	not modelled	13.2	26	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
89	c1zw8A_	Alignment	not modelled	13.0	16	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
90	d1ig4a_	Alignment	not modelled	12.4	24	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: Methyl-CpG-binding domain, MBD
91	c4kt5C_	Alignment	not modelled	12.2	14	PDB header: transcription regulator Chain: C; PDB Molecule: grla; PDBTitle: structure of grlr-grla complex
92	c4v30A_	Alignment	not modelled	12.0	23	PDB header: signaling protein Chain: A; PDB Molecule: cereblon isoform 4; PDBTitle: cereblon isoform 4 from magnetospirillum gryphiswaldense in2 complex with lenalidomide
93	c2anxB_	Alignment	not modelled	12.0	15	PDB header: hydrolase Chain: B; PDB Molecule: lysozyme; PDBTitle: crystal structure of bacteriophage p22 lysozyme mutant l87m
94	d1mswd_	Alignment	not modelled	12.0	33	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: T7 RNA polymerase
95	c3hslX_	Alignment	not modelled	11.9	30	PDB header: replication Chain: X; PDB Molecule: orf59; PDBTitle: the crystal structure of pf-8, the dna polymerase accessory subunit2 from kaposi's sarcoma-associated herpesvirus
96	c1vz0B_	Alignment	not modelled	11.8	26	PDB header: nuclear protein Chain: B; PDB Molecule: chromosome-partitioning protein spo0j; PDBTitle: chromosome segregation protein spo0j from thermus thermophilus
97	c2pncB_	Alignment	not modelled	11.7	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
98	c2jwmA_	Alignment	not modelled	11.5	22	PDB header: plant protein Chain: A; PDB Molecule: kalata-b7; PDBTitle: nmr spatial srtucture of ternary complex kalata b7/mn2+/dpc2 micelle
99	d1w94a1	Alignment	not modelled	11.5	14	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Brix domain