

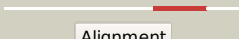

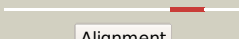



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2015c (-)_2261824_2263080
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	0de2b506099c2092

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		99.3	20	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		99.3	19	PDB header: hydrolase Chain: A; PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eokmcra restriction endonuclease
3	c5mkwA_	 Alignment		99.1	30	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		99.0	16	PDB header: protein transport Chain: S; PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
5	c5h0mA_	 Alignment		98.5	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	c5zmmD_	 Alignment		98.4	25	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		98.3	19	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		97.5	25	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		97.1	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		96.8	21	PDB header: hydrolase Chain: A; PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	d2gykb1	 Alignment		93.6	30	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif

12	c4cmqB_	Alignment		90.4	13	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
13	d2jb0b1	Alignment		88.5	31	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
14	d1vz0a1	Alignment		84.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
15	c3mkyP_	Alignment		80.1	10	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
16	c5ew5C_	Alignment		75.0	25	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
17	c4qkoH_	Alignment		74.9	38	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
18	c4uhpA_	Alignment		72.4	32	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
19	c3mkzU_	Alignment		72.2	11	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
20	c7ceiB_	Alignment		71.2	29	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	c5g2xC_	Alignment	not modelled	67.9	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
22	c1vz0B_	Alignment	not modelled	56.8	12	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome-partitioning protein spo0j; PDBTitle: chromosome segregation protein spo0j from thermus thermophilus
23	d2dlka1	Alignment	not modelled	37.4	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
24	c3plwA_	Alignment	not modelled	28.7	20	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
25	c3cwbQ_	Alignment	not modelled	28.6	24	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
26	d2glia4	Alignment	not modelled	24.8	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
27	d1zfdA_	Alignment	not modelled	24.2	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
28	c4okmA_	Alignment	not modelled	23.4	18	PDB header: transferase Chain: A: PDB Molecule: terpene synthase metal-binding domain-containing protein; PDBTitle: selinadiene synthase apo and in complex with

						diphosphate
29	c1pxeA_	Alignment	not modelled	23.1	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
30	c1va1A_	Alignment	not modelled	23.0	50	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
31	d1a1ia1	Alignment	not modelled	22.2	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
32	d1ncsa_	Alignment	not modelled	21.3	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
33	d1w6ga1	Alignment	not modelled	21.1	16	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
34	d1a1ga1	Alignment	not modelled	20.9	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
35	d2glia5	Alignment	not modelled	20.3	42	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
36	c2yiuE_	Alignment	not modelled	19.4	20	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
37	c1orxA_	Alignment	not modelled	19.3	56	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
38	c1r71B_	Alignment	not modelled	19.1	14	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
39	c4umkA_	Alignment	not modelled	18.9	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: probable chromosome-partitioning protein parb; PDBTitle: the complex of spo0j and pars dna in chromosomal partition system
40	d1r71a_	Alignment	not modelled	18.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
41	d1a1ha1	Alignment	not modelled	17.7	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	c1k48A_	Alignment	not modelled	17.5	56	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
43	c1jzA_	Alignment	not modelled	17.5	56	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
44	d1u86a1	Alignment	not modelled	17.1	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
45	c2fynH_	Alignment	not modelled	17.0	19	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
46	d1ejga_	Alignment	not modelled	15.9	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
47	d1tf6a1	Alignment	not modelled	15.9	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
48	d1f2ig1	Alignment	not modelled	15.8	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
49	c3sztB_	Alignment	not modelled	15.7	14	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
50	d2glia3	Alignment	not modelled	15.6	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
51	d1ubdc3	Alignment	not modelled	15.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
52	d1pt4a_	Alignment	not modelled	15.4	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
53	c4ttnA_	Alignment	not modelled	15.4	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
54	d1n1ua_	Alignment	not modelled	15.3	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1

55	c1n1uA	Alignment	not modelled	15.3	44	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
56	c3t0yA	Alignment	not modelled	15.2	17	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
57	c4ttoA	Alignment	not modelled	15.2	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
58	c2f2iA	Alignment	not modelled	15.2	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
59	c2khaA	Alignment	not modelled	15.1	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
60	c4ttmA	Alignment	not modelled	15.1	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
61	d1tf3a2	Alignment	not modelled	15.1	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
62	d1bhia	Alignment	not modelled	15.0	71	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
63	d1aaya1	Alignment	not modelled	14.9	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
64	c1zrtD	Alignment	not modelled	14.7	19	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
65	c2mn1A	Alignment	not modelled	14.7	38	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
66	c2pncB	Alignment	not modelled	14.3	10	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
67	d1sp2a	Alignment	not modelled	14.1	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
68	c2f2jA	Alignment	not modelled	13.8	36	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
69	c6dhrA	Alignment	not modelled	13.4	44	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
70	c3nctC	Alignment	not modelled	13.1	8	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
71	d1jmna	Alignment	not modelled	13.0	22	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
72	d1nb1a	Alignment	not modelled	13.0	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
73	c1nb1A	Alignment	not modelled	13.0	56	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
74	d2b8ta2	Alignment	not modelled	12.9	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
75	d1w2za1	Alignment	not modelled	12.8	19	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
76	c2lamA	Alignment	not modelled	12.6	56	PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
77	c1kalA	Alignment	not modelled	12.5	56	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
78	d2dika2	Alignment	not modelled	12.3	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
79	c3e4hA	Alignment	not modelled	12.2	44	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
80	c2b8tA	Alignment	not modelled	12.2	23	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
81	c5aj3p	Alignment	not modelled	11.4	29	PDB header: ribosome Chain: P: PDB Molecule: mitoribosomal protein bs16m, mrps16; PDBTitle: structure of the small subunit of the mammalian mitoribosome
						PDB header: transcription

82	c4go1A	Alignment	not modelled	11.4	6	Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
83	d2oqea1	Alignment	not modelled	11.1	16	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
84	d1d6za1	Alignment	not modelled	11.1	16	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
85	c2c10D	Alignment	not modelled	10.9	6	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
86	c1ui7A	Alignment	not modelled	10.8	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
87	c5yixB	Alignment	not modelled	10.6	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
88	c4lfuA	Alignment	not modelled	10.4	8	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
89	c2lurA	Alignment	not modelled	10.4	63	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
90	c2jydA	Alignment	not modelled	10.1	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
91	c2k7gA	Alignment	not modelled	10.0	44	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f
92	c2o8xA	Alignment	not modelled	10.0	26	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
93	d1okha	Alignment	not modelled	9.9	22	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
94	c1d6uB	Alignment	not modelled	9.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
95	d1ubdc4	Alignment	not modelled	9.7	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
96	d1nbla	Alignment	not modelled	9.6	22	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
97	c3higB	Alignment	not modelled	9.5	6	PDB header: oxidoreductase Chain: B: PDB Molecule: amiloride-sensitive amine oxidase; PDBTitle: crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
98	c2kukA	Alignment	not modelled	9.5	31	PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
99	c3loyB	Alignment	not modelled	9.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of a copper-containing benzylamine oxidase from2 hanselula polymorpha