

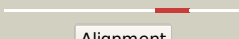

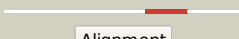
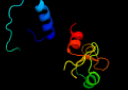

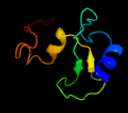








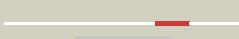





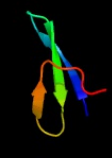





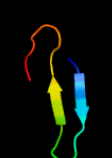




Phyre2

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Description	RVBD0515 (-) _606554_608065
Date	Fri Jul 26 01:50:06 BST 2019
Unique Job ID	61c9e186252034e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		99.0	19	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		98.7	24	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		98.6	15	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eocmcrA restriction endonuclease
4	c5x1hS_	 Alignment		98.5	21	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		97.8	13	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		97.6	26	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		96.9	23	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		96.4	19	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		91.6	29	PDB header: hydrolase Chain: A: PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	d1vz0a1	 Alignment		91.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like

12	d2ho2a1	Alignment		82.8	37	Fold: WW domain-like Superfamily: WW domain Family: WW domain
13	d2gykb1	Alignment		82.7	21	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
14	c3mkyP_	Alignment		81.7	12	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
15	d2jb0b1	Alignment		79.6	27	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
16	c4cmqB_	Alignment		78.8	16	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
17	c3mkzU_	Alignment		77.7	12	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
18	d2ysca1	Alignment		75.6	43	Fold: WW domain-like Superfamily: WW domain Family: WW domain
19	d1r71a_	Alignment		70.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
20	c1r71B_	Alignment		69.3	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
21	d2e45a1	Alignment	not modelled	65.1	36	Fold: WW domain-like Superfamily: WW domain Family: WW domain
22	c4uhpA_	Alignment	not modelled	54.1	22	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
23	c4by2C_	Alignment	not modelled	52.9	22	PDB header: structural protein Chain: C: PDB Molecule: anastral spindle 2, sas 4; PDBTitle: sas-4 (dcpap) tcp domain in complex with a proline rich motif of ana22 (dstil) of drosophila melanogaster
24	c4gkoH_	Alignment	not modelled	52.5	26	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
25	c5ew5C_	Alignment	not modelled	51.5	22	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
26	c7ceiB_	Alignment	not modelled	50.1	26	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
27	c4ld3A_	Alignment	not modelled	50.0	17	PDB header: structural protein, protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structural analysis of the microcephaly protein cpap g-box domain2 suggests a role in centriole elongation.
28	c3plwA_	Alignment	not modelled	48.2	21	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage PDB header: cell cycle

29	c4bxB	Alignment	not modelled	47.0	20	Chain: B; PDB Molecule: cpap; PDBTitle: structure of the wild-type tcp10 domain of danio rerio cpap in complex2 with a peptide of danio rerio stil
30	d2dka1	Alignment	not modelled	44.1	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	c5g2xC	Alignment	not modelled	43.2	19	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
32	c4go1A	Alignment	not modelled	33.7	13	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
33	c1va1A	Alignment	not modelled	32.7	38	PDB header: transcription Chain: A; PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
34	c3t0yA	Alignment	not modelled	32.7	25	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
35	d2glia4	Alignment	not modelled	31.5	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
36	d1a1ia1	Alignment	not modelled	31.2	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
37	d1zfdA	Alignment	not modelled	30.7	56	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
38	d1ncsa	Alignment	not modelled	30.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
39	d1w6ga1	Alignment	not modelled	29.8	31	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
40	c2w48D	Alignment	not modelled	29.1	26	PDB header: transcription Chain: D; PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
41	d1a1ga1	Alignment	not modelled	28.1	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	d1ejga	Alignment	not modelled	26.9	45	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
43	d1bhia	Alignment	not modelled	25.8	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
44	c3szTB	Alignment	not modelled	25.7	17	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
45	c1orxA	Alignment	not modelled	25.5	56	PDB header: antibiotic Chain: A; PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
46	d1a1ha1	Alignment	not modelled	25.1	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
47	d1u86a1	Alignment	not modelled	24.6	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
48	d1jmna	Alignment	not modelled	23.9	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
49	c1pxeA	Alignment	not modelled	23.4	55	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
50	c1jzA	Alignment	not modelled	23.3	56	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
51	d1smf2	Alignment	not modelled	23.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
52	d1tf3a2	Alignment	not modelled	23.1	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
53	c1k48A	Alignment	not modelled	23.0	56	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
54	d1ubdc3	Alignment	not modelled	22.4	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
55	d1f2ig1	Alignment	not modelled	22.2	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2

56	d1aaya1	Alignment	not modelled	21.9	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
57	d2glia3	Alignment	not modelled	21.9	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
58	d2dlka2	Alignment	not modelled	21.7	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
59	d1sp2a_	Alignment	not modelled	20.8	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
60	d1w2za1	Alignment	not modelled	20.8	28	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
61	d1pt4a_	Alignment	not modelled	20.5	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
62	c4ttnA_	Alignment	not modelled	20.3	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
63	c2pncB_	Alignment	not modelled	20.3	19	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
64	c1n1uA_	Alignment	not modelled	20.3	44	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
65	d1n1ua_	Alignment	not modelled	20.3	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
66	c2khaA_	Alignment	not modelled	20.2	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
67	c5xe7A_	Alignment	not modelled	20.2	33	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
68	c4ttoA_	Alignment	not modelled	20.1	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
69	c2mn1A_	Alignment	not modelled	20.1	56	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
70	c4ttmA_	Alignment	not modelled	20.1	56	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
71	c2f2iA_	Alignment	not modelled	20.0	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
72	c3vepA_	Alignment	not modelled	19.8	21	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
73	c2b8tA_	Alignment	not modelled	19.0	21	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
74	c6dhrA_	Alignment	not modelled	18.4	44	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
75	c4ifuA_	Alignment	not modelled	18.2	20	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
76	c2lamA_	Alignment	not modelled	18.0	44	PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
77	c1ui7A_	Alignment	not modelled	17.6	31	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
78	d2glia5	Alignment	not modelled	17.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
79	d1nb1a_	Alignment	not modelled	17.4	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
80	c1nb1A_	Alignment	not modelled	17.4	56	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
81	d1d6za1	Alignment	not modelled	17.1	25	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
82	d2oqea1	Alignment	not modelled	17.0	31	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
83	d1e7oa_	Alignment	not modelled	16.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase

83	v137va_	Alignment	not modelled	16.8	18	sigma factors Family: YlxM/p13-like
84	c3e4hA_	Alignment	not modelled	16.7	44	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
85	d1ubdc4	Alignment	not modelled	16.6	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
86	d1nbla_	Alignment	not modelled	16.6	40	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
87	c2c10D_	Alignment	not modelled	16.3	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
88	c5jhfA_	Alignment	not modelled	16.0	29	PDB header: protein transport Chain: A: PDB Molecule: klth0d11660p; PDBTitle: crystal structure of atg13(17br)-atg13(17lr)-atg17-atg29-atg31 complex
89	c1kalA_	Alignment	not modelled	15.9	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
90	d1ttya_	Alignment	not modelled	15.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
91	d1okha_	Alignment	not modelled	15.7	40	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
92	c4v30A_	Alignment	not modelled	15.7	16	PDB header: signaling protein Chain: A: PDB Molecule: cereblon isoform 4; PDBTitle: cereblon isoform 4 from magnetospirillum gryphiswaldense in2 complex with lenalidomide
93	c5fgmA_	Alignment	not modelled	15.4	30	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
94	c3higB_	Alignment	not modelled	15.2	38	PDB header: oxidoreductase Chain: B: PDB Molecule: amiloride-sensitive amine oxidase; PDBTitle: crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
95	c1d6uB_	Alignment	not modelled	15.2	25	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
96	c2kukA_	Alignment	not modelled	15.1	44	PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
97	d1orla_	Alignment	not modelled	14.9	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
98	c5yixB_	Alignment	not modelled	14.9	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
99	c6j0eB_	Alignment	not modelled	14.9	21	PDB header: transcription Chain: B: PDB Molecule: arsenic responsive repressor arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression