
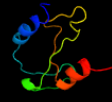

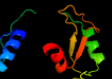

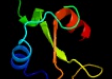

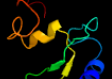

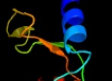








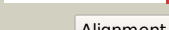



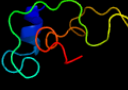

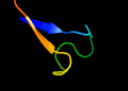


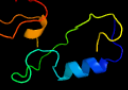
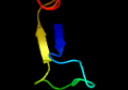




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1148c_(-)_1276305_1277753
Date	Wed Jul 31 22:05:23 BST 2019
Unique Job ID	2ffca56cfb032165

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		99.0	18	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	21	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eokmcra restriction endonuclease
3	c5mkwA_	 Alignment		98.6	13	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	c5h0mA_	 Alignment		97.9	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	23	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	20	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	17	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		96.2	11	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		94.7	11	PDB header: hydrolase Chain: A: PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	d2gykb1	 Alignment		88.5	18	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif

12	c4cmqB_	Alignment		80.5	22	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
13	c3mkyP_	Alignment		80.4	23	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
14	d2jb0b1	Alignment		79.7	19	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
15	d1vz0a1	Alignment		75.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
16	c3mkzU_	Alignment		72.3	22	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
17	c3plwA_	Alignment		54.2	18	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
18	c5ew5C_	Alignment		49.0	16	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
19	c4qkoH_	Alignment		44.9	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
20	d2dlka1	Alignment		40.6	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
21	c7ceiB_	Alignment	not modelled	39.7	16	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
22	c4uhpA_	Alignment	not modelled	39.0	23	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
23	d1a1ga1	Alignment	not modelled	37.0	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
24	c2e1cA_	Alignment	not modelled	36.9	13	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
25	c1nbwA_	Alignment	not modelled	35.9	20	PDB header: hydrolase Chain: A: PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
26	c5g2xC_	Alignment	not modelled	34.5	25	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
27	d1zlda_	Alignment	not modelled	32.8	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
28	d1w6ga1	Alignment	not modelled	31.3	16	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain

29	d1a1a1	Alignment	not modelled	30.7	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
30	d1ncsa	Alignment	not modelled	30.3	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	d1r71a	Alignment	not modelled	30.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
32	c1ilgA	Alignment	not modelled	29.6	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
33	c1r71B	Alignment	not modelled	29.2	23	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
34	c1va1A	Alignment	not modelled	29.1	21	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
35	d1w2za1	Alignment	not modelled	26.4	9	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
36	d1a1ha1	Alignment	not modelled	25.3	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
37	d1u86a1	Alignment	not modelled	25.1	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
38	d1ubdc3	Alignment	not modelled	24.1	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
39	d1sp2a	Alignment	not modelled	23.7	17	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
40	c2pncB	Alignment	not modelled	23.5	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
41	d2glia3	Alignment	not modelled	23.3	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	d1tf3a2	Alignment	not modelled	23.2	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
43	c4go1A	Alignment	not modelled	23.1	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
44	d1f2ig1	Alignment	not modelled	22.9	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
45	d1d6za1	Alignment	not modelled	22.0	19	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
46	d1aaya1	Alignment	not modelled	21.7	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
47	d2oqea1	Alignment	not modelled	21.3	9	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
48	c2cfxD	Alignment	not modelled	20.9	15	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
49	c3d8mA	Alignment	not modelled	20.9	12	PDB header: virus/viral protein Chain: A: PDB Molecule: baseplate protein, receptor binding protein; PDBTitle: crystal structure of a chimeric receptor binding protein from2 lactococcal phages subspecies tp901-1 and p2
50	c3higB	Alignment	not modelled	20.0	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
51	d1bhia	Alignment	not modelled	20.0	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
52	c4czdD	Alignment	not modelled	19.9	15	PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
53	c2c10D	Alignment	not modelled	19.4	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
54	d2glia4	Alignment	not modelled	19.4	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
						Fold: DNA/RNA-binding 3-helical bundle

55	d1zela1	Alignment	not modelled	19.3	28	Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like
56	c1ekmC	Alignment	not modelled	19.3	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 hansenula polymorpha expressed in3 escherichia coli
57	c2w48D	Alignment	not modelled	18.5	24	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
58	c1d6uB	Alignment	not modelled	18.1	19	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
59	c3loyB	Alignment	not modelled	17.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of a copper-containing benzylamine oxidase from2 hansenula polymorpha
60	c3nbbC	Alignment	not modelled	17.0	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
61	c1pxeA	Alignment	not modelled	16.9	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
62	d1nba3	Alignment	not modelled	16.7	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
63	c1ui7A	Alignment	not modelled	16.4	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
64	d2dlka2	Alignment	not modelled	16.1	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
65	c2dbbA	Alignment	not modelled	15.0	21	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
66	c2bsdC	Alignment	not modelled	14.6	18	PDB header: receptor Chain: C: PDB Molecule: receptor binding protein; PDBTitle: structure of lactococcal bacteriophage p2 receptor binding protein
67	c1vz0B	Alignment	not modelled	14.3	20	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome-partitioning protein spo0j; PDBTitle: chromosome segregation protein spo0j from thermus thermophilus
68	d1ubdc4	Alignment	not modelled	14.1	24	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
69	c3pwxB	Alignment	not modelled	14.0	13	PDB header: structural protein Chain: B: PDB Molecule: putative flagellar hook-associated protein; PDBTitle: structure of putative flagellar hook-associated protein from vibrio2 parahaemolyticus
70	c1orxA	Alignment	not modelled	14.0	27	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
71	d1tf6a1	Alignment	not modelled	13.8	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
72	d1ejga	Alignment	not modelled	13.7	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
73	d1jmna	Alignment	not modelled	13.7	20	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
74	c4clvB	Alignment	not modelled	13.4	18	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
75	d2cg4a1	Alignment	not modelled	13.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
76	c3da0C	Alignment	not modelled	12.5	12	PDB header: viral protein Chain: C: PDB Molecule: cleaved chimeric receptor binding protein from PDBTitle: crystal structure of a cleaved form of a chimeric receptor binding2 protein from lactococcal phages subspecies tp901-1 and p2
77	d1tf3a1	Alignment	not modelled	12.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
78	c1ksiA	Alignment	not modelled	12.4	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
79	d2glia5	Alignment	not modelled	10.7	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
80	c3abdY	Alignment	not modelled	10.7	54	PDB header: cell cycle/replication Chain: Y: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal

81	c5o8kB	Alignment	not modelled	10.7	54	PDB header: replication Chain: B: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of mammalian rev7 in complex with rev3 1875-1895
82	c3abdX	Alignment	not modelled	10.6	54	PDB header: cell cycle/replication Chain: X: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
83	c1jzA	Alignment	not modelled	10.4	27	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
84	c1k48A	Alignment	not modelled	10.4	27	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
85	c3abeZ	Alignment	not modelled	9.7	54	PDB header: cell cycle/replication Chain: Z: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of human rev7 in complex with a human rev3 fragment in a2 tetragonal crystal
86	c1zelA	Alignment	not modelled	9.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2827c; PDBTitle: crystal structure of rv2827c protein from mycobacterium tuberculosis
87	c4kunB	Alignment	not modelled	9.7	27	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein lpp1115; PDBTitle: crystal structure of legionella pneumophila lpp1115 / kaib
88	c1ygmA	Alignment	not modelled	9.3	23	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein bsu31320; PDBTitle: nmr structure of mistic
89	c4fjoD	Alignment	not modelled	9.2	54	PDB header: transferase/dna binding protein Chain: D: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of the rev1 ctd-rev3/7-pol kappa rir complex
90	c4ch7A	Alignment	not modelled	9.1	19	PDB header: transcription Chain: A: PDB Molecule: nird-like protein; PDBTitle: crystal structure of the siroheme decarboxylase nirdl
91	c4bgoA	Alignment	not modelled	9.0	7	PDB header: hydrolase Chain: A: PDB Molecule: efem m75 peptidase; PDBTitle: structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
92	d1nbla	Alignment	not modelled	8.9	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
93	c2entA	Alignment	not modelled	8.9	33	PDB header: transcription Chain: A: PDB Molecule: krueppel-like factor 15; PDBTitle: solution structure of the second c2h2-type zinc finger2 domain from human krueppel-like factor 15
94	d1n1ua	Alignment	not modelled	8.6	20	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
95	c1n1uA	Alignment	not modelled	8.6	20	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
96	d1okha	Alignment	not modelled	8.6	30	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
97	d2b8ta2	Alignment	not modelled	8.5	11	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
98	c2f2iA	Alignment	not modelled	8.4	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
99	d1w7ca1	Alignment	not modelled	8.4	13	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain