
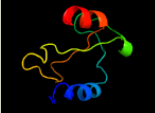
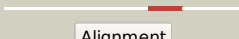

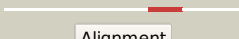


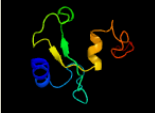







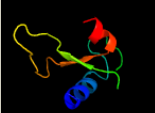





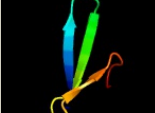

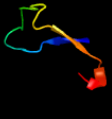






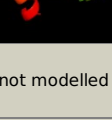


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0393 (-) _472784_474109
Date	Tue Jul 23 14:50:46 BST 2019
Unique Job ID	9de3509d5220c61b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		98.9	15	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		98.4	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		98.3	21	PDB header: hydrolase Chain: A; PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent eokmcra restriction endonuclease
4	c5x1hS_	 Alignment		98.3	18	PDB header: protein transport Chain: S; PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
5	c5h0mA_	 Alignment		97.7	21	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		97.3	7	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		97.1	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		96.1	20	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		95.3	7	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		86.3	20	PDB header: hydrolase Chain: A; PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
11	d2ho2a1	 Alignment		69.2	36	Fold: WW domain-like Superfamily: WW domain Family: WW domain

12	d2gykb1	Alignment		66.4	18	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
13	d2jb0b1	Alignment		62.7	23	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
14	c3vufA	Alignment		60.7	18	PDB header: transferase Chain: A: PDB Molecule: granule-bound starch synthase 1, PDBTitle: crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp
15	c2x6rA	Alignment		59.4	16	PDB header: isomerase Chain: A: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
16	c4rieB	Alignment		58.3	26	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase homolog; PDBTitle: landomycin glycosyltransferase langt2
17	d2ysca1	Alignment		58.0	36	Fold: WW domain-like Superfamily: WW domain Family: WW domain
18	c2xmpB	Alignment		48.4	17	PDB header: sugar binding protein Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
19	d2e45a1	Alignment		43.9	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
20	d3c7bb3	Alignment		37.0	19	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
21	c4cmqB	Alignment	not modelled	33.8	9	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
22	c3plwA	Alignment	not modelled	33.6	34	PDB header: hydrolase Chain: A: PDB Molecule: recombination enhancement function protein; PDBTitle: ref protein from p1 bacteriophage
23	c3tsaA	Alignment	not modelled	32.4	25	PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng
24	c4ambB	Alignment	not modelled	30.6	14	PDB header: transferase Chain: B: PDB Molecule: snogd; PDBTitle: crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater
25	c4by2C	Alignment	not modelled	30.1	25	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
26	c4ld3A	Alignment	not modelled	29.9	20	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.
27	c4uhpA	Alignment	not modelled	28.1	19	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
28	c4qkoH	Alignment	not modelled	27.4	30	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 PDB header: immune system

29	c7ceiB_	Alignment	not modelled	26.5	22	Chain: B; PDB Molecule: protein (colicin e7 immunity protein); PDBTitle: the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
30	d2dlka1	Alignment	not modelled	25.5	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	c4bxB_	Alignment	not modelled	24.6	19	PDB header: cell cycle 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
32	c5ew5C_	Alignment	not modelled	24.5	19	PDB header: hydrolase Chain: C; PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
33	c4bfcA_	Alignment	not modelled	21.2	26	PDB header: transferase Chain: A; PDB Molecule: 3-deoxy-d-manno-octulosonic-acid transferase; PDBTitle: crystal structure of the c-terminal cmp-kdo binding domain of waaa2 from acinetobacter baumannii
34	c5yixB_	Alignment	not modelled	20.9	23	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
35	d1w6ga1	Alignment	not modelled	20.1	28	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
36	c1vw4V_	Alignment	not modelled	19.2	56	PDB header: ribosome Chain: V; PDB Molecule: 54s ribosomal protein l36, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
37	c3u4gA_	Alignment	not modelled	18.9	31	PDB header: transferase Chain: A; PDB Molecule: namn:dmb phosphoribosyltransferase; PDBTitle: the structure of cobt from pyrococcus horikoshii
38	c6gnfC_	Alignment	not modelled	17.3	7	PDB header: transferase Chain: C; PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp
39	c5jhfA_	Alignment	not modelled	16.7	29	PDB header: protein transport Chain: A; PDB Molecule: klth0d11660p; PDBTitle: crystal structure of atg13(17br)-atg13(17lr)-atg17-atg29-atg31 complex
40	c1va1A_	Alignment	not modelled	16.6	38	PDB header: transcription Chain: A; PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
41	c5xvmB_	Alignment	not modelled	16.6	17	PDB header: transferase Chain: B; PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c)
42	c2p6pB_	Alignment	not modelled	16.2	26	PDB header: transferase Chain: B; PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
43	c3wadA_	Alignment	not modelled	15.9	28	PDB header: transferase Chain: A; PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicenistatin
44	d2isya2	Alignment	not modelled	15.8	25	Fold: Iron-dependent repressor protein, dimerization domain Superfamily: Iron-dependent repressor protein, dimerization domain Family: Iron-dependent repressor protein, dimerization domain
45	d1w2za1	Alignment	not modelled	15.5	25	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
46	d1a1ia1	Alignment	not modelled	15.4	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
47	c2b8tA_	Alignment	not modelled	15.1	18	PDB header: transferase Chain: A; PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
48	c5w8sA_	Alignment	not modelled	14.6	24	PDB header: transferase Chain: A; PDB Molecule: lipid a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
49	c5v0tB_	Alignment	not modelled	14.5	17	PDB header: transferase Chain: B; PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an alpha,alpha-trehalose-phosphate synthase (udp-2 forming) from burkholderia xenovorans in complex with glucose-6-3 phosphate
50	c3d0qB_	Alignment	not modelled	14.2	22	PDB header: transferase Chain: B; PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
51	d2glia4	Alignment	not modelled	13.9	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
52	c5g2xC_	Alignment	not modelled	13.8	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
53	d1zfdA_	Alignment	not modelled	13.7	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
54	c2pncB_	Alignment	not modelled	13.4	16	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
55	d2b8ta2	Alignment	not modelled	13.2	21	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
56	d1ncsa	Alignment	not modelled	12.9	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
57	c3iaaB	Alignment	not modelled	12.9	31	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
58	d2oqa1	Alignment	not modelled	12.5	25	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
59	c1pxeA	Alignment	not modelled	12.0	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
60	d1d6za1	Alignment	not modelled	11.7	25	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
61	c2f2jA	Alignment	not modelled	11.3	40	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
62	c5du2B	Alignment	not modelled	11.0	23	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
63	d1a1ha1	Alignment	not modelled	10.9	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
64	c2iyaB	Alignment	not modelled	10.9	19	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
65	d1a1ga1	Alignment	not modelled	10.8	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
66	d1bhia	Alignment	not modelled	10.8	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
67	c1ui7A	Alignment	not modelled	10.6	28	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
68	c4hlnA	Alignment	not modelled	10.5	6	PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltooligosaccharide
69	c3loyB	Alignment	not modelled	10.3	25	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of a copper-containing benzylamine oxidase from2 hansenula polymorpha
70	c2iyfA	Alignment	not modelled	10.3	19	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
71	c4leiB	Alignment	not modelled	10.2	22	PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminytransferase spnp
72	d1rzua	Alignment	not modelled	10.1	27	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
73	d1ejga	Alignment	not modelled	10.1	44	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
74	c3ia7A	Alignment	not modelled	10.0	36	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
75	d1jmna	Alignment	not modelled	9.9	40	Fold: Crambin-like Superfamily: Crambin-like Family: Crambin-like
76	c2c10D	Alignment	not modelled	9.9	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
77	d1u86a1	Alignment	not modelled	9.8	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
78	c3higB	Alignment	not modelled	9.7	31	PDB header: oxidoreductase Chain: B: PDB Molecule: amiloride-sensitive amine oxidase; PDBTitle: crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
79	c1ekmC	Alignment	not modelled	9.7	25	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
80	c1d6uB	Alignment	not modelled	9.7	25	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
						PDB header: antibiotic

81	c1orxA_	Alignment	not modelled	9.6	40	Chain: A; PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
82	c3t5tA_	Alignment	not modelled	9.4	22	PDB header: transferase Chain: A; PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygroscopicus in apo form
83	c3dzcA_	Alignment	not modelled	9.4	20	PDB header: isomerase Chain: A; PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
84	c4ttnA_	Alignment	not modelled	9.3	56	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
85	c2mn1A_	Alignment	not modelled	9.2	38	PDB header: unknown function Chain: A; PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
86	d1tf3a2	Alignment	not modelled	9.2	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
87	c4ttoA_	Alignment	not modelled	9.2	56	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
88	d2iw1a1	Alignment	not modelled	9.2	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
89	c1nbwA_	Alignment	not modelled	9.2	22	PDB header: hydrolase Chain: A; PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
90	c4ttmA_	Alignment	not modelled	9.2	56	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
91	c2khaB_	Alignment	not modelled	9.0	56	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
92	c3othB_	Alignment	not modelled	8.7	33	PDB header: transferase/antibiotic Chain: B; PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
93	c3s29C_	Alignment	not modelled	8.5	19	PDB header: transferase Chain: C; PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
94	c3nbbC_	Alignment	not modelled	8.4	25	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 hansenua polymorpha
95	c2ol5B_	Alignment	not modelled	8.4	12	PDB header: transcription regulator Chain: B; PDB Molecule: pai 2 protein; PDBTitle: crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus
96	d1ubdc3	Alignment	not modelled	8.3	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
97	c6fj3A_	Alignment	not modelled	7.8	32	PDB header: membrane protein Chain: A; PDB Molecule: parathyroid hormone/parathyroid hormone-related peptide PDBTitle: high resolution crystal structure of parathyroid hormone 1 receptor in2 complex with a peptide agonist.
98	d1aaya1	Alignment	not modelled	7.7	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
99	c2kukA_	Alignment	not modelled	7.7	31	PDB header: antiviral protein Chain: A; PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2