
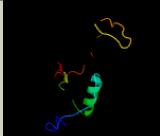



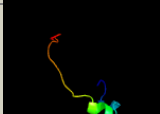












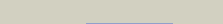






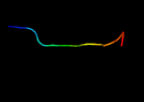







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2019_(-)_2265997_2266413
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	5a468c6bd7f94acf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6b3aA_	 Alignment		47.3	22	PDB header: transferase Chain: A; PDB Molecule: apra methyltransferase 1; PDBTitle: apra methyltransferase 1 - gnat didomain in complex with mn2+ and sam
2	d1o4wa_	 Alignment		38.3	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	c1x31D_	 Alignment		35.4	22	PDB header: oxidoreductase Chain: D; PDB Molecule: sarcosine oxidase delta subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
4	c3tdmD_	 Alignment		30.5	7	PDB header: de novo protein Chain: D; PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
5	c4hh3C_	 Alignment		28.6	17	PDB header: flavoprotein/transcription Chain: C; PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides
6	c3whpA_	 Alignment		28.5	18	PDB header: gene regulation Chain: A; PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
7	c1y80A_	 Alignment		28.1	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
8	d1ng7a_	 Alignment		25.8	24	Fold: Soluble domain of poliovirus core protein 3a Superfamily: Soluble domain of poliovirus core protein 3a Family: Soluble domain of poliovirus core protein 3a
9	c1ng7A_	 Alignment		25.8	24	PDB header: viral protein Chain: A; PDB Molecule: genome polyprotein [core protein p3a]; PDBTitle: the solution structure of the soluble domain of poliovirus2 3a protein
10	c5yz4A_	 Alignment		24.8	18	PDB header: hydrolase Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
11	c6hlwB_	 Alignment		22.5	32	PDB header: viral protein Chain: B; PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)

12	c6ei9A_	Alignment		22.1	17	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
13	c6hltD_	Alignment		21.2	21	PDB header: viral protein Chain: D: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)
14	c4k3zA_	Alignment		21.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: d-erythrose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
15	c2hu4D_	Alignment		19.5	46	PDB header: hydrolase Chain: D: PDB Molecule: neuraminidase; PDBTitle: n1 neuraminidase in complex with oseltamivir 2
16	c4hzvA_	Alignment		19.0	37	PDB header: hydrolase Chain: A: PDB Molecule: neuraminidase; PDBTitle: the crystal structure of influenza a neuraminidase n3
17	c6hmvB_	Alignment		18.4	21	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, lvvy mutant)
18	c4zm6A_	Alignment		16.3	16	PDB header: hydrolase, transferase Chain: A: PDB Molecule: n-acetyl-beta-d glucosaminidase; PDBTitle: a unique gcn5-related glucosamine n-acetyltransferase region exist in2 the fungal multi-domain gh3 beta-n-acetylglucosaminidase
19	d2cyga1	Alignment		16.2	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
20	c4omhA_	Alignment		15.9	30	PDB header: lyase Chain: A: PDB Molecule: geranylgeranyl diphosphate cyclase; PDBTitle: crystal structure of the bacterial diterpene cyclase cotb2 variant2 f149l
21	c4qn3B_	Alignment	not modelled	15.5	46	PDB header: hydrolase Chain: B: PDB Molecule: neuraminidase; PDBTitle: crystal structure of neuraminidase n7
22	c2i2xD_	Alignment	not modelled	14.8	19	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
23	c2htuA_	Alignment	not modelled	14.8	46	PDB header: hydrolase Chain: A: PDB Molecule: neuraminidase; PDBTitle: n8 neuraminidase in complex with peramivir
24	d1vhna_	Alignment	not modelled	14.2	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
25	d3bula2	Alignment	not modelled	13.7	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
26	c4b7qD_	Alignment	not modelled	12.7	38	PDB header: hydrolase Chain: D: PDB Molecule: neuraminidase; PDBTitle: h1n1 2009 pandemic influenza virus: resistance of the i223r2 neuraminidase mutant explained by kinetic and structural analysis
27	d1f8ea_	Alignment	not modelled	12.5	31	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
28	d1ft8a2	Alignment	not modelled	12.3	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Non-canonical RBD domain
						PDB header: viral protein

29	c4k3yA_	Alignment	not modelled	12.3	15	Chain: A; PDB Molecule: neuraminidase; PDBTitle: crystal structure of a subtype n11 neuraminidase-like protein of 2 a/flat-faced bat/peru/033/2010 (h18n11)
30	c5aheA_	Alignment	not modelled	12.2	9	PDB header: isomerase Chain: A; PDB Molecule: PDBTitle: crystal structure of salmonella enterica hisa
31	c3salB_	Alignment	not modelled	12.2	38	PDB header: hydrolase Chain: B; PDB Molecule: neuraminidase; PDBTitle: crystal structure of influenza a virus neuraminidase n5
32	d1vk3a4	Alignment	not modelled	11.9	24	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
33	c1nmbN_	Alignment	not modelled	11.9	31	PDB header: complex (hydrolase/immunoglobulin) Chain: N; PDB Molecule: n9 neuraminidase; PDBTitle: the structure of a complex between the nc10 antibody and influenza2 virus neuraminidase and comparison with the overlapping binding site3 of the nc41 antibody
34	c2qezC_	Alignment	not modelled	11.8	18	PDB header: lyase Chain: C; PDB Molecule: ethanolamine ammonia-lyase heavy chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase heavy chain2 (yp_013784.1) from listeria monocytogenes 4b f2365 at 2.15 a3 resolution
35	c3i8oA_	Alignment	not modelled	11.6	17	PDB header: rna binding protein Chain: A; PDB Molecule: kh domain-containing protein mj1533; PDBTitle: a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
36	c4fvkA_	Alignment	not modelled	11.5	22	PDB header: hydrolase Chain: A; PDB Molecule: neuraminidase; PDBTitle: structural and functional characterization of neuraminidase-like2 molecule n10 derived from bat influenza a virus
37	c6crdG_	Alignment	not modelled	11.2	31	PDB header: viral protein/hydrolase Chain: G; PDB Molecule: tetrabrachion,neuraminidase; PDBTitle: influenza virus neuraminidase subtype n9 (tern) with tetrabrachion2 (tb) domain stalk
38	c2yxba_	Alignment	not modelled	10.7	20	PDB header: isomerase Chain: A; PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
39	c4jgiB_	Alignment	not modelled	10.5	14	PDB header: protein binding Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
40	c2ltmA_	Alignment	not modelled	10.5	17	PDB header: electron transport Chain: A; PDB Molecule: nfu1 iron-sulfur cluster scaffold homolog, mitochondrial; PDBTitle: solution nmr structure of nfu1 iron-sulfur cluster scaffold homolog2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr2876b
41	c1w21D_	Alignment	not modelled	10.2	28	PDB header: hydrolase Chain: D; PDB Molecule: neuraminidase; PDBTitle: structure of neuraminidase from english duck subtype n6 complexed with2 30 mm sialic acid (nana, neu5ac), crystal soaked for 43 hours at 2913 k.
42	c5c4nD_	Alignment	not modelled	9.8	12	PDB header: oxidoreductase Chain: D; PDB Molecule: precorrin-6a reductase; PDBTitle: cobk precorrin-6a reductase
43	c2penE_	Alignment	not modelled	9.6	17	PDB header: chaperone Chain: E; PDB Molecule: orf134; PDBTitle: crystal structure of rbcx, crystal form i
44	d2peqa1	Alignment	not modelled	9.6	17	Fold: RbcX-like Superfamily: RbcX-like Family: RbcX-like
45	d1gtea2	Alignment	not modelled	9.1	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
46	d1ccwa_	Alignment	not modelled	8.8	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
47	c4ot7A_	Alignment	not modelled	8.5	15	PDB header: oxidoreductase Chain: A; PDB Molecule: snadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
48	d1zhva2	Alignment	not modelled	7.9	35	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
49	d2aepa1	Alignment	not modelled	7.5	33	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
50	c2iw0A_	Alignment	not modelled	7.3	21	PDB header: hydrolase Chain: A; PDB Molecule: chitin deacetylase; PDBTitle: structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
51	d1tr9a_	Alignment	not modelled	7.3	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
52	c3tiaC_	Alignment	not modelled	7.2	46	PDB header: hydrolase/hydrolase inhibitor Chain: C; PDB Molecule: neuraminidase; PDBTitle: crystal structure of 1957 pandemic h2n2 neuraminidase complexed with2 laninamivir
53	d1ivga_	Alignment	not modelled	7.2	46	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
54	c4hb0B_	Alignment	not modelled	7.1	14	PDB header: flavoprotein,signaling protein Chain: B; PDB Molecule: appa protein;

54	c9mrvB	Alignment	not modelled	7.1	14	PDBTitle: dark-state structure of appa c20s without the cys-rich region from rb.2 sphaeroides
55	d1lyjb1	Alignment	not modelled	7.1	17	Fold: BRCA2 helical domain Superfamily: BRCA2 helical domain Family: BRCA2 helical domain
56	c3ezxA	Alignment	not modelled	7.1	19	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
57	c6djC	Alignment	not modelled	6.8	32	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of acric2 dimer in complex with partial nme1cas9
58	c5zknA	Alignment	not modelled	6.7	14	PDB header: isomerase Chain: A: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
59	c5ncdA	Alignment	not modelled	6.5	13	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the polysaccharide deacetylase bc1974 from2 bacillus cereus in complex with (2s)-2-amino-5-3 (diaminomethylideneamino)-n-hydroxypentanamide
60	d2py8a1	Alignment	not modelled	6.5	21	Fold: RbcX-like Superfamily: RbcX-like Family: RbcX-like
61	c4alzA	Alignment	not modelled	6.5	17	PDB header: membrane protein Chain: A: PDB Molecule: yop proteins translocation protein d; PDBTitle: the yersinia t3ss basal body component yscd reveals a different2 structural periplasmic domain organization to known homologue prgh
62	d1euca1	Alignment	not modelled	6.2	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
63	c3nmeA	Alignment	not modelled	6.2	13	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
64	d2ggpb1	Alignment	not modelled	6.0	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
65	d1fmfa	Alignment	not modelled	5.9	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
66	d1xhba2	Alignment	not modelled	5.8	4	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
67	c2hxgB	Alignment	not modelled	5.8	5	PDB header: isomerase Chain: B: PDB Molecule: l-arabinose isomerase; PDBTitle: crystal structure of mn2+ bound ecai
68	c4g6cA	Alignment	not modelled	5.8	8	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase 1; PDBTitle: crystal structure of beta-hexosaminidase 1 from burkholderia2 cenocepacia j2315
69	c4kdiC	Alignment	not modelled	5.8	21	PDB header: signaling protein/hydrolase Chain: C: PDB Molecule: ubiquitin thioesterase otu1; PDBTitle: crystal structure of p97/vcp n in complex with otu1 ubxl
70	c3g5IA	Alignment	not modelled	5.8	14	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
71	c2dc1A	Alignment	not modelled	5.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
72	d1koha2	Alignment	not modelled	5.7	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Non-canonical RBD domain
73	c4mj7B	Alignment	not modelled	5.6	19	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
74	c1bmtB	Alignment	not modelled	5.6	19	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
75	c5jppd	Alignment	not modelled	5.6	14	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
76	c2y8uA	Alignment	not modelled	5.4	19	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: a. nidulans chitin deacetylase
77	c4r9xB	Alignment	not modelled	5.4	10	PDB header: metal transport Chain: B: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of putative copper homeostasis protein cutc from2 bacillus anthracis
78	c3a9IB	Alignment	not modelled	5.3	12	PDB header: hydrolase Chain: B: PDB Molecule: poly-gamma-glutamate hydrolase; PDBTitle: structure of bacteriophage poly-gamma-glutamate hydrolase
79	c4gr2A	Alignment	not modelled	5.3	20	PDB header: chaperone Chain: A: PDB Molecule: atrbcx1; PDBTitle: structure of atrbcx1 from arabidopsis thaliana.

80	c3pl0B_	Alignment	not modelled	5.2	36	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution
81	c2py8B_	Alignment	not modelled	5.2	14	PDB header: chaperone Chain: B: PDB Molecule: hypothetical protein rbcx; PDBTitle: rbcx
82	c1mjeA_	Alignment	not modelled	5.2	17	PDB header: gene regulation/antitumor protein/dna Chain: A: PDB Molecule: breast cancer 2; PDBTitle: structure of a brca2-dss1-ssdna complex
83	c5z34A_	Alignment	not modelled	5.1	9	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: the structure of a chitin deacetylase from bombyx mori provide the2 first insight into insect chitin deacetylation mechanism
84	d2axpa1	Alignment	not modelled	5.1	54	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
85	c1mbbA_	Alignment	not modelled	5.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase