


























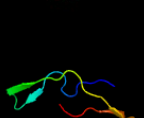





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3215_(entC)_3592251_3593369
Date	Thu Aug 8 16:20:41 BST 2019
Unique Job ID	e5e55da82e086e69

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3os6A_	 Alignment		100.0	39	PDB header: isomerase Chain: A: PDB Molecule: isochorismate synthase dhbc; PDBTitle: crystal structure of putative 2,3-dihydroxybenzoate-specific2 isochorismate synthase, dhbc from bacillus anthracis.
2	c3hwoB_	 Alignment		100.0	41	PDB header: isomerase Chain: B: PDB Molecule: isochorismate synthase entc; PDBTitle: crystal structure of escherichia coli enterobactin-specific2 isochorismate synthase entc in complex with isochorismate
3	d3bzna1	 Alignment		100.0	30	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
4	d1qdlA_	 Alignment		100.0	28	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
5	d2fn0a1	 Alignment		100.0	25	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
6	c3gseA_	 Alignment		100.0	26	PDB header: isomerase Chain: A: PDB Molecule: menaquinone-specific isochorismate synthase; PDBTitle: crystal structure of menaquinone-specific isochorismate synthase from2 yersinia pestis co92
7	c4penA_	 Alignment		100.0	29	PDB header: lyase Chain: A: PDB Molecule: anthranilate synthase component 1; PDBTitle: structure of anthranilate synthase component i (trpe) from2 mycobacterium tuberculosis with inhibitor bound
8	d2g5fa1	 Alignment		100.0	29	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
9	d1l1qa_	 Alignment		100.0	27	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
10	d1i7qa_	 Alignment		100.0	26	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
11	c3r74B_	 Alignment		100.0	22	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383

12	c3h9mA	Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: p-aminobenzoate synthetase, component i; PDBTitle: crystal structure of para-aminobenzoate synthetase, component i from <i>Mycobacterium tuberculosis</i>
13	c2i6yA	Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: anthranilate synthase component i, putative; PDBTitle: structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbti
14	c4grhA	Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: aminodeoxychorismate synthase; PDBTitle: crystal structure of pabb of <i>Stenotrophomonas maltophilia</i>
15	c5kckA	Alignment		100.0	31	PDB header: lyase Chain: A: PDB Molecule: anthranilate synthase component i; PDBTitle: crystal structure of anthranilate synthase component i from <i>Streptococcus pneumoniae</i> tigr4
16	d1k0ga	Alignment		100.0	25	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
17	c3nqkA	Alignment		37.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a structural genomics, unknown function2 (bacova_03322) from <i>Bacteroides ovatus</i> at 2.61 Å resolution
18	d2ffca1	Alignment		29.2	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
19	d1hxra	Alignment		28.0	22	Fold: Mss4-like Superfamily: Mss4-like Family: RabGEF Mss4
20	d2fu5a1	Alignment		27.8	22	Fold: Mss4-like Superfamily: Mss4-like Family: RabGEF Mss4
21	c4anrA	Alignment	not modelled	20.6	40	PDB header: lyase Chain: A: PDB Molecule: soluble lytic transglycosylase b; PDBTitle: crystal structure of soluble lytic transglycosylase sltb12 from <i>Pseudomonas aeruginosa</i>
22	c4aq2l	Alignment	not modelled	19.1	23	PDB header: oxidoreductase Chain: I: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: resting state of homogentisate 1,2-dioxygenase
23	d1qusa	Alignment	not modelled	18.4	30	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
24	c3dupB	Alignment	not modelled	15.7	19	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family hydrolase from <i>Rhodospirillum rubrum</i> atcc 11170
25	c4k6nA	Alignment	not modelled	15.7	10	PDB header: lyase Chain: A: PDB Molecule: aminodeoxychorismate lyase; PDBTitle: crystal structure of yeast 4-amino-4-deoxychorismate lyase
26	d2q8za1	Alignment	not modelled	15.6	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
27	c5n81B	Alignment	not modelled	14.2	14	PDB header: ligase Chain: B: PDB Molecule: tyrocidine synthase 1; PDBTitle: crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
28	c5anzA	Alignment	not modelled	14.2	37	PDB header: hydrolase Chain: A: PDB Molecule: soluble lytic transglycosylase b3; PDBTitle: crystal structure of sltb3 from <i>Pseudomonas aeruginosa</i> .
29	c5nwtM	Alignment	not modelled	14.0	25	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54

						PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
30	d1d5ta2	Alignment	not modelled	13.0	36	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like
31	c2nbpA	Alignment	not modelled	12.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: selenoprotein w; PDBTitle: nmr solution structure of mouse selw
32	c2km1A	Alignment	not modelled	11.8	22	PDB header: protein binding Chain: A: PDB Molecule: protein dre2; PDBTitle: solution structure of the n-terminal domain of the yeast protein dre2
33	d2qdya1	Alignment	not modelled	11.1	12	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
34	c3a10B	Alignment	not modelled	10.9	37	PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
35	c4p55A	Alignment	not modelled	9.8	35	PDB header: dna binding protein Chain: A: PDB Molecule: viral irf2-like protein; PDBTitle: crystal structure of dna binding domain of k11 from kshv
36	c5byhM	Alignment	not modelled	9.6	25	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
37	c5t3pB	Alignment	not modelled	9.5	12	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal coenzyme a diphosphatase nudt7; PDBTitle: crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
38	c2vu4A	Alignment	not modelled	9.0	15	PDB header: photosynthesis Chain: A: PDB Molecule: oxygen-evolving enhancer protein 2; PDBTitle: structure of psbp protein from spinacia oleracea at 1.98 a2 resolution
39	d1ugpa	Alignment	not modelled	8.7	19	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
40	c6a2uA	Alignment	not modelled	8.4	33	PDB header: signaling protein/oxidoreductase Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
41	c6hu9r	Alignment	not modelled	8.4	18	PDB header: oxidoreductase/electron transport Chain: R: PDB Molecule: cytochrome b-c1 complex subunit 7; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
42	d1xe7a	Alignment	not modelled	8.1	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like
43	d2czda1	Alignment	not modelled	7.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
44	d1eyba	Alignment	not modelled	7.8	28	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Homogentisate dioxygenase
45	c1ey2A	Alignment	not modelled	7.8	28	PDB header: oxidoreductase Chain: A: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: human homogentisate dioxygenase with fe(ii)
46	c2jo8B	Alignment	not modelled	7.6	28	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
47	c2lnjA	Alignment	not modelled	7.5	13	PDB header: photosynthesis Chain: A: PDB Molecule: putative uncharacterized protein sll1418; PDBTitle: solution structure of cyanobacterial psbp (cyanop) from synechocystis2 sp. pcc 6803
48	c410nG	Alignment	not modelled	7.5	36	PDB header: transferase Chain: G: PDB Molecule: serine/threonine-protein kinase 3; PDBTitle: crystal structure of stk3 (mst2) sarah domain
49	c5burB	Alignment	not modelled	7.4	28	PDB header: ligase Chain: B: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: o-succinylbenzoate coenzyme a synthetase (mene) from bacillus2 subtilis, in complex with atp and magnesium ion
50	d1v29a	Alignment	not modelled	7.3	17	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
51	d2bcgg3	Alignment	not modelled	7.1	36	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like
52	d1rd5a	Alignment	not modelled	6.4	27	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
53	c4d56A	Alignment	not modelled	6.2	19	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
54	c4bhqA	Alignment	not modelled	6.2	23	PDB header: cell adhesion Chain: A: PDB Molecule: competence protein piln; PDBTitle: structure of the periplasmic domain of the piln type iv2 pilus biogenesis protein from thermus thermophilus
55	d2c1wa1	Alignment	not modelled	6.1	50	Fold: EndoU-like Superfamily: EndoU-like Family: Eukaryotic EndoU ribonuclease

56	c3tfxB_	Alignment	not modelled	6.1	26	PDB header: lyase Chain: B: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
57	c3c66B_	Alignment	not modelled	6.1	27	PDB header: transferase Chain: B: PDB Molecule: poly(a) polymerase; PDBTitle: yeast poly(a) polymerase in complex with fip1 residues 80-105
58	c6bn1A_	Alignment	not modelled	5.9	23	PDB header: signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase hippo; PDBTitle: salvador hippo sarah domain complex
59	c2k27A_	Alignment	not modelled	5.9	19	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
60	c3fuyC_	Alignment	not modelled	5.9	26	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative integron gene cassette protein; PDBTitle: structure from the mobile metagenome of cole harbour salt marsh:2 integron cassette protein hfx_cass1
61	c2zbtB_	Alignment	not modelled	5.7	33	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
62	c1ypxA_	Alignment	not modelled	5.7	6	PDB header: transferase Chain: A: PDB Molecule: putative vitamin-b12 independent methionine synthase family PDBTitle: crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
63	c3qyhG_	Alignment	not modelled	5.7	23	PDB header: lyase Chain: G: PDB Molecule: co-type nitrile hydratase alpha subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-h711 from2 pseudomonas putida.
64	c1gw4A_	Alignment	not modelled	5.6	33	PDB header: high density lipoproteins Chain: A: PDB Molecule: apoa-i; PDBTitle: the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
65	c5dz8A_	Alignment	not modelled	5.5	21	PDB header: cell adhesion Chain: A: PDB Molecule: bspa (bspa_v); PDBTitle: streptococcus agalactiae agi/ii polypeptide bspa variable (v) domain
66	c4lqcA_	Alignment	not modelled	5.4	33	PDB header: ligase Chain: A: PDB Molecule: bile acid-coenzyme a ligase; PDBTitle: crystal structure of a bile acid-coenzyme a ligase (baib) from2 clostridium scindens (vpi 12708) at 2.19 a resolution
67	c2nv2U_	Alignment	not modelled	5.4	27	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
68	c3femB_	Alignment	not modelled	5.3	33	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
69	c4nm0B_	Alignment	not modelled	5.2	47	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of peptide inhibitor-free gsk-3/axin complex
70	c4ccfD_	Alignment	not modelled	5.1	38	PDB header: viral protein Chain: D: PDB Molecule: fusion glycoprotein f0; PDBTitle: structure of respiratory syncytial virus f protein head domain
71	d1n0ea_	Alignment	not modelled	5.0	7	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ