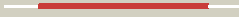


















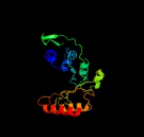




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2178c_aroG_2440340_2441728
Date	Mon Aug 5 13:25:30 BST 2019
Unique Job ID	9dfda8afe7102da9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2b7oa1	 Alignment		100.0	97	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
2	c5hudA	 Alignment		100.0	66	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate (dahp) PDBTitle: non-covalent complex of and dahp synthase and chorismate mutase from2 corynebacterium glutamicum with bound transition state analog
3	c5uxmA	 Alignment		100.0	50	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
4	c6bmcA	 Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: the structure of a dimeric type ii dah7ps associated with pyocyanin2 biosynthesis in pseudomonas aeruginosa
5	c4hsnA	 Alignment		98.5	25	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: crystal structure of dah7ps from neisseria meningitidis
6	d1n8fa	 Alignment		98.3	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
7	d1of8a	 Alignment		98.2	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
8	c3tqkA	 Alignment		98.2	26	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
9	c1ofaB	 Alignment		98.0	25	PDB header: lyase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: crystal structure of the tyrosine-regulated2 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase3 from saccharomyces cerevisiae in complex with4 phosphoenolpyruvate and cobalt(ii)
10	c6agmA	 Alignment		97.9	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase, tyr-sensitive; PDBTitle: molecular basis for feedback inhibition of tyrosine-regulated 3-deoxy-2 d-arabino-heptulosonate-7-phosphate synthase from escherichia coli
11	c4lu0A	 Alignment		96.6	10	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of 2-keto-3-deoxy-d-manno-octulosonate-8-phosphate2 synthase from pseudomonas aeruginosa.

12	c1zcoA_	Alignment		95.9	18	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphoheptonate aldolase; PDBTitle: crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
13	c6mdyC_	Alignment		95.8	14	PDB header: hydrolase Chain: C: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a 2-dehydro-3-deoxyphosphooctonate aldolase from2 legionella pneumophila philadelphia 1
14	c1vs1B_	Alignment		95.7	19	PDB header: transferase Chain: B: PDB Molecule: 3-deoxy-7-phosphoheptulonate synthase; PDBTitle: crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
15	d1vr6a1	Alignment		93.6	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
16	c3stgA_	Alignment		93.0	16	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
17	d2a21a1	Alignment		90.6	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
18	c3nvtA_	Alignment		88.5	16	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
19	c3s6oD_	Alignment		88.1	18	PDB header: hydrolase Chain: D: PDB Molecule: polysaccharide deacetylase family protein; PDBTitle: crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
20	d1d9ea_	Alignment		86.6	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
21	c4z1bA_	Alignment	not modelled	85.1	18	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: structure of h204a mutant kdo8ps from h.pylori
22	c3fs2A_	Alignment	not modelled	84.5	16	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 brucella melitensis at 1.85a resolution
23	c3gr7A_	Alignment	not modelled	83.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
24	c1ofpA_	Alignment	not modelled	81.9	23	PDB header: lyase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: crystal structure of the tyrosine-regulated 3-deoxy-d-arabino-2 heptulosonate-7-phosphate synthase from saccharomyces cerevisiae
25	d1o6oA_	Alignment	not modelled	80.6	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
26	c3sz8D_	Alignment	not modelled	76.6	15	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
27	c6bngB_	Alignment	not modelled	75.4	9	PDB header: transferase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 acinetobacter baumannii
						PDB header: oxidoreductase

28	c3hf3A_	Alignment	not modelled	69.2	20	Chain: A; PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
29	d1z41a1	Alignment	not modelled	68.7	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
30	c4qn9A_	Alignment	not modelled	67.0	16	PDB header: hydrolase Chain: A; PDB Molecule: n-acyl-phosphatidylethanolamine-hydrolyzing phospholipase PDBTitle: structure of human nape-pld
31	c4gtnA_	Alignment	not modelled	66.5	18	PDB header: transferase Chain: A; PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi
32	d1uuma_	Alignment	not modelled	65.4	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
33	c5trwA_	Alignment	not modelled	59.5	22	PDB header: transferase Chain: A; PDB Molecule: pyridoxal kinase pdxy; PDBTitle: crystal structure of pyridoxamine kinase pdxy from burkholderia2 xenovorans
34	c5ocsB_	Alignment	not modelled	59.4	15	PDB header: flavoprotein Chain: B; PDB Molecule: putative nadh-depndent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
35	c3qbuD_	Alignment	not modelled	59.1	20	PDB header: hydrolase Chain: D; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of putative peptidoglycan deactylase (hp0310) from2 helicobacter pylori
36	c3t4cD_	Alignment	not modelled	53.1	14	PDB header: transferase Chain: D; PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 1; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
37	d2nu7b1	Alignment	not modelled	52.2	18	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
38	d1vi9a_	Alignment	not modelled	45.2	24	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
39	c3kruC_	Alignment	not modelled	45.2	21	PDB header: oxidoreductase Chain: C; PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
40	d1ps9a1	Alignment	not modelled	42.7	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
41	c3rxzA_	Alignment	not modelled	39.7	21	PDB header: hydrolase Chain: A; PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
42	c5b6aA_	Alignment	not modelled	39.4	19	PDB header: transferase Chain: A; PDB Molecule: pyridoxal kinase pdxy; PDBTitle: structure of pyridoxal kinasefrom pseudomonas aeruginosa
43	c1tv5A_	Alignment	not modelled	37.7	33	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
44	d1tv5a1	Alignment	not modelled	37.7	33	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
45	c4qg5D_	Alignment	not modelled	37.6	28	PDB header: isomerase Chain: D; PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
46	c5z34A_	Alignment	not modelled	37.6	13	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
47	d2hiya1	Alignment	not modelled	36.8	12	Fold: SP0830-like Superfamily: SP0830-like Family: SP0830-like
48	c6b8sB_	Alignment	not modelled	36.2	15	PDB header: oxidoreductase Chain: B; PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn
49	d1z7aa1	Alignment	not modelled	35.2	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: PA1517-like
50	d1icpa_	Alignment	not modelled	32.0	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
51	c2ymbB_	Alignment	not modelled	31.4	17	PDB header: protein transport Chain: B; PDB Molecule: mit domain-containing protein 1; PDBTitle: structures of mitd1
52	c1ps9A_	Alignment	not modelled	30.6	15	PDB header: oxidoreductase Chain: A; PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
53	c2ymbC_	Alignment	not modelled	29.5	17	PDB header: protein transport Chain: C; PDB Molecule: mit domain-containing protein 1; PDBTitle: structures of mitd1
						PDB header: transferase

54	c3pg8B_	Alignment	not modelled	28.1	19	Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
55	c6qkgB_	Alignment	not modelled	24.4	17	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
56	d1d3ga_	Alignment	not modelled	24.1	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
57	d1xima_	Alignment	not modelled	23.8	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
58	c4q5uC_	Alignment	not modelled	23.7	33	PDB header: calcium binding protein/protein binding Chain: C: PDB Molecule: serine/threonine-protein phosphatase 2b catalytic subunit PDBTitle: structure of calmodulin bound to its recognition site from calcineurin
59	d1vyra_	Alignment	not modelled	23.6	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
60	c4ay8B_	Alignment	not modelled	23.5	17	PDB header: transferase Chain: B: PDB Molecule: methylcobalamin\; coenzyme m methyltransferase; PDBTitle: semet-derivative of a methyltransferase from m. mazei
61	d1ccwa_	Alignment	not modelled	23.3	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
62	d1e3ha5	Alignment	not modelled	23.2	58	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
63	c5wtqB_	Alignment	not modelled	22.7	20	PDB header: chaperone Chain: B: PDB Molecule: proteasome assembly chaperone 4; PDBTitle: crystal structure of human proteasome-assembling chaperone pac4
64	d1lhpa_	Alignment	not modelled	21.7	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
65	c2fptA_	Alignment	not modelled	21.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors
66	c5znsA_	Alignment	not modelled	20.8	17	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: insect chitin deacetylase
67	c2we7A_	Alignment	not modelled	20.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
68	c2ziB_	Alignment	not modelled	20.2	37	PDB header: metal binding protein Chain: B: PDB Molecule: serine/threonine-protein phosphatase 2b PDBTitle: structure of calmodulin complexed with the calmodulin2 binding domain of calcineurin
69	d2o3la1	Alignment	not modelled	19.5	28	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
70	c3k30B_	Alignment	not modelled	19.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiodes simplex
71	d1vfga1	Alignment	not modelled	19.3	46	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like
72	d1eucb1	Alignment	not modelled	19.1	14	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
73	d1kfia2	Alignment	not modelled	19.1	18	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
74	d1ob0a2	Alignment	not modelled	18.7	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
75	c5jp6A_	Alignment	not modelled	18.4	25	PDB header: hydrolase Chain: A: PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
76	d2hh6a1	Alignment	not modelled	17.9	29	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
77	c1y80A_	Alignment	not modelled	17.6	20	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
78	c4a3uB_	Alignment	not modelled	17.5	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh\;flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
79	c2r28D_	Alignment	not modelled	17.2	37	PDB header: metal binding protein/hydrolase Chain: D: PDB Molecule: serine/threonine-protein phosphatase 2b PDBTitle: the complex structure of calmodulin bound to a calcineurin2 peptide
80	d1miwa1	Alignment	not modelled	17.2	38	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like

					Family: Poly A polymerase C-terminal region-like
81	d1ud2a2	Alignment	not modelled	17.0	11 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
82	c6omzA	Alignment	not modelled	16.7	16 PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
83	d2iw0a1	Alignment	not modelled	16.2	14 Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
84	c3bv6D	Alignment	not modelled	15.7	33 PDB header: hydrolase Chain: D: PDB Molecule: metal-dependent hydrolase; PDBTitle: crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold
85	d1k47a2	Alignment	not modelled	15.6	8 Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Phosphomevalonate kinase (PMK)
86	c4muoB	Alignment	not modelled	15.5	16 PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein ybib; PDBTitle: the trpd2 enzyme from e.coli: ybib
87	c3hvyC	Alignment	not modelled	15.4	15 PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase family protein, ynbb b.subtilis PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
88	c3mbjA	Alignment	not modelled	15.2	9 PDB header: transferase Chain: A: PDB Molecule: putative phosphomethylpyrimidine kinase; PDBTitle: crystal structure of a putative phosphomethylpyrimidine kinase2 (bt_4458) from bacteroides thetaiotaomicron vpi-5482 at 2.10 a3 resolution (rhombohedral form)
89	c2yewL	Alignment	not modelled	15.2	23 PDB header: virus Chain: I: PDB Molecule: e2 envelope glycoprotein; PDBTitle: modeling barmah forest virus structural proteins
90	d1v1ha1	Alignment	not modelled	14.9	31 Fold: Triple beta-spiral Superfamily: Fibre shaft of virus attachment proteins Family: Adenovirus
91	c2wltA	Alignment	not modelled	14.7	15 PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: the crystal structure of helicobacter pylori l-asparaginase at 1.4 a2 resolution
92	c5b42A	Alignment	not modelled	14.7	30 PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
93	c5il0B	Alignment	not modelled	14.0	16 PDB header: rna binding protein Chain: B: PDB Molecule: mettl14; PDBTitle: crystal structural of the mettl3-mettl14 complex for n6-adenosine2 methylation
94	c1miyB	Alignment	not modelled	13.9	38 PDB header: translation, transferase Chain: B: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
95	c3ufxG	Alignment	not modelled	13.9	7 PDB header: ligase Chain: G: PDB Molecule: succinyl-coa synthetase beta subunit; PDBTitle: thermus aquaticus succinyl-coa synthetase in complex with gdp-mn2+
96	c4jicB	Alignment	not modelled	13.6	22 PDB header: oxidoreductase Chain: B: PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
97	d1f76a	Alignment	not modelled	13.5	19 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
98	c1vfgB	Alignment	not modelled	13.3	46 PDB header: transferase/rna Chain: B: PDB Molecule: poly a polymerase; PDBTitle: crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
99	c5du2B	Alignment	not modelled	13.3	33 PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase