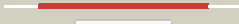



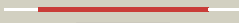


















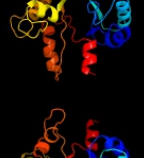


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2498c_(citE)_2812365_2813186
Date	Wed Aug 7 12:50:12 BST 2019
Unique Job ID	3f053cd394eecbae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6arbA_	 Alignment		100.0	100	PDB header: lyase Chain: A: PDB Molecule: citrate lyase subunit beta-like protein; PDBTitle: crystal structure of protein cite from mycobacterium tuberculosis in2 complex with magnesium, pyruvate and coenzyme a
2	c4l7zC_	 Alignment		100.0	28	PDB header: lyase Chain: C: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of chloroflexus aurantiacus malyl-coa lyase
3	c5vxsF_	 Alignment		100.0	35	PDB header: lyase Chain: F: PDB Molecule: citrate lyase subunit beta-like protein, mitochondrial; PDBTitle: crystal structure analysis of human clybl in apo form
4	c4roqA_	 Alignment		100.0	31	PDB header: lyase Chain: A: PDB Molecule: malyl-coa lyase/beta-methylmalyl-coa lyase; PDBTitle: crystal structure of malyl-coa lyase from methylobacterium extorquens
5	c4l9zA_	 Alignment		100.0	33	PDB header: lyase Chain: A: PDB Molecule: malyl-coa lyase; PDBTitle: crystal structure of rhodobacter sphaeroides malyl-coa lyase in2 complex with magnesium, oxalate, and coa
6	c3r4iB_	 Alignment		100.0	24	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of a citrate lyase (bx_e_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
7	c3pugA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: haloferax volcanii malate synthase native at 3mm glyoxylate
8	d1u5ha_	 Alignment		100.0	98	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
9	c3qqwC_	 Alignment		100.0	24	PDB header: lyase Chain: C: PDB Molecule: putative citrate lyase; PDBTitle: crystal structure of a putative lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
10	c1u5vA_	 Alignment		100.0	98	PDB header: lyase Chain: A: PDB Molecule: cite; PDBTitle: structure of cite complexed with triphosphate group of atp form2 mycobacterium tuberculosis
11	c3qllB_	 Alignment		100.0	37	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of ripc from yersinia pestis

12	c1sgjB	Alignment		100.0	32	PDB header: lyase Chain: B; PDB Molecule: citrate lyase, beta subunit; PDBTitle: crystal structure of citrate lyase beta subunit
13	d1sgja	Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
14	c3cuzA	Alignment		100.0	22	PDB header: transferase Chain: A; PDB Molecule: malate synthase a; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
15	c3cuxA	Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: malate synthase; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
16	d1dxea	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
17	c4tv6A	Alignment		100.0	22	PDB header: lyase Chain: A; PDB Molecule: 2-dehydro-3-deoxyglucarate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
18	c4mf4F	Alignment		100.0	25	PDB header: lyase Chain: F; PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpai aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
19	c4b5sB	Alignment		100.0	19	PDB header: lyase Chain: B; PDB Molecule: 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; PDBTitle: crystal structures of divalent metal dependent pyruvate aldolase,2 hpai, in complex with pyruvate
20	c2v5jB	Alignment		100.0	18	PDB header: lyase Chain: B; PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
21	c1izcA	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A; PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
22	d1izca	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
23	c6r62A	Alignment	not modelled	100.0	23	PDB header: lyase Chain: A; PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of a class ii pyruvate aldolase from sphingomonas2 wittichii rw1 in complex with hydroxypyruvate
24	c2vvtA	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A; PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
25	c3qz6A	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A; PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
26	c5vfbB	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B; PDB Molecule: malate synthase g; PDBTitle: 1.36 angstrom resolution crystal structure of malate synthase g from2 pseudomonas aeruginosa in complex with glycolic acid.
27	d1e0ta2	Alignment	not modelled	99.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
28	d1n8ia	Alignment	not modelled	99.9	23	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G

29	d1d8ca_	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
30	d1a3xa2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
31	d1pkla2	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
32	d2g50a2	Alignment	not modelled	99.7	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
33	d1liua2	Alignment	not modelled	99.7	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
34	c4fxjB_	Alignment	not modelled	99.4	19	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes m1/m2; PDBTitle: structure of m2 pyruvate kinase in complex with phenylalanine
35	c1e0tD_	Alignment	not modelled	99.2	20	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
36	c4imaD_	Alignment	not modelled	99.0	19	PDB header: transferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: the structure of c436m-hpyk in complex with citrate/mn/atp/fru-1,6-bp
37	d1h6za1	Alignment	not modelled	99.0	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
38	c2hroA_	Alignment	not modelled	99.0	19	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-length enzyme i of the pts system from <i>Staphylococcus carnosus</i>
39	c3khdC_	Alignment	not modelled	99.0	18	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
40	c5ws9C_	Alignment	not modelled	99.0	20	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase (pyk) from <i>Mycobacterium tuberculosis</i> in complex with 2 oxalate, ATP and allosteric activator AMP
41	c6du6D_	Alignment	not modelled	98.9	18	PDB header: transferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of the pyruvate kinase (pk1) from the mosquito <i>Aedes aegypti</i>
42	c1a3wB_	Alignment	not modelled	98.9	19	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from <i>Saccharomyces cerevisiae</i> complexed with fbp, pg, 2 mn2+ and k+
43	c1t5aB_	Alignment	not modelled	98.9	19	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
44	c1pkjB_	Alignment	not modelled	98.9	18	PDB header: transferase Chain: B: PDB Molecule: protein (pyruvate kinase); PDBTitle: the structure of <i>Leishmania</i> pyruvate kinase
45	c2hwgA_	Alignment	not modelled	98.9	19	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
46	c3e0vB_	Alignment	not modelled	98.9	19	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from <i>Leishmania mexicana</i> in 2 complex with sulphate ions
47	c2vgbB_	Alignment	not modelled	98.9	18	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
48	c1aqfB_	Alignment	not modelled	98.9	21	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
49	c3qtgA_	Alignment	not modelled	98.9	22	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from <i>Pyrobaculum aerophilum</i>
50	c2e28A_	Alignment	not modelled	98.8	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from <i>Bacillus stearothermophilus</i>
51	c2bg5C_	Alignment	not modelled	98.8	20	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter <i>Tengcongensis</i> pep: sugar3 phosphotransferase system (pts)
52	c3t07D_	Alignment	not modelled	98.8	18	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of <i>S. aureus</i> pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
53	c1h6zA_	Alignment	not modelled	98.7	22	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from <i>Trypanosoma brucei</i>
54	c3khdA_	Alignment	not modelled	98.7	17	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.

55	c3eoeC	Alignment	not modelled	98.7	20	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
56	d1vbga1	Alignment	not modelled	98.7	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
57	c3ma8A	Alignment	not modelled	98.6	14	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
58	c1vbhA	Alignment	not modelled	98.6	19	PDB header: transferase Chain: A: PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
59	c2olsA	Alignment	not modelled	98.5	16	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
60	c1kblA	Alignment	not modelled	98.4	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
61	d1kbla1	Alignment	not modelled	98.4	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
62	c3odmE	Alignment	not modelled	98.3	17	PDB header: lyase Chain: E: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: archaeal-type phosphoenolpyruvate carboxylase
63	c1jqoA	Alignment	not modelled	96.0	20	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
64	d1jqoa	Alignment	not modelled	96.0	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
65	d1jqna	Alignment	not modelled	95.9	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
66	c5nc8B	Alignment	not modelled	82.1	18	PDB header: transport protein Chain: B: PDB Molecule: potassium efflux system protein; PDBTitle: shewanella denitrificans kef ctd in amp bound form
67	d2hmva1	Alignment	not modelled	73.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
68	c2bdqA	Alignment	not modelled	72.6	15	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
69	c3lyeA	Alignment	not modelled	63.2	19	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
70	d1lssa	Alignment	not modelled	54.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
71	c4g65A	Alignment	not modelled	45.0	17	PDB header: transport protein Chain: A: PDB Molecule: trk system potassium uptake protein trka; PDBTitle: potassium transporter peripheral membrane component (trka) from vibrio2 vulnificus
72	c2c3zA	Alignment	not modelled	44.7	17	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
73	c3fa4D	Alignment	not modelled	44.1	18	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
74	c3c85A	Alignment	not modelled	39.9	7	PDB header: transport protein Chain: A: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
75	d1xi3a	Alignment	not modelled	35.3	16	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
76	c3eywA	Alignment	not modelled	34.3	19	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
77	d1qopa	Alignment	not modelled	31.6	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
78	c3fwzA	Alignment	not modelled	27.7	17	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ybal; PDBTitle: crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
79	d1lid1a	Alignment	not modelled	27.4	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
80	c4lsbA	Alignment	not modelled	25.4	14	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315

81	c1fcbA	Alignment	not modelled	24.2	13	PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
82	c2r94B	Alignment	not modelled	23.5	20	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
83	c6btmD	Alignment	not modelled	23.2	16	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
84	d1i4na	Alignment	not modelled	23.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
85	c2w91A	Alignment	not modelled	22.1	15	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-n-acetylglucosaminidase d; PDBTitle: structure of a streptococcus pneumoniae family 85 glycoside2 hydrolase, endo-d.
86	d1a53a	Alignment	not modelled	21.6	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
87	c4mg4G	Alignment	not modelled	21.4	13	PDB header: unknown function Chain: G: PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
88	c2g1uA	Alignment	not modelled	21.4	13	PDB header: transport protein Chain: A: PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
89	d1a0ea	Alignment	not modelled	21.4	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
90	d1o4ua1	Alignment	not modelled	21.3	14	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
91	c3gdbA	Alignment	not modelled	21.1	15	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein spr0440; PDBTitle: crystal structure of spr0440 glycoside hydrolase domain,2 endo-d from streptococcus pneumoniae r6
92	c5butG	Alignment	not modelled	21.0	13	PDB header: membrane protein Chain: G: PDB Molecule: ktr system potassium uptake protein a,ktr system potassium PDBTitle: crystal structure of inactive conformation of ktrab k+ transporter
93	c4e6zA	Alignment	not modelled	19.0	17	PDB header: transport protein Chain: A: PDB Molecule: apicoplast tic22, putative; PDBTitle: tic22 from plasmodium falciparum
94	c2ze3A	Alignment	not modelled	18.8	10	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
95	c4hpfB	Alignment	not modelled	18.3	13	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: potassium channel subfamily u member 1; PDBTitle: structure of the human slo3 gating ring
96	d2fy8a1	Alignment	not modelled	16.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
97	c6bmaA	Alignment	not modelled	16.4	15	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
98	c4gx5D	Alignment	not modelled	15.6	18	PDB header: transport protein Chain: D: PDB Molecule: trka domain protein; PDBTitle: gsuk channel
99	c3fhaD	Alignment	not modelled	15.6	31	PDB header: hydrolase Chain: D: PDB Molecule: endo-beta-n-acetylglucosaminidase; PDBTitle: structure of endo-beta-n-acetylglucosaminidase a