

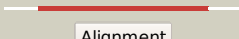

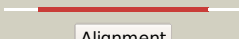





















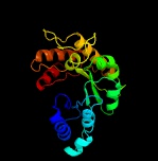






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1837c_glcB_2084763_2086988
Date	Fri Aug 2 13:30:45 BST 2019
Unique Job ID	3b0396c2214edd06

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5vfbB_	 Alignment		100.0	69	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.
2	d1n8ia_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
3	d1d8ca_	 Alignment		100.0	57	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
4	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
5	c3cuxA_	 Alignment		100.0	20	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
6	c4roqA_	 Alignment		99.9	21	PDB header: lyase Chain: A: PDB Molecule: malyl-coa lyase/beta-methylmalyl-coa lyase; PDBTitle: crystal structure of malyl-coa lyase from methylobacterium extorquens
7	c5vxsF_	 Alignment		99.9	21	PDB header: lyase Chain: F: PDB Molecule: citrate lyase subunit beta-like protein, mitochondrial; PDBTitle: crystal structure analysis of human clybl in apo form
8	c4l9zA_	 Alignment		99.9	20	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
9	c4l7zC_	 Alignment		99.8	21	PDB header: lyase Chain: C: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of chloroflexus aurantiacus malyl-coa lyase
10	c3pugA_	 Alignment		99.8	16	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: haloferax volcanii malate synthase native at 3mm glyoxylate
11	c6arbA_	 Alignment		99.7	24	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

12	c3qllB	Alignment		99.6	22	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of ripc from yersinia pestis
13	c3r4iB	Alignment		99.6	18	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
14	c1u5vA	Alignment		99.6	25	PDB header: lyase Chain: A: PDB Molecule: cite; PDBTitle: structure of cite complexed with triphosphate group of atp form2 mycobacterium tuberculosis
15	c3qqwC	Alignment		99.6	17	PDB header: lyase Chain: C: PDB Molecule: putative citrate lyase; PDBTitle: crystal structure of a putative lyase (reut_b4148) from ralstonia2 eutropha jmp1.34 at 2.44 a resolution
16	d1u5ha	Alignment		99.5	26	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpal aldolase
17	c1sgjB	Alignment		99.5	17	PDB header: lyase Chain: B: PDB Molecule: citrate lyase, beta subunit; PDBTitle: crystal structure of citrate lyase beta subunit
18	d1sgja	Alignment		99.5	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpal aldolase
19	c2hroA	Alignment		96.6	18	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-length enzyme i of the pts system from2 staphylococcus carnosus
20	c2hwgA	Alignment		96.6	15	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
21	c2bg5C	Alignment	not modelled	96.5	18	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
22	c4tv6A	Alignment	not modelled	96.5	15	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyglucarate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
23	d1dxea	Alignment	not modelled	96.2	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpal aldolase
24	c6r62A	Alignment	not modelled	96.1	16	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
25	c4mf4F	Alignment	not modelled	96.0	17	PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpal aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
26	c3qz6A	Alignment	not modelled	95.9	12	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
27	c4b5sB	Alignment	not modelled	95.1	20	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
28	c2v5iB	Alignment	not modelled	95.0	10	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid

28	c2v9jB	Alignment	not modelled	93.0	19	aldolase; PDB header: lyase
29	c2vwtA	Alignment	not modelled	94.5	13	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
30	d1vbga1	Alignment	not modelled	93.8	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
31	c1h6zA	Alignment	not modelled	92.1	16	PDB header: transferase Chain: A; PDB Molecule: pyruvate phosphate dikinase; PDBTitle: 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
32	d1h6za1	Alignment	not modelled	91.3	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
33	d1izca	Alignment	not modelled	91.1	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpal aldolase
34	c1izcA	Alignment	not modelled	91.1	17	PDB header: lyase Chain: A; PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
35	c2olsA	Alignment	not modelled	90.1	14	PDB header: transferase Chain: A; PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
36	d1e0ta2	Alignment	not modelled	90.0	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
37	d1kbla1	Alignment	not modelled	87.4	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
38	c1vbhA	Alignment	not modelled	86.6	18	PDB header: transferase Chain: A; PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
39	c1kblA	Alignment	not modelled	80.7	19	PDB header: transferase Chain: A; PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
40	d1a3xa2	Alignment	not modelled	74.2	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
41	d1liua2	Alignment	not modelled	60.9	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
42	d2g50a2	Alignment	not modelled	58.3	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
43	d1pkla2	Alignment	not modelled	55.5	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
44	d1rg6a	Alignment	not modelled	51.9	27	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
45	d1zela1	Alignment	not modelled	50.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like
46	d1mzha	Alignment	not modelled	44.7	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
47	c3pdmP	Alignment	not modelled	44.7	20	PDB header: virus Chain: P; PDB Molecule: coat protein; PDBTitle: hibiscus latent singapore virus
48	c5mrwG	Alignment	not modelled	42.3	27	PDB header: hydrolase Chain: G; PDB Molecule: potassium-transporting atpase kdpc subunit; PDBTitle: structure of the kdpcfbc complex
49	d1vtmp	Alignment	not modelled	40.3	12	Fold: Four-helical up-and-down bundle Superfamily: TMV-like viral coat proteins Family: TMV-like viral coat proteins
50	d1ei7a	Alignment	not modelled	40.1	16	Fold: Four-helical up-and-down bundle Superfamily: TMV-like viral coat proteins Family: TMV-like viral coat proteins
51	d1ub3a	Alignment	not modelled	35.4	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
52	c4hffB	Alignment	not modelled	34.6	14	PDB header: hydrolase Chain: B; PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of the type vi effector-immunity complex tae4-tai42 from salmonella typhimurium
53	c3ng3A	Alignment	not modelled	33.5	24	PDB header: lyase Chain: A; PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
54	c2kz6A	Alignment	not modelled	31.5	23	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2

55	c3ngjC_	Alignment	not modelled	28.6	11	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
56	d1gsma1	Alignment	not modelled	27.9	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
57	d1ic8a2	Alignment	not modelled	27.0	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
58	d1vcva1	Alignment	not modelled	26.6	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
59	c2q4oA_	Alignment	not modelled	23.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at2g37210/t2n18.3; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
60	d2q4oa1	Alignment	not modelled	23.9	24	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
61	c2gu1A_	Alignment	not modelled	21.7	37	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
62	c5xqgC_	Alignment	not modelled	20.8	20	PDB header: lyase Chain: C: PDB Molecule: pcrglx protein; PDBTitle: crystal structure of a pl 26 exo-rhamnogalacturonan lyase from2 penicillium chrysogenum complexed with unsaturated galacturonosyl3 rhamnose
63	c5ux5C_	Alignment	not modelled	20.5	19	PDB header: oxidoreductase/transferase Chain: C: PDB Molecule: bifunctional protein proline utilization a (puta); PDBTitle: structure of proline utilization a (puta) from corynebacterium2 freiburgense
64	c4gkgA_	Alignment	not modelled	20.4	43	PDB header: signaling protein Chain: A: PDB Molecule: c4-dicarboxylate transport sensor protein dctb; PDBTitle: crystal structure of the s-helix linker
65	c5dbul_	Alignment	not modelled	19.9	19	PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis
66	c4xbsA_	Alignment	not modelled	19.2	17	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
67	c5uz9D_	Alignment	not modelled	19.0	64	PDB header: immune system/rna Chain: D: PDB Molecule: crispr-associated protein csy3; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
68	c4uw8F_	Alignment	not modelled	18.7	23	PDB header: viral protein Chain: F: PDB Molecule: l-shaped tail fiber protein; PDBTitle: structure of the carboxy-terminal domain of the bacteriophage t5 l-2 shaped tail fiber with its intra-molecular chaperone domain
69	c3bd1B_	Alignment	not modelled	18.6	16	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
70	c3oa3A_	Alignment	not modelled	18.3	13	PDB header: lyase Chain: A: PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
71	c6b3nA_	Alignment	not modelled	18.2	31	PDB header: protein binding Chain: A: PDB Molecule: nleg5-1; PDBTitle: solution structure of the n-terminal domain of the effector nleg5-12 from escherichia coli o157:h7 str. sakai
72	c2pxgA_	Alignment	not modelled	17.4	18	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein; PDBTitle: nmr solution structure of omla
73	c2zzxD_	Alignment	not modelled	17.1	16	PDB header: transport protein Chain: D: PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in2 complex with lactate
74	c2zc2A_	Alignment	not modelled	16.6	12	PDB header: replication Chain: A: PDB Molecule: dnad-like replication protein; PDBTitle: crystal structure of dnad-like replication protein from streptococcus2 mutans ua159, gi 24377835, residues 127-199
75	d1z21a1	Alignment	not modelled	15.9	12	Fold: Type III secretion system domain Superfamily: Type III secretion system domain Family: YopR Core
76	d1vj7a2	Alignment	not modelled	15.9	33	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: RelA/SpoT domain
77	d1ev7a_	Alignment	not modelled	15.6	25	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease NaeI
78	c3ty8A_	Alignment	not modelled	15.3	21	PDB header: transferase Chain: A: PDB Molecule: polynucleotide 2',3'-cyclic phosphate phosphodiesterase / PDBTitle: crystal structure of c. thermocellum pnkp ligase domain apo form
79	d1t35a_	Alignment	not modelled	15.0	12	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like

80	d1gyxa_	Alignment	not modelled	14.8	21	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
81	d1wuua1	Alignment	not modelled	14.7	11	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
82	c3hlzA_	Alignment	not modelled	14.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bt_1490; PDBTitle: crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution
83	c4e6nC_	Alignment	not modelled	13.7	21	PDB header: protein binding Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of bacterial pnkp-c/hen1-n heterodimer
84	c4hfkB_	Alignment	not modelled	13.6	16	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the type vi effector-immunity complex tae4-tai42 from enterobacter cloacae
85	c2zkru_	Alignment	not modelled	13.4	33	PDB header: ribosomal protein/rna Chain: U: PDB Molecule: rna expansion segment es41; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
86	d1u04a1	Alignment	not modelled	13.0	80	Fold: SH3-like barrel Superfamily: PAZ domain Family: PAZ domain
87	d2jn4a1	Alignment	not modelled	12.7	21	Fold: NifT/FixU barrel-like Superfamily: NifT/FixU-like Family: NifT/FixU
88	c2jn4A_	Alignment	not modelled	12.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein fixu, nifT; PDBTitle: solution nmr structure of protein rp4601 from rhodospseudomonas2 palustris. northeast structural genomics consortium target rpt2;3 ontario center for structural proteomics target rp4601.
89	d1o0ya_	Alignment	not modelled	12.7	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
90	c2vy2A_	Alignment	not modelled	12.7	41	PDB header: transcription Chain: A: PDB Molecule: protein leafy; PDBTitle: structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter
91	d1umya_	Alignment	not modelled	12.6	15	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
92	c3mpoD_	Alignment	not modelled	12.3	28	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
93	c6f9aA_	Alignment	not modelled	12.2	21	PDB header: sugar binding protein Chain: A: PDB Molecule: er quality-control lectin; PDBTitle: solution structure of the mrh domain of yos9 complexed with alpha3,2 alpha6-man5
94	c5wamA_	Alignment	not modelled	12.2	27	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor bame; PDBTitle: structure of bame from neisseria gonorrhoeae
95	c6fk3B_	Alignment	not modelled	12.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure and function of aldehyde dehydrogenase from thermus2 thermophilus: an enzyme with an evolutionarily-distinct c-terminal3 arm (recombinant full-length protein in complex with propanal)
96	c3da5A_	Alignment	not modelled	11.9	78	PDB header: rna binding protein Chain: A: PDB Molecule: argonaute; PDBTitle: crystal structure of piwi/argonaute/zwillie(paz) domain from2 thermococcus thioireducens
97	d1sv0c_	Alignment	not modelled	11.8	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain
98	c4a1eT_	Alignment	not modelled	11.5	42	PDB header: ribosome Chain: T: PDB Molecule: rpl24; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
99	d2ipqx1	Alignment	not modelled	11.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: STY4665 C-terminal domain-like