Supporting Information

UDP-Galactopyranose Mutase in Nematodes

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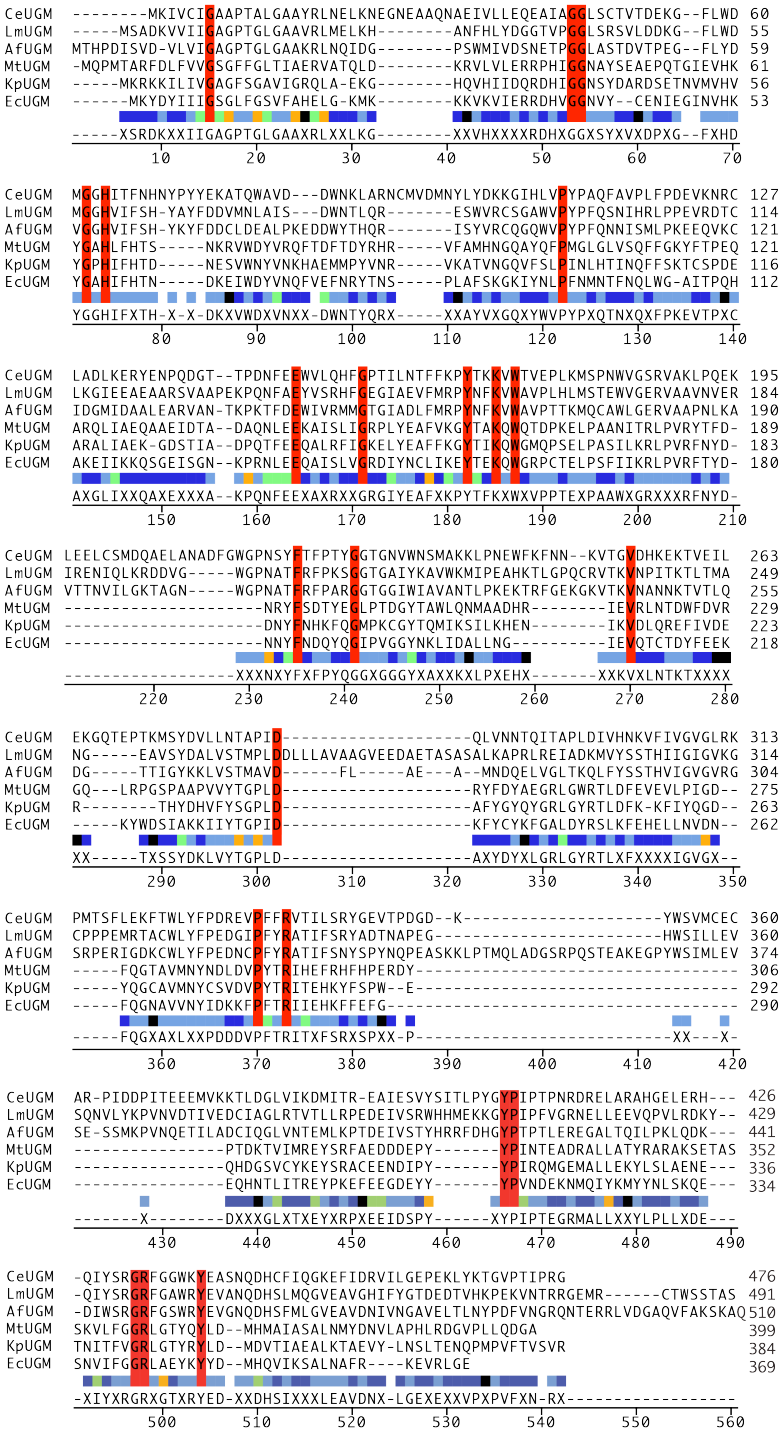

Figure S1. Clustal W analysis of UGM proteins.

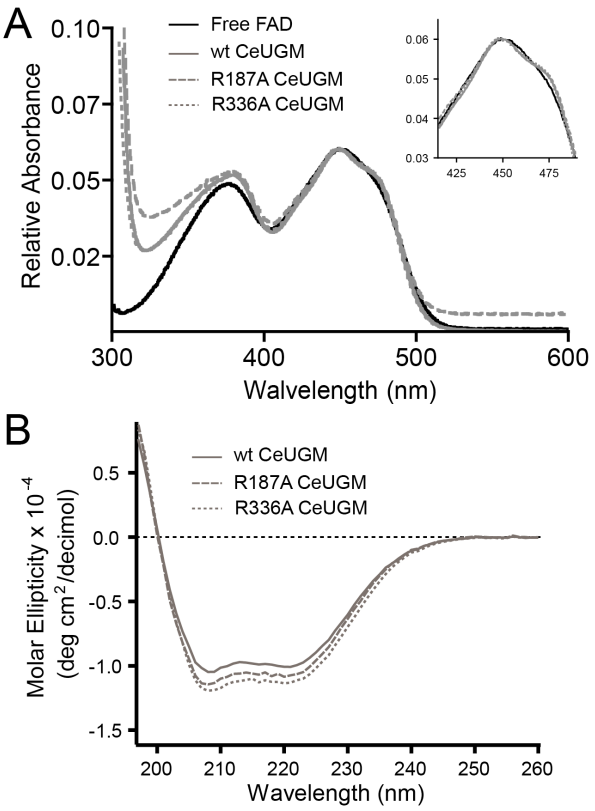

Figure S2. Spectrophotometric analysis of wild-type CeUGM and mutants. (A) UV-visible spectrum of free FAD, wild-type (wt) CeUGM, R187A CeUGM variant, and R336A CeUGM variant. Inset trace shows region of the spectra that is sensitive to chemical environment of the flavin and is diagnostic of bound cofactor. (B) Circular dichroism spectra for wild-type CeUGM, R187A CeUGM variant, and R336A CeUGM variant. Baseline scans of buffer solution were subtracted from all spectra, and data were converted to molar ellipticity for accurate comparison between samples.

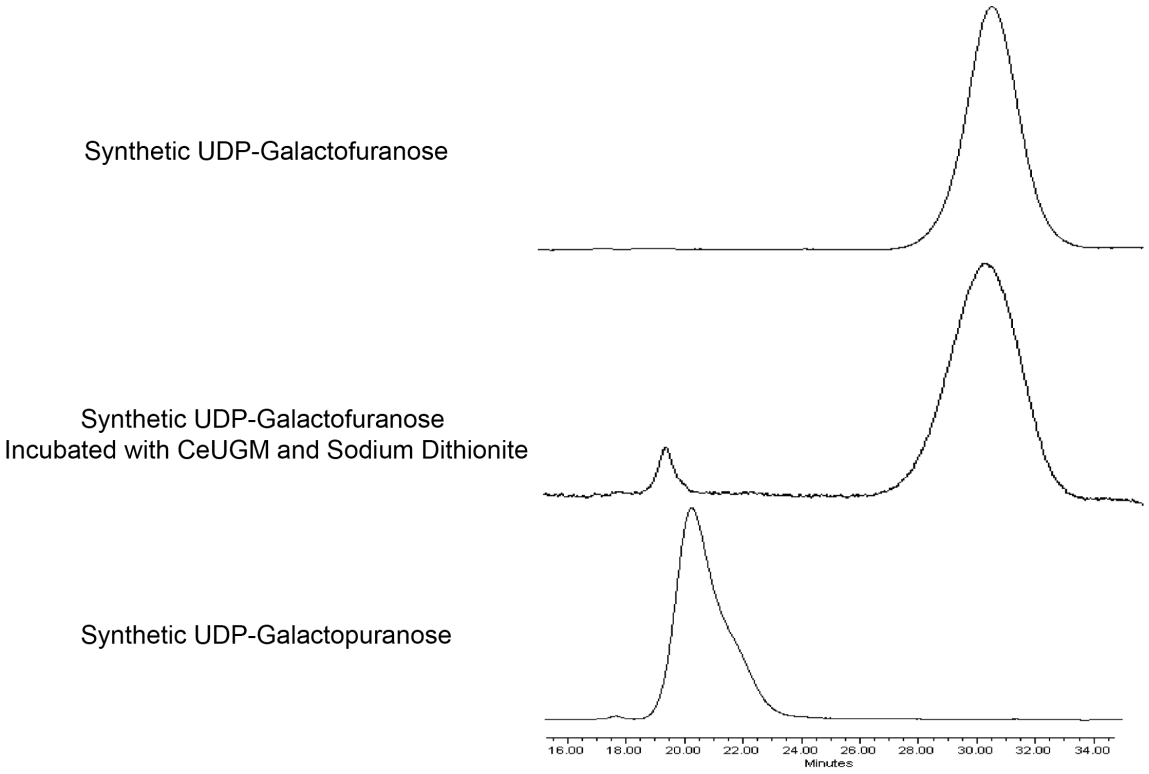

Figure S3. CeUGM catalytic activity. Incubation of UDP-Gal*f*, CeUGM, and the reducing agent sodium dithionite results in formation of a product with a similar retention time as synthetic UDP-Gal*p* (CalBioChem, La Jolla, CA).

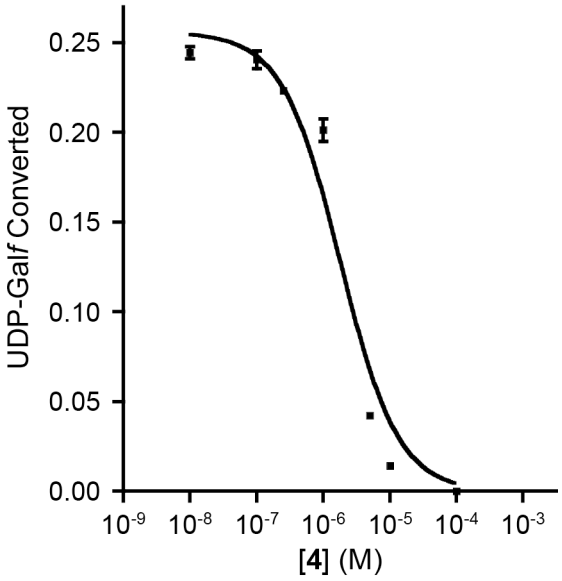

Figure S4. Inhibition of CeUGM as a function of increasing concentrations of compound **4**.

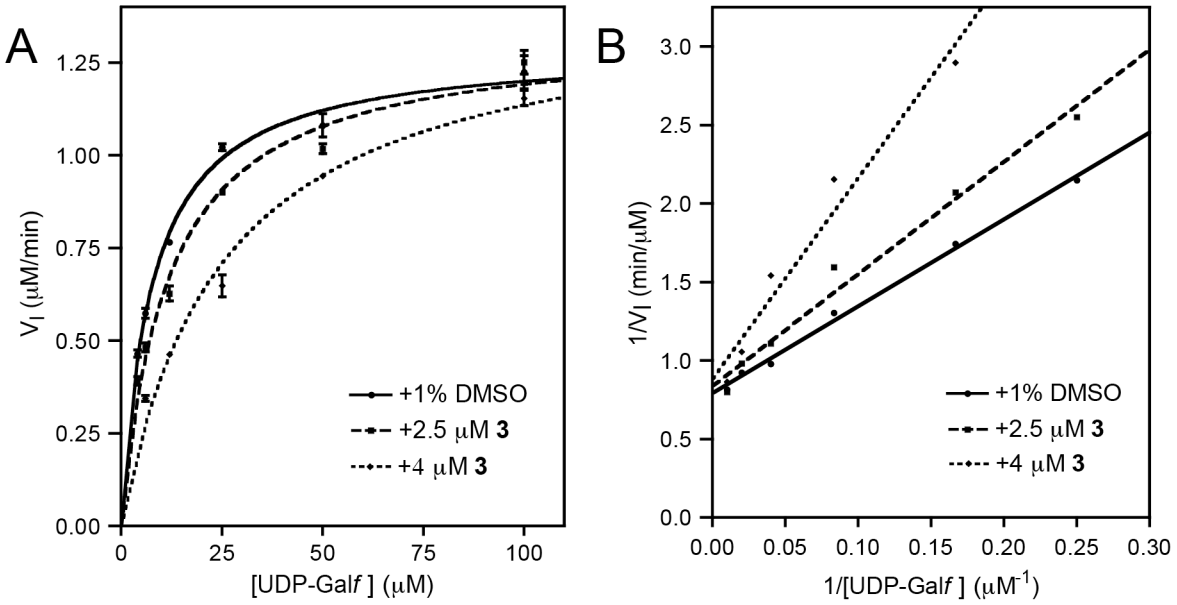

Figure S5. Competitive inhibition of CeUGM by compound **3**. (A) Initial velocity analysis of CeUGM in the presence of increasing concentrations of compound **3**. Error bars represent the standard deviation of triplicate measurements. (B) Double reciprocal analysis of the data presented in (A).

Table S1. Oligonucleotide Primer Sequences Used to Generate Point Mutants of CeUGM[a]

R187A	5'-CTCCAAATTGGGTTGGATCTGCTGTTGCTAAGCTTCCAC-3'
R336A	5'-CCCAGATCGTGAAGTTCCATTCTTCGCTGTCACAATTCTCAGC-3'

[a]The primer described below and its reverse complement (sequence not shown) were used together in a single PCR reaction to generate each mutant. The codon changed during the reaction is underlined.

Table S2. Active Site Resides That Appear Conserved Between CeUGM and MtUGM

C. elegans	*M. tuberculosis*
H64	H65
Y167	Y161
W172	W166
R187	R180
Y219	Y191
R336	R292
E359	E315
Y404	Y328
Y438	Y366