**Supporting Information**

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**Figure S1**: Enhanced lysis of a *pgi* mutant. Overnight cultures of the indicated strains were plated on LB agar (+/-)glucose and the lysis indicator CPRG (see text for details) and imaged after 18 hours of growth.

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**Figure S2**: Ability of Δ*pgi* to grow on various carbon sources. A) Growth curves with M9 minimal media and the indicated sole carbon sources. SEM plotted. B) Serial dilutions of overnight cultures grown in M9 + 0.2%CAA plated on M9 agar supplemented with the indicated carbon sources and grown for 18 hours at 37°C. C) Growth curves with M9 minimal media, designated carbon sources, and 0.2% glucose. SEM plotted. D) Serial dilutions of overnight cultures grown in M9 + 0.2%CAA plated on M9 agar supplemented with the designated carbon sources and 0.2% glucose.

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AI-generated content may be incorrect.

**Figure S3***: In vitro* biochemical abundance of specified metabolites. A. UDP-GlcNAc levels measured with 125mM G6P addition. SEM plotted with 3 replicates displayed. B. Intermediate GlcNAc1P levels measured after increasing levels of GlcN1P and constant G6P addition. C. UDPGlcNAc levels measured after increasing levels of GlcN1P and constant G6P addition. SD plotted with 3 replicates displayed.

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**Figure S4**: Structural alignments of GlmU. A) Multiple amino-acid sequence alignments of *M.Tb, E.coli,* and *V. cholerae* with conserved residues denoted, using Clustal. B) GlmU monomer structural alignment. GlmUVC is blue, GlmUEC is depicted in orange, and GlmUMtb is in teal. RMSD, root mean squared deviation, is a measure of how closely two alignments match; RMSD < 2.5 is a reasonable alignment. C) Percent Identity Matrix, created by Clustal2.1 shows alignment similarity across species.

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**Figure S5**: Predicted molecular models of GlmU. A) Predicted models of VCH GlmU with glucosamine-1P with interacting residues denoted, length of bonds, pTM and ipTM scores. Model #3 was the model used above. B) Predicted models of VCH GlmU with glucose-1P with interacting residues denoted, length of bonds, pTM and ipTM scores. Model #4 was the model used above. Highlighted in green are the same interacting residues as the substrate GlcN-1P. C) Predicted models of VCH GlmU with glucose-6P with interacting residues denoted, length of bonds, pTM and ipTM scores. Model #1 was the model used above. Highlighted in green are the same interacting residues as the substrate GlcN-1P. D) PAE plot and confidence model generated for VCH GlmU + Gln-1P model #0. E) Molecular modeling of GlmU binding glucose-6P (red) and the associated polar interactions.

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Table S1: Strain list used in this study.

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Table S2: Plasmids and oligos used in this study.