Table S1. Bacterial strains used in this study.

species	strain	relevant genotype	source
S. Typhimurium	14028s	Wild-type	ATCC
S. Typhimurium	KAM31	Δ*gfrR::kan*	(27)
S. Typhimurium	KAM67	Δ*gfrR*	(27)
S. Typhimurium	KAM32	Δ*gfrAB::kan*	(27)
S. Typhimurium	KAM42	Δ*gfrAB*	(27)
S. Typhimurium	GLS01	Δ*gfrE::kan*	this study
S. Typhimurium	GLS03	Δ*gfrE*	this study
S. Typhimurium	GLS02	Δ*gfrF::kan*	this study
S. Typhimurium	GLS04	Δ*gfrF*	this study
S. Typhimurium	KAM91	Δ*ptsH::kan*	(27)
S. Typhimurium	KAM95	Δ*ptsH*	(27)
S. Typhimurium	GLS05	Δ*ldcC::kan*	this study
S. Typhimurium	KAM129	Δ*ldcC*	this study
S. Typhimurium	DM2591	Δ*cadA::mudJ*	D. Downs
S. Typhimurium	KAM136	Δ*cadA::mudJ* Δ*ldcC*	this study
S. Typhimurium	GLS06	Δ*patA::kan*	this study
S. Typhimurium	KAM130	Δ*patA*	this study
S. Typhimurium	GLS07	Δ*patD::kan*	this study
S. Typhimurium	KAM131	Δ*patD*	this study
S. Typhimurium	GLS08	Δ*gabT::kan*	this study
S. Typhimurium	KAM133	Δ*gabT*	this study
S. Typhimurium	PBK01	Δ*hisC::kan*	this study
S. Typhimurium	PBK02	Δ*hisC*	this study
S. Typhimurium	ACB01	Δ*rpoN*	A. Bono
E. coli	BL21 (DE3)	F– *ompT gal dcm lon hsdSB(rB-mB-)* λ(DE3 [*lacI lac*UV5-T7 gene 1 *ind1 sam7 nin5*])	(18)
E. coli	KAM216	BL21/DE3λ/pACYC184+*plyE*/pET21a+*gfrE*	this study
E. coli	KAM217	BL21/DE3λ/pACYC184+*plyE*/pET21a+*gfrF*	this study

Table S2. Plasmids used in this study.

Plasmid	Relevant characteristics	Ref.
pKD46	expresses λ phage recombinase genes γ, β and exo from arabinose-inducible P*araB* promoter; temperature-sensitive replicon	(21)
pKD4	template plasmid used to generate amplicons for inactivation of target genes in the λ Red system	(21)
pCP20	expresses FLP enzyme for removal of kan gene flanked by FRT sites; temperature-sensitive replicon	(35)
pET21a	vectors carries an N-terminal T7 Tag sequence and T7 promoter	Novagen
pET21a+*gfrE*	carries *S*. Typhimurium *gfrE* under control of T7 promoter in pET21a	this study
pET21a+*gfrF*	carries *S*. Typhimurium *gfrF* under control of T7 promoter in pET21a	this study

Table S3. Primers used in this study.

Sequence	Experiment
5'-ATTTTCGGTTCCTGGATAGGGTTATTTTATGTGTAGGCTGGAGCTGCTTC-3'	*gfrE* knock out λ red
5'-CAGGTACTCGTCCTGATTAAAACCCAACATCATATGAATATCCTCCTTA-3'	*gfrE* knock out λ red
5'-TTAAAAGAGAATGTCATATATGCCGGGTCATATGAATATCCTCCTTA-3'	*gfrF* knock out λ red
5'-CGATTTCGATCGCGTTTTAAAAAGTAAAATTGTGTAGGCTGGAGCTGCTTC-3'	*gfrF* knock out λ red
5'-GCCTGGGCCGATGCATGGAAGGCATTGTAATGTGTAGGCTGGAGCTGCTTC-3'	*ldcC* knock out λ red
5'-GATGTGATGAACCTGTTTTAATCCCAGCATCATATGAATATCCTCCTTA-3	*ldcC* knock out λ red
5'-GCCTGCCTACTATGAGCC-3'	*ldcC* flanking
5'-GATGTGATGAACCTGTTTTAATC-3'	*ldcC* flanking
5'-TTTCGGTTCCTGGATAGG-3'	*gfrEF* flanking
5'-TGGAGATCAAAGTGGTGAATG-3'	*gfrEF* flanking
5'-TGAAAACTACGCGCAATATGCTGGCGTAAATGTGTAGGCTGGAGCTGCTTC-3'	*hisC* knock out λ red
5'-GTTCTACGCAGGCGGTCTGTTGCAGGGCATCATATGAATATCCTCCTTA-3'	*hisC* knock out λ red
5'-CGCGTAAACGCCCTCAAG-3'	*hisC* flanking
5'-CCGGTCGATGAAAAGATACTTC-3'	*hisC* flanking
5'-ATCGAGAAGCGAACGCTAAACCATGAGGAATGTGTAGGCTGGAGCTGCTTC-3'	*patA* knock out λ red
5'-GGATAAGCACAGCGCCATCCGGCATCGTTTCATATGAATATCCTCCTTA-3'	*patA* knock out λ red
5'-ACGCACTGAATCTCATCG-3'	*patA* flanking
5'-TGGTGATTGTGATGGGATTC-3'	*patA* flanking
5'-AGCGGCGGCCCGTTCGCCGGAAATCGATTATGTGTAGGCTGGAGCTGCTTC-3'	*patD* knock out λ red

5’-GGATCATTTACTGTTCAGAAAAATCGTGAACATATGAATATCCTCCTTA-3’	*patD* knock out λ red
5’-GTCAGCTCACAACCTGAC-3’	*patD* flanking
5’-CGCAGCAAGTACTCAAAGG-3’	*patD* flanking
5’-GAAATCAAATATATGTGCATCGGCCTTTAATGTGTAGGCTGGAGCTGCTTC-3’	*gabT* knock out λ red
5’-ACGTCGCCACCCGACGCTGCTTATTGGACACATATGAATATCCTCCTTA-3’	*gabT* knock out λ red
5’-GTTCCAAATACGGCATCGAAG-3’	*gabT* flanking
5’-CCGGATAAGACAGTTACGTCG-3’	*gabT* flanking
5’-CATATGATGTCACCAACCATGCTG-3’	GfrE purification
5’-AAGCTTGATTTTACTTTTTAAAACGCGATCG-3’	GfrE purification
5’-CATATGATGTTGGGTTTTAATCAGGACG-3’	GfrF purification
5’-AAGCTTATAATCGAACTGACGGTAGTAACG-3’	GfrF purification

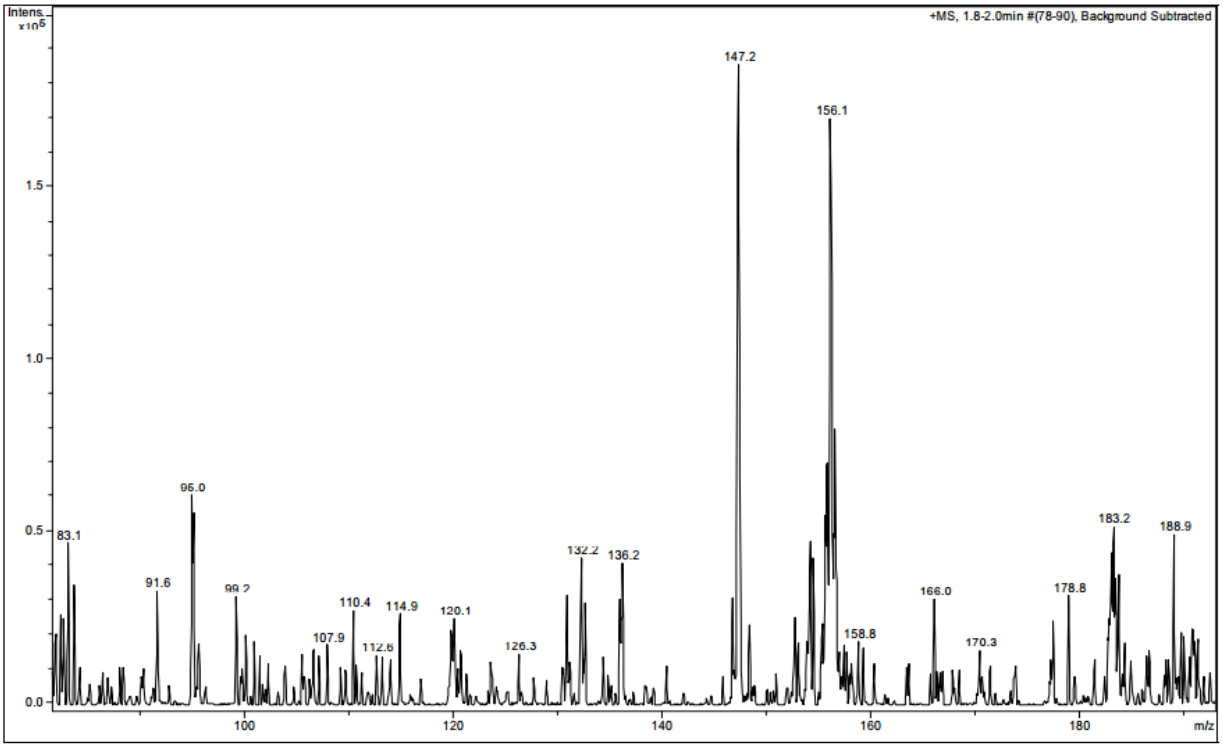

Figure S1. Mass spectrum of combined extracellular and intracellular fractions of S. Typhimurium cells grown in minimal medium containing fructoselysine as the sole carbon and nitrogen source. The mass spectrum revealed prominent peaks with the mass expected for lysine (m/z 147.2, $(M+1)^+$) and histidine (m/z 156.1, $(M+1)^+$). Both of these peaks were absent in the mass spectrum of extracts prepared from cells grown with arabinose and ammonium.

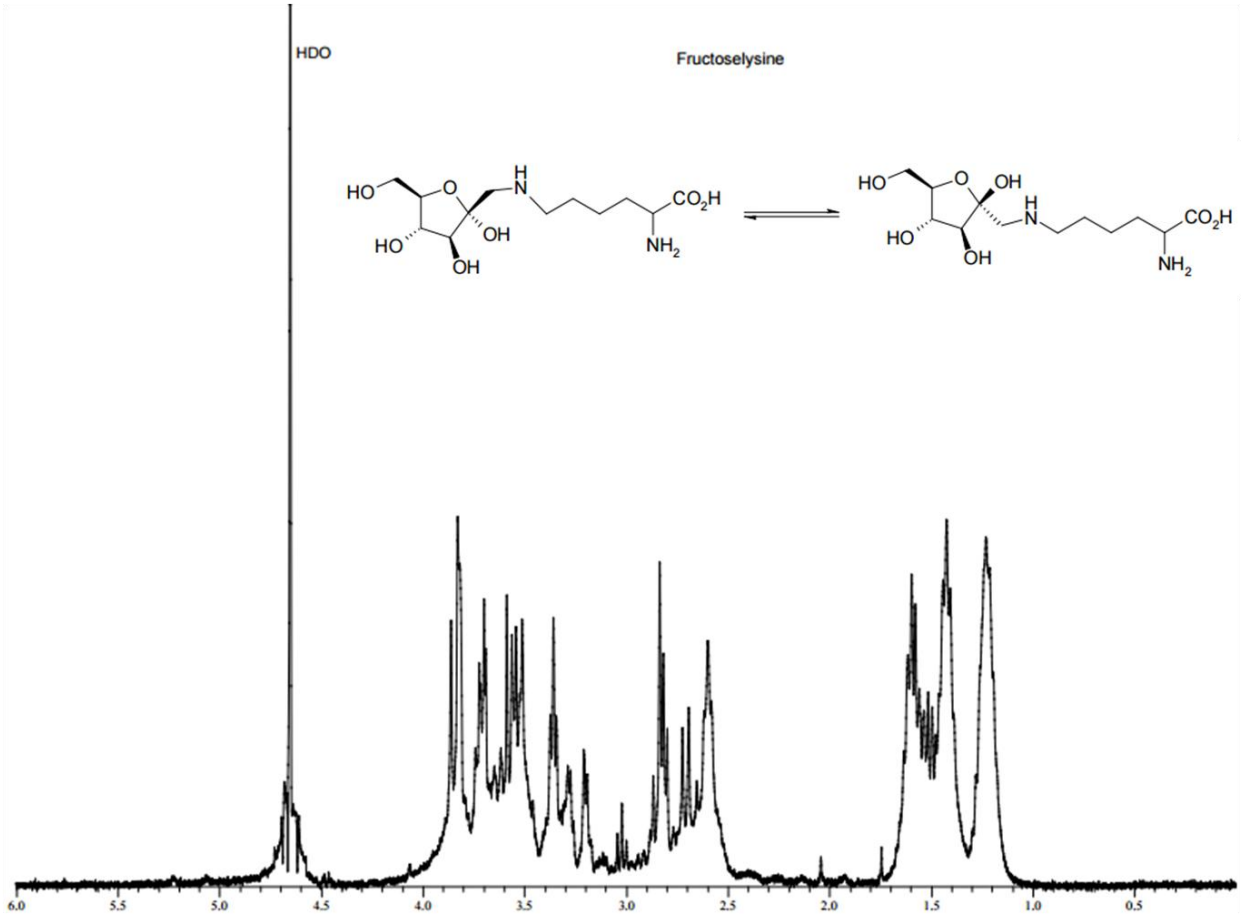

Figure S2. H^1-NMR of fructoselysine. The H^1-NMR spectrum was similar to that reported by Wiame *et al*. (8). The structures of fructoselysine with the sugar in the alpha (right) and beta (left) forms are shown.

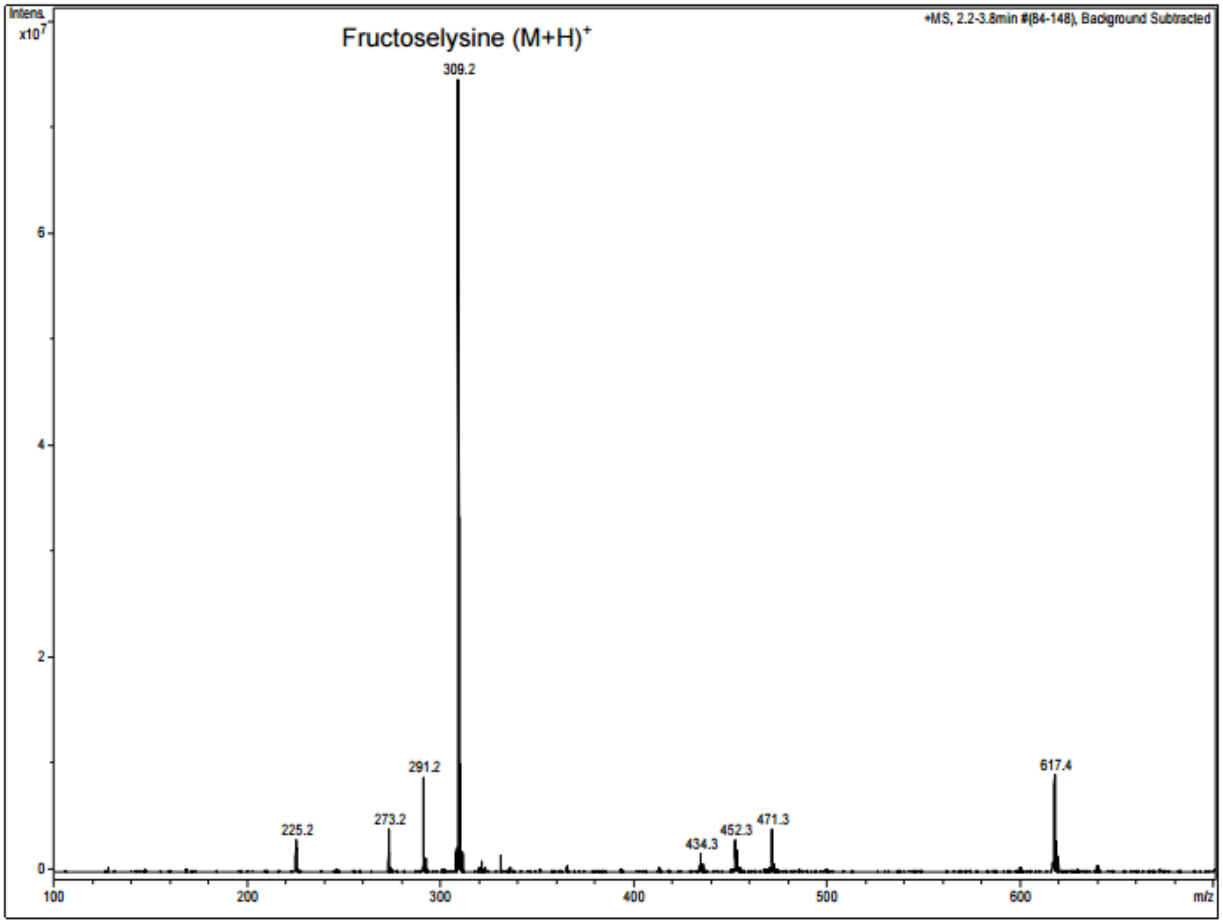

Figure S3. Mass spectrum of fructoselysine. A prominent peak with the expected mass for fructoselysine (m/z 309, $(M+1)^+$) was observed in the mass spectrum of a sample of the final product from the fructoselysine synthesis. Note that there are not significant amounts of the reacting materials in the preparation: Boc-lysine (m/z 247.3, $(M+1)^+$); glucose (m/z 181.2, $(M+1)^+$); lysine (m/z 147.2, $(M+1)^+$).

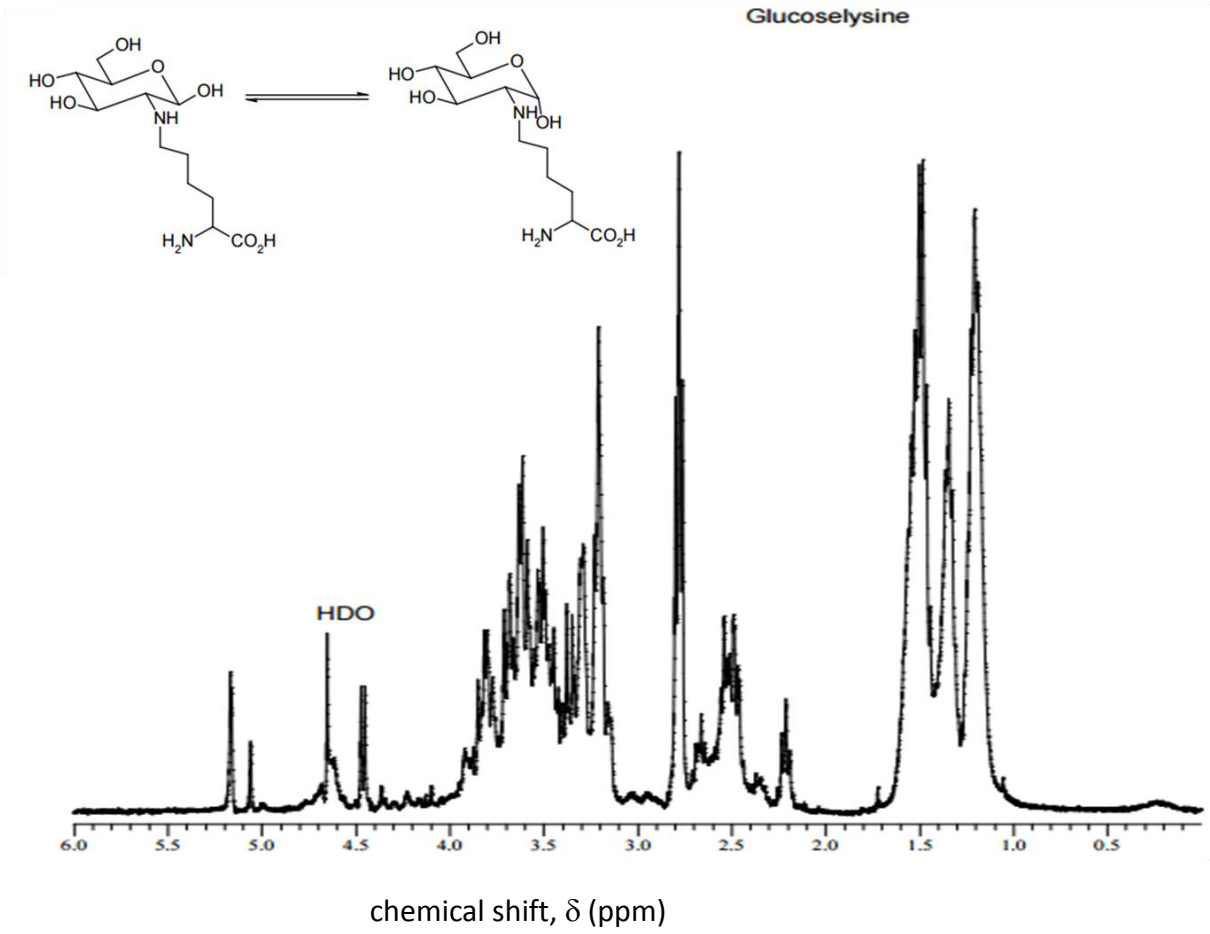

Figure S4. H^1-NMR of glucoselysine. The H^1-NMR spectrum was as expected and included the two signals corresponding to the anomeric proton of glucose (δ = 5.2 and 5.1). The structures of glucoselysine with the sugar in the alpha (right) and beta (left) forms are shown.

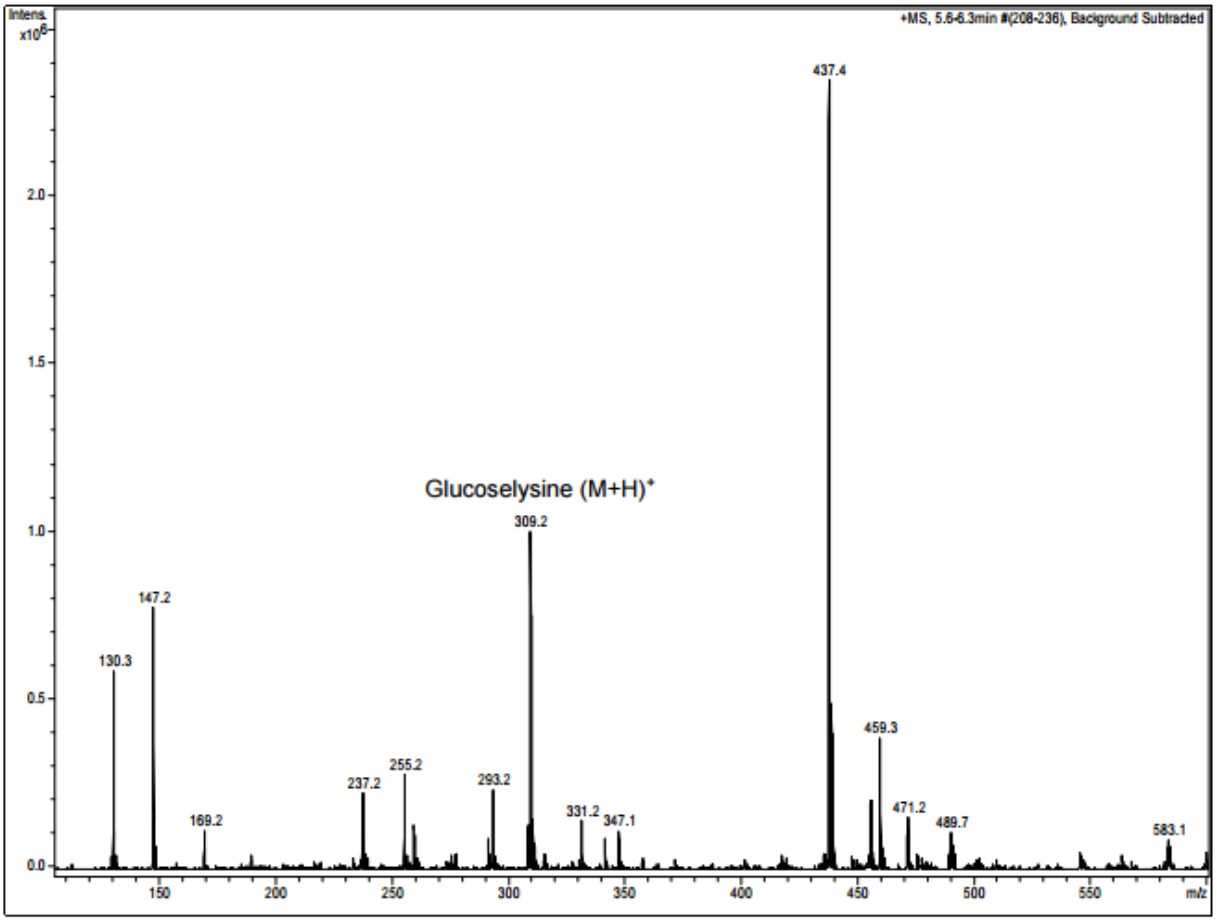

Figure S5. Mass spectrum of glucoselysine. A peak with the expected mass for glucoselysine (m/z 309, $(M+1)^+$) was observed in a sample of the final product from the glucoselysine synthesis. Although there are not significant amounts of the reacting materials: Boc-lysine (m/z 247.3, $(M+1)^+$) or fructose (m/z 181.2, $(M+1)^+$), there does appear to be some lysine (m/z 147.2, $(M+1)^+$) in the final product.

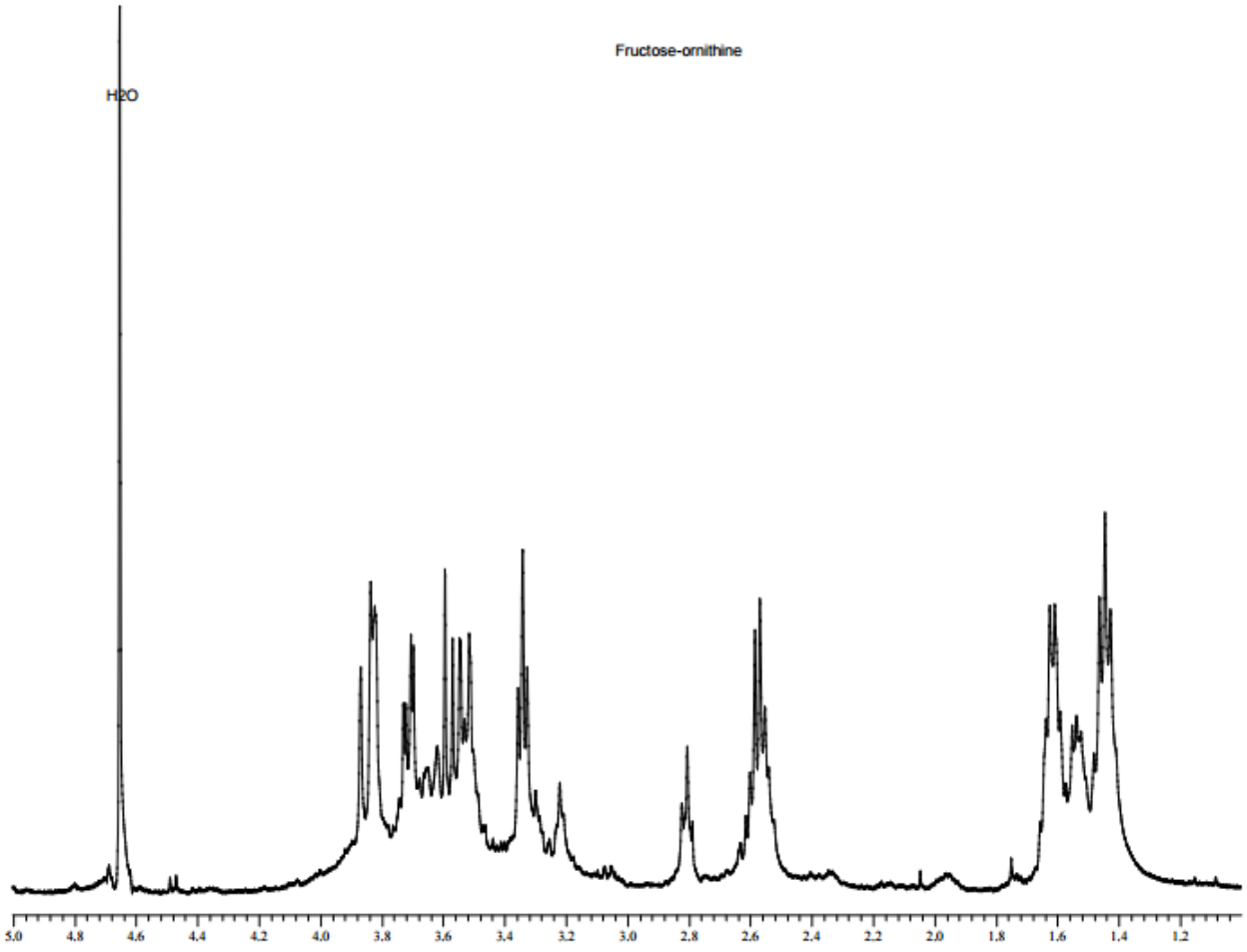

Figure S6. H^1-NMR of fructose-ornithine. The H^1-NMR of the fructose-ornithine preparation was as expected.

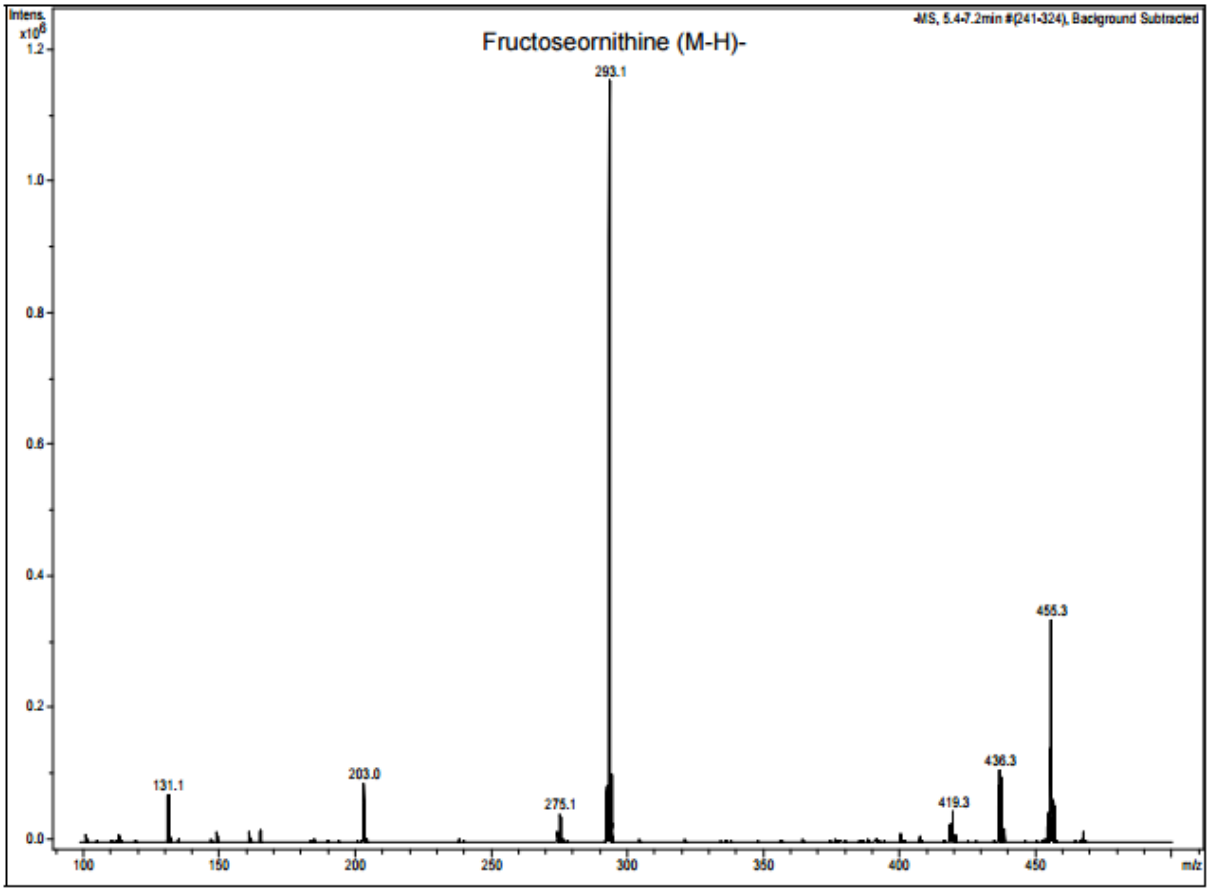

Figure S7. Mass spectrum of fructose-ornithine. A prominent peak with the expected mass for fructose-ornithine (m/z 291, $(M-1)^-$) was observed in the final product of the fructose-ornithine synthesis. There appeared to be some ornithine (m/z 131.1, $(M-1)^-$) in the final product.

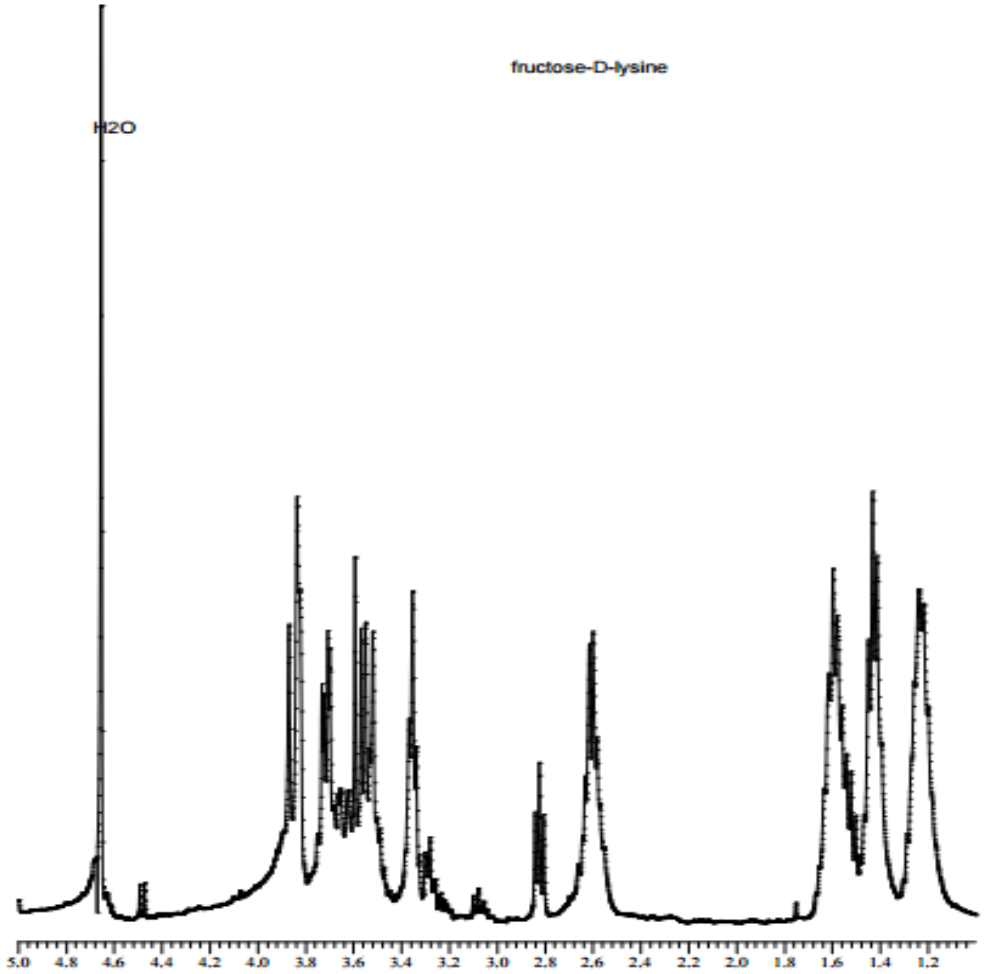

Figure S8. H^1-NMR of fructose-D-lysine. The H^1-NMR spectrum was similar to that for fructose-L-lysine reported by Wiame *et al*. (8).

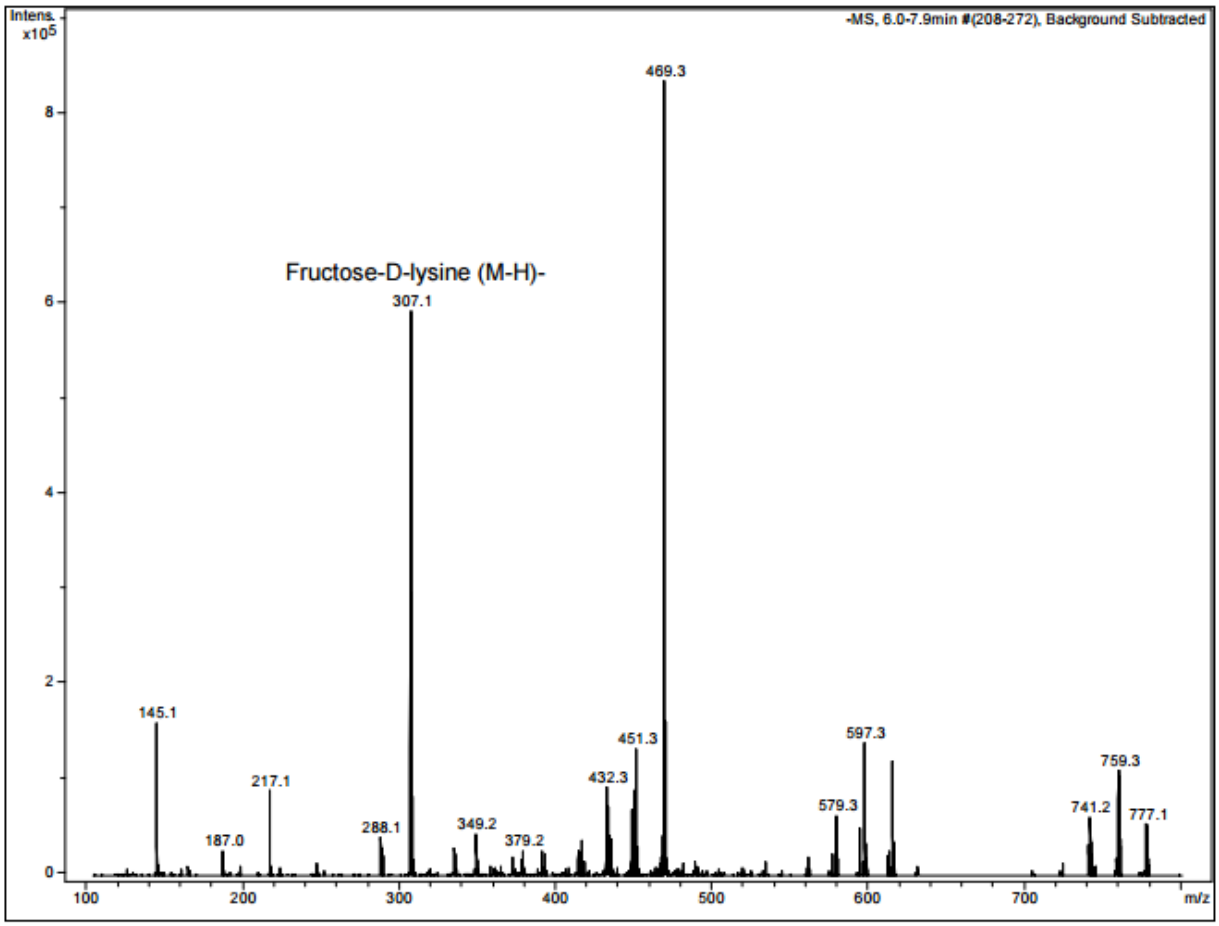

Figure S9. Mass spectrum of fructose-D-lysine. A prominent peak with the expected mass for fructose-D-lysine (m/z 307.1, $(M-1)^-$) was observed in the final product from the fructose-D-lysine synthesis. The final product appeared to have some unreacted lysine (m/z 145.1, $(M-1)^-$).