Supplemental Figure Legends:

Supplemental 1. Amino acid sequence alignment of the RgtA, B, C, and D polypeptides. The alignment was performed using the multiple sequence alignment scoring matrix BLOSUM 62 application in the Clone Manager program. Shaded letters represent sequence identity.

Supplemental 2. Relationship of RgtE to ArnC, FlmF1 and FlmF2. The RgtE amino acid sequence shares similar qualities with known bactoprenyl glycosyl transferases that function in the synthesis of monosaccharide lipid donors which are utilized in the biosynthesis of LPS. Like the known glycosyl transferases ArnC, FlmF1,and FlmF2, the RgtE amino acid sequence contains a glycosyl transferase 2 (GT2) domain which contains the signature DXD catalytic motif followed by two signature putative C-terminal transmembrane (TM) domains. The enzymes are likely anchored to the inner membrane by the transmembrane domains leaving the catalytic domain (GT2) exposed to the cytoplasmic/inner membrane interface.

Supplemental 3. Amino acid sequence alignment of the *R. leguminosarum* bv. *viciae* RgtD and putative RgtD proteins in *Caulobacter crescentus* CB15 and *Aquifex aeolicus* VF5. Alignments were made in the Clone Manager program using the BLOSUM 62 matrix scoring system. Shaded letters are identical amino acids. The putative RgtD peptides share over 50% similarity (positives) with the *Rhizobium* RgtD and are share highly conserved regions towards the N-terminus.

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Summary of Percent Matches:
   Ref:  RgtA(RL1469)          1 to    499   (   499 aa)      --
     2:  RgtB(RL1468)          1 to    494   (   494 aa)      45%
     3:  RgtC(RL1471)          1 to    501   (   501 aa)      59%
     4:  RgtD(RL0684)          1 to    473   (   473 aa)      21%


RgtA(RL1469)          1 MLERATRTIKTAGLLLAAYFVL-NIVLRIVLPHSLELDEAEQSFFSQYLLAGYGPQPPFY
RgtB(RL1468)          1 MTESNRRDISWIFALLAAYFVL-QVGVRLATSHSLDLDEAEQAFRSQWLAAGYGPQPPFY
RgtC(RL1471)          1 MLERITRSITSASIFLAAYFLL-NIALRIALPHTLDLDEAEQSFYSQYLLAGYGPQPPFY
RgtD(RL0684)          1 MSPR-------SGLLIVLGFTLWRVVMLNFDATDFFVDEAQYWFWSQNLDLGYYSKPPMI

RgtA(RL1469)         60 NWMQYAVVSVTGIS-------IGALIVPKNILLFLSYLFYGLAGRRVLKDEALAAVGMLA
RgtB(RL1468)         60 NWLQYTVFQFAGVS-------LTALSIVKNLLLFISYLLYGLTARLVLRDKALVAIATLG
RgtC(RL1471)         60 NWIQYAIVSVTGIS-------MWVLSVPKNIILFGCYLFYGLAAREVLKSRSLAALAMLS
RgtD(RL0684)         54 AWVIRAMTELSGSNAIYWIRLLGPLIHMAAALVLMK------TAKRFVGPEIEGWTG-AT

RgtA(RL1469)        113 LITLPQVSYMAQQDLTHTTALLFASSLFLYGFFRTLDRPDMASYLLLGLATGIGLISKYN
RgtB(RL1468)        113 LLTIPQMAFEMQRDLTHTVAVFFSASIFFYGFIRSLKQPSLASYLIAGIGIGFGLLAKYN
RgtC(RL1471)        113 LITLPQVGLMAQRELTHTVALLFATSLFLFGFFRTLRQPTIGSYLLIGIATGIGLISKYN
RgtD(RL0684)        107 YITLPGVA-LSSVFFSTDVILLFFIAIALLAYFGLTQRRSVGLALVMGLGVGLAFLTKYA

RgtA(RL1469)        173 FALMPVVALIAILPDAEWRRRALDWRMLAAITVALVIVLPHAVWLQGNLAFASSDTLVK-
RgtB(RL1468)        173 FAILPAAALIAALSDARLRPRIFDWRLGLTAAVALVITLPHLFWLKDNLDFATARTLEK-
RgtC(RL1471)        173 FAILPFAALIAVLPEREWRSRLIDWRLLPAAVLAILIVLPHALWLPDNLASASAPTLER-
RgtD(RL0684)        166 VLFVVPGGAIALLLIPAARIAVRD--VIIAVAVAAVVALPNLWW---NL--QHDNTTVRH

RgtA(RL1469)        232 ---MAAGS---EPAGAVRIGKGLLAFLVAIIAFAALPVVIFA---ATFRRD--FVRALSA
RgtB(RL1468)        232 ---MTASG---DASYLTQVAMGVSSLALAIISFAALTVAVFA---IVFGKS--LRPALGS
RgtC(RL1471)        232 ---MTADPGHLAPAGLPRIGQGLLSLVIAVLGFVALPIVLIA---AAFRRDSRVFRALSS
RgtD(RL0684)        219 TQDIAHWS---ELGINLRRGLEFFAAQFGVVG----PIIFFAMLWAVYR----MIRGRSD

RgtA(RL1469)        281 GNRWTGMMERMML-ASLAGIALIVLFTGSTTVRERWLDPFLL---VLPIYFLAKMQAAGL
RgtB(RL1468)        281 GSEWTRLLERMML-VFLAGILLLIVFGGAAGIKDRWLVPMLF---ILPLYFCLKIEAAGV
RgtC(RL1471)        286 SSPMIRVIERMMV-ISLLAFVGVVLFAGASDIHERWLDPCLL---VLLIYLFLKLETADI
RgtD(RL0684)        268 DR------EKMLVWLSMPVVLLITLQATVAKAYANWAVTAYVAGTILAVWLLYLKWPKGL

RgtA(RL1469)        337 DLSAGLRRFRPVLPVLMACVLIALGFRVVGAGLIGTY-SRPNVPMAGFAREMTRQAEPAL
RgtB(RL1468)        337 ETGKALRRFIPVVAVIMIGVPAALYGSVAAARFTGHY-ERLNRPYAGMLEILRKQAEPAA
RgtC(RL1471)        342 DLSAGLARFRPVVPVFMVVILSILLFRIVGIQYIGTY-TRTNVPFSGYVAELTATRKPVL
RgtD(RL0684)        322 RLSLTINGIASLL-FPLATIFPHQLLLPNGDALMKRYLGRAEVSRE--AAALATQAGTDI

RgtA(RL1469)        396 VIASDTYIGGNMRLQFPDVPVVIPDFPAPGIP-AY--------AEAKGPVLIVWRGKKTA
RgtB(RL1468)        396 ILAGDSLLAGNLRQDIPGVPILSADY--PGFN-PD--------LTSRRPLLLVWLLPK--
RgtC(RL1471)        401 IVAGTKFIAGNMRLQFPDVPVVIPFFPGPGVP-EY--------ADAKGPVLVIWRGE---
RgtD(RL0684)        379 IVTDNRDMVADLFYTLRDASYRIYARAPAGLPESYYEQEFALPADITGKVLFLTDGAFTC

RgtA(RL1469)        447 TAADAVMPERFSSALTAAGIALQEIGSLSLPYYFGRQGDNFALGYAWVRPETR
RgtB(RL1468)        443 GGSEALPPDMAEWLQANLGTSAPEASVIDVPYFYGRGDDRYRFGYAWVNQPG-
RgtC(RL1471)        449 TADDPTISPGFANDLVKSGIHLPELKTLTLPYLFGDGKRSFSIGYSWVEGGAK
RgtD(RL0684)        439 ATE---TPEVLKNWQPTEG------------NYKGKTLSIYKVSATCLAP---
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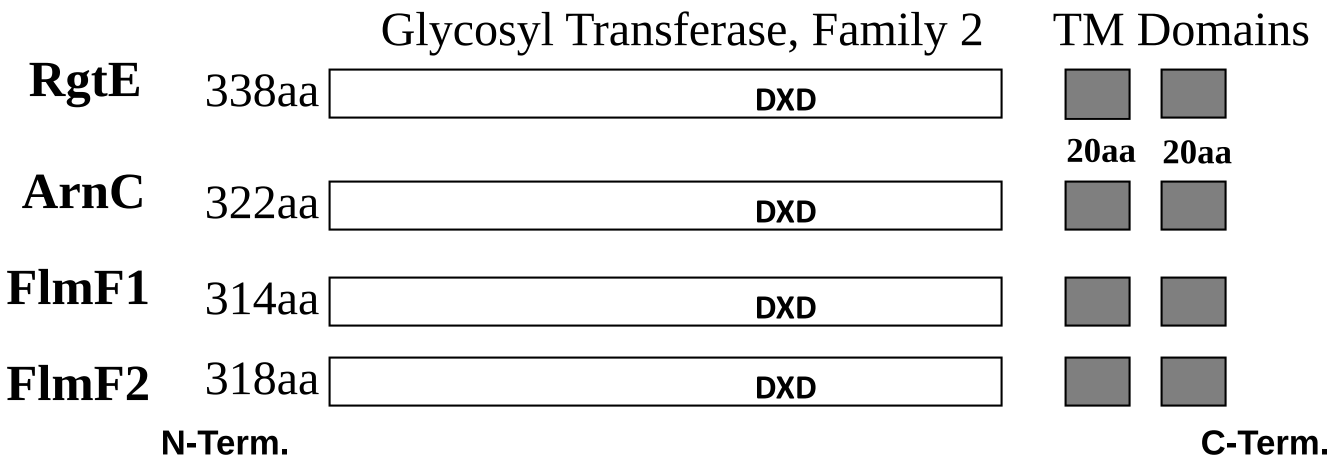
Supp1

Strains	**Related Enzymes**	**Reaction**
Rhizobium leguminosarum	RgtE, 100% i.d.	UDP-D-GalA → Dod-P-GalA
Escherichia coli	ArnC, 32% i.d.	UDP-L-AraNFormyl → Und-P-L-AraNFormyl
Francisella novicida	FlmF1, 24% i.d.	UDP-D-GalNAc → Und-P-D-GalNAc
	FlmF2, 23% i.d.	UDP-D-Glc → Und-P-D-Glc



Supp2

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Summary of Percent Matches:
   Ref:  Rl RgtD(RL0684)        1 to    473   (    473 aa)      --
     2:  Aq RgtD(aq_765)        1 to    480   (    480 aa)      27%
     3:  Cc RgtD(CC_0209)       1 to    524   (    524 aa)      29%


Rl RgtD(RL0684)       1 -------MSP-------RSGLLIVLG--FTLWRVVMLNFDATDFFVDEAQYWFWSQNLDL
Aq RgtD(aq_765)       1 -----------------MFGLALLINTFFLVFRVLYVLFYPVDLSPEEAQYWDWSRHLDL
Cc RgtD(CC_0209)      1 MQTAPDASSPPIENRAWRLTLLMIGG--LTIVRLAALFLTPLELYPDEAQYWLWSRELAF

Rl RgtD(RL0684)      45 GYYSKPPMIAWVIRAMTELSGSNAIYWIRLLGPLIHMAAALVLMKTAKRFVGPEIEGWTG
Aq RgtD(aq_765)      44 SYYSKPPMVAYMNFLSTHVFG-NTELGVRINAILLSFLLSLITYFFAKKLFSEKVAFVAS
Cc RgtD(CC_0209)     59 GYFSKPPMIAWLIWATTQIGDTEA--WVRLSAPFLHGATALVIHRIARRLYG----GWAG

Rl RgtD(RL0684)     105 ----ATYITLPGVALSSVFFSTDVILLFFIAIALLAYFGL---TQRRSVGLALVMGLGVG
Aq RgtD(aq_765)     103 ----VVPNLFTGFSINSVLFTTDSPLIFFWALSVISFYFA---IEKNTLSLWILTGVFSG
Cc RgtD(CC_0209)    113 LAAAAIYSLMPGVVLSSGLIATDAPLLFFLSLTVWAYVSLPDASARRRYALAAGMGAALG

Rl RgtD(RL0684)     158 LAFLTKYAVLFVVPGGAIALLLIPAARIAVRDVIIAVAVAA--VVALPNLWWNLQHDNTT
Aq RgtD(aq_765)     156 LAFLSKYPAVFLLPLGILYLYLTKKELLKDLKIFSSVLVAF--LIALPVLIWNAKHDFIS
Cc RgtD(CC_0209)    173 LAFLSKYAAVYALGSVALHFAISSEARRRWSPALVGLFIVAFALVLAPNLLWNAANQFST

Rl RgtD(RL0684)     216 VRHTQDIAHWSELGI-NLRRGLEFFAAQFGVVGPIIFFAMLW-AVYRMIRGRSDDREKML
Aq RgtD(aq_765)     214 FKHVSNLAQKHAHFP-NFSTFFEYLGGQVLLLSVIPFFFVLY-GWVRTFK----ERNKRL
Cc RgtD(CC_0209)    233 VKHTAANANWNAHQLFNVRELIEFVGSQFGVFGPVPFAVLIGGAIWLGVKRKLQSPDLLL

Rl RgtD(RL0684)     274 VWL---SMPVVLLITLQATVAKAYANWAVTAYVAGTIL-AVWLLYLKWPKGLR-LSLTIN
Aq RgtD(aq_765)     268 IFLTTFSLPVFLFFAFLSLKKRVYANWAGFGYYTASIL-FAY-YFLKSPKSLKFLTLILS
Cc RgtD(CC_0209)    293 LCF---ALPPLIVVAGEAFVSRANANWAGAAFVSGSVIVAGWLLRWNARRWLI-GGLVLQ

Rl RgtD(RL0684)     329 GIASLLFPLATIFPH----QLLLPNGDALMKRYLG-----RAEVSREAAALATQAGTDII
Aq RgtD(aq_765)     326 AFLTLLLHFTPLFDYLGLRNLLPPKRDPA-KLLVG-----WEDLGKEVGRFYT--GKELI
Cc RgtD(CC_0209)    349 AAFAAFFVACMVNPKVAD-AAGLSNG---FKRVRGWDQTVEAVIARVREEQALRGPLSAV

Rl RgtD(RL0684)     380 VTDNRDMVADL-FYTLRDASYRIYARAPA-------GLPESYYEQEFALPADITGK-VLF
Aq RgtD(aq_765)     378 FSTAYQISAELAFYV--PGNPRTYVFHVN-------RYTQYYLWREGL--KNFKGKDAVF
Cc RgtD(CC_0209)    405 AMDDRFVYNAA-AYYGRD--YFGQPGAPPLRMWVHEAYPQNQAETETPLDADYGRR-ALI

Rl RgtD(RL0684)     431 LT-DGAFTCAT----ETPEVLKNWQPTEG---------NYKGKTLSIYKVS----A----
Aq RgtD(aq_765)     427 VS-YGGVPKEVMRSFEGKEFLKEVRVVWR---------NQVVRKFYIYKLKNFKGE----
Cc RgtD(CC_0209)    461 VSLEGGY---------RPEIEQDFKAVSGLQIARVRLDKTRSRRVDLFIAE----GFAPL

Rl RgtD(RL0684)     469 -----TCLAP-------
Aq RgtD(aq_765)     473 -----FYENPKGY----
Cc RgtD(CC_0209)    508 PRDPITGLPPKPKTAAR
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Supp3