Supplementary Information for the manuscript entitled:

## Biochemical evidence for an alternate pathway in N-linked glycoprotein biosynthesis

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## **Supplementary Results**



**Supplementary Figure 1:** Coomassie-stained SDS-PAGE and Western blot analysis of purified proteins using antibodies specific to an N-terminal T7 or C-terminal His tag. (1) AglK (2) AglC (3) AglB.

## A

AglK Alg5	(1) (1)	MRALRFLIENRNTVFFTLLVALVLSLYLLVYLFSHTPRPPYPEELKYIADEKGHEVSRALPNLNEHQDDE
AglK	(3)	DKLIYLIIPAYNEEKMIKNVVNNLQNHNYDNIIIVDDGSKDNTYKIMKELEEESKQNNNNNNNN
Alg5	(71)	EIFLSVVIPSYNETGRILLMLTDAISFLKEKYGSRWEIVIVDDGSTDNTTQYCLKICKEQFKLN
AglK	(67)	NNNKVIA <mark>IK</mark> HE <mark>ON</mark> KGV <mark>GGA</mark> TIT <mark>G</mark> LKKAYELGADIAVTF <mark>DADG</mark> QHAPDDIAKVTQPIINDSKE
Alg5	(135)	-YEQFRI <mark>IK</mark> FS <mark>ON</mark> RGK <mark>GGA</mark> VRQ <mark>G</mark> FLHIRGKYGLFADADGASKFSDVEKLIDAISKIETSSTDLKTTK
AglK	(129)	YVV <mark>GSR</mark> IKNPKEFKNMPLTKKVGNLGLSFITFLLGGYYVTDSOSGLRAFSKSALKVLSEQLRAKRYE
Alg5	(201)	PAVAI <mark>GSR</mark> AHMVNTEAVIKRSMIRNCLMYGFHTLVFIFGIRSIKDTOCGFKLENRAAILKIFPYLHTEGWI
AglK	(196)	TCSEALIIAKKNKLNIGEVPIKTIYTEYSMARGTNVMIGFKIFYRULMLKMGKVLD
Alg5	(272)	FDVEILILAIRKRIQIEEIPISWHEVDGSKMALAIDSIKMAKDUVIIRMAYLLGIYRDNKKC
в		
_		
AglK	(1)	-MADKLIYLII <mark>PAYNE</mark> EKM <mark>IKNV</mark> VNNLQNHNYDNIIIIVDDGSKDNTYKIMKELEEESKQNNNNNNN
AglJ	(1)	MPTPDAVCILT <mark>PTYNE</mark> AETIADVISDYRDEGFANVLVIDGGSTDGTRELAEDAGAHVVVQSGSGKG
AglK	(1)	-MADKLIYLIIPAYNEEKMIKNVVNNLQNHNYDNIIIVDDGSKDNTYKIMKELEEESKQNNNNNNN
AglJ	(1)	MPTPDAVCILTPTYNEAETIADVISDYRDEGFANVLVIDGGSTDGTRELAEDAGAHVVVQSGSGKG
AglK	(66)	NNNNKVIAIKHEQNKGVGGATITGLKKAYELGADIAVTFDADGQHAPDDIAKVIQP
AglJ	(67)	QAVREAVEDHIQAPYVLMLDGDGTYEATDATKMLDPLTEGYDHVIGDRFADMRPGAMTRLNRVGNR
AglK	(1)	-MADKLIYLIIPAYNEEKMIKNVVNNLQNHNYDNIIIVDDGSKDNTYKIMKELEEESKQNNNNNNN
AglJ	(1)	MPTPDAVCILTPTYNEAETIADVISDYRDEGFANVLVIDGGSTDGTRELAEDAGAHVVVQSGSGKG
AglK	(66)	NNNNKVIAIKHEQNKGVGGATITGLKKAYELGADTAVTFDADGQHAPDDIAKVIQP
AglJ	(67)	QAVREAVEDHIQAPYVLMLDGDGTYEATDATKMLDPLTEGYDHVIGDRFADMRPGAMTRLNRVGNR
AglK	(122)	IINDSKEYVVGSRIKNPKEFKNMPLTKKVGNLGLSFITFLLGGYYV
AglK	(133)	IINRAFAFIHGQDFRDILSGYRAFTRESFLDMTLTSDGFGIETEMAVECAKRCIKTTVVPTTYYPR
AglK	(1)	-MADKLIYLIIPAYNEEKMIKNVVNNLQNHNYDNIIIVDDGSKDNTYKIMKELEEESKQNNNNNNN
AglJ	(1)	MPTPDAVCILTPTYNEAETIADVISDYRDEGFANVLVIDGGSTDGTRELAEDAGAHVVVQSGSGKG
AglK	(66)	NNNNKVIAIKHEQNKGVGGATITGLKKAYELGADTAVTEDADGQHAPDDIAKVIQP
AglJ	(67)	QAVREAVEDHIQAPYVLMLDGDGTYEATDATKMLDPLTEGYDHVTGDRFADMRPGAMTRLNRVGNR
AglK	(122)	IINDSKEYVVGSRIKNPKEFKNMPLTKKVGNLGLSFITFLLGGYYV
AglJ	(133)	IINRAFAFIHGQDFRDILSGYRAFTRESFLDMTLTSDGFGIETEMAVECAKRGIKTTVVPTTYYPR
AglK	(168)	TD-SQSGLRAFSKSALKVISEQLRAKRYETCSEALIIAKKNKLNIGEVPIK
AglJ	(199)	PDGSDTNLDPIRDGGIIFUELYRRAKTNNPLFYFGSVGFASTATGLGLALYVAYEWVVRSISHEVI
AglK AglJ AglK AglJ AglK AglJ AglK AglJ AglK AglJ	<pre>(1) (1) (66) (67) (122) (133) (168) (199) (218) (265)</pre>	

С

AglK	(1)	MADKLIYLIIPAYNEEKMIKNVVNNLQNHNYDNIIIVDDGSKDNTYKIMKELEEESKQNNNNN
MMP1170	(1)	MEKNDIFVVIPAYNEEKMIKNTLINLKSHGYENIIVVDDGSRDNTSKIAISEE
AglK	(64)	NNNNNNKVIAIKHEQNKGVGGATITGLKKAYELGADIAVTFDADGQHAPDDIAKVIQPIINDS
MMP1170	(54)	VIVCKHIINRGLGGALKTGLKCAVKYNPKVIVTFDADGQHDPEDIFKVSEPILEDS
AglK	(127)	KEYVVGSRIKNPKEFKNMPLTKK <mark>VGNLGL</mark> SFITFLLGGYYVTDSQSGLRAFSKSALKVLSEQL
MMP1170	(110)	FDVVVGSRLIDENELKNMPLIKKIGNWGLNFITYLMGGRMVTDSQGGLRAFSYDAAEIVSKQL
AglK	(190)	RAKRYETCSEALIIAKKNKLNIGEVPIKTIYTEYSMARGTNVMIGFKIFYRLLMLKMGKVLD
MMP1170	(173)	KSNRYEVSSEFIVLFKKNNLKFKEVPIKTIYTEYSMARGTNVITGFKILFKLLIQKLI

**Supplementary Figure 2:** Alignment of AglK from *M. voltae* with (A) the dolichyl-phosphate  $\beta$ -glucosyltransferase (DPG) Alg5 from *S. cerevisiae*, (B) AglJ from *H. volcanii*, or (C) MMP1170 from *M. maripaludis*. Residues highlighted in black indicate sequence identity (25% for Alg5, 18% for AglJ, and 60% for MMP1170) and those in gray and black denote sequence similarity (53% for Alg5, 43% for AglJ, and 79% for MMP1170). The alignment was performed using ClustalW.



**Supplementary Figure 3**: ESI-MS (negative ion mode) of purified Dol-P-GlcNAc (calcd.  $[M-H]^{-}$  = 1050.8). The (C55) Dol-linked product was enriched during HPLC purification



**Supplementary Figure 4**: (A) <sup>1</sup>H NMR spectrum of Dol-P-GlcNAc. (B) (i) Expansion of the <sup>31</sup>P decoupled <sup>1</sup>H NMR spectrum of the anomeric proton for Dol-P-GlcNAc, a doublet with a coupling constant of 3.4 Hz ( $J_{1,2}$ ). (ii) Expansion of the <sup>1</sup>H NMR spectrum of the anomeric proton for Dol-P-GlcNAc, a doublet of doublets with coupling constants of 3.4 ( $J_{1,2}$ ) and 6.4 ( $J_{1,P}$ ) Hz.



**Supplementary Figure 5**: Capillary electrophoresis of AglK reaction products after aqueous extractions of the reaction mixture in order to identify the nucleotide product as UDP. In each case, (1) UDP, (2) UMP, or (3) UDP-GlcNAc was spiked into the reaction mixture in order to identify the nucleotide peak. CE was performed on a Hewlett-Packard 3D CE system. A bare silica capillary (75  $\mu$ m x 80 cm) was used with a detector distance of 72 cm. The running buffer was 25 mM sodium tetraborate (pH 9.5). The capillary was conditioned before each run with a 0.4 M NaOH wash for 2 min, H<sub>2</sub>O for 2 min, and running buffer for 2 min. Samples were introduced by pressure injection for 16 s at 30 mbar, and the separation was performed at 25 kV and monitored at 254 nm.



**Supplementary Figure 6**: (A) ESI-MS (negative ion mode) of *M. maripaludis* lipid extraction after HPLC purification, where calcd.  $[M-2H+Na]^{-} = 1692.0$  and  $[M-2H]^{2^{-}} = 834.5$ . (B) Structure of the  $\alpha$ - and  $\omega$ -saturated Dol-P-trisaccharide, ManNAc3NAm(6Thr)A- $\beta$ 1,4-Glc-2,3-diNAcA- $\beta$ 1,3-GalNAc-P-Dol. (C) TLC of (C55) Dol-P (1-2), *M. maripaludis* lipid extract (4-5), and co-spot (3). The Dol-P-trisaccharide purified by HPLC is indicated by an arrow.



**Supplementary Figure 7**: ESI-MS (negative ion mode) of Dol-P-GlcNAc-Glc-2,3-diNAcA (calcd. [M-H]<sup>-</sup> = 1308.8).



**Supplementary Figure 8**: ESI-MS (positive ion mode) of the glycopeptide produced by AglB (calcd.  $[M+H]^+ = 1875.8$ ).



**Supplementary Figure 9**: Synthesis of (C55-60) Dol-PP-GlcNAc (1) and (C85-105) Dol-PP-GlcNAc. Reagents and conditions: (a) Ac<sub>2</sub>O, pyr; (b) HN(CH<sub>3</sub>)<sub>2</sub>, CH<sub>3</sub>CN; (c) dibenzyl *N*,*N*-phosphoramidite, 1,2,4-triazole, CH<sub>2</sub>Cl<sub>2</sub>; (d) 1% H<sub>2</sub>O<sub>2</sub>, -78 °C; (e) Pd(OH)<sub>2</sub>/C, H<sub>2</sub>, NEt<sub>3</sub>; (f) CDI, DMF; (g) MeOH, then Dol-P (C55-60 or C85-105), CH<sub>2</sub>Cl<sub>2</sub>; (h) 1% NaOMe/MeOH.

**Supplementary Table 1**: (A) Dol-P-GlcNAc (B) <sup>1</sup>H and <sup>13</sup>C NMR assignments (ppm) and coupling constants (Hz) for the dolichyl portion of Dol-P-GlcNAc. (C) <sup>1</sup>H and <sup>13</sup>C NMR assignments (ppm) and coupling constants (Hz) for the GlcNAc portion of Dol-P-GlcNAc.



В	Dolichyl-Phosph	nate		lsop
lsoprene uni	t Methyl group	s δC	δ <b>H</b>	
α	H CH <sub>3</sub> (cis)	20.0	0.79	
β <b>to</b> ω-3	H CH <sub>3</sub> (cis)	23.2	1.55	
<b>ω-1, ω-2</b>	H CH <sub>3</sub> (trans)	16.0, 17.6	1.55	lsop
ω	H CH <sub>3</sub> (cis) CH <sub>3</sub> (trans)	25.8 ( <i>cis</i> ), 15.5 ( <i>trans</i> )	1.55	
lsoprene uni	t Methylene grou	up δC	δΗ	
α	PO-CH2	64.9	3.86	(
α	<b>н₂с</b> <	37.5	1.29	
α	PO-CH <sub>2</sub> (cis	37.9	1.39, 1.62	
$\beta$ to $\omega$		26.6	2.01	
β <b>to</b> ω-3	H CH <sub>2</sub> (cis)	32.1	1.98	
<b>ω-1</b> , ω-2	H CH <sub>2</sub> (trans)	39.7	1.94	

oprene unit	Methine groups	δC	δΗ
α	РОСҢ	29.1	1.28
β <b>to</b> ω-3		124.4	5.06
ω to ω-2	H CH <sub>3</sub> (trans)	129.9	5.09
oprene unit	Quaternary carbor	is δC	
oprene unit α		<b>is</b> δ <b>C</b> 135.5	
ρ <b>prene unit</b> α β to ω-3	Quaternary carbon $H \rightarrow C^{H_3(cis)}$ $H \rightarrow C^{CH_3(ris)}$ $H \rightarrow C^{CH_3(trans)}$	<b>is</b> δ <b>C</b> 135.5 134.9	

CH<sub>3</sub> (trans)

GIcNAc

## С

Proton	δ <b>Η (Hz)</b>	Carbon	δC
H-1 (J <sub>1,2</sub> )	5.36 (3.4)	C-1	94.2
H-1 (J <sub>1,P</sub> )	5.36 (6.4)		
H-2 (J <sub>2,3</sub> )	3.89 (9.4)	C-2	54.0
H-3 (J <sub>3,4</sub> )	3.63 (10.0)	C-3	71.5
H-4	3.26	C-4	67.7
H-5	3.82	C-5	73.7
H-6 (J <sub>5,6</sub> )	3.53 (7.6)	C-6	62.3
H-6 (J <sub>6,6'</sub> )	3.53 (9.9)		
H-6'	3.91		
		C=O	171.3
CH <sub>3</sub>	1.96		22.6