

University of Groningen

## Impact of *Lactobacillus plantarum* Sortase on Target Protein Sorting, Gastrointestinal Persistence, and Host Immune Response Modulation

Remus, Daniela M.; Bongers, Roger S.; Meijerink, Marjolein; Fusetti, Fabrizia; Poolman, Berend; de Vos, Paulus; Wells, Jerry M.; Kleerebezem, Michiel; Bron, Peter A.

*Published in:*  
Journal of Bacteriology

*DOI:*  
[10.1128/JB.01321-12](https://doi.org/10.1128/JB.01321-12)

**IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.**

*Document Version*  
Publisher's PDF, also known as Version of record

*Publication date:*  
2013

[Link to publication in University of Groningen/UMCG research database](#)

*Citation for published version (APA):*

Remus, D. M., Bongers, R. S., Meijerink, M., Fusetti, F., Poolman, B., de Vos, P., ... Bron, P. A. (2013). Impact of *Lactobacillus plantarum* Sortase on Target Protein Sorting, Gastrointestinal Persistence, and Host Immune Response Modulation. *Journal of Bacteriology*, 195(3), 502-509. DOI: 10.1128/JB.01321-12

### Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

### Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

**Table S2:** Significant fold-changes (False discovery rate  $\leq 0.05$ ) of gene expression in response to *srtA* gene deletion

Gene ID	Gene name	Function	fold change
lp_0076	fusA1	elongation factor G	-100
lp_0077	lp_0077	unknown	-19
lp_0078	lp_0078	transport protein	-10
lp_0080	lp_0080	acetyltransferase, GNAT family (putative)	-13
lp_0915	lp_0915	phage protein	82
lp_1196	lp_1196	integrase/recombinase	-23
lp_1197	cps2A	polysaccharide biosynthesis protein, chain length regulator (putative)	62
lp_1198	cps2B	polysaccharide biosynthesis protein; regulator	22
lp_1199	cps2C	polysaccharide biosynthesis protein; phosphatase (putative)	23
lp_1200	cps2D	UDP N-acetyl glucosamine 4-epimerase, NAD dependent	12
lp_1201	cps2E	priming glycosyltransferase	16
lp_1202	cps2F	glycosyltransferase	13
lp_1203	cps2G	polysaccharide biosynthesis protein	10
lp_1204	cps2H	polysaccharide polymerase	12
lp_1205	cps2I	oligosaccharide transporter (flippase)	6
lp_1206	cps2J	Glycosyltransferase	3
lp_1207	cps2K	polysaccharide biosynthesis protein (putative)	3
lp_1386	lp_1386	cation efflux protein (putative)	-2
lp_3444	lp_3444	transcription regulator, Crp family	3
lp_3634	lp_3634	alpha-1,2-mannosidase (putative)	7