

University of Groningen

Bacillus subtilis YqjG is required for genetic competence development

Saller, Manfred J.; Otto, Andreas; Lahpor, Greetje; Becher, Doerte; Hecker, Michael;
Driessen, Arnold

Published in:
Proteomics

DOI:
[10.1002/pmic.201000435](https://doi.org/10.1002/pmic.201000435)

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:
2011

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

Citation for published version (APA):

Saller, M. J., Otto, A., Berrelkamp-Lahpor, G. A., Becher, D., Hecker, M., & Driessen, A. J. M. (2011). Bacillus subtilis YqjG is required for genetic competence development. Proteomics, 11(2), 270-282. DOI: 10.1002/pmic.201000435

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.

PROTEOMICS

Supporting Information for Proteomics

DOI 10.1002/pmic.201000435

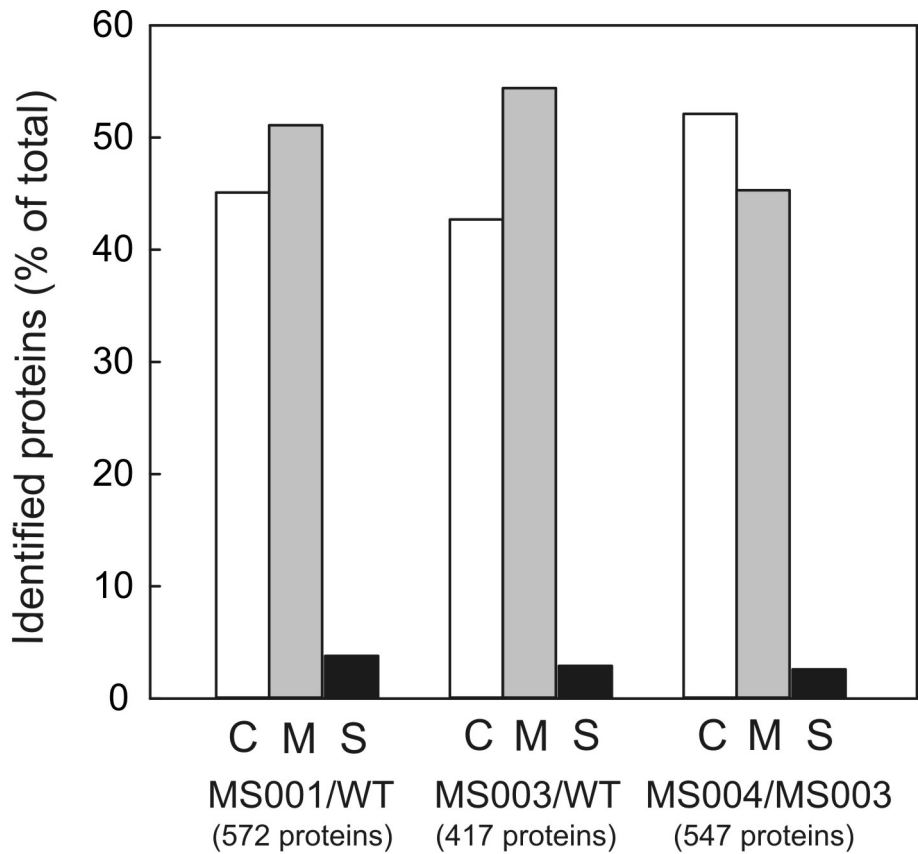
Manfred J. Saller, Andreas Otto, Greetje A. Berrelkamp-Lahpor,

Dörte Becher, Michael Hecker and Arnold J. M. Driessen

***Bacillus subtilis* YqjG is required for genetic competence development**

Supplementary data:

Supplementary Fig. 1. Distribution of the proteins identified by mass-spectrometry. The cellular localization of the proteins identified and quantified by mass-spectrometry were predicted by LocateP (29). C: cytoplasmic proteins, M: membrane proteins, S: secreted proteins. The bar diagram shows the data obtained by the comparison of MS001 and MS003 versus the wild type and a comparison between MS004 versus MS003 as described in the results section.



Supplementary Table 1

Overview of all identified and quantified proteins. All identified and quantified proteins are listed according to their functional classification. Additionally, the protein identification number, a brief protein description and the LocateP-predicted localization are indicated. Changes in protein amounts are expressed as log₂ ratios.