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## Less is more: Genome-reduced *Bacillus subtilis* for protein production

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DOI:  
[10.33612/diss.146898256](https://doi.org/10.33612/diss.146898256)

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

*Publication date:*  
2020

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*Citation for published version (APA):*  
Aguilar Suarez, R. (2020). *Less is more: Genome-reduced Bacillus subtilis for protein production*. University of Groningen. <https://doi.org/10.33612/diss.146898256>

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## References

1. Albalat, R. & Cañestro, C. Evolution by gene loss. *Nat. Rev. Genet.* **17**, 379–391 (2016).
2. Kortschak, R. D., Samuel, G., Saint, R. & Miller, D. J. EST analysis of the cnidarian *Acropora milleporai* reveals extensive gene loss and rapid sequence divergence in the model invertebrates. *Curr. Biol.* **13**, 2190–2195 (2003).
3. Wolf, Y. I. & Koonin, E. V. Genome reduction as the dominant mode of evolution. *BioEssays* **35**, 829–837 (2013).
4. Hedrick, P. W. Population genetics of malaria resistance in humans. *Heredity (Edinb.)* **107**, 283304 (2011).
5. Hodgson, J. A. et al. Natural selection for the Duffy-null allele in the recently admixed people of Madagascar. *Proc. R. Soc. B Biol. Sci.* **281**, (2014).
6. Wendel, J. F. Genome evolution in polyploids. *Plant Mol. Biol.* **42**, 225–249 (2000).
7. Initial sequencing and analysis of the human genome. *Nature* **412**, 565–566 (2001).
8. Puigbò, P., Lobkovsky, A. E., Kristensen, D. M., Wolf, Y. I. & Koonin, E. V. Genomes in turmoil: Quantification of genome dynamics in prokaryote supergenomes. *BMC Med.* **12**, 1–19 (2014).
9. Ziehe, D., Dünschede, B. & Schünemann, D. From bacteria to chloroplasts: Evolution of the chloroplast SRP system. *Biol. Chem.* **398**, 653–661 (2017).
10. Gil, R., Sabater-Muñoz, B., Latorre, A., Silva, F. J. & Moya, A. Extreme genome reduction in *Buchnera* spp.: Toward the minimal genome needed for symbiotic life. *Proc. Natl. Acad. Sci.* **99**, 4454–4458 (2002).
11. Charlat, S. et al. Male-killing bacteria trigger a cycle of increasing male fatigue and female promiscuity. *Curr. Biol.* **17**, 273–277 (2007).
12. Hutchison, C. A. et al. Design and synthesis of a minimal bacterial genome. *Science* **351**, (2016).
13. Gibson, D. G. et al. Creation of a bacterial cell controlled by a chemically synthesized genome. *Science* **329**, 52–56 (2010).
14. Hashimoto, M. et al. Cell size and nucleoid organization of engineered *Escherichia coli* cells with a reduced genome. *Mol. Microbiol.* **55**, 137–149 (2005).
15. Kobayashi, K. et al. Essential *Bacillus subtilis* genes. *Proc. Natl. Acad. Sci.* **100**, 4678–4683 (2003).
16. Komatsu, M., Uchiyama, T., Omura, S., Cane, D. E. & Ikeda, H. Genome-minimized *Streptomyces* host for the heterologous expression of secondary metabolism. *Proc. Natl. Acad. Sci.* **107**, 2646–2651 (2010).
17. Wirth, N. T. & Nikel, P. I. Engineering reduced-genome strains of *Pseudomonas putida* for product valorization. *Minimal Cells Des. Constr. Biotechnol. Appl.* 69–93 (2020) doi:10.1007/978-3-030-31897-0\_3.
18. Petzold, C. J., Chan, L. J. G., Nhan, M. & Adams, P. D. Analytics for metabolic engineering. *Front. Bioeng. Biotechnol.* **3**, 1–11 (2015).
19. Gustavsson, M. & Lee, S. Y. Prospects of microbial cell factories developed through systems metabolic engineering. *Microb. Biotechnol.* **9**, 610–617 (2016).
20. Zhao, L. et al. Construction of second generation protease-deficient hosts of *Bacillus subtilis* for secretion of foreign proteins. *Biotechnol. Bioeng.* **116**, 2052–2060 (2019).
21. Blattner, C. et al. Enhanced production of recombinant CRM197 in *Escherichia coli*. Patent (2017).
22. Rousset, F. et al. Genome-wide CRISPR-dCas9 screens in *E. coli* identify essential genes and phage host factors. *PLoS Genet.* **14**, 1–28 (2018).
23. Glass, J. I. et al. Essential genes of a minimal bacterium. *Proc. Natl. Acad. Sci.* **103**, 425–430 (2006).
24. Suthers, P. F., Zomorodi, A. & Maranas, C. D. Genome-scale gene/reaction essentiality and synthetic lethality analysis. *Mol. Syst. Biol.* **5**, 1–17 (2009).
25. Gibson, D. G. et al. Complete chemical synthesis, assembly, and cloning of a *Mycoplasma genitalium* genome. *Science* **319**, 1215–1220 (2008).
26. Reuß, D. R. et al. Large-scale reduction of the *Bacillus subtilis* genome: consequences for the transcriptional network, resource allocation, and metabolism. *Genome Res.* **27**, 289–299 (2017).
27. Murakami, K. et al. Large scale deletions in the *Saccharomyces cerevisiae* genome create strains with altered regulation of carbon metabolism. *Appl. Microbiol. Biotechnol.* **75**, 589–597 (2007).
28. Hirokawa, Y. et al. Genetic manipulations restored the growth fitness of reduced-genome *Escherichia coli*. *J. Biosci. Bioeng.* **116**, 52–58 (2013).

29. Stülke, J. & Zhu, B. The minimal genome project for *Bacillus subtilis*. <http://www.minibacillus.org/> (2020).
30. Komatsu, M. et al. Engineered *Streptomyces avermitilis* host for heterologous expression of biosynthetic gene cluster for secondary metabolites. *ACS Synth. Biol.* **2**, 384–396 (2013).
31. Mizoguchi, H., Sawano, Y., Kato, J. I. & Mori, H. Superpositioning of deletions promotes growth of *Escherichia coli* with a reduced genome. *DNA Res.* **15**, 277–284 (2008).
32. Shen, X. et al. Developing genome-reduced *Pseudomonas chlororaphis* strains for the production of secondary metabolites. *BMC Genomics* **18**, 1–14 (2017).
33. Pohl, S. et al. Proteomic analysis of *Bacillus subtilis* strains engineered for improved production of heterologous proteins. *Proteomics* **13**, 3298–3308 (2013).
34. Wu, S. C. et al. Functional production and characterization of a fibrin-specific single-chain antibody fragment from *Bacillus subtilis*: Effects of molecular chaperones and a wall-bound protease on antibody fragment production. *Appl. Environ. Microbiol.* **68**, 3261–3269 (2002).
35. Ara, K. et al. *Bacillus* minimum genome factory: effective utilization of microbial genome information. *Biotechnol. Appl. Biochem.* **46**, 169–178 (2007).
36. Manabe, K. et al. Combined effect of improved cell yield and increased specific productivity enhances recombinant enzyme production in genome-reduced *Bacillus subtilis* strain MGB874. *Appl. Environ. Microbiol.* **77**, 8370–8381 (2011).
37. Westers, H. et al. Genome engineering reveals large dispensable regions in *Bacillus subtilis*. *Mol. Biol. Evol.* **20**, 2076–2090 (2003).
38. Baumgart, M. et al. Construction of a prophage-free variant of *Corynebacterium glutamicum* ATCC 13032 for use as a platform strain for basic research and industrial biotechnology. *Appl. Environ. Microbiol.* **79**, 6006–6015 (2013).
39. Wenzel, M. & Altenbuchner, J. Development of a markerless gene deletion system for *Bacillus subtilis* based on the mannose phosphoenolpyruvate-dependent phosphotransferase system. 1942–1949 (2015) doi:10.1099/mic.o.000150.
40. Stoebel, D. M., Dean, A. M. & Dykhuizen, D. E. The cost of expression of *Escherichia coli* lac operon proteins is in the process, not in the products. *Genetics* **178**, 1653–1660 (2008).
41. WHO. Thirteenth General Programme of Work. 1–54 (2019).
42. Lipsitch, M. & Siber, R. How can vaccines contribute to solving the antimicrobial resistance problem? *MBio* **7**, 1–8 (2016).
43. Fowler, V. G. & Proctor, R. A. Where does a *Staphylococcus aureus* vaccine stand? *Clin. Microbiol. Infect.* **20**, 66–75 (2014).
44. van den Berg, S. et al. A human monoclonal antibody targeting the conserved staphylococcal antigen IsaA protects mice against *Staphylococcus aureus* bacteremia. *Int. J. Med. Microbiol.* **305**, 55–64 (2015).
45. Hoekstra, H. et al. A human monoclonal antibody that specifically binds and inhibits the staphylococcal complement inhibitor protein SCIN. *Virulence* **0**, 1–13 (2017).
46. Rosman, C. W. K. et al. Ex vivo tracer efficacy in optical imaging of *Staphylococcus aureus* nuclease activity. *Sci. Rep.* **8**, 1–8 (2018).
47. Hemmerich, J., Noack, S., Wiechert, W. & Oldiges, M. Microbioreactor systems for accelerated bioprocess development. *Biotechnol. J.* **13**, 1–9 (2018).
48. Kunst, F. et al. The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. *Nature* **390**, 249–256 (1997).
49. Buescher, J. M. et al. Global network reorganization during dynamic adaptations of *Bacillus subtilis* metabolism. *Science*. **335**, 1099–1103 (2012).
50. Nicolas, P. et al. Condition-dependent transcriptome reveals high-level regulatory architecture *Bacillus subtilis*. *Science*. **335**, 1103–1106 (2012).
51. Tanaka, K. et al. Building the repertoire of dispensable chromosome regions in *Bacillus subtilis* entails major refinement of cognate large-scale metabolic model. *Nucleic Acids Res.* **41**, 687–699 (2013).
52. Hohmann, H., van Dijk, J. M., Krishnappa, L. & Pragá, Z. *Host Organisms: Bacillus subtilis*. *Industrial Biotechnology* (Wiley-VCH Verlag GmbH, 2016). doi:10.1002/9783527807796.ch7.
53. Reuß, D. R., Commichau, F. M., Gundlach, J., Zhu, B. & Stülke, J. The blueprint of a minimal cell: mini*Bacillus*. *Microbiol. Mol. Biol. Rev.* **80**, 955–987 (2016).
54. Li, Y. et al. Characterization of genome-reduced *Bacillus subtilis* strains and their application for the production of guanosine and thymidine. *Microb. Cell Fact.* **15**:94, 1–15 (2016).
55. Stephenson, K. & Harwood, C. R. Influence of a cell-wall-associated protease on production of alpha-amylase by *Bacillus subtilis*. *Appl. Environ.*

## References

- Microbiol.* **64**, 2875–2881 (1998).
56. Krishnappa, L., Monteferrante, C. G., Neef, J., Dreisbach, A. & van Dijl, J. M. Degradation of extracytoplasmic catalysts for protein folding in *Bacillus subtilis*. *Appl. Environ. Microbiol.* **80**, 1463–1468 (2014).
  57. Westers, H. et al. The CsxRS two-component regulatory system controls a general secretion stress response in *Bacillus subtilis*. *FEBS J.* **273**, 3816–3827 (2006).
  58. Neef, J. et al. Versatile vector suite for the extracytoplasmic production and purification of heterologous His-tagged proteins in *Lactococcus lactis*. *Appl. Microbiol. Biotechnol.* **99**, 9037–9048 (2015).
  59. Bongers, R. S. et al. Development and characterization of a Subtilin-Regulated Expression System in *Bacillus subtilis*: strict control of gene expression by addition of subtilin. *Appl. Environ. Microbiol.* **71**, 8818–24 (2005).
  60. Palva, I. Molecular cloning of  $\alpha$ -amylase gene from *Bacillus amyloliquefaciens* and its expression in *B. subtilis*. *Gene* **19**, 81–87 (1982).
  61. Gilbert, C., Howarth, M., Harwood, C. R. & Ellis, T. Extracellular self-assembly of functional and tunable protein conjugates from *Bacillus subtilis*. *ACS Synth. Biol.* **6**, 957–967 (2017).
  62. Darmon, E. et al. A novel class of heat and secretion stress-responsive genes is controlled by the autoregulated CsxRS two-component system of *Bacillus subtilis*. *J. Bacteriol.* **184**, 5661–5671 (2002).
  63. Hyrylainen, H. L. et al. A novel two-component regulatory system in *Bacillus subtilis* for the survival of severe secretion stress. *Mol. Microbiol.* **41**, 1159–1172 (2001).
  64. Krishnappa, L. et al. Extracytoplasmic proteases determining the cleavage and release of secreted proteins, lipoproteins, and membrane proteins in *Bacillus subtilis*. *J. Proteome Res.* **12**, 4101–4110 (2013).
  65. Antelmann, H. et al. The extracellular proteome of *Bacillus subtilis* under secretion stress conditions. *Mol. Microbiol.* **49**, 143–156 (2003).
  66. Zweers, J. C., Wiegert, T. & van Dijl, J. M. Stress-responsive systems set specific limits to the overproduction of membrane proteins in *Bacillus subtilis*. *Appl. Environ. Microbiol.* **75**, 7356–7364 (2009).
  67. Reilman, E., Mars, R. A. T. T., van Dijl, J. M. & Denham, E. L. The multidrug ABC transporter BmrC/BmrD of *Bacillus subtilis* is regulated via a ribosome-mediated transcriptional attenuation mechanism. *Nucleic Acids Res.* **42**, 11393–11407 (2014).
  68. Neef, J., Koedijk, D. G. A. M., Bosma, T., van Dijl, J. M. & Buist, G. Efficient production of secreted staphylococcal antigens in a non-lysing and proteolytically reduced *Lactococcus lactis* strain. *Appl. Microbiol. Biotechnol.* **98**, 10131–10141 (2014).
  69. Botella, E. et al. pBaSysBioII: An integrative plasmid generating *gfp* transcriptional fusions for high-throughput analysis of gene expression in *Bacillus subtilis*. *Microbiology* **156**, 1600–1608 (2010).
  70. Nepal, S. et al. An ancient family of mobile genomic islands introducing cephalosporinase and carbapenemase genes in *Enterobacteriaceae*. *Virulence* **9**, 1377–1389 (2018).
  71. Szybalski, W. In Vivo and in Vitro Initiation of Transcription. in *Control of Gene Expression* (eds. Kohn, A. & Shatky, A.) 23–24 (Springer US, 1974). doi:10.1007/978-1-4684-3246-6\_3.
  72. Elowitz, M. B. & Leibler, S. A synthetic oscillatory network repressilator. *Nature* **403**, 335–338 (2000).
  73. Gardner, T. S., Cantor, C. R. & Collins, J. J. Construction of a genetic toggle switch in *Escherichia coli*. *Nature* **403**, 339–342 (2000).
  74. Ro, D. K. et al. Production of the antimalarial drug precursor artemisinic acid in engineered yeast. *Nature* **440**, 940–943 (2006).
  75. Agapakis, C. M. et al. Insulation of a synthetic hydrogen metabolism circuit in bacteria. *J. Biol. Eng.* **4**, 1–15 (2010).
  76. Fredens, J. et al. Total synthesis of *Escherichia coli* with a recoded genome. *Nature* **569**, 514–518 (2019).
  77. Venetz, J. E. et al. Chemical synthesis rewriting of a bacterial genome to achieve design flexibility and biological functionality. *Proc. Natl. Acad. Sci.* **116**, 8070–8079 (2019).
  78. Parekh, S., Vinci, V. A. & Strobel, R. J. Improvement of microbial strains and fermentation processes. *Appl. Microbiol. Biotechnol.* **54**, 287–301 (2000).
  79. Lee, S. Y., Mattanovich, D. & Villaverde, A. Systems metabolic engineering, industrial biotechnology and microbial cell factories. *Microb. Cell Fact.* **11**, (2012).
  80. Makino, T., Skretas, G. & Georgiou, G. Strain engineering for improved expression of recombinant proteins in bacteria. *Microb. Cell Fact.* **10**, 1–10 (2011).

81. Lee, S. Y., Lee, D.-Y. & Kim, T. Y. Systems biotechnology for strain improvement. *Trends Biotechnol.* **23**, 349–358 (2005).
82. Chen, Z., Wilmanns, M. & Zeng, A. P. Structural synthetic biotechnology: From molecular structure to predictable design for industrial strain development. *Trends Biotechnol.* **28**, 534–542 (2010).
83. Aggarwal, K. & Lee, K. H. Functional genomics and proteomics as a foundation for systems biology. *Briefings Funct. Genomics Proteomics* **2**, 175–184 (2003).
84. Malmström, J. et al. Proteome-wide cellular protein concentrations of the human pathogen *Leptospira interrogans*. *Nature* **460**, 762–765 (2009).
85. Maaß, S. et al. Efficient, global-scale quantification of absolute protein amounts by integration of targeted mass spectrometry and two-dimensional gel-based proteomics. *Anal. Chem.* **83**, 2677–2684 (2011).
86. Maaß, S. et al. Highly precise quantification of protein molecules per cell during stress and starvation responses in *Bacillus subtilis*. *Mol. Cell. Proteomics* **13**, 2260–2276 (2014).
87. Muntel, J. et al. Comprehensive absolute quantification of the cytosolic proteome of *Bacillus subtilis* by data independent, parallel fragmentation in liquid chromatography/mass spectrometry (LC/MSE). *Mol. Cell. Proteomics* **13**, 1008–1019 (2014).
88. Wiśniewski, J. R. & Rakus, D. Multi-enzyme digestion FASP and the 'Total Protein Approach' based absolute quantification of the *Escherichia coli* proteome. *J. Proteomics* **109**, 322–331 (2014).
89. van Dijk, J. M. & Hecker, M. *Bacillus subtilis*: from soil bacterium to super-secreting cell factory. *Microb. Cell Fact.* **12**, 3 (2013).
90. Zweers, J. C. et al. Towards the development of *Bacillus subtilis* as a cell factory for membrane proteins and protein complexes. *Microb. Cell Fact.* **7**, 10 (2008).
91. Schallmey, M., Singh, A. & Ward, O. P. Developments in the use of *Bacillus* species for industrial production. *Can. J. Microbiol.* **50**, 1–17 (2004).
92. Westers, L., Westers, H. & Quax, W. J. *Bacillus subtilis* as cell factory for pharmaceutical proteins: A biotechnological approach to optimize the host organism. *Biochim. Biophys. Acta - Mol. Cell Res.* **1694**, 299–310 (2004).
93. Aguilar Suárez, R., Stülke, J. & van Dijk, J. M. Less is more: Toward a genome-reduced *Bacillus* cell factory for 'difficult proteins'. *ACS Synth. Biol.* **8**, 99–108 (2019).
94. Antelo-Varela, M. et al. Ariadne's thread in the analytical labyrinth of membrane proteins: integration of targeted and shotgun proteomics for global absolute quantification of membrane proteins. *Anal. Chem.* **91**, 11972–11980 (2019).
95. Pohl, S. & Harwood, C. R. Heterologous protein secretion by *Bacillus* species. From the cradle to the grave. *Advances in Applied Microbiology* vol. 73 (Elsevier Inc., 2010).
96. Rahmer, R., Heravi, K. M. & Altenbuchner, J. Construction of a super-competent *Bacillus subtilis* 168 using the PmtIA-comKS inducible cassette. *Front. Microbiol.* **6**, 1–11 (2015).
97. Bradford, M. M. A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Anal. Biochem.* **72**, 248–254 (1976).
98. Bonn, F. et al. Picking vanished proteins from the void: How to collect and ship/share extremely dilute proteins in a reproducible and highly efficient manner. *Anal. Chem.* **86**, 7421–7427 (2014).
99. Abràmoff, M. D., Magalhães, P. J. & Ram, S. J. Image processing with ImageJ Part II. *Biophotonics Int.* **11**, 36–43 (2005).
100. Eymann, C. et al. A comprehensive proteome map of growing *Bacillus subtilis* cells. *Proteomics* **4**, 2849–2876 (2004).
101. Tyanova, S., Temu, T. & Cox, J. The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. *Nat. Protoc.* **11**, 2301–2319 (2016).
102. Cox, J. et al. Andromeda: A peptide search engine integrated into the MaxQuant environment. *J. Proteome Res.* **10**, 1794–1805 (2011).
103. Schwanhäusser, B. et al. Global quantification of mammalian gene expression control. *Nature* **473**, 337–342 (2011).
104. Perez-Riverol, Y. et al. The PRIDE database and related tools and resources in 2019: Improving support for quantification data. *Nucleic Acids Res.* **47**, D442–D450 (2019).
105. Deutsch, E. W. et al. The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. *Nucleic Acids Res.* **45**, 1100–1106 (2017).
106. Tyanova, S. et al. The Perseus computational platform for comprehensive analysis of (prote)omics data. *Nat. Methods* **13**, 731–740 (2016).
107. MacLean, B. et al. Skyline: An open source

## References

- document editor for creating and analyzing targeted proteomics experiments. *Bioinformatics* **26**, 966–968 (2010).
108. Goosens, V. J. et al. Novel twin-arginine translocation pathway-dependent phenotypes of *Bacillus subtilis* unveiled by quantitative proteomics. *J. Proteome Res.* **12**, 796–807 (2013).
  109. Jongbloed, J. D. H. et al. Two minimal Tat translocases in *Bacillus*. *Mol. Microbiol.* **54**, 1319–1325 (2004).
  110. Tusnády, G. E. & Simon, I. The HMMTOP transmembrane topology prediction server. *Bioinformatics* **17**, 849–850 (2001).
  111. Papanastasiou, M. et al. The *Escherichia coli* peripheral inner membrane proteome. *Mol. Cell. Proteomics* **12**, 599–610 (2012).
  112. García-Pérez, A. N. et al. From the wound to the bench: Exoproteome interplay between wound-colonizing *Staphylococcus aureus* strains and co-existing bacteria. *Virulence* **9**, 363–378 (2018).
  113. Palva, I. et al. Secretion of interferon by *Bacillus subtilis*. *Gene* **22**, 229–235 (1983).
  114. Mäder, U., Schmeisky, A. G., Flórez, L. A. & Stülke, J. SubtiWiki -A comprehensive community resource for the model organism *Bacillus subtilis*. *Nucleic Acids Res.* **40**, 1278–1287 (2012).
  115. Hyryläinen, H. L. et al. Penicillin-binding protein folding is dependent on the PrsA peptidyl-prolyl cis-trans isomerase in *Bacillus subtilis*. *Mol. Microbiol.* **77**, 108–127 (2010).
  116. Percy, M. G. & Gründling, A. Lipoteichoic acid synthesis and function in Gram-positive bacteria. *Annu. Rev. Microbiol.* **68**, 81–100 (2014).
  117. Neuhaus, F. C. & Baddiley, J. A Continuum of anionic charge: structures and functions of d-alanyl-teichoic acids in Gram-positive bacteria. *Microbiol. Mol. Biol. Rev.* **67**, 686–723 (2003).
  118. Eiamphungporn, W. & Helmann, J. D. The *Bacillus subtilis*  $\sigma$ M regulon and its contribution to cell envelope stress responses. *Mol. Microbiol.* **67**, 830–848 (2008).
  119. Hyryläinen, H. L., Sarvas, M. & Kontinen, V. P. Transcriptome analysis of the secretion stress response of *Bacillus subtilis*. *Appl. Microbiol. Biotechnol.* **67**, 389–396 (2005).
  120. Glick, B. Metabolic load and heterologous gene expression. *Biotechnol. Adv.* **13**, 247–261 (1995).
  121. Tjalsma, H. et al. Proteomics of protein secretion by *Bacillus subtilis*: Separating the ‘secrets’ of the secretome. *Microbiol. Mol. Biol.* **68**, 207–233 (2004).
  122. Bolhuis, A. et al. SecDF of *Bacillus subtilis*, a molecular siamese twin required for the efficient secretion of proteins. *J. Biol. Chem.* **273**, 21217–21224 (1998).
  123. Tsirigotaki, A., De Geyter, J., Šoštarić, N., Economou, A. & Karamanou, S. Protein export through the bacterial Sec pathway. *Nat. Rev. Microbiol.* **15**, 21 (2016).
  124. van Wely, K. H. M., Swaving, J., Freudl, R. & Driessen, A. J. M. Translocation of proteins across the cell envelope of Gram-positive bacteria. *FEMS Microbiol. Rev.* **25**, 437–454 (2001).
  125. Chen, J. et al. Combinatorial Sec pathway analysis for improved heterologous protein secretion in *Bacillus subtilis*: identification of bottlenecks by systematic gene overexpression. *Microb. Cell Fact.* **14**, 92 (2015).
  126. Saller, M. J. et al. *Bacillus subtilis* YqjG is required for genetic competence development. *Proteomics* **11**, 270–282 (2011).
  127. Hahne, H. et al. A comprehensive proteomics and transcriptomics analysis of *Bacillus subtilis* salt stress adaptation. **192**, 870–882 (2010).
  128. Dreisbach, A. et al. Monitoring of changes in the membrane proteome during stationary phase adaptation of *Bacillus subtilis* using in vivo labeling techniques. *Proteomics* **8**, 2062–2076 (2008).
  129. Lopez, D., Vlamakis, H. & Kolter, R. Generation of multiple cell types in *Bacillus subtilis*. *FEMS Microbiol. Rev.* **33**, 152–163 (2009).
  130. Dubnau, D. & Losick, R. Bistability in bacteria. *Mol. Microbiol.* **61**, 564–572 (2006).
  131. Kearns, D. B. & Losick, R. Cell population heterogeneity during growth of *Bacillus subtilis*. *Genes Dev.* **19**, 3083–3094 (2005).
  132. Bolhuis, A. et al. Evaluation of bottlenecks in the late stages of protein secretion in *Bacillus subtilis*. *Appl. Environ. Microbiol.* **65**, 2934–2941 (1999).
  133. von Heijne, G. & Abrahmsen, L. Species-specific variation in signal peptide design. *FEBS Lett.* **244**, 439–446 (1989).
  134. von Heijne, G. Life and death of a signal peptide. *Nature* **396**, 111–113 (1998).
  135. Tjalsma, H. et al. Functional analysis of the secretory precursor processing machinery of *Bacillus subtilis*: Identification of a eubacterial homolog of archaeal and eukaryotic signal peptidases. *Genes Dev.* **12**, 2318–2331 (1998).
  136. Guest, R. L., Wang, J., Wong, J. L. & Raivio, T. L. A bacterial stress response regulates respiratory



- protein complexes to control envelope stress adaptation. *J. Bacteriol.* **199**, 1–14 (2017).
137. Hyryläinen, H. L. et al. D-alanine substitution of teichoic acids as a modulator of protein folding and stability at the cytoplasmic membrane/cell wall interface of *Bacillus subtilis*. *J. Biol. Chem.* **275**, 26696–26703 (2000).
  138. Hughes, A. H., Hancock, I. C. & Baddiley, J. The function of teichoic acids in cation control in bacterial membranes. *Biochem. J.* **132**, 83 LP–93 (1973).
  139. Reardon-Robinson, M. E. & Ton-That, H. Disulfide-bond-forming pathways in Gram-positive bacteria. *J. Bacteriol.* **198**, 746–754 (2016).
  140. Bolhuis, A., Venema, G., Quax, W. J., Bron, S. & van Dijk, J. M. Functional analysis of paralogous thiol-disulfide oxidoreductases in *Bacillus subtilis*. *J. Biol. Chem.* **274**, 24531–24538 (1999).
  141. Pósfai, G., Umenhoffer, K., Kolisnychenko, V., Stahl, B. & Sharma, S. S. Emergent properties of reduced-genome *Escherichia coli*. *J. Chem. Inf. Model.* **312**, 1044–1047 (2006).
  142. Wittmann, C. & Liao, J. C. *Industrial Biotechnology*. (Wiley-VCH Verlag GmbH, 2017).
  143. Antelo-Varela, M. et al. Membrane modulation of super-secreting ‘midiBacillus’ expressing the major *Staphylococcus aureus* antigen -a mass-spectrometry based absolute quantification approach. *Front. Bioeng. Biotechnol.* **8**, (2020).
  144. Zhu, B. & Stülke, J. SubtiWiki in 2018: From genes and proteins to functional network annotation of the model organism *Bacillus subtilis*. *Nucleic Acids Res.* **46**, D743–D748 (2018).
  145. Grasso, S., van Rijk, T. & van Dijk, J. M. GP4: an integrated Gram-Positive Protein Prediction Pipeline for subcellular localization mimicking bacterial sorting. <http://gp4.hpc.rug.nl> (2020).
  146. Noone, D., Howell, A., Collery, R. & Devine, K. M. YkdA and YvtA, HtrA-like serine proteases in *Bacillus subtilis*, engage in negative autoregulation and reciprocal cross-regulation of ykdA and yvtA gene expression. *J. Bacteriol.* **183**, 654–663 (2001).
  147. Wilson, D. N. & Nierhaus, K. H. The weird and wonderful world of bacterial ribosome regulation. *Crit. Rev. Biochem. Mol. Biol.* **42**, 187–219 (2007).
  148. Schmidt, A. et al. The quantitative and condition-dependent *Escherichia coli* proteome. *Nat. Biotechnol.* **34**, 104–110 (2016).
  149. Dennis, P. P. & Bremer, H. Modulation of chemical composition and other parameters of the cell at different exponential growth rates. *EcoSal Plus* **3**, (2008).
  150. Vitikainen, M. et al. Quantitation of the capacity of the secretion apparatus and requirement for PrsA in growth and secretion of  $\alpha$ -amylase in *Bacillus subtilis*. *J. Bacteriol.* **183**, 1881–1890 (2001).
  151. Zanen, G. et al. Proteomic dissection of potential signal recognition particle dependence in protein secretion by *Bacillus subtilis*. *Proteomics* **6**, 3636–3648 (2006).
  152. Liu, Y. et al. The production of extracellular proteins is regulated by ribonuclease III via two different pathways in *Staphylococcus aureus*. *PLoS One* **6**, (2011).
  153. Eymann, C., Homuth, G., Scharf, C. & Hecker, M. *Bacillus subtilis* functional Genomics: Global characterization of the stringent response by proteome and transcriptome analysis. *J. Bacteriol.* **184**, 2500–2520 (2002).
  154. Schäfer, H. & Turgay, K. Spx, a versatile regulator of the *Bacillus subtilis* stress response. *Curr. Genet.* **65**, 871–876 (2019).
  155. Duarte, V. & Latour, J. M. PerR vs OhrR: Selective peroxide sensing in *Bacillus subtilis*. *Mol. Biosyst.* **6**, 316–323 (2010).
  156. Rojas-Tapias, D. F. & Helmann, J. D. Stabilization of *Bacillus subtilis* Spx under cell wall stress requires the anti-adaptor protein YirB. *PLoS Genet.* **14**, 1–22 (2018).
  157. Yu, N. Y. et al. PSORTb 3.0: Improved protein subcellular localization prediction with refined localization subcategories and predictive capabilities for all prokaryotes. *Bioinformatics* **26**, 1608–1615 (2010).
  158. Bateman, A. et al. UniProt: The universal protein knowledgebase. *Nucleic Acids Res.* **45**, D158–D169 (2017).
  159. Cox, J. et al. Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. *Mol. Cell. Proteomics* **13**, 2513–2526 (2014).
  160. Metsalu, T. & Vilo, J. ClustVis: A web tool for visualizing clustering of multivariate data using Principal Component Analysis and heatmap. *Nucleic Acids Res.* **43**, W566–W570 (2015).
  161. Heberle, H., Meirelles, V. G., da Silva, F. R., Telles, G. P. & Minghim, R. InteractiVenn: A web-based tool for the analysis of sets through Venn diagrams. *BMC Bioinformatics* **16**, 1–7 (2015).
  162. Cowan, D. A. & Burton, S. G. *Biocatalysts and Enzyme Technology*. *Macromolecular Chemistry*

## References

- and Physics vol. 206 (2005).
163. Bakshi, B. R. Toward sustainable chemical engineering: The role of process systems engineering. *Annu. Rev. Chem. Biomol. Eng.* **10**, 265–288 (2019).
  164. Rugbjerg, P., Sarup-Lytzen, K., Nagy, M. & Sommer, M. O. A. Synthetic addiction extends the productive life time of engineered *Escherichia coli* populations. *Proc. Natl. Acad. Sci.* **115**, 2347–2352 (2018).
  165. Unthan, S. et al. Chassis organism from *Corynebacterium glutamicum* - a top-down approach to identify and delete irrelevant gene clusters. *Biotechnol. J.* **10**, 290–301 (2015).
  166. Sharma, S. S., Blattner, F. R. & Harcum, S. W. Recombinant protein production in an *Escherichia coli* reduced genome strain. *Metab. Eng.* **9**, 133–141 (2007).
  167. Earl, A. M., Losick, R. & Kolter, R. Ecology and genomics of *Bacillus subtilis*. *Trends Microbiol.* **16**, 269–275 (2008).
  168. Fischer, E. & Sauer, U. Large-scale in vivo flux analysis shows rigidity and suboptimal performance of *Bacillus subtilis* metabolism. *Nat. Genet.* **37**, 636–640 (2005).
  169. Price, M. N., Wetmore, K. M., Deutschbauer, A. M. & Arkin, A. P. A comparison of the costs and benefits of bacterial gene expression. *PLoS One* **11**, 1–22 (2016).
  170. Moya, A. et al. Toward minimal bacterial cells: Evolution vs. design. *FEMS Microbiol. Rev.* **33**, 225–235 (2009).
  171. Geißler, M. et al. Evaluation of surfactin synthesis in a genome reduced *Bacillus subtilis* strain. *AMB Express* **9**, (2019).
  172. Chung, C. T., Niemela, S. & Miller, R. One-step preparation of competent *Escherichia coli*: Transformation and storage of bacterial cells in the same solution. *Proc. Natl. Acad. Sci.* **86**, 2172–2175 (1989).
  173. Spizizen, J. Transformation of biochemically deficient strains of *Bacillus subtilis* by deoxyribonucleate. *Proc. Natl. Acad. Sci.* **44**, 1072–1078 (1958).
  174. Kohlstedt, M. et al. Adaptation of *Bacillus subtilis* carbon core metabolism to simultaneous nutrient limitation and osmotic challenge: A multi-omics perspective. *Environ. Microbiol.* **16**, 1898–1917 (2014).
  175. Handtke, S. et al. *Bacillus pumilus* KatX2 confers enhanced hydrogen peroxide resistance to a *Bacillus subtilis* PkatA: KatX2 mutant strain. *Microb. Cell Fact.* **16**, 1–9 (2017).
  176. Bolten, C. J., Kiefer, P., Letisse, F., Portais, J. C. & Wittmann, C. Sampling for metabolome analysis of microorganisms. *Anal. Chem.* **79**, 3843–3849 (2007).
  177. Krömer, J. O., Fritz, M., Heinzle, E. & Wittmann, C. In vivo quantification of intracellular amino acids and intermediates of the methionine pathway in *Corynebacterium glutamicum*. *Anal. Biochem.* **340**, 171–173 (2005).
  178. Kohlstedt, M. A multi-omics perspective on osmoadaptation and osmoprotection in *Bacillus subtilis*. *Univ. des Saarlandes* 129 (2014).
  179. Meyer, H., Liebeke, M. & Lalk, M. A protocol for the investigation of the intracellular *Staphylococcus aureus* metabolome. *Anal. Biochem.* **401**, 250–259 (2010).
  180. Russell, J. B. & Cook, G. M. Energetics of bacterial growth balance of anabolic and catabolic reactions. *Microbiol. Rev.* **59**, 1–15 (1995).
  181. Sarvas, M., Harwood, C. R., Bron, S. & Van Dijl, J. M. Post-translocational folding of secretory proteins in Gram-positive bacteria. *Biochim. Biophys. Acta - Mol. Cell Res.* **1694**, 311–327 (2004).
  182. Kabisch, J. et al. Characterization and optimization of *Bacillus subtilis* ATCC 6051 as an expression host. *J. Biotechnol.* **163**, 97–104 (2013).
  183. Wang, Y. et al. Deleting multiple lytic genes enhances biomass yield and production of recombinant proteins by *Bacillus subtilis*. *Microb. Cell Fact.* **13**, 1–11 (2014).
  184. Lieder, S., Nikel, P. I., de Lorenzo, V. & Takors, R. Genome reduction boosts heterologous gene expression in *Pseudomonas putida*. *Microb. Cell Fact.* **14**, 1–14 (2015).
  185. Paczia, N. et al. Extensive exometabolome analysis reveals extended overflow metabolism in various microorganisms. *Microb. Cell Fact.* **11**, 1–14 (2012).
  186. Manabe, K. et al. Improved production of secreted heterologous enzyme in *Bacillus subtilis* strain MGB874 via modification of glutamate metabolism and growth conditions. *Microb. Cell Fact.* **12**, 1–10 (2013).
  187. Kabisch, J. et al. Metabolic engineering of *Bacillus subtilis* for growth on overflow metabolites. *Microb. Cell Fact.* **12**, 1 (2013).
  188. Goelzer, A. & Fromion, V. Resource allocation in living organisms. *Biochem Soc Trans* **15**, 945–952 (2017).
  189. Borkowski, O. et al. Translation elicits a growth rate-dependent, genome-wide, differential



- protein production in *Bacillus subtilis*. *Mol. Syst. Biol.* **12**, 870 (2016).
190. Billerbeck, S., Calles, B., Müller, C. L., De Lorenzo, V. & Panke, S. Towards functional orthogonalisation of protein complexes: Individualisation of GroEL monomers leads to distinct quasihomogeneous single rings. *ChemBioChem* **14**, 2310–2321 (2013).
  191. Yu, B. J. et al. Minimization of the *Escherichia coli* genome using a Tn5-targeted Cre/loxP excision system. *Nat. Biotechnol.* **20**, 1018–1023 (2002).
  192. Sleator, R. D. The story of *Mycoplasma mycoides* JCVI-syn1.0. *Bioeng. Bugs* **1**, 231–234 (2010).
  193. Giga-Hama, Y., Tohda, H., Takegawa, K. & Kumagai, H. *Schizosaccharomyces pombe* minimum genome factory. *Biotechnol. Appl. Biochem.* **46**, 147 (2007).
  194. Karcagi, I. et al. Indispensability of horizontally transferred genes and its impact on bacterial genome streamlining. *Mol. Biol. Evol.* **33**, 1257–1269 (2016).
  195. Tilburg, A. Y. Van et al. Mini*Bacillus* PG10 as a convenient and effective production host for lantibiotics. *ACS Synth. Biol.* (2020) doi:10.1021/acssynbio.0c00194.
  196. Bernal-Cabas, M. et al. Functional association of the stress-responsive LiaH protein and the minimal TatAyCy protein translocase in *Bacillus subtilis*. *Biochim. Biophys. Acta - Mol. Cell Res.* **1867**, 118719 (2020).
  197. Umenhoffer, K. et al. Genome-wide abolishment of mobile genetic elements using genome shuffling and CRISPR/Cas-assisted MAGE allows the efficient stabilization of a bacterial chassis. *ACS Synth. Biol.* **6**, 1471–1483 (2017).
  198. Choi, J. W., Yim, S. S., Kim, M. J. & Jeong, K. J. Enhanced production of recombinant proteins with *Corynebacterium glutamicum* by deletion of insertion sequences (IS elements). *Microb. Cell Fact.* **14**, 1–12 (2015).
  199. Martínez-García, E., Jatsenko, T., Kivisaar, M. & de Lorenzo, V. Freeing *Pseudomonas putida* KT2440 of its proviral load strengthens endurance to environmental stresses. *Environ. Microbiol.* **17**, 76–90 (2015).
  200. Stouthamer, A. H. A theoretical study on the amount of ATP required for synthesis of microbial cell material. *Antonie Van Leeuwenhoek* **39**, 545–565 (1973).
  201. Martínez-García, E., Nikel, P. I., Chavarría, M. & de Lorenzo, V. The metabolic cost of flagellar motion in *Pseudomonas putida* KT2440. *Environ. Microbiol.* **16**, 291–303 (2014).
  202. Wu, S. C. & Wong, S. L. Engineering of a *Bacillus subtilis* strain with adjustable levels of intracellular biotin for secretory production of functional streptavidin. *Appl. Environ. Microbiol.* **68**, 1102–1108 (2002).
  203. Olmos-Soto, J. & Contreras-Flores, R. Genetic system constructed to overproduce and secrete proinsulin in *Bacillus subtilis*. *Appl. Microbiol. Biotechnol.* **62**, 369–373 (2003).
  204. Lee, S. J., Kim, D. M., Bae, K. H., Byun, S. M. & Chung, J. H. Enhancement of secretion and extracellular stability of staphylokinase in *Bacillus subtilis* by *wprA* gene disruption. *Appl. Environ. Microbiol.* **66**, 476–480 (2000).
  205. Acevedo-Rocha, C. G., Fang, G., Schmidt, M., Ussery, D. W. & Danchin, A. From essential to persistent genes: A functional approach to constructing synthetic life. *Trends Genet.* **29**, 273–279 (2013).
  206. Koo, B. et al. Construction and analysis of two genome-scale deletion libraries for *Bacillus subtilis*. *Cell Syst.* **4**, 291–305.e7 (2017).
  207. Képès, F. Periodic transcriptional organization of the *E. coli* genome. *J. Mol. Biol.* **340**, 957–964 (2004).
  208. Edwards, J. S. & Palsson, B. O. The *Escherichia coli* MG1655 in silico metabolic genotype: Its definition, characteristics, and capabilities. *Proc. Natl. Acad. Sci.* **97**, 5528–5533 (2000).
  209. Pfeifer, E., Gätgens, C., Polen, T. & Frunzke, J. Adaptive laboratory evolution of *Corynebacterium glutamicum* towards higher growth rates on glucose minimal medium. *Sci. Rep.* **7**, 1–14 (2017).
  210. Choe, D. et al. Adaptive laboratory evolution of a genome-reduced *Escherichia coli*. *Nat. Commun.* **10**, (2019).
  211. Nishimura, I., Kurokawa, M., Liu, L. & Ying, B.-W. Coordinated changes in mutation and growth rates induced by genome reduction. *MBio* **8**, 1–10 (2017).
  212. Oesterreich, B. et al. Characterization of the biological anti-staphylococcal functionality of hUK-66 IgG1, a humanized monoclonal antibody as substantial component for an immunotherapeutic approach. *Hum. Vaccines Immunother.* **10**, 926–937 (2014).
  213. Lorenz, U. et al. Functional antibodies targeting IsaA of *Staphylococcus aureus* augment host immune response and open new perspectives for antibacterial therapy. *Antimicrob. Agents Chemother.* **55**, 165–173 (2011).

## Abbreviations

ADP	Adenosine diphosphate
AEC	Adenylate energy charge
AMP	Adenosine monophosphate
AUC	Area under the curve
ATP	Adenosine triphosphate
CHIPS	Chemotaxis inhibitory protein
DBT cycle	Design, Build, Test cycle
DCW	Dry cell weight
FDR	False discovery rate
HPLC	High-performance liquid chromatography
iBAQ	Intensity-based absolute quantification algorithm
IsaA	Immunodominant <i>Staphylococcus aureus</i> antigen A
KDa	Kilo Dalton
LB	Lysogenic broth
LC/MS	Liquid chromatography–mass spectrometry
LDS-PAGE	Lithium dodecyl sulfate-polyacrylamide gel electrophoresis
LFQ	Label-free quantification intensities
LTA	Lipoteichoic acid
MS	Mass Spectrometry
Nuc	Nuclease
PBPs	Penicillin binding proteins
PCA	Principal component analysis
PG	Peptidoglycan
PMM	Pumilus minimal media
OD <sub>600</sub>	Optical density at 600 nm
SCIN	Staphylococcal complement inhibitor
SDS	Sodium dodecyl sulphate
SDS-PAGE	SDS-polyacrylamide gel electrophoresis
SMM	Spizizen minimal media
SRM	Selected Reaction Monitoring
TCA	Trichloroacetic acid
TE buffer	Tris EDTA buffer
TEAB buffer	Tetraethylammonium bromide buffer
TMD	Transmembrane domain
UPS2	Universal Proteomics Standard
Y <sub>X/S</sub>	Biomass yields on substrate

## Acknowledgments

If I dive deep in my memories, without any doubt, my life as a PhD candidate has been the best period of my life. That being said, I am profoundly thankful to my promoter **Jan Maarten** for giving me the opportunity to be part of MolBac. Jan Maarten, I met you for the first time during my master's studies when you were a guest lecturer in the biotechnology course. Only one lecture and a short talk afterwards were enough to leave the room thinking 'I would like to work with him, he seems to be a nice supervisor and a good person. That hunch was right. I went to MolBac for a short master's project, and here I am with a PhD thesis. Thank you for allowing me the opportunity to present my work at different venues and to go to Saarbrücken and Greifswald. I am happy that the work done abroad culminated in two chapters of this thesis. The freedom, trust and support that you gave me in my scientific and personal life are prized. I admire the positive, hard-working, reliable, enthusiastic and sensible person that you are. I am always curious to learn your tips and tricks, about research and life, and discover what else is part of what I call 'JM's magic'. I hope I can continue learning more of it. **Rita**, Groningen is a napkin, isn't it? Thank you for the pleasant chats in Groningen and at the conferences. I am also glad you joined the non-official MolBac outings. Fortunately, we all landed safely in the first one. **Girbe**, thank you for being my co-promoter, the suggestions during the *Bacillus* clubs, the translation of the Dutch summary and the fun Sinterklaas parties.

The work described in this thesis could not have been done without the support of several people. I would like to thank prof. **Dörte Becher** and prof. **Christoph Wittmann** for opening the doors of their labs. I would like to thank **Sandra**, **Minia** and **Michael** for the super-fast and efficient way of working. Sandra, thank you for help with the Voronoi treemaps. Minia and Michael, thank you for making my research stay so productive, you are incredible. I really enjoyed working in the lab with you. Minia, que alegría me da cada vez que te veo, que maja eres. Mucho éxito en Suiza y con el pequeño Antonio. Michael, I learned a lot from you, the experience at iSBio really enriched me, thank you so much. Prof. **Josef Alterbuchter**, thank you for providing so many strains and plasmids, it was nice to meet you in the UK.

I would like to thank the assessment committee, prof. **Ken-ichi Yoshida**, prof. **Gert-Jan Euverink** and prof. **Dirk-Jan Scheffers**, for reading and approving my thesis. Ken-ichi your presentations of applied microbiology are always inspiring. Dirk-Jan thank you for your support with the PhD-related topics in the council.

After the approval of the thesis, the next step is the PhD defence. Fortunately, I will have good company on this special day, thanks to my deluxe paranymphs **Sjouke**, **Bimal** and **Edisa**. Sjouke, I had so much fun preparing Jolanda's cabaret with you and Lianne, these are fun memories. Thank you for your willingness to help everyone, and even come all the way to our house just to drill a hole in the wall. Thank you for your invariable good mood and sharing the koffie verslaafdheid. **Bimal**, we met at the

beginning of your PhD and it has been fun to be around you since then. You always have interesting stories, and you are enthusiastic and full of energy. Especially when Solomon and Tim were in the lab to potentiate it. I am also glad that you managed to complement the phenotype of the S313 story. Thank you for the squash tips and mountain biking trips, which I really enjoyed. Bimal and Pragy, thank you for delicious dinners and the invitation to the wedding. Our time in Nepal was a unique experience. Pragy, thank you for your kindness and for being a wonderful host. All the best with your future projects. Edisa, no tengo palabras para agradecer la gran amistad que me has brindado desde hace tantos años. Gracias por venir a ‘estudiar’ a Groningen solo para seguir ‘hechando el chal’ de cerca conmigo. Gracias por estar ahí cuando más lo he necesitado, he inclusive ir a media noche a mi casa para escuchar mis dilemas y conflictos internos. En otras palabras, eres la mejor.

During these last couple of years, I have spent most of my time at MolBac. As such, I would like to thank all the people who have been part of MolBac and contributed to make it a nice, friendly, cosy and sometimes chaotic place to be. The list of members is long but I would like to address some people. My life at MolBac started as a MSc student where I began to work with Jolanda after I asked Jan Maarten to work with the most experienced person. Jolanda, I am glad that you were my supervisor and my bench-buddy. It has been enjoyable to work with you. Thank you for your help with ideas and answering my questions, some experiments and the Nederlands-donderdag together with Sjouke. I learned from you that ‘5 minutes late is bad planning’. Solomon, thank you for sharing your desk when I did not have my own. Xin, thank you for the nice conversations, the ping-pong lessons and the dinners. I am happy that Xin’s fan club was a success. Jolien, thank you for giving me a pleasant place to live. All the best in your new job at the UMCG. Francisco, gracias por tu disposición para ayudar y tus buenos consejos sobre otros temas sobre la vida fuera del laboratorio. Rense, thank you for the inspiration to take cold showers. It really helps me to wake up completely every morning. I can recommend it to anyone, cold showers work better than coffee. I also would like to thank Dennis, Carien, Mehdi, Eleni for the nice food at the Sinterklaas parties. Laura, gracias por crear conciencia sobre el medio ambiente. Marco, thank you for the ping pong games. Lisanne, thank you for the wonderful crafts, you have natural talent for it. Ayşegül, I also like your drawings. Maybe we should start an Arts club. Tobias, thank you for taking care of the duties in the lab and changing my view of animal prints. Elisa, thank you for the nice talks and I hope that we go biking again. Yan-Yan, Lu and Min, thank you for the nice hot-pot evenings and the high tea time. Min, we will get the driver’s license soon. Mafalda, Lisanne and Marjolein, thank you for making the office so cosy that I even moved there. Hermie, thank you for hosting the Sinterklaas parties. Marines, me divertí mucho haciendo el cabaret de Andrea contigo y Adriana. Gracias por tu sincera amistad. Adriana, gracias por las buenas pláticas y la agradable compañía. Andrea, Yaremit y Gaby, gracias por hacerme sentir en casa y ser un pedacito de ese México que añoro, las quiero mucho. Andrea, muchas gracias por consentirme

siempre, y ayudarme cuando me lástime mi mano, te deseo lo mejor. **Yaremit**, nos va a faltar tu alegría, siempre es muy agradable y divertido plática contigo. Ya me tocará visitarte del otro lado de la frontera. **Gaby**, siempre tan amenas esas pláticas mientras tomamos café. Gracias por las incontables cenas con sabor a México. Gracias a **Oli y Román**, por soportar todo el escándalo que hacemos a veces en tu casa.

To my students **Mireia, Max, Simone** and **Robert**, thank you for your help with the S313 and the genome-reduced strains projects. **César**, fue muy agradable que estuvieras aquí. Espero pronto termines la tesis de doctorado. **Ana**, gracias por tu interés en los chasis de *Bacillus*. Aysegül y yo te visitaremos en España para la fiesta. I also would like to thank **Niels** for the help with the MALDI-TOF. **Sigrid** and **Monika**, for the incredibly fast help determining the plasmid copy number. **Elias**, muchas gracias por preparar tan buenos SOP's y explicarme sobre ellos, y tu idea de disfrazarnos junto con Andrea. **Paola**, thank you for helping me setting CLC. **Ank**, thank you for the nice follow up and tracking of my packages. **Marina**, gracias por la ayuda con el ensayo de la nucleasa y la comida española. **Venus**, muchas gracias por ayudarme con mis dudas sobre Jupiter notebook y data visualization. Venus e **Iris**, gracias por el delicioso mezcal y el suministro de epazote.

An important element in my life is food. Thus, I would like to thank **Giorgio, Stefano, Larissa, Suruchi** and **Margarita** for the more than abundant and frequent dinners. Giorgio, your raviolis are the best. Thank you for all the food and cooking lessons. Have you ever thought about becoming the competitor of Giallo Z.? Stefano, thank you for the good conversations and the cooking lessons. Larissa, thank you for sharing the German cuisine with us. Suruchi, the cappuccinos after the Sunday morning swimming were the best. Thank you for being such a caring person, especially these last days of my PhD, and for the wonderful Nepalese food. Margarita, gracias por las cenas en tu casa. Tu 7-layer dip es adictivo. Muchas gracias por tu apoyo especialmente estas últimas semanas. Te deseo lo mejor. I would like to thank **Alberto, Arjen, Jelmer, Simone** and **Yanglei** for all the international dinners, the paintball and escape room sessions. It was always so much happiness and fun with you. Alberto and Arjen, thank you for offering me your house for one week when I did not have accommodation. Both of you have helped me a lot in different ways, thanks.

Since mental health is a recurrent topic during PhD life, I would like to thank the people that contributed to keep my mind on the safe side through running and climbing. First to my running buddies, **Tomas, Francis, Usma** and **Rita**. Thank you for the many kilometres of philosophical conversations. The crematorium is just the starting point. Tomas, thank you for your friendship and never-ending energy to run. All the best in Enschede with Angelique and Eloise. Francis, thank you for the pandoros, not for nothing 'la panza avanza'. Usma, besides a passionate runner you are so generous and a great cook, thank you for sharing your delicious food. Rita, I am glad you started running, I hope we go for many more km. Secondly to my climbing buddies, **Tim, Vania**



and **Pavol**. Tim, thank you for your positive vibes. Vania, además de escalar, me alegra que también compartimos clases de pole dance. Te deseo lo mejor en Boston. Pavol, thank you for the climbing tips and for pushing me to try more difficult routes than I had in mind. I also would like to thank **Mathijs** for organizing the cool mountain biking trips.

A mis mejores amigos **Cone**, **Chana** y **Fractal**, con ustedes es diversión garantizada. Gracias por el ameno buzón de quejas las tardes de domingo y por ayudarme en los procesos democráticos de la vida. Gracias por todos los gratos recuerdos que hemos creado desde hace ya media vida. A ustedes también les debo mi salud mental. San Cone de los terrenitos, dame unos meritos. Fractal, espero sigas siendo tan sensato como antes. **Miko** gracias por tu amistad y tu apoyo desde que llegue a Groningen, eres uno de mis mejores amigos. Gracias por las largas pláticas sobre lo bizarro que es este mundo, además de microbiología. **Sam** y **Lety**, otro poquito más y ya serán dos décadas de ‘C.B.’. Muchas gracias por estar al pendiente pese a la distancia y el tiempo. Gracias por su amistad. **Eli**, gracias por animarte a viajar conmigo en Europa nunca olvidare todas las aventuras que tuvimos y lo mucho que nos hemos divertido desde la época de los nakamas.

**Manolo**, gracias por tu tutoría durante mi estancia en MolGen y por tu compañía durante nuestro viaje a Granada. Hiciste que nuestra estancia en Granada fuera más especial. **Danae**, madrina mía, espero verte como toda una PI dentro de poco. Fue muy divertido ir a Walibi. Quizá finalmente el siguiente año Edisa y yo te visitemos. **Cesar**, gracias por la hospitalidad en Edimburgo. **Mami-san**, thank you, the dinners with **Eli** and for the amazing Japanese dinners that you host at your place. Thank you for all the super relaxing evenings outside Groningen and for organizing the dinner where I met Pieter.

Mijn lieve **Pieter**, what a joy has been these years sharing stories, dreams and memories with you. I have enjoyed so much living and traveling with you. Thank you for taking care of me so well and for making me laugh so much. ‘Tú lo sabes todo’ and you know when I need your help without asking. Thank your patient and help with my Dutch. I am sure you will manage to speak Spanish with the suegros soon. Thank you for the surprises, especially when you brought my brother to Groningen. I have never been so astonished in my life, you are wonderful. I admire your talent, curiosity and creativity, which have also boosted that side of me. So, let’s work on atelier de snijhoek. I am really happy with you and I am looking forward to our new adventures, trips -Japan, YTQ moments, and much more. I just want to say that you make my hearth so warm and happy!

Ik ben blij dat je een geweldig familie heeft. **Marjolijn**, **Pien**, **Roos** en **Rutger**, bedankt voor de gezelligheid. Ik voel me welkom met jullie. Marjolein, mijn lieve schoonmoeder, je bent altijd vriendelijk en lief. Bedankt voor het zorgen voor mij, de taartjes en de gezelligheid. Roos en Rutger, bedankt voor de vlinders interesse. Pien, bedankt voor de uitnodigingen voor de musea, het uitleggen van kunst, en speciaal voor de opening van de tentoonstelling in Utrecht.

Finalmente, quiero agradecer a quienes han estado a mi lado toda la vida, mi familia. Recuerdo con mucha alegría todos los buenos momentos que hemos pasado juntos y todo el apoyo que me han brindado. Mamá y papá, yo no podría estar aquí si no fuera por ustedes que me han brindado su amor, apoyo y confianza desde pequeña. Ni que decir de la libertad que me dieron. Al final no fui a Francia, pero sí a Holanda, una de las mejores decisiones en mi vida. Los quiero tanto a los dos y espero con mucho anhelo verlos pronto. Los extraño mucho. Gracias a mis hermanos, Erick y Ruco, por cuidar de mamá y papá, la ayuda y los buenos consejos sobre la vida. También gracias a Paty y Lika por estar pendiente de mí y de mi familia, los quiero como mis hermanas.

Thank you all for being part of my life.

Rocío  
November 2020



## List of Publications

- Bernal-Cabas, M., Miethke, M., Antelo-Varela, M., **Aguilar Suárez, R.**, Neef, J., Schön, L., Gabarrini, G., Otto, A., Becher, D., Wolf, D., & van Dijl, J. M. (2020). Functional association of the stress-responsive LiaH protein and the minimal TatAyCy protein translocase in *Bacillus subtilis*. *Biochimica et Biophysica Acta - Molecular Cell Research*, 1867(8), [118719].
- Antelo-Varela, M., **Aguilar Suárez, R.**, Bartel, J., Bernal-Cabas, M., Stobernack, T., Sura, T., van Dijl, J. M., Maaß, S., & Becher, D. (2020). Membrane modulation of super-secreting ‘midi*Bacillus*’ expressing the major *Staphylococcus aureus* antigen -A Mass-Spectrometry-based absolute quantification approach. *Frontiers in Bioengineering and Biotechnology*, 8, [143].
- **Aguilar Suarez, R.**, Stülke, J., & van Dijl, J. (2019). Less is more: towards a genome-reduced *Bacillus* cell factory for ‘difficult proteins’. *ACS Synthetic Biology*, 8(1), 99-108.
- Heuker, M., Sijbesma, J. W. A., **Aguilar Suárez, R.**, de Jong, J. R., Boersma, H. H., Luurtsema, G., Elsinga, P. H., Glaudemans, A. W. J. M., van Dam, G. M., van Dijl, J. M., Slart, R. H. J. A., & van Oosten, M. (2017). In vitro imaging of bacteria using (18)F-fluorodeoxyglucose micro positron emission tomography. *Scientific Reports*, 7, [4973].
- Mendoza-Martínez, C., Correa-Basurto, J., Nieto-Meneses, R., Márquez-Navarro, A., **Aguilar-Suárez, R.**, Montero-Cortes, M. D., Noguera-Torres, B., Suárez-Contreras, E., Galindo-Sevilla, N., Rojas-Rojas, Á., Rodríguez-Lezama, A., & Hernández-Luis, F. (2015). Design, synthesis and biological evaluation of quinazoline derivatives as anti-trypanosomatid and anti-plasmodial agents. *European Journal of Medicinal Chemistry*, 96, 296-307.

## Biography

Rocío Aguilar Suárez studied chemistry, bacteriology and microbiology at the National Polytechnic Institute in Mexico City. After the culmination of her bachelor's programme with a thesis she received her bachelor's degree with a distinction in 2011. The research described in her bachelor's thesis focused on the assessment of antimalarial activity of quinazoline derivatives in a murine model. In addition to her studies, she was also involved in policy activities. After her graduation, she did a research stay at the Center of Research and Advanced Studies, campus Merida in Mexico, where she worked with prof. Leopoldina Aguirre Macedo,



and worked on petroleum hydrocarbon-degrading bacteria. Later, she moved to the Netherlands to pursue a master's degree in molecular biology and biotechnology at the University of Groningen. During her studies she joined the molecular genetics research group of prof. Oscar Kuipers at the Groningen Institute Biomolecular Sciences & Biotechnology, where she worked on lantibiotic production in *Lactococcus lactis*. Consecutively, Rocío joined to the Molecular bacteriology research group of prof. Jan Maarten van Dijk at the University Medical Center Groningen, where she worked on the role of a small regulatory RNA in *Bacillus subtilis*. After receiving her master's degree in 2014, she became a PhD candidate at the University of Groningen where she worked on the development of genome-reduced *Bacillus subtilis* strains for protein production under the guidance of prof. Jan Maarten van Dijk. During her PhD trajectory, she did a research stay at the Microbial Proteomics research group of prof. Dörte Becher at the University of Greifswald in Germany, followed by a research stay at the Institute for Systems biotechnology of prof. Christoph Wittmann at Saarland University in Germany. The results of this collaborative work are described in the present thesis. Besides her research activities, she participated in the policy activities as a member of the University Council of the University of Groningen.

