

NINA DOMBROWSKI

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<https://ndombrowski.github.io/>

EDUCATION & TRAINING

Bioinformatician	31/08/2023-current
University of Amsterdam (UvA), Amsterdam, Netherlands	
Postdoctoral Research Scholar	01/08/2018-31/08/2023
Royal Netherlands Institute for Sea Research (NIOZ), Texel, Netherlands	
Postdoctoral Research Scholar	01/08/2015-31/07/2018
University of Texas at Austin, Port Aransas, USA	
Doctoral Degree in Biology	14/03/2012/-15/04/2015
Max-Planck Institute for Plant Breeding Research, Cologne, Germany	
Thesis: 'Structural and functional analysis of the root microbiome of <i>Arabidopsis thaliana</i> and relative species'	
Diploma Degree (equivalent to Master of Science, MSc)	01/07/2010-24/11/2011
Leibniz Institute for Plant Biochemistry, Halle, Germany	
Thesis: 'Polysomal mRNA profiling of auxin responsive transcriptomes in different cell types of <i>Arabidopsis thaliana</i> '	
University Student	01/09/2006-24/11/2011
Martin Luther University Halle-Wittenberg, Halle, Germany	
Research Assistant	01/08/2008-30/06/2010
Leibniz Institute for Plant Biochemistry, Halle, Germany	

FELLOWSHIPS & GRANTS

Co-PI: JGI Community Science Program (CSP) Sequencing Grant	2017
PI: JGI Community Science Program (CSP) Sequencing Grant	2016
University of Texas Marine Science Institute Travel Grant	2016, 2017
International Max Planck Research School IMPRS Fellowship	01/02/2012-01/04/2015

ATTENDED CONFERENCES: Talks

EMBO Workshop Molecular biology of archaea <i>‘Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on evolution ‘</i> Frankfurt, Germany	08/08/2022
Utrecht Bioinformatics Center (UBC) seminar series <i>‘Using genomic approaches to illuminate the deep roots of archaea’</i> Virtual Meeting	02/04/2021
Gordon Research Seminar (GRS) archaea <i>‘Ultra-small archaea – a diverse and deep-branching archaeal lineage?’</i> , Talk, Les Diablerets, Switzerland	20-21/07/2019
Bioinformatics & Systems Biology (BioSB) Conference <i>‘Using genomic approaches to illuminate the deep roots of archaea’</i> Lunteren, Netherlands	02/04/2019
Royal Dutch Society of Microbiology (KNVM) meeting <i>‘Ultra-small archaea: A deep-branching lineage?’</i> Arnhem, Netherlands	26/03/2019
Next generation genomics symposium <i>‘How metagenomics has changed our view on archaeal diversity’</i> , Invited talk, Helsinki, Finland	23/10/2018
6th International Symposium on Microbial Ecology (ISME) <i>‘Comparative metagenomics uncovers the functional potential of bacteria from deep-sea hydrothermal vent and estuary sediments’</i> , Montreal, Canada	21/08/2016
3rd Annual Southeastern Biogeochemistry Symposium <i>‘Metabolic pathways of hydrocarbon-degrading bacteria from the Deepwater Horizon oil’</i> Knoxville, USA	12/03/2016

Research Cruises

Co-Chief Scientist , R/V Pelagia, Hydrothermal vents North of Iceland	07/2021
Participating Scientist , R/V Pelagia, Rainbow vent field in the Mid-Atlantic Ridge, Azores	06/2019-07/2019
Participating Scientist , R/V Pelagia, Heraklion (Greece)-Lymassol (Cyprus)	08/2018

TEACHING & OUTREACH

Lecturer 2-day Practical ‘ <u>Microbial Ecology: Sequence Data Analysis</u> ’ Training for BSc level students University of Amsterdam (UvA), Lecturer	12/2025
Lecturer 2-day Practical ‘ <u>Big Biological Data Analysis: De novo transcriptomics</u> ’ Training for MSc level students University of Amsterdam (UvA), Lecturer	11/2025
Lecturer at the Workshop series ‘ <i>Bioinformatics for marine biologists</i> ’ Royal Netherlands Institute for Sea Research (NIOZ), NL Organized and lectured three sessions: Phylogenomics, Metagenomics, and Introduction to the Tidyverse for graduate and undergraduate students.	02/2023-current
10 week workshop series ‘ <i>Bioinformatics for marine biologists</i> ’ Training for PhD level students Lectures given: Basic Introduction into the Command Line, Basic Introduction into Awk, Phylogenomics, Metagenomics Royal Netherlands Institute for Sea Research (NIOZ), Organizer and Lecturer	14/01/2021-22/04/2021
2-day Workshop ‘ <i>R for beginners</i> ’ Training for R beginners (undergraduate to senior researchers) Royal Netherlands Institute for Sea Research (NIOZ), TA	21-22/11/2019
10 week workshop series ‘ <i>Bioinformatics in marine sciences</i> ’ Training for PhD level students Lectures given: Basic Introduction into the Command Line, Basic Introduction into Awk, Phylogenomics Royal Netherlands Institute for Sea Research (NIOZ), Organizer and lecturer	01/09/2019-01/12/2019
Undergraduate class MNS193 ‘ <i>Genomics in Ocean Sciences</i> ’ Training for undergraduate level students Guest lecturer on genomic binning UT Austin Marine Science Institute, Guest lecturer	26/10/2017
Seminar series ‘ <i>Molecular biology</i> ’ Lectures given: Introduction to the command line, Introduction to the HPC, The tree of life, Phylogeny UT Austin Marine Science Institute, Organizing committee & lecturer	01/01/2016-20/12/2016
Undergraduate class ‘ <i>Marine Microbial Ecology</i> ’ Guest lecturer on oil-degrading marine microbial communities UT Austin Marine Science Institute, Guest lecturer	13/04/2016
ECOGEO Workshop ‘ <i>Omics Training: Introduction to Environmental Omics</i> ’, U. Hawai‘i Mānoa, Guest lecturer on phylogenomics Material: http://www.earthcube.org/group/ecogeo/omicsvm	24/07/2016

PUBLICATIONS

* shared first authors

2025

Huang WC, **Dombrowski N**, Mahendrarajah TA, Wahl N, Stamatakis A, Szöllősi GJ, et al. Phylogenetic reconciliation supports a methanogenic ancestor of the Archaea and a derived origin for host-associated lineages. **bioRxiv**; 2025 p. 2025.11.11.687807.

<https://www.biorxiv.org/content/10.1101/2025.11.11.687807v1>

Hamm JN, **Dombrowski N**, Valentin-Alvarado LE, Greening C, Williams TA, Spang A. Caliditerrarchaeota, a new sister to Nanohaloarchaeota, provides insights into the evolution of DPANN halophily. **bioRxiv**; 2025. p. 2025.08.05.668663.

<https://www.biorxiv.org/content/10.1101/2025.08.05.668663v1>

2024

Hamm JN, Liao Y, von Kűgelgen A, **Dombrowski N**, Landers E, Brownlee C, et al. The parasitic lifestyle of an archaeal symbiont. **Nat Commun**. 2024 July 31;15(1):6449.

<https://www.nature.com/articles/s41467-024-49962-y>

Moody ERR, lvarez-Carretero S, Mahendrarajah TA, Clark JW, Betts HC, **Dombrowski N**, et al. The nature of the last universal common ancestor and its impact on the early Earth system.

Nat Ecol Evol 2024; 8: 1654–1666. <https://www.nature.com/articles/s41559-024-02461-1>

van Duijnhoven HJ, **Dombrowski N**, Kuperus P, Aires T, Coelho MAG, Silva J, et al. Draft genome of the marine bacterium *Alteromonas gracilis* strain J4 isolated from the green

coenocytic alga *Caulerpa prolifera*. **Microbiology Resource Announcements** 2024; 13: e00184-24. <https://journals.asm.org/doi/full/10.1128/mra.00184-24>

2023

van der Gulik PTS, Egas M, Kraaijeveld K, **Dombrowski N**, Groot AT, Spang A, Hoff W, Gallie Jenna. On distinguishing between canonical tRNA genes and tRNA gene fragments in prokaryotes. **RNA Biology** 2023; 20: 48–58.

<https://www.tandfonline.com/doi/full/10.1080/15476286.2023.2172370>

Vaksmaa A, Polerecky L, **Dombrowski N**, Kienhuis MVM, Posthuma I, Gerritse J, et al. Polyethylene degradation and assimilation by the marine yeast *Rhodotorula mucilaginosa*.

ISME Communications 2023; 3: 68. <https://www.nature.com/articles/s43705-023-00267-z>

Mahendrarajah TA, Moody ERR, Schrempf D, Sznth LL, **Dombrowski N**, Davn AA, et al. ATP synthase evolution on a cross-braced dated tree of life. **Nat Commun** 2023; 14: 7456.

<https://www.nature.com/articles/s41467-023-42924-w>

Eme L, Tamarit D, Caceres EF, Stairs CW, De Anda V, Schön ME, Seitz KW, **Dombrowski N**, et al. Inference and reconstruction of the heimdallarchaeal ancestry of eukaryotes. **Nature** 2023; 618: 992–999. <https://www.nature.com/articles/s41586-023-06186-2>

2022

Krause S, Gfrerer S, von Kűgelgen A, Reuse C, **Dombrowski N**, Villanueva L, et al. The importance of biofilm formation for cultivation of a Micrarchaeon and its interactions with its Thermoplasmatales host. **Nat Commun** 2022; 13: 1735. <https://www.nature.com/articles/s41467-022-29263-y>

Moody ER, Mahendrarajah TA, **Dombrowski N**, Clark JW, Petitjean C, Offre P, Szűllősi GJ, Spang A, Williams TA. An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. **eLife** 2022; 11: e66695. <https://elifesciences.org/articles/66695>

Langwig MV, De Anda V, **Dombrowski N**, Seitz KW, Rambo IM, Greening C, Teske AP, Baker BJ. Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. **ISME Journal** 2022; 16: 307–320. <https://www.nature.com/articles/s41396-021-01057-y>

2021

De Anda V, Chen L-X, **Dombrowski N**, Hua Z-S, Jiang H-C, Banfield JF, Li WJ, Baker BJ. Brockarchaeota, a novel archaeal phylum with unique and versatile carbon cycling pathways. **Nature Communications** 2021; 12: 2404. <https://www.nature.com/articles/s41467-021-22736-6>

Mayer T, Mari A, Almario J, Murillo-Roos M, Syed M. Abdullah H, **Dombrowski N**, Hacquard S, Kemen EM, Agler MT. Obtaining deeper insights into microbiome diversity using a simple method to block host and nontargets in amplicon sequencing. **Molecular Ecology Resources** 2021; 21: 1952–1965. <https://onlinelibrary.wiley.com/doi/10.1111/1755-0998.13408>

Suominen S, **Dombrowski N**, Sinninghe Damsté JS, Villanueva L. A diverse uncultivated microbial community is responsible for organic matter degradation in the Black Sea sulphidic zone. **Environmental Microbiology** 2021; 23: 2709–2728. <https://sfamjournals.onlinelibrary.wiley.com/doi/full/10.1111/1462-2920.14902>

2020

Dombrowski N, Williams TA, Sun J, Woodcroft BJ, Lee J-H, Minh BQ, et al. Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. **Nature Communications** 2020; 11: 3939. <https://www.nature.com/articles/s41467-020-17408-w>

Reysenbach A-L, John ES, Meneghin J, Flores GE, Podar M, **Dombrowski N**, et al. Complex subsurface hydrothermal fluid mixing at a submarine arc volcano supports distinct and highly diverse microbial communities. **PNAS** 2020; 117: 32627–32638. <https://www.pnas.org/doi/10.1073/pnas.2019021117>

Suominen S, **Dombrowski N**, Damsté JSS, Villanueva L. A diverse uncultivated microbial community is responsible for organic matter degradation in the Black Sea sulphidic zone. **Environmental Microbiology** 2020.

<https://sfamjournals.onlinelibrary.wiley.com/doi/full/10.1111/1462-2920.14902>

Rambo IM, **Dombrowski N**, Constant L, Erdner D, Baker BJ. Metabolic relationships of uncultured bacteria associated with the microalgae *Gambierdiscus*. **Environmental Microbiology** 2020; **22**: 1764–1783.

<https://sfamjournals.onlinelibrary.wiley.com/doi/full/10.1111/1462-2920.14878>

Baker BJ, De Anda V, Seitz KW, **Dombrowski N**, Santoro AE, Lloyd KG. Diversity, ecology and evolution of Archaea. **Nature Microbiology** 2020; 1–14.

<https://www.nature.com/articles/s41564-020-0715-z>

2019

Schwank K, Bornemann TLV, **Dombrowski N**, Spang A, Banfield JF, Probst AJ. An archaeal symbiont-host association from the deep terrestrial subsurface. **The ISME Journal** 2019; 1.

<https://www.nature.com/articles/s41396-019-0421-0>

Spang A, Stairs CW, **Dombrowski N**, Eme L, Lombard J, Caceres EF, Greening C, Baker B, Ettema T. Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism. **Nature Microbiology** 2019; 1.

<https://www.nature.com/articles/s41564-019-0406-9>

Dombrowski N, Lee J-H, Williams TA, Offre P, Spang A. Genomic diversity, lifestyles and evolutionary origins of DPANN archaea. **FEMS Microbiol Lett** 2019; 366.

<https://academic.oup.com/femsle/article/366/2/fnz008/5281434>

Seitz KW, **Dombrowski N**, Eme L, Spang A, Lombard J, Sieber JR, Teske A, Ettema T, Baker B. Asgard archaea capable of anaerobic hydrocarbon cycling. **Nature Communications** 2019; 10: 1822. <https://www.nature.com/articles/s41467-019-09364-x>

Steen AD, Kevorkian RT, Bird JT, **Dombrowski N**, Baker BJ, Hagen SM, Mulligan K, Schmidt J, Webber A, Royalty T, Alperin M. Kinetics and Identities of Extracellular Peptidases in Subsurface Sediments of the White Oak River Estuary, North Carolina. **Appl Environ Microbiol** 2019; 85.

2018

Dombrowski N, Teske AP, Baker BJ. Expansive microbial metabolic versatility and biodiversity in dynamic Guaymas Basin hydrothermal sediments. **Nature Communications** 2018; **9**: 4999. <https://www.nature.com/articles/s41467-018-07418-0>

Garrido-Oter R*, Nakano RT*, **Dombrowski N***, Ma K-W, McHardy AC, Schulze-Lefert P. Modular Traits of the Rhizobiales Root Microbiota and Their Evolutionary Relationship with Symbiotic Rhizobia. **Cell Host & Microbe** 2018; 24: 155-167.e5. [https://www.cell.com/cell-host-microbe/abstract/S1931-3128\(18\)30318-4](https://www.cell.com/cell-host-microbe/abstract/S1931-3128(18)30318-4)

Chen L-X, Méndez-García C, **Dombrowski N**, Servín-Garcidueñas LE, Eloë-Fadrosh EA, Fang B-Z, Luo, Z-H, Tan S, Zhi X-Y, Hua Z-S, Martinez-Romero E, Woyke T, Huang L-N, Sánchez J, Peláez AI, Ferrer M, Baker BJ, Shu W-S.. Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. **The ISME Journal** 2017. <https://www.nature.com/articles/s41396-017-0002-z>

2017

Heijden MGA van der, **Dombrowski N**, Schlaeppi K. Continuum of root–fungal symbioses for plant nutrition. **PNAS** 2017. <http://www.pnas.org/content/early/2017/10/20/1716329114.extract>

Dombrowski N, Seitz KW, Teske AP and Baker, BJ.. Genomic insights into potential interdependencies in microbial hydrocarbon and nutrient cycling in hydrothermal sediments. **Microbiome** 2017; 5, 106. <https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-017-0322-2>

Dombrowski N, Schlaeppi K, Agler MT, Hacquard S, Kemen E, Garrido-Oter R, Wunder J, Coupland G and Schulze-Lefert P.. Root microbiota dynamics of perennial *Arabis alpina* are dependent on soil residence time but independent of flowering time. **ISME J** 2017; 11: 43–55. <http://www.nature.com/ismej/journal/v11/n1/full/ismej2016109a.html>

2016

Dombrowski N, Donaho JA, Gutierrez T, Seitz KW, Teske AP, Baker BJ.. Reconstructing metabolic pathways of hydrocarbon-degrading bacteria from the Deepwater Horizon oil spill. **Nature Microbiology** 2016; 16057. <http://www.nature.com/articles/nmicrobiol201657>

Steen AD, Kevorkian RT, Bird JT, **Dombrowski N**, Baker BJ, Hagen SM, *et al.*. Extracellular peptidases in subsurface sediments of the White Oak River estuary, NC, suggest microbial community adaptation to oxidize degraded organic matter. **bioRxiv** 2016; 80671. <https://www.biorxiv.org/content/early/2016/11/21/080671>

Agler MT, Mari A, **Dombrowski N**, Hacquard S, Kemen EM.. New insights in host-associated microbial diversity with broad and accurate taxonomic resolution. **bioRxiv** 2016; 050005. <http://www.biorxiv.org/content/early/2016/04/23/050005>

2015

Bai Y, Müller DB, Srinivas G, Garrido-Oter R, Potthoff E, Rott M, **Dombrowski N**, Münch P, Spaepen S, Remus-Emserman M, Hüttel B, McHardy A, Vorhold JA, Schulze-Lefert P, Pieterse CMJ. Functional overlap of the *Arabidopsis* leaf and root microbiota. **Nature** 2015; 528: 364–369.

<http://www.nature.com/nature/journal/vaop/ncurrent/full/nature16192.html>

Zamioudis, C, Korteland, J, Van Pelt, JA, van Hamersveld, M. **Dombrowski, N**, Bai, Y, Hanson, J, Van Verk, MC, Ling, H-Q, Schulze-Lefert, P. Rhizobacterial volatiles and photosynthesis-related signals coordinate MYB72 expression in *Arabidopsis* roots during onset of induced systemic resistance and iron-deficiency responses. **Plant J** 2015; 84, 309–322.

<http://onlinelibrary.wiley.com/doi/10.1111/tpj.12995/abstract>

2014

Schlaeppli K, **Dombrowski N**, Oter RG, Themaat EVL van, Schulze-Lefert P.. Quantitative divergence of the bacterial root microbiota in *Arabidopsis thaliana* relatives. **PNAS** 2015; 111: 585–592.

<http://www.pnas.org/content/early/2013/12/26/1321597111.abstract>

Book chapters

2021

Dombrowski N, Mahendrarajah T, Gross ST, Eme L, Spang A. Archaea. Practical Handbook of Microbiology, 4th ed. 2021. CRC Press.

2019

Blohs M, Moissl-Eichinger C, Mahnert A, Spang A, **Dombrowski N**, Krupovic M, Klingl A. Archaea - An Introduction, 4th ed. 2019. UK: Elsevier.