

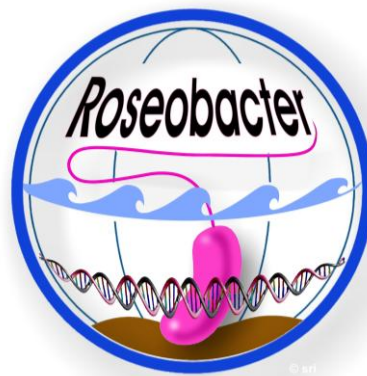
ANNEX I

Transregional Collaborative Research Centre (TRR 51)

**Ecology, Physiology and Molecular Biology
of the *Roseobacter* Group:**

**Towards a Systems Biology Understanding of a
Globally Important Group of Marine Bacteria**

**Final Report
2010-2022**



Coordinating University



Complete list of publications of TRR51

1. Arahal DR, Busse H-J, Bull CT, Christensen H, Chuvochina M, Dedysh SN, Fournier P-E, Konstantinidis KT, Parker CT, Rosselló-Móra R, Ventosa A, **Göker M** (2023) Judicial Opinion 128. *Internat J System Evol Microbiol* 73: 5797 (<https://doi:10.1099/ijsem0.005797>). [A6]
2. Aßhauer KP, **Wemheuer B**, **Daniel R**, Meinicke P (2015) Tax4Fun: predicting functional profiles from metagenomic 16S rRNA data. *Bioinformatics* 31: 2882-2884 (<https://doi.org/10.1093/bioinformatics/btv287>). [Z02]
3. **Bakenhus I**, **Dlugosch L**, **Billerbeck S**, **Giebel HA**, **Milke F**, **Simon M** (2017) Composition of total and cell-proliferating bacterioplankton community in early summer in the North Sea – roseobacters are the most active component. *Frontiers in Microbiology* 8:1771. (<https://doi:0.3389/fmicb.2017.01771>) [A1]
4. **Bakenhus I**, **Dlugosch L**, **Giebel HA**, **Beardsley C**, **Simon M**, **Wietz M** (2018) Distinct biogeographic patterns of bacterioplankton composition and single-cell activity between the subtropics and Antarctica. *Environ Microbiol* 20/8, Special Issue: 3100-3108 (<https://doi.org/10.1111/1462-2920.14383>). [A1]
5. **Bakenhus I**, **Voget S**, **Poehlein A**, **Brinkhoff T**, **Daniel R**, **Simon M** (2018) Genome sequence of *Planktotalea frisia* type strain (SH6-1T), a representative of the *Roseobacter* group isolated from the North Sea during a phytoplankton bloom. *Stand Gen Sci* 13: 7, (<https://doi.org/10.1186/s40793-018-0311-5>) [A1, Z02]
6. **Bakenhus I**, **Wemheuer B**, **Akyol P**, **Giebel HA**, **Dlugosch L**, **Daniel R**, **Simon M** (2019) Distinct relationships between fluorescence *in situ* hybridization- and rRNA gene- and amplicon-based sequencing data of bacterioplankton lineages. *System Appl Microbiol* 42/5: article 126000 (<https://doi.org/10.1016/j.syapm.2019.06.005>). [A1, Z02]
7. **Balmonte JP**, **Simon M**, **Giebel HA**, **Arnosti C** (2021) A sea change in microbial enzymes: Heterogeneous latitudinal and depth-related gradients in bulk water and particle-associated enzymatic activities from 30°S to 59°N in the Pacific Ocean. *Limnol Oceanogr* 66: 3489-3507 (<https://doi.org/10.1002/lno.11894>). [A1]
8. **Balmonte JP**, **Giebel HA**, **Arnosti C**, **Simon M**, **Wietz M** (2024) Distinct bacterial succession and functional response to algal bloom in the South, Equatorial, and North Pacific Ocean. *Environ Microbiol* 26:e16594 (<https://DOI:10.1111/1462-2920.16594>) [A1]
9. **Bartling P**, **Brinkmann H**, **Bunk B**, **Overmann J**, **Göker M**, **Petersen J** (2017) The composite 259-kb plasmid of *Martellella mediterranea* DSM 17316^T – a natural replicon with functional RepABC modules from *Rhodobacteraceae* and *Rhizobiaceae*. *Frontiers in Microbiology* 8: 1787. (<https://doi:10.3389/fmicb.2017.01787>). [A5, A6, A7]
10. **Bartling P**, **Vollmers J**, **Petersen J** (2018). The first world swimming championships of roseobacters - Phylogenomic insights into an exceptional motility phenotype. *Syst. Appl. Microbiol.* 41: 544-55 (<https://doi.org/10.1016/j.syapm.2018.08.012>). [A5]
11. **Bartsch, A.**, **Bunk, B.**, **Haddad, I.**, **Klein, J.**, **Münch, R.**, **Johl, T.**, **Kärst, U.**, **Jänsch, L.**, **Jahn, D.** & **Retter, I** (2012) GeneReporter - Sequence based document retrieval and annotation *Bioinformatics*, **27**: 1034-1035 (<https://doi.org/10.1093/bioinformatics/btr047>). [A7, INF]
12. **Behringer, M.**, **Plötzky, L.**, **Baabe, D.**, **Zaretske, M.-K.**, **Schweyen, P.**, **Bröring, M.**, **Jahn, D.**, & **Härtig, E.** (2020) *RirA* of *Dinoroseobacter shibae* senses iron via a [3Fe-4S]₁₊ cluster coordinated by three cysteine residues. *Biochem J* 477: 191–212 (<https://doi.org/10.1042/BCJ20180734>). [B5]
13. **Beier, N**, **Kucklick, M**, **Fuchs, S.**, **Mustafayeva, S.**, **Behringer, M.**, **Härtig, E.**, **Jahn, D.**, & **Engelmann, S.** (2021) Adaptation of *Dinoroseobacter shibae* to oxidative stress and

- the specific role of RirA, PLOS ONE, 16, e0248865 (<https://doi.org/10.1371/journal.pone.0248865>). [C6, B5]
14. **Bercovici SK, Dittmar T, Niggemann J** (2022) The detection of bacterial exometabolites in marine dissolved organic matter through ultrahigh-resolution mass spectrometry. *Limnol Oceanogr: Methods* 20: 350-360 (<https://doi.org/10.1002/lom3.10491>). [A8]
 15. **Bercovici SK, Wiemers M, Dittmar T, Niggemann J** (2023) Disentangling Biological Transformations and Photodegradation Processes from Marine Dissolved Organic Matter Composition in the Global Ocean. *Environ Sci Technol* 57: 20975-21484 (<https://doi.org/10.1021/acs.est.3c05929>) [A8]
 16. **Bercovici SK, Dittmar T, Niggemann J** (2023) Processes in the surface ocean regulate dissolved organic matter distributions in the deep. *Global Biogeochemical Cycles* 37: e2023GB007740. (<https://doi.org/10.1029/2023GB007740>) [A8]
 17. **Bergen, N., P. Krämer J. Romberg, A. Wichels, G. Gerlach, T. Brinkhoff.** 2022. Shell disease syndrome is associated with reduced and shifted epibacterial diversity on the carapace of the crustacean *Cancer pagurus*. *Microbiology Spectrum* 10: e0341922. (<https://doi:10.1128/spectrum.03419-22>). [B2]
 18. **Berger M, Brock N, Liesegang H, Dogs M, Preuth I, Simon M, Dickschat J, Brinkhoff T** (2012) Genetic analysis of the upper phenylacetate catabolic pathway in the production of tropodithietic acid by *Phaeobacter gallaeciensis*. *Appl Environ Microbiol* 78(10): 3539-3551. (<https://DOI:10.1128/AEM.07657-11>). [A1, B2, B7]
 19. **Berger M, Neumann A, Schulz S, Simon M, Brinkhoff T** (2011) Tropodithietic acid production in *Phaeobacter gallaeciensis* is regulated by N-acyl homoserine lactone-mediated quorum sensing. *J Bacteriol* 193: 6576–6585 (<https://doi:10.1128/JB.05818-11>). [A1, B2, C2]
 20. **Beyersmann PG, Chertkov O, Petersen J, Fiebig A, Chen A, Pati A, Ivanova NN, Lapidus A, Goodwin LA, Chain P, Detter JC, Rohde M, Gronow S, Kyrpides NC, Woyke T, Simon M, Göker M, Klenk H-P, Brinkhoff T** (2013) Genome sequence of *Phaeobacter caeruleus* type strain (DSM 24564), a surface-associated member of the marine *Roseobacter* clade. *Standards in Genomic Sciences* 8: 403-419 (<https://doi:10.4056/sigs.3927626>). [A1, A5, A6, B2]
 21. **Beyersmann PG, Tomasch J, Son K, Stocker R, Göker M, Wagner-Döbler I, Simon M, Brinkhoff T** (2017) Dual function of tropodithietic acid as antibiotic and signaling molecule in quorum sensing. *Scientific Reports*, 7: 730 (<https://doi:10.1038/s41598-017-00784-7>). [A1, A6, B2, B4]
 22. **Billerbeck S, Wemheuer B, Voget S, Poehlein A, Giebel HA, Brinkhoff T, Gram L, Jeffrey WH, Daniel R, Simon M** (2016) Biogeography and environmental genomics of the *Roseobacter* group affiliated pelagic CHAB-I-5 lineage. *Nature Microbiol.* 1: Article no. 16063 (<https://DOI:10.1038/NMICROBIOL.2016.63>). [A1, B2, Z02]
 23. **Billerbeck S, Orchard J, Tindall BJ, Giebel, HA, Brinkhoff, T, Simon M** (2015) Description of *Octadecabacter temperatus* sp. nov., isolated from the southern North Sea, emended description of the genus *Octadecabacter* and reclassification of *Octadecabacter jejudonensis* (Park & Yoon, 2014) as *Pseudooctadecabacter jejudonensis* gen. nov., comb. nov. *Int. J. Syst. Evol. Microbiol.* 65: 1967-1974 (<https://DOI:10.1038/NMICROBIOL.2016.63>). [A1, B2]
 24. **Birmes L, Freese HM & Petersen J** (2021) RepC_{soli}: a novel promiscuous plasmid type of Rhodobacteraceae mediates horizontal transfer of antibiotic resistances in the ocean. *Environ Microbiol.* 23: 5395-5411 ((<https://doi.org/10.1111/1462-2920.15380>). [A5, A8]
 25. **Bischoff V, Bunk B, Meier-Kolthoff J, Spröer C, Poehlein A, Dogs M, Nguyen M, Petersen J, Daniel R, Overmann J, Göker M, Simon M, Brinkhoff T, Moraru C**

- (2019) Cobaviruses – a new globally distributed phage group infecting Rhodobacteraceae in marine ecosystems. *ISME J*: 13, 1404–1421 (<https://doi.org/10.1038/s41396-019-0362-7>). [A1, A5, A6, A7, B2, B6, Z02]
26. **Blaženović, I.**, Kind, T., Torbašinović, H., Obrenović, S., Mehta, S.S., Tsugawa, H., Wermuth, T., Schauer, N., Jahn, M., Biedendieck, R., **Jahn, D.**, Fiehn, O. (2017) Comprehensive comparison of in silico MS/MS fragmentation tools of the CASMI contest: database boosting is needed to achieve 93% accuracy. *J. Cheminform.*, **9**: **32** (<https://link.springer.com/article/10.1186/s13321-017-0219-x>). [INF]
 27. **Blaženović, I.**, Kind, T., Sa, M., Ji, J., Vaniya, A., Wancewicz, B., Roberts, B., Torbasinovic, H., Lee, T., Mehta, S., Showalter, M., Song, H., Kwok, J., **Jahn, D.**, Kim, J. & Fiehn, O. (2019) Structure annotation of all mass spectra in untargeted metabolomics. *Anal. Chem.*, **91**: 2155-2162 (<https://doi.org/10.1021/acs.analchem.8b04698>). [INF]
 28. **Breider S, Freese HM, Spröer C, Simon M, Overmann J, Brinkhoff T** (2017) *Phaeobacter porticola* sp. nov., an antibiotic producing bacterium isolated from a harbor in the southern North Sea. *Int J Syst Evol Microbiol* **67**, 2153-2159 (<https://doi.org/10.1099/ijsem.0.001879>). [A1, A8, B2]
 29. **Breider S, Scheuner C, Schumann P, Fiebig A, Petersen J, Pradella S, Klenk H-P, Brinkhoff T, Göker M** (2014) Genome-scale data suggest reclassifications in the *Leisingera-Phaeobacter* cluster including proposals for *Sedimentitalea* gen. nov. and *Pseudophaeobacter* gen. nov. *Frontiers in Microbiology* **5**: 416 (<https://doi.org/10.3389/fmicb.2014.00416>). [A1, A5, A6, B2]
 30. **Breider S, Teshima H, Petersen J, Fiebig A, Chertkov O, Dalingault H, Chen A, Pati A, Goodwin LA, Chain P, Detter JC, Ivanova NN, Lapidus A, Rohde M, Tindall BJ, Kyrpides NC, Woyke T, Simon M, Göker M, Klenk HP, Brinkhoff T** (2014) Complete genome sequence of *Leisingera nanhaiensis* strain DSM 24252^T isolated from marine sediment. *Standards in Genomic Sciences* **9**: 687-703 (<https://doi.org/10.4056/sigs.3828824>). [A1, A5, A6, B2]
 31. **Breider S, Sehar S, Berger, M, Thomas T, Brinkhoff, T, Egan S** (2019) Genome sequence of *Epibacterium ulvae* strain DSM 24752^T, an indigoidine-producing, macroalga-associated member of the marine Roseobacter group. *Environ. Microbiome.* **14**: Article Number: UNSP **4** (<https://link.springer.com/article/10.1186/s40793-019-0343-5>). [B2]
 32. **Brinkmann H, Göker M, Koblížek M, Wagner-Döbler I, Petersen J** (2018) Horizontal operon transfer, plasmids and the evolution of photosynthesis in *Rhodobacteraceae*. *The ISME Journal* **12**: 1994-2010 (<https://doi.org/10.1038/s41396-018-0150-9>). [A5, A6, B4]
 33. **Brock NL, Citron CA, Zell C, Berger M, Wagner-Döbler I, Petersen J, Brinkhoff T, Simon M, Dickschat J** (2013) Isotopically labeled sulfur compounds and synthetic selenium and tellurium analogues to study sulfur metabolism in marine bacteria. *Beilstein J Org Chem* **9**: 942-950 (<https://doi.org/10.3762/bjoc.9.108>). [A5, B2, B4, B7]
 34. **Brock NL, Nikolay, A, Dickschat, JS** (2014) Biosynthesis of the Antibiotic Tropodithietic Acid by the Marine Bacterium *Phaeobacter inhibens*, *ChemComm* **50**, 5487-5489 (<https://doi.org/10.1039/C4CC01924E>). [B7]
 35. **Brock NL, Menke, M, Klapschinski, TA, Dickschat JS** (2014) Marine Bacteria from the Roseobacter Clade Produce Sulfur Volatiles via Amino Acid and Dimethylsulfoniopropionate Catabolism, *Org. Biomol. Chem.* **2014**, **12**, 4318-4323 (<https://doi.org/10.1039/C4OB00719K>) [B7]
 36. **Broy S, Chen C, Hoffmann T, Brock, NL, Nau-Wagner G, Jebbar M, Smits SHJ, Dickschat, JS, Bremer E** (2015) Abiotic Stress Protection by Ecologically Abundant DMSP and its Natural and Synthetic Derivatives: Insights from *Bacillus subtilis*, *Environ. Microbiol.*, **17**, 2362-2378 (<https://doi.org/10.1111/1462-2920.12698>). [B7]

37. **Bruns H**, Crüsemann M, Letzel A-C, Alanjary M, McInerney JO, Jensen PR, **Schulz S**, Moore BS, Ziemert N (2018) Function-related replacement of bacterial siderophore pathways. *ISME J* 12: 320-329 (<https://doi.org/10.1038/ismej.2017.137>). [C2]
38. **Bruns H**, Herrmann J, Müller R, **Wang H**, **Wagner Döbler I**, **Schulz S** (2018) Oxygenated *N*-Acyl Alanine Methyl Esters (NAMEs) from the Marine Bacterium *Roseovarius tolerans* EL-164. *J Nat Prod* 81:131–139 (<https://doi.org/10.1021/acs.jnatprod.7b00757>). [B4, C2]
39. **Bruns H**, **Thiel V**, **Voget S**, **Patzelt D**, **Daniel R**, **Wagner-Döbler I**, **Schulz S** (2013) *N*-acylated alanine methyl esters (NAMEs) from *Roseovarius tolerans*, structural analogs of quorum-sensing autoinducers, *N*-acylhomoserine lactones. *Chem Biodivers* 10:1559–1573 (<https://doi.org/10.1002/cbdv.201300210>). [B4, C2, Z02]
40. **Bruns H.**, **Ziesche**, L, N. Taniwal K, **Wolter**, L, **Brinkhoff**, T, Herrmann J, Müller R, **Schulz**. S (2018) *N*-acylated amino acid methyl esters from marine Roseobacter group bacteria. *Beilstein J. Org. Chem.* 14: 2964–2973. (<https://doi:10.3762/bjoc.14.276>). [B2, C2]
41. **Bruns S**, **Wienhausen G**, Scholz-Böttcher B, Wilkes H (2022) Simultaneous quantification of all B vitamins and selected biosynthetic precursors in seawater and bacteria by means of different mass spectrometric approaches. *Anal Bioanal Chem* 414: 7839-7854 (<https://doi:10.3762/bjoc.14.276>). [A8]
42. **Bruns S**, **Wienhausen G**, Scholz-Böttcher B, Heyen S, Wilkes H (2023) Method development and quantification of all B vitamins and selected biosynthetic precursors in winter and spring samples from the North Sea and de novo synthesized by *Vibrio campbellii*. *Mar Chem* 256: 104300 (<https://doi.org/10.1016/j.marchem.2023.104300>) [A8]
43. **Buddruhs N**, Chertkov O, **Petersen J**, Fiebig A, Chen A, Pati A, Ivanova NN, Lapidus A, Goodwin LA, Chain P, Detter JC, Gronow S, Kyrpides NC, Woyke T, **Göker M**, **Brinkhoff T**, **Klenk H-P** (2013). Complete genome sequence of the marine methyl-halide oxidizing *Leisingera methylohalidivorans* type strain (DSM 14336), a member of the *Roseobacter* clade. *Standards in Genomic Sciences* 9: 128-141 (<https://doi:10.4056/sigs.4297965>). [A5, A6, B2]
44. **Buddruhs N**, **Pradella S**, **Göker**, M, **Päucher**, O, Pukall R, Spröer C, Schumann P, **Petersen**, J, **Brinkhoff T** (2013) Molecular and phenotypic analyses reveal the non-identity of the *Phaeobacter gallaeciensis* type strain deposits CIP 105210^T and DSM 17395. *Int. J. Syst. Evol. Microbiol.* 63: 4340–4349 (<https://doi.org/10.1099/ijs.0.053900-0>). [A5, A6, B2]
45. **Burkhardt I**, **Lauterbach L**, **Brock**, NL, **Dickschat**, JS (2017) Chemical Differentiation of Three DMSP Lyases from the Marine Roseobacter group, *Org. Biomol. Chem.* 15, 4432-4439 (<https://doi.org/10.1039/C7OB00913E>). [B7]
46. **Czech L**, Höppner A, Kobus S, Seubert A, **Riclea**, R, **Dickschat**, JS, Heider J, Smits SHJ, Bremer E (2019) Illuminating the catalytic core of ectoine synthase through structural and biochemical analysis, *Sci. Rep.* 9, 364 (<https://doi.org/10.1038/s41598-018-36247-w>). [B7]
47. **Celik E**, M. Maczka M, N. Bergen N, T. **Brinkhoff T**, S. **Schulz S**, J. S. **Dickschat**, JS (2017) Metabolism of 2,3-dihydroxypropane-1-sulfonate by marine bacteria, *Org. Biomol. Chem.* 15, 2919-2922 (<https://doi.org/10.1039/C7OB00357A>). [B2, B7, C2]
48. **Chang, A.**, **Jeske**, L., **Ulbrich**, S., **Hofmann**, J., **Koblitz**, J., **Schomburg**, I., **Neumann-Schaal**, M., **Jahn**, D. & **Schomburg**, D. (2020) BRENDA, the ELIXIR Core Data Resource in 2021: New Developments and Update. *Nucleic Acids Res.*, 49:D498-D508 (<https://doi.org/10.1093/nar/gkaa1025>). [C3, INF]

49. **Chhalodia AK**, Rinkel J, Konvalinkova D, **Petersen J**, **Dickschat JS** (2021) Identification of volatiles from six marine *Celeribacter* strains, *Beilstein J. Org. Chem.* 17, 420-430 (<https://doi.org/10.3762/bjoc.17.38>). [A5, B7]
50. **Chhalodia AK**, **Dickschat JS** (2021) Breakdown of 3-(Allylsulfonio)propanoates in Bacteria from the *Roseobacter* Group Yields Garlic Oil Constituents, *Beilstein J. Org. Chem.* 17, 569-580 (<https://doi.org/10.3762/bjoc.17.51>). [B7]
51. **Chhalodia AK**, **Dickschat JS** (2023) Discovery of Dimethylsulfoxonium Propionate Lyases – A Missing Enzyme Relevant to the Global Sulfur Cycle, *Org. Biomol. Chem.*, 21, 3083-3089 (<https://doi.org/10.1039/D2OB02288E>). [B7]
52. **Chhalodia AK**, **Dickschat JS** (2024) The Stereochemical Course of DmdC, an Enzyme Involved in the Degradation of Dimethylsulfoniopropionate. *ChemBiochem* early access (<https://DOI10.1002/cbic.202300795>) [B7]
53. Crenn K, **Bunk B**, Spröer C, **Overmann J**, Jeanthon C (2019) Complete genome sequence of the *Silicimonas algicola* type strain, a representative of the marine *Roseobacter* group isolated from the cell surface of the marine diatom *Thalassiosira delicatula*. *Microbiol Resour Announc* 8, e00108-19 (<https://doi.org/10.1128/mra.00108-19>). [A7]
54. Crenn K, Serpin D, Lepleux C, Spröer C, **Bunk B**, **Overmann J**, Jeanthon C (2016) *Silicimonas algicola* gen. nov., sp. nov., a novel member of the *Roseobacter* clade isolated from the cell surface of the marine diatom *Thalassiosira delicatula*. *Int J Syst. Evol Microbiol* 66, 4580-4588 (<https://doi.org/10.1099/ijsem.0.001394>). [A7]
55. **Daniel R**, **Simon M**, **Wemheuer B** (2018) Editorial: Molecular ecology and genetic diversity of the *Roseobacter* clade. *Front Microbiol* 9, 1185 (<https://doi.org/10.3389/fmicb.2018.01185>). [A1, Z02]
56. **De Corte D**, Varela MM, Louro AM, **Bercovici SK**, Valencia-Vila J, Sintes E, Baltar F, Rodríguez-Ramos T, **Simon M**, Bode A, **Dittmar T**, **Niggemann J** (2023) Zooplankton-derived dissolved organic matter composition and its bioavailability to natural prokaryotic communities. *Limnol Oceanogr* 68: 336-347 (<https://doi.org/10.1002/lno.12272>). [A7]
57. **Dickschat JS**, Rabe P, **Citron CA** (2015) The Chemical Biology of Dimethylsulfoniopropionate, *Org. Biomol. Chem.* 13, 1954-1968 (<https://doi.org/10.1039/C4OB02407A>). [B7]
58. **Dickschat JS**, Rinkel J, Klapschinski T, **Petersen J** (2017). Characterisation of the L-cysteine β -lyase PatB from *Phaeobacter inhibens*: an enzyme involved in the biosynthesis of the marine antibiotic tropodithietic acid. *ChemBioChem*. 18: 2260–2267 (<https://doi.org/10.1002/cbic.201700358>). [A5, B7]
59. **Dlugosch L**, **Poehlein A**, **Wemheuer B**, Pfeiffer B, Badewien TH, **Daniel R**, **Simon M** (2022) Significance of gene variants for the functional biogeography of the near-surface Atlantic Ocean microbiome. *Nature Comm* 13: 456 (<https://doi.org/10.1038/s41467-022-28128-8>). [A1, Z02]
60. **Dlugosch L**, Bunse C, **Bunk B**, Böttcher L, **Tran Quoc Den**, **Dittmar T**, Hartmann M, **Heinrichs M**, Hintz NH, Mori C, **Niggemann J**, Spröer C, Striebel M, **Simon M**. (2023) Naturally-induced biphasic phytoplankton spring bloom reveals rapid and distinct substrate and bacterial community dynamics. *FEMS Microbiol Ecol* 99: 1-14 (<https://doi.org/10.1093/femsec/fiad078>). [A1, A2, A7, A8, C7]
61. **Dogs M**, Teshima H, **Petersen J**, Fiebig A, Chertkov O, Daligault H, Chen A, Pati A, Goodwin LA, Chain P, Detter JC, Ivanova NN, Lapidus A, Rohde M, Gronow S, Kyrpides NC, Woyke T, **Simon M**, **Klenk H-P**, **Göker M**, **Brinkhoff T** (2013) Genome sequence of *Phaeobacter daeponensis* type strain (DSM 23529), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of *Phaeobacter daeponensis*. *Standards in Genomic Sciences* 9: 142-159 (<https://doi:10.4056/sigs.4287962>). [A1, A5, A6, B2]

62. **Dogs M, Voget S, Teshima H, Petersen J, Fiebig A**, 12 co-authors, **Simon M, Klenk HP, Göker M, Brinkhoff T** (2013) Genome sequence of *Phaeobacter inhibens* type strain (T5^T), a secondary-metabolite producing member of the marine *Roseobacter* clade, and emendation of the species *Phaeobacter inhibens*. *Stand Genomic Sci*, 9: 334-350 (<https://DOI:10.4056/sigs.4448212>). [A1, A5, A6, B2]
63. **Dogs M, Wemheuer B, Wolter, L, Bergen N, Daniel R, Simon, M, Brinkhoff. T** (2017) *Rhodobacteraceae* on the marine brown alga *Fucus spiralis* are predominant and show physiological adaptation to an epiphytic lifestyle. *Syst. Appl. Microbiol.* 40: 370-382 (<https://doi.org/10.1016/j.syapm.2017.05.00>) [A1, B2, Z02]
64. Dougan KE, Deng ZL, **Wöhlbrand L, Reuse C, Bunk B, Chen Y, Hartlich J, Hiller K, John U, Kalvelage J, Mansky J, Neumann-Schaal M, Overmann J, Petersen J, Sanchez S, Schmidt-Hohagen K, Shah S, Spröer C, Sztajer H, Wang H, Bhattacharya D, Rabus R, Jahn D, Chan CX, Wagner-Döbler I** (2023) Evolution of resilience against heat stress in a red-tide dinoflagellate. *Genome Biology* 24: 265 (<https://doi.org/10.1186/s13059-023-03107-4>) [A5, A7, B4, B5, C3, C5]
65. **Drüppel K, Hensler M, Trautwein K, Koßmehl S, Wöhlbrand L, Schmidt-Hohagen K, Ulbrich M, Bergen N, Meier-Kolthoff JP, Göker M, Klenk H-P, Schomburg D, Rabus RA** (2014) Pathways and substrate-specific regulation of amino acid degradation in *Phaeobacter inhibens* DSM 17395 (archetype of the marine *Roseobacter* clade). *Environmental Microbiology* 16: 218-138 (<https://doi:10.1111/1462-2920.12276>). [A6, B2, C1, C3]
66. Duan Y, Toplak M, Hou A, **Brock, NL, Dickschat, JS, Teufel R** (2021) A flavoprotein dioxygenase steers bacterial tropone biosynthesis via coenzyme A-ester oxygenolysis and ring epoxidation, *J. Am. Chem. Soc.*, 143, 10413-10421 (<https://doi.org/10.1021/jacs.1c04996>). [B7]
67. **Dudek, C.-A, Jahn, D.** (2022) PRODORIC: state-of-the-art database of prokaryotic gene regulation. *Nucleic Acids Res.*, 50(D1):D295-D302 (<https://doi.org/10.1021/jacs.1c04996>). [INF]
68. **Ebert M, Laaß S, Burghartz M, Petersen J, Koßmehl S, Wöhlbrand L, Rabus R, Wittmann C, Tielen P, Jahn D** (2013) Transposon mutagenesis identified chromosomal and plasmid genes essential for adaptation of the marine bacterium *Dinoroseobacter shibae* to anaerobic conditions. *J Bacteriol* 195: 4769-4777 (<https://doi.org/10.1128/jb.00860-13>). [A5, B5, C1, C4, C5]
69. **Ebert M., Laass S., Thürmer A., Roselius L., Eckweiler D., Daniel R., Härtig E., Jahn D.** (2017) FnrL and three Dnr regulators are used for the metabolic adaptation to low oxygen tension in *Dinoroseobacter shibae*. *Front Microbiol* 8: 642, (<https://doi.org/10.3389/fmicb.2017.00642>) [B5, Z02]
70. **Ebert M., Schweyen P., Bröring M., Laass S, Härtig E, Jahn, D.** (2017) Heme and nitric oxide binding by the transcriptional regulator DnrF from the marine bacterium *Dinoroseobacter shibae* increases napD promoter affinity. *J. Biol. Chem.*, 292: 15468-15480 (<https://doi.org/10.1074/jbc.M117.79872>). [B5]
71. **Eckweiler, D., Dudek, C.-A., Hartlich, J., Broetje, D, Jahn, D.** (2017) PRODORIC2: the bacterial gene regulation database in 2018. *Nucleic Acids Res.* 46:D320-D326 (<https://doi.org/10.1093/nar/gkx1091>). [INF]
72. **Fiebig A, Pradella S, Petersen J, Michael V, Päuker O, Rohde M, Göker M, Klenk H-P, Wagner-Döbler I** (2013) Genome of the marine alphaproteobacterium *Hoeflea phototrophica* type strain (DFL-43^T). *Standards in Genomic Sciences* 7: 440-444 (<https://doi:10.4056/sigs.3486982>). [A5, A6, B4]
73. **Fiebig A, Pradella S, Petersen J, Päuker O, Michael V, Lünsdorf H, Göker M, Klenk H-P, Wagner-Döbler I** (2013) Genome of the R-body producing marine alphaproteobacterium *Labrenzia alexandrii* type strain (DFL-11^T). *Standards in Genomic Sciences* 7: 413-426 (<https://doi:10.4056/sigs.3456959>). [A5, A6, B4]

74. **Fiebig A, Riedel T, Gronow S, Klenk H-P, Göker M** (2013) Genome sequence of the reddish-pigmented *Rubellimicrobium thermophilum* type strain (DSM 16684^T), a member of the *Roseobacter* clade. *Standards in Genomic Sciences* 8: 480-490 (<https://doi.org/10.4056/sigs.4247911>). [A6, B4]
75. **Frank O, Göker M, Pradella S, Petersen J** (2015) Ocean's twelve: Flagellar and biofilm chromids in the multipartite genome of *Marinovum algicola* DG898 exemplify functional compartmentalization. *Environmental Microbiology* 17: 4019-4034 (<https://doi.org/10.1111/1462-2920.12947>). [A5, A6]
76. **Frank O, Michael V, Päuker O, Boedeker C, Jogler C, Rohde M, Petersen J** (2015). Plasmid curing and the loss of grip - The 65-kb replicon of *Phaeobacter inhibens* DSM 17395 is required for biofilm formation, motility and the colonization of marine algae. *Syst. Appl. Microbiol.* 38: 120–127 (<https://doi.org/10.1016/j.syapm.2014.12.001>). [A5]
77. **Frank O, Pradella S, Rohde M, Scheuner C, Klenk H-P, Göker M, Petersen J** (2014). Complete genome sequence of the *Phaeobacter gallaeciensis* type strain CIP 105210^T (= DSM 26640^T = BS107^T). *Stand. Genomic Sci.* 9: 914–932 (<https://doi.org/10.4056/sigs.5179110>). [A5, A6]
78. **Freese H, Daligault H, Petersen J, Pradella S, Fiebig A, Davenport KW, Teshima H, Chen A, Pati A, Ivanova NN, Goodwin LA, Chain P, Detter JC, Rohde M, Gronow S, Kyrpides NC, Woyke T, Brinkhoff T, Göker M, Overmann J, Klenk H-P** (2013) Genome sequence of the phage-gene rich marine *Phaeobacter arcticus* type strain DSM 23566. *Standards in Genomic Sciences* 8: 450-464 (<https://doi.org/10.4056/sigs.383362>). [A5, A6, A7, B2]
79. **Freese HM, Methner A, Overmann J** (2017) Adaptation of biofilm bacteria to the open ocean: A genomically distinct subpopulation of *Phaeobacter gallaeciensis* colonizes Pacific mesozooplankton. *Front Microbiol* 8, 1659 (<https://doi.org/10.3389/fmicb.2017.01659>). [A7]
80. **Freese HM, Ringel V, Overmann J, Petersen J** (2022). Beyond the ABCs - Discovery of three new plasmid types in *Rhodobacterales* (RepQ, RepY, RepW). *Microorganisms* 10: 738 (<https://doi.org/10.3390/microorganisms10040738>). [A5, A7]
81. **Freese HM, Sikorski J, Bunk B, Scheuner C, Meier-Kolthoff JP, Spröer C, Gram L, Overmann J** (2017) Trajectories and drivers of genome evolution in surface-associated marine *Phaeobacter*. *Genome Biol Evol* 9, 3297-3311 (<https://doi.org/10.1093/gbe/evx249>). [A6, A7]
82. **Giebel HA, Arnosti C, Badewien TH, Bakenhus I, Balmonte JP, Billerbeck S, Dlugosch L, Henkel R, Kuerzel B, Meyerjürgens J, Milke F, Voss D, Wienhausen G, Wietz M, Winkler H, Wolterink M, Simon M** (2021) Microbial growth and organic matter cycling in the Pacific Ocean along a latitudinal transect between subarctic and subantarctic waters. *Front Mar Sciences* 8: 764383. (<https://doi.org/10.3389/fmars.2021.764383>). [A1, A8]
83. **Giebel HA, Kalhoefer D, Gahl-Janssen R, Choo YJ, Lee K, Cho JC, Tindall BJ, Rhiel E, Beardsley C, Aydogmus ÖO, Voget S, Daniel R, Simon M, Brinkhoff T** (2013) *Planktomarina temperata* gen. nov., sp. nov., belonging to the globally distributed RCA cluster of the marine *Roseobacter* clade, isolated from the German Wadden Sea. *Int J Syst Evol Microbiol* 63: 4207–4217 (<https://doi.org/10.1099/ijs.0.053249-0>). [A1, B2]
84. **Giebel HA, Wolterink M, Brinkhoff T, Simon M** (2019) Complementary energy acquisition via aerobic anoxygenic photosynthesis and carbon monoxide oxidation by *Planktomarina temperata* of the *Roseobacter* group. *FEMS Microb Ecol* 95/5: fiz050 (<https://doi.org/10.1093/femsec/fiz050>). [A1]
85. **Giebel, H.-A., F. Klotz, S. Voget, A. Poehlein, K. Grosser, A. Teske, T. Brinkhoff.** 2016. Draft genome sequence of the marine *Rhodobacteraceae* strain O3.65,

- cultivated from oil-polluted seawater of the Deepwater Horizon oil spill. *Stand. Genomic Sci.* 11: 81 (<https://DOI:10.1186/s40793-016-0201-7>) [A1, B2, Z02]
86. **Göker M** (2021) What can genome analysis offer for bacteria? Pp. 255-281 in: Bridge, P., Smith, D., Stackebrandt, E. (eds), *Trends in the systematics of bacteria and fungi*. CAB International, Wallingford (<http://dx.doi.org/10.1079/9781789244984.0255>). [A6]
 87. **Göker M** (2022a) Solving the remaining problems with names of classes. Request for an Opinion. *Internat J System Evol Microbiol* 72: 5605 (<https://doi:10.1099/ijsem0.005605>). [A6]
 88. **Göker M** (2022b) Filling the gaps: missing taxon names at the ranks of class, order and family. *Internat J System Evol Microbiol* 72: 5638 (<https://doi:10.1099/ijsem0.005638>). [A6]
 89. **Göker M, Klenk H-P** (2013) Phylogeny-driven target selection for genome-sequencing (and other) projects. *Standards in Genomic Sciences* 8: 360-374 (<https://doi:10.4056/sigs.3446951>). [A6]
 90. **Gómez-Consarnau L, González JM, Riedel T, Jaenicke S, Wagner-Döbler I, Sañudo-Wilhelmy SA, Fuhrman JA** (2016) Proteorhodopsin light-enhanced growth linked to vitamin-B1 acquisition in marine Flavobacteria. *ISME J* 10:1102-12. (<https://doi:10.1038/ismej.2015.196>). [B4]
 91. **Gram L, Rasmussen BB, Wemheuer B, Bernbom N, Ng YY, Porsby CH, Breider S, Brinkhoff T** (2015) *Phaeobacter inhibens* from the *Roseobacter* clade has an environmental niche as a surface colonizer in harbors. *Syst Appl Microbiol* 38: 483-493 (<https://doi.org/10.1016/j.syapm.2015.07.006>). [B2, Z02]
 92. **Hahnke S, Brock NL, Zell C, Simon M, Dickschat JS, Brinkhoff T** (2013) Physiological diversity of *Roseobacter* clade bacteria co-occurring during a phytoplankton bloom in the North Sea. *System Appl Microbiol* 36: 39–48 (<https://doi.org/10.1016/j.syapm.2012.09.004>). [A1, B2, B7]
 93. **Hahnke S, Sperling M, Langer T, Wichels A, Gerds G, Beardsley C, Brinkhoff T, Simon M** (2013) Distinct seasonal growth patterns of the bacterium *Planktotalea frisia* in the North Sea and specific interaction with phytoplankton algae. *FEMS Microbiol Ecol* 86: 185-199 (<https://doi.org/10.1111/1574-6941.12151>). [A1, B2]
 94. **Hansen CT, Niggemann J, Giebel H-A, Simon M, Bach W, Dittmar T** (2019) Biodegradability of hydrothermally altered deep-sea dissolved organic matter. *Mar Chem*, 217: 103706 (<https://doi.org/10.1016/j.marchem.2019.103706>). [A1, A8]
 95. **Harig T, Schlawis C, Ziesche L, Pohlner M, Engelen B, Schulz S** (2017) Nitrogen-containing volatiles from marine *Salinispora pacifica* and *Roseobacter*-group bacteria. *J Nat Prod ASAP*, doi.org/10.1021/acs.jnatprod.7b00789. [A2, C2]
 96. **Harig T, Schlawis C, Ziesche L, Pohlner M, Engelen B, Schulz S** (2017) Nitrogen-Containing Volatiles from Marine *Salinispora pacifica* and *Roseobacter*-Group Bacteria. *J Nat Prod* 80: 3289–3295 (<https://doi.org/10.1021/acs.jnatprod.7b00789>). [A2, C2]
 97. **Heinrichs ME, De Corte D, Engelen B, Pan D.** (2021). An Advanced Protocol for the Quantification of Marine Sediment Viruses via Flow Cytometry. *Viruses* 13:102; doi.org/10.3390/v13010102. [A2]
 98. **Heinrichs ME, Heyerhoff B, Arslan-Gatz BS, Seidel M, Niggemann J, Engelen B** (2022) Deciphering the virus signal within the marine dissolved organic matter pool. *Front Microbiol* 13: 863686. (doi.org/10.3389/fmicb.2022.863686) [A2, A8]
 99. **Heinrichs ME, Tebbe DA, Wemheuer B, Niggemann J, Engelen B** (2020) Impact of viral lysis on the composition of bacterial communities and dissolved organic matter in deep-sea sediments. *Viruses* 12, 922; doi.org/10.3390/v12090922. [A8, B2]

100. **Heyerhoff B, Engelen B, & Bunse C.** (2022). Auxiliary metabolic gene functions in pelagic and benthic viruses of the Baltic Sea. *Front Microbiol* 13. 863620. doi.org/10.3389/fmicb.2022.863620. [A2]
101. Hofner B, Boccuto L, **Göker M** (2015) Controlling false discoveries in high-dimensional situations: Boosting with stability selection. *BMC Bioinformatics* 16: 144 (<https://doi.org/10.1186/s12859-015-0575-3>). [A6]
102. **Hollensteiner J, Poehlein A, Daniel R** (2019) Complete genome sequence of *Marinobacter* sp. strain JH2, isolated from seawater of the Kiel Fjord. *Microbiol Res Announc* 8: e00596-19 (<https://doi.org/10.1128/mra.00596-19>). [Z02]
103. **Hollensteiner J, Schneider D, Poehlein A, Daniel R** (2020) Complete genome of *Roseobacter ponti* DSM 106830T. *Genome Biol Evol* 12: 1013-1018 8 (<https://doi.org/10.1093/gbe/evaa114>). [Z02]
104. **Hollensteiner J, Wemheuer F, Schneider D, Pfeiffer B, Wemheuer B** (2023) Extraction of total DNA and RNA from marine filter samples and generation of a universal cDNA as universal template for marker gene studies. *Methods Mol Biol* 2555: 13-21 (https://link.springer.com/protocol/10.1007/978-1-4939-6691-2_2). [Z02]
105. **Hollensteiner J, Schneider D, Poehlein A, Himmelbach A, Daniel R** (2023) Metagenome-assembled genomes from particle-associated microbial communities in the mesopelagic zone of the Pacific Ocean. *Microbiology Resource Announcements*, ahead of print. <https://doi.org/10.1128/MRA.00614-23> [Z02]
106. **Hollensteiner J, Schneider D, Poehlein A, Brinkhoff T, Daniel R** (2023) Pan-genome analysis of six *Paracoccus* type strain genomes reveal lifestyle traits. *PLOS ONE* 18: e0287947 (<https://DOI10.1371/journal.pone.0287947>). [B2, Z02]
107. **Hördt A, García-López M, Meier-Kolthoff JP, Schleuning M, Weinhold LM, Tindall BJ, Gronow S, Kyrpides NC, Woyke T, Göker M** (2020) Analysis of 1,000+ type-strain genomes substantially improves taxonomic classification of *Alphaproteobacteria* *Frontiers in Microbiology* 11: 468 (<https://doi.org/10.3389/fmicb2020.00468>). [A6]
108. Jacob M, Thomas PM, **Giebel HA, Billerbeck S, Simon M, Striebel M, Dlugosch L** (2024) Cross-domain biodiversity effects: linking diatom species and intraspecific richness, bacterial diversity, and biomass production. *ISME Comm*, online first (<https://doi.org/10.1093/ismeco/ycae046>). [A1]
109. **Kalhoefer D., Thole, S, Voget, S, Lehmann R, Liesegang H, Wollher A, Daniel, R, Simon M, Brinkhoff. T** (2011). Comparative genome analysis and genome-guided physiological analysis of *Roseobacter litoralis*. *BMC Genomics*. 12: 324. (<https://DOI:10.1186/1471-2164-12-324>). [A1, B2, Z02]
110. Kallscheuer N, Jeske O, Sandargo B, ..., **Petersen J, ..., Jogler C** (2020). The planctomycete *Stieleria maiorica* Mal15^T employs stieleriacines to alter the species composition in marine biofilms. *Commun Biol*. 3: 303 (<https://doi.org/10.1038/s42003-020-0993-2>). [A5]
111. **Kalvelage J, Wöhlbrand L, Schoon R-A, Zink F-M, Correll C, Senkler J, Eubel H, Hoppenrath M, Rhiel E, Braun H-P, Winklhofer M, Klingl A, Rabus R** (2023) The enigmatic nucleus of the marine dinoflagellate *Prorocentrum cordatum*. *mSphere* (<https://doi.org/10.1128/msphere.00038-23>). [C5]
112. **Kalvelage J, Wöhlbrand L, Senkler J, Schumacher J, Ditz N, Bischof K, Winklhofer M, Klingl A, Braun HP, Rabus R** (2024) Conspicuous chloroplast with light harvesting-photosystem I/II megacomplex in marine *Prorocentrum cordatum*. *Plant Physiol* 00: 1–20 (<https://doi.org/10.1093/plphys/kiad052>). [C5]
113. **Kanukollu S, Voget S, Pohlner M, Vandieken V, Petersen J, Kyrpides NC, Woyke T, Shapiro N, Göker M, Klenk H-P, Cypionka H, Engelen B** (2016) Genome sequence of *Shimia* sp. SK013, a representative of the *Roseobacter* group isolated from marine

- sediment. *Standards in Genomic Sciences* 11: 25 (<https://doi:10.1186/s40793-016-0143-0>). [A2, A5, A6, B1]
114. **Kanukollu S, Wemheuer B, Herber J, Billerbeck S, Lucas J, Daniel R, Simon M, Cypionka H, Engelen B** (2016) Distinct compositions of free-living, particle-associated and benthic communities of the Roseobacter group in the North Sea. *FEMS Microbiol Ecol.* 92/1: fiv145 (<https://doi:10.1093/femsec/fiv145>). [A1, A2, B1, Z02]
 115. Kappler U, Davenport KW, Beatson S, Lucas S, Lapidus A, Copeland A, Berry KW, Rio TGD, Hammon N, Dalin E, Tice H, Pitluck S, Richardson P, Bruce D, Goodwin LA, Han C, Tapia R, Detter JC, Chang Y-J, Jeffries CD, Land M, Hauser L, Kyrpides NC, **Göker M, Ivanova NN, Klenk H-P, Woyke T** (2012) Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium *Starkeya novella* type strain (ATCC 8093^T). *Stand Genomic Sci* 7: 44-58 (<https://doi:10.4056/sigs.3006378>). [A6]
 116. Kielkowski P, **Brock, NL Dickschat, JS, Hocek M** (2013) Nucleobase Protection Strategy for Gene Cloning and Expression, *ChemBioChem*, 14, 801-804 (<https://doi.org/10.1002/cbic.201300127>). [B7]
 117. **Kirchhoff C, Cypionka H** (2017) Boosted membrane potential as bioenergetic response to anoxia in *Dinoroseobacter shibae*. *Front Microbiol* 8: 695, doi.org/10.3389/fmicb.2017.00695. [B1]
 118. **Kirchhoff C, Cypionka H** (2017) Propidium ion enters viable cells with high membrane potential during live-dead staining. *J Microbiol Methods* 142:79-82, doi.org/10.1016/j.mimet.2017.09.011. [B1]
 119. **Kirchhoff C, Ebert M, Jahn D, Cypionka H** (2018) Chemiosmotic energy conservation in *Dinoroseobacter shibae*: Proton translocation driven by aerobic respiration, denitrification and photosynthetic light reaction. *Front Microbiol* 9: 903, (<https://doi.org/10.3389/fmicb.2018.00903>). [B1, B5]
 120. **Klingner A, Bartsch A, Dogs M, Wagner-Döbler I, Jahn D, Simon M, Brinkhoff T, Becker J, Wittmann C** (2015) Large-scale ¹³C flux profiling reveals conservation of the Entner-Doudoroff pathway as a glycolytic strategy among marine bacteria that use glucose. *Appl Environ Microbiol* 81/7: 2408-2422 (<https://doi.org/10.1128/AEM.03157-14>). [A1, B2, B4, B5, C4]
 121. Klein, J., Leupold, S., Biegler, I., Biedendieck, R., **Münch, R. & Jahn, D.** (2012) TLM-Tracker: Software for cell segmentation, tracking and lineage analysis in time-lapse microscopy movies. *Bioinformatics*, 28: 2276-2277 (<https://doi.org/10.1093/bioinformatics/bts424>). [B1]
 122. **Kleist S, Ulbrich M, Bill N, Schmidt-Hohagen K, Geffers R, Schomburg D.** (2017) Dealing with salinity extremes and nitrogen limitation - an unexpected strategy of the marine bacterium *Dinoroseobacter shibae*. *Environ Microbiol.* 19: 894-908. (<https://doi:10.1111/1462-2920.13266>). [C3]
 123. **Klotz F, Brinkhoff T, Freese HM, Wietz M, Teske A, Simon M, Giebel HA** (2018) *Tritonibacter horizontis* gen. nov., sp. nov., a member of the Rhodobacteraceae, isolated from the Deepwater Horizon oil spill. *Int J Syst Evol Microbiol* 68: 736-744. (<https://DOI10.1099/ijsem.0.002573>). [A1, A7, B2]
 124. Koch H, Dürwald A, Schweder T, **Noriega-Ortega B, Vidal-Melgosa S, Hehemann J-H, Dittmar T, Freese HM, Becher D, Simon M & Wietz M** (2019) Biphasic cellular adaptations and ecological implications of *Alteromonas macleodii* degrading a mixture of algal polysaccharides. *ISME J* 13: 92-103 (<https://doi.org/10.1038/s41396-018-0252-4>). [A1, A7, A8]
 125. Koch H, **Freese HM, Hahnke RL, Simon M, Wietz M** (2019) Adaptations of *Alteromonas* sp. 76-1 to polysaccharide degradation: A CAZyme plasmid for ulvan degradation and two alginolytic systems. *Front Microbiol* 10: 504 (<https://doi.org/10.3389/fmicb.2019.00504>). [A1, A7]

126. Koch H, Germscheid N, **Freese H**, **Noriega-Ortega BE**, Lücking D, **Berger M**, Qiu G, Marzinelli E, Campbell A, Steinberg PD, **Overmann J**, **Dittmar T**, **Simon M**, Wietz M (2020) Genomic, metabolic and phenotypic variability shapes ecological differentiation and intraspecies interactions of *Alteromonas macleodii*. *Sci Reports*, 10: 809 (<https://doi.org/10.1038/s41598-020-57526-5>). [A1, A7, A8]
127. Kohn T, Heuer A, Jogler M, Vollmers J, Boedeker C, **Bunk B**, Rast P, Borchert D, Glöckner I, **Freese H**, **Klenk H-P**, **Overmann J**, Kaster A-K, Rohde M, Wiegand S, Jogler C (2016) *Fuerstia marisgermanicae* gen. nov., sp. nov., an unusual member of the phylum Planctomycetes from the German Wadden Sea. *Front Microbiol* 7: 2079 (<https://doi.org/10.3389/fmicb.2016.02079>). [A6, A7]
128. **Koppenhöfer S**, **Tomasch J**, Ringel V, **Birmes L**, **Brinkmann H**, Spröer C, Jarek M, **Wang H**, **Pradella S**, **Wagner-Döbler I**, **Petersen J** (2022). The sixth element: a 102-kb RepABC plasmid of xenologous origin modulates chromosomal gene expression in *Dinoroseobacter shibae*. *mSystems* 7: e0026422. (<https://doi.org/10.1128/msystems.00264-22>) [A5, B4]
129. **Koppenhöfer S**, **Wang H**, Scharfe M, Kaefer V, **Wagner-Döbler I**, **Tomasch J**. (2019) Integrated Transcriptional Regulatory Network of Quorum Sensing, Replication Control, and SOS Response in *Dinoroseobacter shibae*. *Front Microbiol*. 12: 803. (<https://doi.org/10.3389/fmicb.2019.00803>). [A5, B4]
130. **Koßmehl S**, **Wöhlbrand L**, **Drüppel K**, Feenders C, Blasius B, **Rabus R*** (2013) Subcellular protein localization (cell envelope) in *Phaeobacter inhibens* DSM 17395. *Proteomics* 13: 2743-2760 (<https://doi.org/10.1002/pmic.201300112>). [C1]
131. **Koteska D**, Marter P, Huang S, **Pradella S**, **Petersen J**, **Schulz S** (2022) Volatiles of the Apicomplexan Alga *Chromera velia* and Associated Bacteria. *ChemBioChem* 24: e202200530 (<https://doi.org/10.1002/cbic.202200530>). [A5, C2]
132. **Koteska D**, Sanchez Garcia S, Wagner-Döbler I, **Schulz S** (2022) Identification of Volatiles of the Dinoflagellate *Prorocentrum cordatum*. *Mar Drugs* 20: 371 (<https://doi.org/10.3390/md20060371>). [B4, C2]
133. **Koteska D**, Wang H, Wagner-Döbler I, **Schulz S** (2023) Outer membrane vesicles of *Dinoroseobacter shibae* transport a volatile aldehyde. *Front Ecol Evol* 11: 1102159 (<https://doi.org/10.3389/fevo.2023.1102159>). [B4, C2]
134. Kopejtká K, **Tomasch J**, **Bunk B**, Spröer C, **Wagner-Döbler I**, Koblížek M (2018) The complete genome sequence of *Rhodobaca barguzinensis* alga05 (DSM 19920) documents its adaptation for life in soda lakes. *Extremophiles*: 22: 839-849. (<https://doi.org/10.1007/s00792-018-1041-8>). [A7, B4]
135. **Laass S**, **Kleist S**, **Bill N**, **Drüppel K**, **Koßmehl S**, **Wöhlbrand L**, **Rabus R**, Klein J, Rohde M, Bartsch A, **Wittmann C**, **Schmidt-Hohagen K**, **Tielen P**, **Jahn D**, **Schomburg D** (2014) Gene regulatory and metabolic adaptation processes of *Dinoroseobacter shibae* DFL12T during oxygen depletion. *J Biol Chem* 289: 13219–13231. (<https://doi.org/10.1074/jbc.M113.545004>). [C1, C3, C4, C5]
136. Lau SCK, **Riedel T**, **Fiebig A**, Han J, Huntemann M, **Petersen J**, Ivanova NN, Markowitz V, Woyke T, **Göker M**, Kyrpides NC, **Klenk H-P**, Qian P-Y (2015) Genome sequence of the pink-pigmented marine bacterium *Loktanella hongkongensis* type strain (UST950701-009P^T), a representative of the *Roseobacter* group. *Standards in Genomic Sciences* 10: 51 (<https://doi.org/10.1186/s40793-015-0050-9>). [A5, A6, B4]
137. **Leinberger, J.**, **F. Milke**, M. Christodoulou, A. **Poehlein**, J. Caraveo-Patino, A. Teske, **T. Brinkhoff** (2022) Microbial epibiotic community of the deep-sea galatheid squat lobster *Munidopsis alvisca*. *Sci. Rep.* 12:: 2675 (<https://doi.org/10.1038/s41598-022-06666-x>). [A1, B2, Z02]
138. **Leinberger, J.**, J. **Holste**, B. **Bunk**, H.M. **Freese**, C. Sproeer, L. **Dlugosch**, A.C. Kueck, S. **Schulz**, **T. Brinkhoff** (2021) High potential for secondary metabolite

- production of *Paracoccus marcusii* CP157, isolated from the crustacean *Cancer pagurus*. *Frontiers Microbiol.*, 12: 688754 (<https://doi.org/10.3389/fmicb.2021.688754>). [A7, B2, C2, C7]
139. Liu Y, Brinkhoff T, Berger M, Poehlein A, Voget S, Paoli L, Sunagawa S, Amann R, Simon M (2023) Metagenome assembled genomes reveal greatly expanded taxonomic and functional diversification of the abundant marine *Roseobacter* RCA cluster. *Microbiome* 11:265 (<https://doi.org/10.1186/s40168-023-01644-5>). [A1, B2, Z02]
 140. Liu Y, Brinkhoff T, Simon M (2025) Ecogenomics and functional biogeography of the *Roseobacter* group in the global oceans based on 653 MAGs and SAGs. *Microbiome* 13: 247 (<https://doi.org/10.1186/s40168-025-02259-8>). [A1, B2]
 141. Ludewig-Klingner AK, Michael V, Jarek M, Brinkmann H, Petersen J (2018). Distribution and evolution of peroxisomes in alveolates (Apicomplexa, dinoflagellates, ciliates). *Genome Biol. Evol.* 10: 3531–3543 (<https://doi.org/10.1093/gbe/evx250>). [A5]
 142. Majzoub M, Beyersmann PG, Simon M, Thomas T, Brinkhoff T, Egan S (2019) *Phaeobacter inhibens* controls bacterial community assembly on a marine diatom. *FEMS Microb Ecol* 95/6: fiz060 (<https://doi.org/10.1093/femsec/fiz060>). [A1, B2]
 143. Majzoub ME, McElroy K, Maczka M, Schulz S, Thomas T, Egan S (2021) Genomic Evolution of the Marine Bacterium *Phaeobacter inhibens* during Biofilm Growth. *Appl Environ Microbiol* 87: e0076921 (<https://doi.org/10.1128/AEM.00769-21>). [C2]
 144. Majzoub ME, McElroy K, Maczka M, Thomas T, Egan S (2018) Causes and Consequences of a Variant Strain of *Phaeobacter inhibens* With Reduced Competition. *Front Microbiol* 9: 2601 (<https://doi.org/10.3389/fmicb.2018.02601>). [C2]
 145. Mansky J, Wang H, Ebert M, Tomasch J, Härtig E, Jahn D, Wagner-Döbler I (2022) The influence of genes on the “killer plasmid” of *Dinoroseobacter shibae* on its symbiosis with the dinoflagellate *Prorocentrum minimum*. *Front Microbiol* 12: 804767 (<https://doi.org/10.3389/fmicb.2021.804767>). [B4, B5]
 146. Mansky J, Wang H, Wagner-Döbler I, Tomasch J (2024) The effect of site-specific recombinases XerCD on the removal of over-replicated chromosomal DNA through outer membrane vesicles in bacteria. *Microbiology Spectrum*, early access (<https://DOI10.1128/spectrum.02343-23>) [B4]
 147. Marter P, Huang S, Brinkmann H, Pradella S, Jarek M, Rohde M, Bunk B, Petersen J (2021). Filling the gaps in the cyanobacterial tree of life – Metagenome analysis of *Stigonema ocellatum* DSM 106950, *Chlorogloea purpurea* SAG 13.99 and *Gomphosphaeria aponina* DSM 107014. *Genes* 12: 389 (<https://doi.org/10.3390/genes12030389>). [A5, A7]
 148. Meier-Kolthoff JP, Göker M (2017) VICTOR: Genome-based phylogeny and classification of prokaryotic viruses. *Bioinformatics* 2017: 1-9 (<https://doi:10.1093/bioinformatics/btx440>). [A6]
 149. Meier-Kolthoff JP, Göker M (2019) TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. *Nat Commun* 10: 2182 (<https://doi:10.1038/s41467-019-10210-3>). [A6]
 150. Meier-Kolthoff JP, Hahnke RL, Petersen J, Scheuner C, Michael V, Fiebig A, et al. (2014). Complete genome sequence of DSM 30083T, the type strain (U5/41^T) of *Escherichia coli*, and a proposal for delineating subspecies in microbial taxonomy. *Stand. Genomic Sci.* 9: 2 (<https://doi.org/10.1186/1944-3277-9-2>). [A5, A6]
 151. Meier-Kolthoff JP, Sardà Carbasse J, Peinado-Olarte RL, Göker M (2022) TYGS and LPSN: a database tandem for fast and reliable genome-based classification and

- nomenclature of prokaryotes. *Nucleic Acids Research*, 50: D801-D807 (<https://doi.org/10.1093/nar/gkab902>). [A6]
152. Merder J, Röder H, **Dittmar T**, Feudel U, Freund JA, Gerds G, Kraberg A, **Niggemann J** (2021) Dissolved organic compounds with synchronous dynamics share chemical properties and origin. *Limnol Oceanogr* 66: 4001-4016 (<https://doi.org/10.1002/lno.11938>). [A8]
 153. **Michael V**, **Frank O**, **Bartling P**, **Scheuner C**, **Göker M**, **Brinkmann H**, **Petersen J** (2016) Biofilm-plasmids with a rhamnose operon are essential determinants of the “swim-or-stick” lifestyle in roseobacters. *ISME J* 10: 2498–2513 (<https://doi.org/10.1038/ismej.2016.30>). [A5, A6]
 154. **Milici M**, Deng ZL, **Tomasch J**, Decelle J, Wos-Oxley M, **Wang H**, Jáuregui R, Plumeier I, **Giebel HA**, Badewien T, **Wurst M**, Pieper D, **Simon M**, **Wagner-Doebler I** (2016) Co-occurrence analysis of microbial taxa in the Atlantic Ocean reveals high connectivity in the free-living bacterioplankton. *Frontiers Microbiol.* 7: 649 (<https://doi.org/10.3389/fmicb.2016.00649>). [A1, B4]
 155. **Milici M**, **Tomasch J**, Wos-Oxley M, Decelle J, Jáuregui R, **Wang H**, Deng ZL, Plumeier I, **Giebel HA**, Badewien T, **Wurst M**, Pieper DH, **Simon M**, **Wagner-Doebler I** (2016) Bacterioplankton biogeography in the Atlantic Ocean: a case study of the distance-decay relationship. *Frontiers Microbiol.* 7: 590 (<https://doi.org/10.3389/fmicb.2016.00590>). [A1, B4]
 156. **Milici M**, **Tomasch J**, Wos-Oxley ML, **Wang H**, Jáuregui R, Camarinha-Silva A, Deng ZL, Plumeier I, **Giebel HA**, **Wurst M**, Pieper DH, **Simon M**, **Wagner-Döbler I** (2016) Low diversity of planktonic bacteria in the tropical ocean. *Scientific Reports* 6: 19054 (<https://DOI:10.1038/srep19054>). [A1, B4]
 157. **Milici M**, Vital M, **Tomasch J**, Badewien TH, **Giebel H-A**, Plumeier I, **Wang H**, Pieper DH, **Wagner-Döbler I**, **Simon M**. (2017) Diversity and community composition of particle-associated and free-living bacteria in mesopelagic and bathypelagic Southern Ocean water masses: evidence of dispersal limitation in the Bransfield strait. *Limnol Oceanogr* 62: 1080-1095 (<https://doi.org/10.1002/lno.10487>). [A1, B4]
 158. **Milke F**, **Sanchez-Garcia S**, **Dlugosch L**, McNichol J, Fuhrman JA, **Simon M**, **Wagner-Döbler I** (2022) Composition and biogeography of planktonic pro- and eukaryotic communities in the Atlantic Ocean: primer choice matters. *Front Microbiol.* 13: 895875 (<https://doi.org/10.3389/fmicb.2022.895875>). [A1, B4]
 159. **Milke F**, **Wagner-Doebler I**, **Wienhausen G**, **Simon M** (2022) Selection, drift and community interactions shape microbial biogeographic patterns in the Pacific Ocean. *ISME J* 16: 2653–2665. (<https://doi.org/10.1038/s41396-022-01318-4>). [A1, A8, B4]
 160. **Milke F**, Meyerjürgens J, **Simon M** (2023) Ecological mechanisms and current systems shape the modular structure of the global oceans’ prokaryotic seascape. *Nature Comm* 14: 6141 (<https://doi.org/10.1038/s41467-023-41909-z>). [A1]
 161. **Mitulla M**, Dinasquet J, Guillemette R, **Simon M**, Azam F, Wietz M (2016) Response of bacterial communities from California coastal waters to alginate particles and an alginolytic *Alteromonas macleodii* strain. *Environ Microbiol* 18: 4369–4377 (<https://doi.org/10.1111/1462-2920.13314>). [A1]
 162. **Moraru, C.** (2023) VirClust-A Tool for Hierarchical Clustering, Core Protein Detection and Annotation of (Prokaryotic) Viruses. *Viruses* 15: 1007 (<https://doi.org/10.3390/v15041007>). [B6]
 163. **Münch, R.**, **Klein, J.**, **Jahn, D.** (2011): Prediction and Analysis of Gene Regulatory Networks in Prokaryotic Genomes. *Bioinformatics - Experimental Biology Systems* ISBN 978-953-307-280-7. InTech - Open Access Publisher. [INF]
 164. **Neumann A**, **Patzelt D**, **Wagner-Döbler I**, **Schulz S** (2013) Identification of new *N*-acylhomoserine lactone signalling compounds of *Dinoroseobacter shibae* DFL-12^T by

- overexpression of *luxI* genes. *ChemBioChem* 14: 2355–2361 (<https://doi.org/10.1002/cbic.201300424>). [B4, C2]
165. Neumann AM, Balmonte JP, **Berger M**, **Giebel HA**, Arnosti C, **Voget S**, **Simon M**, **Brinkhoff T**, Wietz M (2015) Different utilization of alginate and other algal polysaccharides by marine *Alteromonas macleodii* ecotypes. *Environ Microbiol* 17: 3857–3868 (<https://doi.org/10.1111/1462-2920.12862>). [A1, B2, Z02]
 166. **Noriega-Ortega BE**, **Wienhausen G**, Mentges A, **Dittmar T**, **Simon M**, **Niggemann J** (2019) Does the chemodiversity of bacterial exometabolomes sustain the chemodiversity of marine dissolved organic matter? *Front Microbiol* 10: 215 (<https://doi.org/10.3389/fmicb.2019.00215>). [A8]
 167. Osterholz H, **Niggemann J**, **Giebel HA**, **Simon M**, **Dittmar T** (2015) Inefficient microbial production of refractory dissolved organic matter in the ocean. *Nature Comm* 6: 7422 (<https://doi.org/10.1038/ncomms8422>). [A1, A8]
 168. Osterholz H, Singer G, **Wemheuer B**, **Daniel R**, **Simon M**, **Niggemann J**, **Dittmar T** (2016) Deciphering associations between dissolved organic molecules and bacterial communities in a pelagic marine system. *ISME J* 7: 1717–1730 (<https://doi.org/10.1038/ismej.2015.231>). [A1, A8, Z02]
 169. Öztürk B, Werner J, **Meier-Kolthoff JP**, **Bunk B**, Spröer C, Springael D (2020) Comparative genomics suggests mechanisms of genetic adaptation toward the catabolism of the phenylurea herbicide linuron in *Variovorax*. *Genome Biol Evol* 12: 827–841 (<https://doi:10.1093/gbe/evaa085>). [A6, A7]
 170. Parte AC, Sardà Carbasse J, **Meier-Kolthoff JP**, Reimer LC, **Göker M** (2020) List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. *International Journal of Systematic and Evolutionary Microbiology*, 70: 5607–5612 (<https://doi:10.1099/ijsem.0.004332>). [A6]
 171. **Patzelt D**, **Michael V**, **Päucker O**, **Ebert M**, **Tielen P**, **Jahn D**, **Tomasch J**, **Petersen J**, **Wagner-Döbler I** (2016) Gene flow across genus barriers - Conjugation of *Dinoroseobacter shibae*'s 191-kb killer plasmid into *Phaeobacter inhibens* and AHL-mediated expression of type IV secretion systems. *Front Microbiol* 7: 742 (<https://doi.org/10.3389/fmicb.2016.00742>). [A5, B4, B5]
 172. **Patzelt D**, **Wang H**, **Buchholz I**, Rohde M, Gröbe L, **Pradella S**, **Neumann A**, **Schulz S**, **Heyber S**, **Münch K**, **Münch R**, **Jahn D**, **Wagner-Döbler I**, **Tomasch J** (2013) You are what you talk: Quorum sensing induces individual morphologies and cell division modes in *Dinoroseobacter shibae*. *ISME J* 7: 2274–2286 (<https://doi.org/10.1038/ismej.2013.107>). [A5, B4, B5, C2, INF]
 173. Penesyanyan, A., **Breider, S**, Schumann P, Tindall BJ, S. Egan S, **Brinkhoff, T** (2013). *Epibacterium ulvae* gen. nov., sp. nov., epibiotic bacteria isolated from the surface of a marine alga. *Int. J. Syst. Evol. Microbiol.* 63: 1589–1596 (<https://doi.org/10.1099/ijms.0.042838-0>). [B2]
 174. **Petersen J** (2011). Phylogeny and compatibility: plasmid classification in the genomics era. *Arch Microbiol* 193: 313–321 (<https://doi.org/10.1007/s00203-011-0686-9>). [A5]
 175. **Petersen J**, Brinkmann H, **Berger M**, **Brinkhoff T**, **Päucker O**, **Pradella S** (2011). Origin and evolution of a novel DnaA-like plasmid replication type in *Rhodobacteraceae*. *Mol. Biol. Evol.* 28: 1229–1240 (<https://doi.org/10.1093/molbev/msq310>). [A5, B2]
 176. **Petersen J**, Brinkmann H, **Bunk B**, **Michael V**, **Päucker O**, **Pradella S** (2012). Think pink: photosynthesis, plasmids and the Roseobacter clade. *Env. Microbiol.* 14: 2661–2672 (<https://doi.org/10.1111/j.1462-2920.2012.02806.x>). [A5, A7]
 177. **Petersen J**, **Frank O**, **Göker M**, **Pradella S** (2013). Extrachromosomal, extraordinary and essential--the plasmids of the Roseobacter clade. *Appl Microbiol Biotechnol.* 97: 2805–2815 (<https://doi:10.1007/s00253-013-4746-8>). [A5, A6]

178. **Petersen J**, Ludewig AK, **Michael V**, **Bunk B**, Jarek M, Baurain D, et al. (2014). *Chromera velia*, endosymbioses and the Rhodoplex hypothesis - Plastid evolution in cryptophytes, alveolates, stramenopiles, and haptophytes (CASH lineages). *Genome Biol. Evol.* 6: 666–684 (<https://doi.org/10.1093/gbe/evu043>). [A5, A7]
179. **Petersen J**, Vollmers J, Ringel V, **Brinkmann H**, Ellebrandt-Sperling C, Spröer C, Howat A, Murrell C, Kaster AK (2019). A marine plasmid hitchhiking vast phylogenetic and geographic distances. *Proc Nat. Acad. Sci USA.* 116: 20568-20573 (<https://doi.org/10.1073/pnas.1905878116>). [A5]
180. **Petersen J**, **Wagner-Döbler I** (2017). Plasmid transfer in the ocean - A case study from the roseobacter group. *Front. Microbiol.* 8: 1350 (<https://doi.org/10.3389/fmicb.2017.01350>). [A5, B4]
181. Pinto M, Zenner PP, Langer TM, Harrison J, **Simon M**, Varela MM, Herndl GJ (2020) Putative degraders of low-density polyethylene-derived compounds are ubiquitous members of plastic-associated bacterial communities in the marine environment. *Environ Microbiol* 22: 4779-479 (<https://doi:10.1111/1462-2920.15232>). [A1]
182. **Pohlner M**, Degenhardt J, **von Hoyningen-Huene AJE**, **Wemheuer B**, Erlmann N, Schnetger B, Badewien TH, **Engelen B** (2017) The biogeographical distribution of benthic Roseobacter group members along a Pacific transect is structured by nutrient availability within the sediments and primary production in different oceanic provinces. *Front Microbiol* 8: 2550, (doi.org/10.3389/fmicb.2017.02550). [A2, Z02]
183. **Pohlner M**, **Dlugosch L**, **Wemheuer B**, Mills H, **Engelen B**, Reese BK (2019) The Majority of Active *Rhodobacteraceae* in Marine Sediments Belong to Uncultured Genera: A Molecular Approach to Link Their Distribution to Environmental Conditions. *Front Microbiol* 10: 659, (doi.org/10.3389/fmicb.2019.00659). [A1, A2]
184. **Pohlner M**, Marshall I, Schreiber L, **Cypionka H**, **Engelen B** (2017) Draft genome sequence of *Pseudoruegeria* sp. SK021, a representative of the marine Roseobacter group, isolated from North Sea sediment. *Genome Announc* 5: e00541-17, (doi.org/10.1128/genomeA.00541-17). [A2, B1]
185. **Pradella S**, **Päuker O**, **Petersen J** (2010). Genome organization of the marine Roseobacter clade member *Marinovum algicola*. *Arch Microbiol* 192: 115-126 (<https://doi.org/10.1007/s00203-009-0535-2>). [A5]
186. **Pucelik S**, **Becker M**, **Heyber S**, **Wöhlbrand L**, **Rabus R**, **Jahn D**, **Härtig E** (2024) The blue light-dependent LOV-protein LdaP of *Dinoroseobacter shibae* acts as antirepressor of the PpsR repressor, regulating photosynthetic gene cluster expression. *Front Microbiol* 15: 1351297. (<https://doi.org/10.3389/fmicb.2024.1351297>) [B5, C1]
187. Rabe P, Klapschinski TA, **Brock, NL**, **Citron, CA**, D'Alvise P, Gram L, **Dickschat, JS** (2014). Synthesis and Bioactivity of Analogs of the Marine Antibiotic Tropodithietic Acid, *Beilstein J Org Chem.*, 10: 1796-1801 (<https://doi.org/10.3762/bjoc.10.188>). [B7]
188. **Rex R**, **Bill N**, **Schmidt-Hohagen K**, **Schomburg D** ((2013) Swimming in light: a large-scale computational analysis of the metabolism of *Dinoroseobacter shibae*. *PLoS Comput Biol.* 9: e1003224. ((<https://doi:0.1371/journal.pcbi.1003224>)). [C3]
189. **Riclea R**, Gleitzmann J, Bruns H, Junker C, Schulz S, **Dickschat, JS** (2012) Algicidal Lactones from the Marine Roseobacter Clade Bacterium *Ruegeria pomeroyi*, *Beilstein J. Org. Chem*, 8, 941-950 (<https://doi.org/10.3762/bjoc.8.106>). [B7, C2]
190. **Reimer LC**, **Will SE**, **Schomburg D** (2017) The fate of lysine: Non-targeted stable isotope analysis reveals parallel ways for lysine catabolization in *Phaeobacter inhibens*. *PLoS ONE* 12: e0186395. (<https://doi:10.1371/journal.pone.0186395>). [C3]
191. **Riedel T**, **Fiebig A**, **Göker M**, **Klenk H-P** (2014) Complete genome sequence of the bacteriochlorophyll a-containing *Roseobacterium elongatum* type strain (DSM 19469), a representative of the *Roseobacter* clade isolated from Australian coast sand.

- Standards in Genomic Sciences 9: 840-854 (<https://doi:10.4056/sigs.5541028>). [A6, B4]
192. **Riedel T, Fiebig A, Han J, Huntemann M, Spring S, Petersen J, et al.** (2014). Genome sequence of the *Wenxinia marina* type strain (DSM 24838^T), a representative of the Roseobacter group isolated from oilfield sediments. *Stand. Genomic Sci.* 9: 855–865 (<https://doi:10.4056/sigs.5601028>). [A5, B4]
 193. **Riedel T, Fiebig A, Petersen J, Gronow S, Göker M, Klenk H-P** (2013) Genome sequence of the *Litoreibacter arenae* type strain (DSM 19593^T), a member of the *Roseobacter* clade isolated from sea sand. *Standards in Genomic Sciences* 9: 117-127 (<https://doi:10.4056/sigs.4258318>). [A5, A6, B4]
 194. **Riedel T, Gómez-Consarnau L, Tomasch J, Martin M, Jarek M, González JM, Spring S, Rohlf s M, Brinkhoff T, Cypionka H, Göker M, Fiebig A, Klein J, Goesmann A, Fuhrman JA, Wagner-Döbler I** (2013) Genomics and physiology of a marine flavobacterium encoding a proteorhodopsin and a xanthorhodopsin-like protein. *PLoS One.* 8: e57487. (<https://doi:10.1371/journal.pone.0057487>). [A6, B1, B2, B4]
 195. **Riedel T, Rohlf s M, Buchholz I, Wagner-Döbler I, Reck M.** (2013) Complete sequence of the suicide vector pJP5603. *Plasmid.* 04-7. *Plasmid* 69: 104-107. (<https://doi:10.1016/j.plasmid.2012.07.005>). [B4]
 196. **Riedel T, Spring S, Fiebig A, Petersen J, Göker M, Klenk H-P.** (2014). Genome sequence of the pink to light reddish-pigmented *Rubellimicrobium mesophilum* type strain (DSM 19309^T), a representative of the Roseobacter group isolated from soil, and emended description of the species. *Stand Genomic Sci.* 9: 902–913 (<https://doi.org/10.4056/sigs.5621012>). [A5, A6, B4]
 197. **Riedel T, Spring S, Fiebig A, Petersen J, Kyrpides NC, Göker M, et al.** (2014). Genome sequence of the exopolysaccharide-producing *Salipiger mucosus* type strain (DSM 16094^T), a moderately halophilic member of the Roseobacter clade. *Stand. Genomic Sci.* 9: 1331–1343 (<https://doi:10.4056/sigs.4909790>). [A5, A6, B4]
 198. **Riedel T, Spring S, Fiebig A, Scheuner C, Petersen J, Göker M.** (2015). Genome sequence of the *Roseovarius mucosus* type strain (DSM 17069^T), a bacteriochlorophyll a -containing representative of the marine Roseobacter group isolated from the dinoflagellate *Alexandrium ostenfeldii*. *Stand. Genomic Sci.* 10: 17 (<https://doi:10.1186/1944-3277-10-17>). [A5, A6, B4]
 199. **Riedel T, Teshima H, Petersen J, Fiebig A, Davenport KW, Daligault H, Erkkila T, Gu W, Munk AC, Xu Y, Chen A, Pati A, Ivanova NN, Goodwin LA, Chain P, Detter JC, Rohde M, Gronow S, Kyrpides NC, Woyke T, Göker M, Brinkhoff T, Klenk H-P** (2013) Genome sequence of the *Leisingera aquimarina* type strain (DSM 24565), a member of the marine *Roseobacter* clade rich in extrachromosomal elements. *Standards in Genomic Sciences* 8: 389-402 (<https://doi:10.4056/sigs.3858183>). [A5, A6, B2, B4]
 200. **Riedel T, Tomasch J, Buchholz I, Jacobs J, Kollenberg M, Gerdts G, Wichels A, Brinkhoff T, Cypionka H, Wagner-Döbler I.** (2010) Constitutive expression of the proteorhodopsin gene by a flavobacterium strain representative of the proteorhodopsin-producing microbial community in the North Sea. *Appl Environ Microbiol.* 76: 3187-97. (<https://doi:10.1128/AEM.02971-09>). [B1, B2, B4]
 201. **Roselius, L., Langemann, D., Müller, J., Hense, B., Filges, S., Jahn, D, Münch, R.** (2014) Modeling and analysis of a gene-regulatory feed-forward loop with basal expression of the second regulator. *J Theoret Biol.*, 363:290-299 (<https://doi.org/10.1016/j.itbi.2014.08.043>). [INF]
 202. **Ruppersberg HS, Goebel MR, Kleinert SI, Wünsch D, Trautwein K, Rabus R** (2017) Photometric determination of ammonium and phosphate in seawater medium using a

- microplate reader. *J Mol Microbiol Biotechnol* 27:73-80 (<https://doi.org/10.1159/000454814>). [C1]
203. **Sanchez-Garcia S, Wang H, Wagner-Döbler I.** (2022) The microbiome of the dinoflagellate *Prorocentrum cordatum* in laboratory culture and its changes at higher temperatures. *Front Microbiol.* 13: 952238. (<https://doi.org/10.3389/fmicb.2022.952238>) [B4]
204. Schober I, **Bunk B**, Carril G, **Freese HM**, Ojeda N, Riedel T, **Meier-Kolthoff JP**, **Göker M**, Spröer C, Flores-Herrera PA, Nourdin-Galindo G, Gómez F, Cárdenas C, Vásquez-Ponce F, Labra A, Figueroa J, Olivares Pacheco J, Nübel U, **Sikorski J**, Marshall SH, **Overmann J** (2023) Ongoing diversification of the global fish pathogen *Piscirickettsia salmonis* through genetic isolation and transposition bursts. *ISME J* 17: 2247-2258, (<https://doi.org/10.1038/s41396-023-01531-9>). [A6, A7]
205. Schulz A, Hermann L, Freibert S, Bönig T, Hoffmann T, **Riclea, R**, **Dickschat, JS**, Heider J, Bremer E (2017) Transcriptional regulation of ectoine catabolism in response to multiple metabolic and environmental cues, *Environ Microbiol* 19: 4599-4619 (<https://doi.org/10.1111/1462-2920.13924>). [B7]
206. **Schulz S, Biwer P, Harig T, Koteska D, Schlawis C** (2020) Chemical Ecology of Bacterial Volatiles. In: Liu H-W, Begley TP (eds) *Comprehensive natural products III*. Elsevier, Amsterdam, pp 161–178. [C2]
207. **Schulz S, Dickschat JS, Kunze B, Wagner-Dobler I, Diestel R, Sasse F** (2010) Biological Activity of Volatiles from Marine and Terrestrial Bacteria. *Mar Drugs* 8: 2976–2987 ((<https://doi.org/10.3390/md8122976>). [B4, B7, C2]
208. **Schulz S, Hötling S** (2015) The use of the lactone motif in chemical communication. *Nat Prod Rep* 32: 1042–1066 (<https://doi.org/10.1039/C5NP00006H>). [C2]
209. **Schulz S, Schlawis C, Koteska D, Harig T, Biwer P** (2020) Structural Diversity of Bacterial Volatiles. In: Ryu C-M, Weisskopf L, Piechulla B (eds) *Bacterial Volatile Compounds as Mediators of Airborne Interactions*. Springer Singapore, Singapore, pp 93–121 (https://doi.org/10.1007/978-981-15-7293-7_3). [C2]
210. Segev E, Wyche TP, Kim KH, **Petersen J**, Ellebrandt C, Vlamakis H, et al. (2016). Dynamic metabolic exchange governs a marine algal-bacterial interaction. *eLife* 5: e17473 (<https://doi.org/10.7554/eLife.17473>). [A5]
211. Shevshuk, O., **Roselius, L.**, Günther, G., **Klein, J.**, **Jahn, D.**, Steinert, M. & **Münch, R.** (2012) InFiRe - a novel computational method for the identification of insertion sites in transposon mutagenized bacterial genomes. *Bioinformatics*, 28:306-310 (<https://doi.org/10.1093/bioinformatics/btr672>). [B5, INF]
212. Silvano E, Yang M, **Wolterink M, Giebel HA, Simon M, Scanlan DJ, Zhao Y, Chen Y** (2020) Lipidomic analysis of roseobacters of the pelagic RCA cluster and their response to phosphorus limitation. *Front Microbiol* 11: 552135. (<https://doi.org/10.3389/fmicb.2020.552135>) [A1]
213. Simmonds P, Adriaenssens EM, Zerbini FM, Abrescia NGA, Aiewsakun P, Alfenas-Zerbini P, Bao Y, Barylski J, Drost C, Duffy S, Duprex WP, Dutilh BE, Elena SF, Garcia ML, Junglen S, Katzourakis A, Koonin EV, Krupovic M, Kuhn JH, Lambert AJ, Lefkowitz EJ, Lobočka M, Lood C, Mahony J, **Meier-Kolthoff JP**, Mushegian AR, Oksanen HM, Poranen MM, Reyes-Munoz A, Robertson DL, Roux S, Rubino L, Sabanadzovic S, Siddell S, Skern T, Smith DB, Sullivan MB, Suzuki N, Turner D, Van Doorslaer K, Vandamme AM, Varsani A, Vasilakis N (2023) Four principles to establish a universal virus taxonomy. *PLoS Biol* 21: e3001922 (<https://doi.org/10.1371/journal.pbio.3001922>). [A6]
214. Simon C, **Daniel R** (2010) Construction of small-insert and large-insert metagenomic libraries. *Meth Mol Biol* 668: 39-50 (https://doi.org/10.1007/978-1-60761-823-2_2). [Z02]

215. Simon C, **Daniel R** (2011) Metagenome analyses: past and future trends. *Appl Environ Microbiol* 77: 1153–1161 (<https://doi.org/10.1128/AEM.02345-10>). [Z02]
216. **Simon M** (2017) Roommates in space and time. *Nature Microbiol* 2: 17122 (<https://doi.org/10.1038/nmicrobiol.2017.122>). [A1]
217. **Simon M, Billerbeck S, Kessler D, Selje N, Schlingloff A** (2012) Bacterioplankton communities in the Southern Ocean: Composition and growth response to various substrate regimes. *Aquat Microb Ecol* 68: 13–28 (<https://doi.org/10.3354/ame01597>). [A1]
218. **Simon M, Scheuner C, Meier-Kolthoff JP, Brinkhoff T, Wagner-Döbler I, Ulbrich M, Klenk HP, Schomburg D, Petersen J, Göker M.** (2017) Phylogenomics of *Rhodobacteraceae* reveals evolutionary adaptation to marine and non-marine habitats. *ISME J* 11: 1483-1499 (<https://doi:10.1038/ismej.2016.198>). [A1, A5, A6, B2, B4, C3]
219. Smith AF, Silvano E, **Päucker O**, Guillonneau R, Quareshy M, Murphy A, Mausz MA, Stirrup R, Rihtman B, Aguilo-Ferretjans MA, Brandsma J, **Petersen J**, Scanlan DJ, Yin Chen Y (2021). A novel class of sulfur-containing aminolipids widespread in marine roseobacters. *ISME J* 25: 2440-2453 (<https://doi.org/10.1038/s41396-021-00933-x>). [A5]
220. Sonnenschein EC, Broughton C, Phippen W, Nielsen KF, Mateiu RV, Melchiorson J, Gram L, **Overmann J, Freese HM** (2017) *Phaeobacter piscinae* sp. nov., a novel species of the Roseobacter group and potential aquaculture probiont. *Int J Syst Evol Microbiol* 67: 4559-4564 (<https://doi.org/10.1099/ijsem.0.002331>). [A7]
221. **Soora M, Cypionka H** (2013) Light enhances survival of *Dinoroseobacter shibae* during long-term starvation. *PLoS ONE* 8: e83960. (<doi.org/10.1371/journal.pone.0083960>) [B1]
222. **Soora M, Tomasch J, Wang H, Michael V, Petersen J, Engelen B, Wagner-Doebler I, Cypionka H** (2015) Oxidative stress and starvation in *Dinoroseobacter shibae*: The role of extrachromosomal elements. *Front Microbiol* 6:233. (<doi.org/10.3389/fmicb.2015.00233>) [A2, A5, B1, B4]
223. **Srinivas S, Berger M, Brinkhoff T, Niggemann J** (2022) Impact of quorum sensing and tropodithietic acid production on the exometabolome of *Phaeobacter inhibens*. *Front Microbiol* 13: 917969 (<https://doi.org/10.1099/ijsem.0.002331>). [A8, B2]
224. Steinert G, **Wemheuer B**, Janussen D, Erpenbeck D, **Daniel R, Simon M, Brinkhoff T, Schupp P** (2019) Prokaryotic diversity and community patterns in Antarctic continental shelf sponges. *Front Mar Sci* 6: 297 (<https://doi.org/10.3389/fmars.2019.00297>). [A1, B2, Z02]
225. **Strijkstra A, Trautwein K, Roesler S, Feenders C, Danzer D, Riemenschneider U, Blasius B, Rabus R** (2016) High performance CCD camera system for digitalisation of 2D DIGE gels. *Proteomics* 16: 1975-1979 (<https://doi.org/10.1002/pmic.201500385>). [C1, C7]
226. **Sultana S, Bruns S, Wilkes H, Simon M, Wienhausen G** (2023) Vitamin B₁₂ is not shared by all marine prototrophic bacteria with their environment. *The ISME Journal*; (<https://doi.org/10.1038/s41396-023-01391-3>). [A8]
227. **Tebbe DA, Geihser S, Wemheuer B, Daniel R, Schäfer H, Engelen B** (2022) Seasonal and Zonal Succession of Bacterial Communities in North Sea Salt Marsh Sediments, *Microorganisms*, 10: 859. (<doi.org/10.3390/microorganisms10050859>) [A2, Z02]
228. **Tebbe DA, Gruender C, Dlugosch L, Löhmus K, Rolfes S, Könneke M, Chen Y, Engelen B, Schäfer H** (2023) Microbial drivers of DMSO reduction and DMS-dependent methanogenesis in saltmarsh sediments. *ISME J* 17: 2340-2351 (<https://doi.org/10.1038/s41396-023-01539-1>). [A1, A2, C7]
229. **Thiel V, Brinkhoff T, Dickschat JS, Wickel S, Grunenberg J, Wagner-Döbler I, Simon M, Schulz S** (2010) Identification and biosynthesis of tropone derivatives and

- sulfur volatiles produced by bacteria of the marine Roseobacter clade. *Org Biomol Chem.* 8: 234-46. (<https://doi.org/10.1039/b909133e>) [A1, B2, B4, B7, C2]
230. **Thole S., Kalhoefer, D, Voget, S, Berger, M, Engelhardt T, Liesegang H, Wollher A, Kjelleberg S, Daniel, R, Simon M, T, Brinkhoff. T** (2012) *Phaeobacter gallaeciensis* genomes from globally opposite locations reveal high similarity of adaptation to surface life. *ISME J.* 6: 2229–2244 (<https://doi.org/10.1038/ismej.2012.62>). [A1, B2, Z02]
231. **Tomasch J, Gohl R, Bunk B, Diez MS, Wagner-Döbler I** (2011) Transcriptional response of the photoheterotrophic marine bacterium *Dinoroseobacter shibae* to changing light regimes. *ISME J* 5: 1957-68. (<https://doi.org/10.1038/ismej.2011.68>). [A7, B4]
232. **Tomasch J, Ringel V, Wang H, Freese HM, Bartling P, Brinkmann H, Vollmers J, Jarek M, Wagner-Döbler I, Petersen J** (2022). Fatal affairs - conjugational transfer of a dinoflagellate-killing plasmid between marine *Rhodobacterales*. *Microb Genom* 8: 000787 (<https://doi.org/10.1099/mgen.0.000787>). [A5, A7, B4]
233. **Tomasch J, Wang H, Hall ATK, Patzelt D, Preusse M, Petersen J, et al.** (2018). Packaging of *Dinoroseobacter shibae* DNA into gene transfer agent particles is not random. *Genome Biol. Evol.* 10: 359–369 (<https://doi.org/10.1093/gbe/evy005>). [A5, B4]
234. **Tran Quoc D, Neu T, Sultana S, Giebel HA, Simon M, Billerbeck S** (2023) Distinct glycoconjugate cell surface structures make the pelagic diatom *Thalassiosira rotula* an attractive habitat for bacteria. *J Phycol.* 59: 309–322 (<https://doi.org/10.1111/jpy.13308>). [A1, A8]
235. **Tran Quoc D, Milke F, Niggemann J, Simon M** (2023) The diatom *Thalassiosira rotula* induces distinct growth responses and colonization patterns of Roseobacteraceae, Flavobacteria and Gammaproteobacteria. *Environ Microbiol* 25: 3536-3555, (<https://doi.org/10.1111/1462-2920.16506>). [A1, A8]
236. **Trautwein K, Feenders C, Hulsch R, Ruppertsberg HS, Strijkstra A, Kant M, Vagts J, Wünsch D, Michalke B, Maczka M, Schulz S, Hillebrand H, Blasius B, Rabus R** (2017) Non-Redfield, nutrient synergy, and flexible internal elemental stoichiometry in a marine bacterium. *FEMS Microbiol Ecol* 93: fix059 (<https://doi.org/10.1093/femsec/fix059>). [C1, C2, C7]
237. **Trautwein K, Hensler M, Wiegmann K, Skorubskaya E, Wöhlbrand L, Wünsch D, Hinrichs C, Feenders C, Müller C, Schell K, Ruppertsberg H, Vagts J, Koßmehl S, Steinbüchel A, Schmidt-Kopplin P, Wilkes H, Hillebrand H, Blasius B, Schomburg D, Rabus R** (2018) The marine bacterium *Phaeobacter inhibens* secures external ammonium by rapid buildup of intracellular nitrogen stocks. *FEMS Microbiol Ecol* 94: fiy154 (<https://doi.org/10.1093/femsec/fiy154>). [C1, C3, C7]
238. **Trautwein K, Will SE, Hulsch R, Maschmann U, Wiegmann K, Hensler M, Michael V, Ruppertsberg H, Wünsch D, Feenders C, Neumann-Schaal M, Kaltenhäuser S, Ulbrich M, Schmidt-Hohagen K, Blasius B, Petersen J, Schomburg D, Rabus R** (2016) Native plasmids restrict growth of *Phaeobacter inhibens* DSM 17395: Energetic costs of plasmids assessed by quantitative physiological analyses. *Environ Microbiol* 18: 4817-4829 (<https://doi.org/10.1111/1462-2920.13381>). [A5, C1, C3, C7]
239. **Voget S, Billerbeck, Simon, M, Daniel R** (2015). Closed genome sequence of *Octadecabacter temperatus* SB1, the first mesophilic species of the genus *Octadecabacter*. *Genome Announc* 3: e01051-15. (<https://doi.org/10.1128/genomeA.01051-15>). [A1, Z02]
240. **Voget S, Bruns H, Wagner-Döbler I, Schulz S, Daniel R** (2015) Draft Genome Sequence of *Roseovarius tolerans* EL-164, a Producer of *N*-Acylated Alanine Methyl Esters and *N*-Acylhomoserine Lactones. *Genome Announc* 3:15 (<https://doi.org/10.1128/genomeA.01096-15>). [B4, Z02]

241. **Voget S, Valerio SMD, von Hoyningen-Huene AJE, Natramilarasu PK, Vollheyde K, Xiao S, Daniel R** (2015) Genome sequence of *Jannaschia aquimarina* GSW-M26, a member of the Roseobacter clade. *Genome Announc* 3: e00353-15 (<https://doi.org/10.1128/genomea.00353-15>). [Z02]
242. **Voget S, Wemheuer B, Brinkhoff T, Vollmers J, Dietrich S, Giebel HA, Beardsley C, Sardemann C, Bakenhus I, Billerbeck S, Daniel R, Simon M** (2015) Adaptation of an abundant *Roseobacter* RCA organism to pelagic systems revealed by genomic and transcriptomic analyses. *ISME J* 9: 371-384 (<https://doi.org/10.1038/ismej.2014.134>). [A1, Z02]
243. Vollmers J, **Voget S, Dietrich S, Gollnow K, Smits M, Meyer K, Brinkhoff T, Simon M, Daniel R** (2013) Poles apart: Extreme genome plasticity and a new xanthorhodopsin-like gene family in the genomes of *Octadecabacter arcticus* 238 and *Octadecabacter antarcticus* 307. *PLoS One* 8: e63422 (<https://doi.org/10.1371/journal.pone.0063422>). [A1, Z02]
244. **Wagner-Döbler I.** (2016) Biofilm transplantation in the deep sea. *Mol Ecol.* 25:1905-1907. (<https://doi:10.1111/mec.13612>). [B4]
245. **Wagner-Döbler I, Ballhausen B, Berger M, Brinkhoff T, Buchholz I, Bunk B, Cypionka H, Daniel R, Drepper T, Gerdt G, Hahnke S, Han C, Jahn D, Kalhoefer D, Kiss H, Klenk HP, Kyrpides N, Liebl W, Liesegang H, Meincke L, Pati A, Petersen J, Piekarski T, Pommerenke C, Pradella S, Pukall R, Rabus R, Stackebrandt E, Thole S, Thompson L, Tielen P, Tomasch J, von Jan M, Wanphrut N, Wichels A, Zech H, Simon M.** (2010). The complete genome sequence of the algal symbiont *Dinoroseobacter shibae* – a hitchhiker’s guide to life in the sea. *ISME J.* 4: 61–77 (<https://doi.org/10.1038/ismej.2009.94>). [A1, A5, A6, B1, B2, B4, B5, C1]
246. **Wang H, Beier N, Boedeker C, Sztajer H, Henke P, Neumann-Schaal M, Mansky J, Rohde M, Overmann J, Petersen J, Klawonn F, Kucklick M, Engelmann S, Tomasch J, Wagner-Döbler I.** (2021). *Dinoroseobacter shibae* outer membrane vesicles are enriched for the chromosome dimer resolution site *dif*. *mSystems* 6: e00693-20 (<https://doi.org/10.1128/msystems.00693-20>). [A5, A7, B4, C6]
247. **Wang H, Tomasch J, Michael V, Bhujju S, Jarek M, Petersen J, et al.** (2015). Identification of genetic modules mediating the Jekyll and Hyde interaction of *Dinoroseobacter shibae* with the dinoflagellate *Prorocentrum minimum*. *Front. Microbiol.* 6: 1262 (<https://doi:10.3389/fmicb.2015.01262>). [A5, B4]
248. **Wang H, Tomasch J, Jarek M, Wagner-Döbler I** (2014) A dual-species co-cultivation system to study the interactions between Roseobacters and dinoflagellates. *Front Microbiol.* 25: 311. (<https://doi:10.3389/fmicb.2014.00311>). [B4]
249. **Wang H, Ziesche L, Frank O, Michael V, Martin M, Petersen J, Schulz S, Wagner-Döbler I, Tomasch J** (2014) The CtrA phosphorelay integrates differentiation and communication in the marine alphaproteobacterium *Dinoroseobacter shibae*. *BMC Genomics* 15: 130 (<https://doi.org/10.1186/1471-2164-15-130>). [A5, B4, C2]
250. **Weiten A, Kalvelage K, Neumann-Schaal M, Buschen R, Scheve S, Winkhofer M, Rabus R** (2022) Nanomolar responsiveness of marine *Phaeobacter inhibens* DSM 17395 toward carbohydrates and amino acids. *Microb Physiol* 32: 108-121 (<https://doi.org/10.1159/000524702>). [C1]
251. **Wemheuer B, Güllert S, Billerbeck S, Giebel H-A, Voget S, Simon M, Daniel R** (2014) Impact of a phytoplankton bloom on the diversity of the active bacterial community in the southern North Sea as revealed by metatranscriptomic approaches. *FEMS Microbiol Ecol* 87: 378-389 (<https://DOI:10.1111/1574-6941.12230>). [A1, Z02]
252. **Wemheuer B, Wemheuer F, Daniel R** (2012) RNA-based assessment of diversity and composition of active archaeal communities in the German Bight. *Archaea* 2012: 695826 (<https://doi.org/10.1155/2012/695826>) [Z02]

253. **Wemheuer B**, Wemheuer F, Hollensteiner J, **Meyer F-D**, **Voget S**, **Daniel R** (2015) The green impact: bacterioplankton response towards a phytoplankton spring bloom in the southern North Sea assessed by comparative metagenomic and metatranscriptomic approaches. *Front Microbiol* 6: 805 (<https://doi.org/10.3389/fmicb.2015.00805>). [Z02]
254. **Wemheuer B**, Wemheuer F, Meier D, **Billerbeck S**, **Giebel HA**, **Simon M**, Scherber C, **Daniel R** (2017) Linking compositional and functional predictions to decipher the biogeochemical significance in DFAA turnover of abundant bacterioplankton lineages in the North Sea. *Microorganisms* 5: 68. (<https://doi.org/10.3390/microorganisms5040068>). [A1, Z02]
255. Wemheuer F, Taylor JA, **Daniel R**, Johnston E, Meinicke P, Thomas T, **Wemheuer B** (2020) Tax4Fun2: prediction of habitat-specific functional profiles and functional redundancy based on 16S rRNA gene sequences. *Environ Microbiome* 15: 11 (<https://doi.org/10.1186/s40793-020-00358-7>). [Z02]
256. Wemheuer F, von Hoyningen-Huene AJE, **Pohlner M**, Degenhardt J, **Engelen B**, **Daniel R**, **Wemheuer B** (2019) Primary Production in the Water Column as Major Structuring Element of the Biogeographical Distribution and Function of Archaea in Deep-Sea Sediments of the Central Pacific Ocean. *Archaea* 2019, 3717239, doi.org/10.1155/2019/3717239. [A2, Z02]
257. **Wichmann H**, **Brinkhoff T**, **Simon M**, Richter-Landsberg C (2016) Dimethylsulfoniopropionate promotes process outgrowth in neural cells and exerts protective effects against tropodithietic acid. *Marine Drugs* 14: 89 (<https://doi.org/10.3390/md14050089>). [A1, B2]
258. **Wichmann H**, Vocke F, **Brinkhoff T**, **Simon M**, Richter-Landsberg C (2015) Cytotoxic effects of tropodithietic acid on mammalian clonal cell lines of neuronal and glial origin. *Mar Drugs* 13: 7113–7123 (<https://doi.org/10.3390/md13127058>). [A1, B2]
259. **Wiegmann K**, **Hensler M**, **Wöhlbrand L**, **Ulbrich M**, **Schomburg D**, **Rabus R** (2014) Carbohydrate catabolism in *Phaeobacter inhibens* DSM 17395, member of the marine *Roseobacter* clade. *Appl Environ Microbiol* 80: 4725-4737 (<https://doi.org/10.1128/AEM.00719-14>). [C1, C3]
260. **Wienhausen G**, Bittner MJ, Paerl RW (2022) Key knowledge gaps to fill at the cell-to-ecosystem level in marine B-vitamin cycling. *Front Mar Sci* 9: 876726 (<https://doi.org/10.3389/fmars.2022.876726>). [A8]
261. **Wienhausen G**, Bruns S, **Sultana S**, Groon LA, Wilkes H, **Simon M** (2022) The overlooked role of a biotin precursor for marine bacteria - desthiobiotin as an escape route for biotin auxotrophy. *ISME J* 16: 2599-2609 (<https://doi.org/10.1038/s41396-022-01304-w>). [A8]
262. **Wienhausen G**, **Dlugosch L**, Jarling R, Wilkes H, **Giebel HA** **Simon M** (2022) Availability of vitamin B₁₂ and its lower ligand intermediate alpha-ribazole impact prokaryotic and protist communities in oceanic systems. *ISME J* 16: 2002–2014 (<https://doi.org/10.1038/s41396-022-01250-7>). [A1, A8, C7]
263. **Wienhausen G**, **Moraru C**, Bruns S, **Tran Quoc D**, **Sultana S**, Wilkes H, **Dlugosch L**, Azam F, **Simon M** (2024) Ligand crossfeeding resolves bacterial vitamin B₁₂ auxotrophies. *Nature* 629: 886-892, <https://doi.org/10.1038/s41586-024-07396-y>. [A1, A8, B6, C7]
264. **Wienhausen G**, **Noriega-Ortega BE**, **Niggemann J**, **Dittmar T**, **Simon M** (2017) The exometabolome of two model strains of the *Roseobacter* group: A marketplace of microbial metabolites. *Frontiers in Microbiol.* 8: 1985. (<https://doi.org/10.3389/fmicb.2017.01985>). [A8]
265. Wiese J, Imhoff JF, Horn H, Borchert E, Kyrpidis NC, **Göker M**, Klenk H-P, Woyke T, Hentschel U (2020) Genome analysis of the marine bacterium *Kiloniella laminariae* and

- first insights into comparative genomics with related *Kiloniella* species. Archives of Microbiology 202: 815-824 (<https://doi.org/10.1007/s00203-019-01791-0>). [A6]
266. Wietz M, **Wemheuer** B, Simon H, **Giebel** HA, Seibt MA, **Daniel** R, **Brinkhoff** T, **Simon** M (2015) Bacterial community dynamics during polysaccharide degradation at contrasting sites in the Southern and Atlantic Oceans. Environ Microbiol 17: 3822-3831 (<https://doi.org/10.1111/1462-2920.12842>). [A1, B2, Z02]
267. **Will** SE, **Neumann-Schaal** M, **Heydorn** RL, **Bartling** P, **Petersen** J, **Schomburg** D (2017). The limits to growth – energetic burden of the endogenous antibiotic tropodithietic acid in *Phaeobacter inhibens* DSM 17395. PLoS One 12: e0177295 (<https://doi.org/10.1371/journal.pone.0177295>). [A5, C3]
268. **Wöhlbrand** L, **Feenders** C, Nachbaur J, Freund H, **Engelen** B, Wilkes H, Brumsack H-J, **Rabus** R (2017) Impact of extraction methods on metaproteomic analyses of marine sediments. Proteomics 17: 1700241 (<https://doi.org/10.1002/pmic.201700241>). [A2, C1, C7]
269. **Wöhlbrand** L, **Rabus** R, **Blasius** B, **Feenders** C (2017) Influence of nanoLC column and gradient length as well as MS/MS frequency and sample complexity on shotgun protein identification of marine bacteria. J Mol Microbiol Biotechnol 27: 199-212 (<https://doi.org/10.1159/000478907>). [C1, C7]
270. **Wöhlbrand** L, **Wemheuer** B, **Feenders** C, **Ruppersberg** HS, **Hinrichs** C, **Blasius** B, **Daniel** R, **Rabus** R (2017) Complementary metaproteomic approaches to assess the bacterioplankton response toward a phytoplankton spring bloom in the Southern North Sea. Front Microbiol 8: 442 (<https://doi.org/10.3389/fmicb.2017.00442>). [C1, C7, Z02]
271. **Wolter** LA, Mitulla M, Kalem J, **Daniel** R, **Simon** M, Wietz M (2021) CAZymes in *Maribacter dokdonensis* 62-1 from the Patagonian shelf: Genomics and physiology compared to related flavobacteria and a co-occurring *Alteromonas* strain. Front Microbiol 12: 628055 (<https://doi.org/10.3389/fmicb.2021.628055>). [A1, B2, Z02]
272. **Wolter** LA, Wietz M, **Ziesche** L, **Breider** S, **Leinberger** J, **Poehlein** A, **Daniel** R, **Schulz** S, **Brinkhoff** T (2021) Pseudoceanicola algae sp. nov., isolated from the marine macroalga *Fucus spiralis*, shows genomic and physiological adaptations for an algae-associated lifestyle. Syst Appl Microbiol 44: 126166 (<https://doi.org/10.1016/j.syapm.2020.126166>). [B2, C2, Z02]
273. **Wünsch** D, **Scheve** S, **Weiten** A, **Kalvelage** K, **Rabus** (2022) Luciferase-based determination of ATP/NAD(H) pools in a marine (environmental) bacterium. Microb Physiol 32: 122-134 (<https://doi.org/10.1159/000522414>) [C1]
274. **Wünsch** D, **Strijkstra** A, **Wöhlbrand** L, **Freese** HM, **Scheve** S, **Hinrichs** C, **Trautwein** K, **Maczka** M, **Petersen** J, **Schulz** S, **Overmann** J, **Rabus** R* (2020) Global response of *Phaeobacter inhibens* DSM 17395 to deletion of its 262-kb chromid encoding antibiotic synthesis. Microbial Physiol 30: 9-24 (<https://doi.org/10.1159/000522414>). [A5, A8, C1, C2]
275. **Wünsch** D, **Trautwein** K, **Scheve** S, **Hinrichs** C, **Feenders** C, **Blasius** B, **Schomburg** D, **Rabus** R (2019) Amino acid and sugar catabolism in the marine bacterium *Phaeobacter inhibens* DSM 17395 from an energetic viewpoint. Appl Environ Microbiol 85: e02095-19 (<https://doi.org/10.1128/AEM.02095-19>). [C1, C3, C7]
276. Xue X, **Sztajer** H, **Buddruhs** N, **Petersen** J, Rohde M, Talay SR, **Wagner-Döbler** I (2011). Lack of the delta subunit of RNA polymerase increases virulence related traits of *Streptococcus mutans*. PLoS One 6: e20075 (<https://doi.org/10.1371/journal.pone.0020075>). [A5, B4]
277. Zech H, Echtermeyer C, **Wöhlbrand** L, Blasius B, **Rabus** R (2011) Biological versus technical variability in 2D DIGE experiments with environmental bacteria. Proteomics 11: 3380-3389 (<https://doi.org/10.1002/pmic.201100071>). [C1]

278. Zech H, Hensler M, Koßmehl S, Drüppel K, Wöhlbrand L, Trautwein K, Hulsch R, Maschmann U, Colby T, Schmidt J, Reinhardt R, Schmidt-Hohagen K, Schomburg D, Rabus R (2013) Adaptation of *Phaeobacter inhibens* DSM 17395 to growth with complex nutrients. *Proteomics* 13: 2851-2868 (<https://doi.org/10.1002/pmic.201200513>). [C1, C3]
279. Zech H, Hensler M, Koßmehl S, Drüppel K, Wöhlbrand L, Trautwein K, Colby T, Schmidt J, Reinhardt R, Schmidt-Hohagen K, Schomburg D, Rabus R (2013) Dynamics of amino acid utilization in *Phaeobacter inhibens* DSM 17395. *Proteomics* 13: 2869-2885 (<https://doi.org/10.1002/pmic.201200560>). [C1, C3]
280. Zhan Y, Huang S, Voget S, Simon M, Chen F (2016) A novel *Roseobacter* phage possesses features of podoviruses, siphoviruses, prophages and gene transfer agents. *Scientific Reports* 6: 30372 (<https://DOI:10.1038/srep30372>). [A1, Z02]
281. Ziesche L, Bruns H, Dogs M, Wolter L, Mann F, Wagner-Döbler I, Brinkhoff T, Schulz S (2015) Homoserine Lactones, Methyl Oligohydroxybutyrates, and Other Extracellular Metabolites of Macroalgae-Associated Bacteria of the *Roseobacter* Clade: Identification and Functions. *ChemBioChem* 16: 2094–2107 (<https://doi.org/10.1002/cbic.201500189>). [B2, B4, C2]
282. Ziesche L, Rinkel J, Dickschat JS, Schulz S (2018) Acyl group specificity of AHL-synthases involved in Quorum-sensing in *Roseobacter* group bacteria, *Beilstein J. Org. Chem.*, 14, 1309-1316 (<https://doi.org/10.3762/bjoc.14.112>). [B7, C2]
283. Ziesche L, Wolter L, Wang H, Brinkhoff T, Pohlner M, Engelen B, Wagner-Döbler I, Schulz S (2019) An Unprecedented Medium-Chain Diunsaturated N-acylhomoserine Lactone from Marine *Roseobacter* Group Bacteria. *Mar. Drugs* 17: 20. (doi.org/10.3390/md17010020). [A2, B2, B4, C2]
284. Zucker F, Bischoff V, Ndela EO, Heyerhoff B, Poehlein A, Freese H, Roux S, Simon M, Enault F & Moraru C (2022). New Microviridae isolated from *Sulfitobacter* reveals two cosmopolitan subfamilies of ssDNA phages infecting marine and terrestrial Alphaproteobacteria, *Virus Evolution* 8: veac070, (<https://doi.org/10.1093/ve/veac070>). [A1, A2, A7, B6]

Publications without peer review

285. Dlugosch L, Poehlein A, Wemheuer B, Pfeiffer B, Giebel HA, Daniel R, Simon M (2021) Nitrogen availability drives gene length of dominant prokaryotes and diversity of genes acquiring Nitrogen-species in oceanic systems. *BioRxiv* (<https://doi.org/10.1101/2021.01.10.426031>). [A1, Z02]
286. Dudek, C. A., Overmann, J, Jahn, D. (2023) Vorhersage bakterieller Genregulation. *BIOspektrum* 19: 252-254 (<https://doi.org/10.1007/s12268-023-1931-x>). [A8, INF]
287. Piekarski, T., Jahn, D. & Tielen, P. (2011) Marine Mikrobiologie: Etablierung genetischer Werkzeuge für Bakterien der *Roseobacter*-Gruppe. *BIOspektrum* 04/11 (<https://doi.org/10.1007/s12268-011-0064-9>). [B5, INF]
288. Rabus, R., Engelmann, S., Jahn, D., Petersen, J., Schomburg, D., Schulz, S, Wagner-Döbler, I. (2016) Systembiologie der marinen *Roseobacter*-Gruppe. *Systembiologie*, 11: 16-19. [A5, C1, C2, C3, C5]
289. Voget S, Göker M, Brinkhoff T (2014) Genomik: Grundlage zum Verständnis des Erfolgs von *Roseobacter*-Gruppe. *BIOspektrum* 20: 279.282 (<https://doi.org/10.1007/s12268-014-0441-2>). [A6, B2, Z02]