

**2024:**

**Böhm JW, Zübert C, Kahlenberg G, Jochner-Oette S, Kube M.** Load of the ash dieback pathogen *Hymenoscyphus fraxineus* differs in soil. *J Plant Dis Prot* (2024). *In press*

**Zübert C, Kube M.** Differential gene expression of *Hymenoscyphus fraxineus* grown on *Fraxinus excelsior* and *F. mandshurica* supplemented media. *J Plant Dis Prot* (2024).

**Böhm JW, Huettel B, Schneider B, Kube M.** 2024. The complete genome of “*Candidatus* Phytoplasma fraxini” AshY1 from the ash yellows group. *Microbiol Resour Announc* 13:e00318-24.

**Toth R, Ilic A-M, Huettel B, Duduk B, Kube M.** Divergence within the Taxon ‘*Candidatus* Phytoplasma asteris’ Confirmed by Comparative Genome Analysis of Carrot Strains. *Microorganisms*. 2024; 12(5):1016. <https://doi.org/10.3390/microorganisms12051016>

**2023:**

Duduk B, Ćurčić Ž, Stepanović J, **Böhm JW**, Kosovac A, Rekanović E, **Kube M.** Prevalence of a '*Candidatus* Phytoplasma solani'-Related Strain Designated as New 16SrXII-P Subgroup over '*Candidatus* Arsenophonus phytopathogenicus' in Sugar Beet in Eastern Germany. *Plant Dis*. 2023 Dec;107(12):3792-3800.

**Böhm JW, Duceck D, Duduk B, Schneider B, Kube M.** Genome Comparison of '*Candidatus* Phytoplasma rubi' with Genomes of Other 16SrV Phytoplasmas Highlights Special Group Features. September 2023, *Applied Microbiology* 3(3):1083-1100

**Böhm, J.W., Duceck, D., Zübert, C., Carminati, G., Schneider, B., Duduk, B., Kube, M.** First insights into the genome of '*Candidatus* Phytoplasma rubi' highlight effector protein repertoire of 16SrV phytoplasmas. 2023, *Phytopathogenic Mollicutes*, 13 (1), pp. 11-12.

Duduk B, Kosovac A, Stepanovic J, Rekanovic E, Curcic Z, **Böhm JW, Kube M**, Vuckovic N, Duduk N, Vico I. Phytoplasma, proteobacterium and fungus in single and mixed infections of sugar beet in central Europe. 2023, *Phytopathogenic Mollicutes*, 13 (1), pp. 97-98.

**Duceck D, Zübert C, Böhm JW, Carminati G, Schneider B, Kube M.** Complete Genome of “*Candidatus* Phytoplasma rubi” RS, a Phytopathogenic Bacterium Associated with Rubus Stunt Disease. *Microbiol Resource Announcements*. 2023 May 17;12(5): e0130322. doi: 10.1128/mra.01303-22.

**2022:**

Ulrich K, Becker R, Behrendt U, **Kube M**, Schneck V, Ulrich A. Physiological and genomic characterisation of *Luteimonas fraxinea* sp. nov., a bacterial species associated with trees tolerant to ash dieback. *ScienceDirect. Systematic and Applied Microbiology*. Volume 45, Issue 4, July 2022, 126333. doi: 10.1016/j.syapm.2022.126333.

Bertaccini A, Arocha-Rosete Y, Contaldo N, Duduk B, Fiore N, Montano HG, **Kube M**, ... Revision of the 'Candidatus Phytoplasma' species description guidelines. *Int J Syst Evol Microbiol.* 2022 Apr;72(4). DOI: 10.1099/ijsem.0.005353

**Zübert C, Ilic AM, Duduk B, Kube M.** The Genome Reduction Excludes the Ribosomal Rescue System in *Acholeplasmataceae*. *Microbial Physiology*, 2022 Jan 31, pp. 45-56, DOI: 10.1159/000520450

## 2021:

**Zübert C. and Kube M.** Application of TaqMan Real-Time PCR for Detecting 'Candidatus Arsenophonus Phytopathogenicus' Infection in Sugar Beet. *Pathogens* 2021, 10,(11) 1466. <https://doi.org/10.3390/pathogens10111466>

Ćurčić, Ž., Kosovac, A., Stepanović, J., ...**Kube, M.**, Duduk, B. Multilocus genotyping of 'candidatus phytoplasma solani' associated with rubbery taproot disease of sugar beet in the pannonian plain, *Microorganisms*, 2021, 9(9), 1950

Ulrich K, **Kube M**, Becker R, Schneck V, Ulrich A. Genomic Analysis of the Endophytic *Stenotrophomonas* Strain 169 Reveals Features Related to Plant-Growth Promotion and Stress Tolerance. *Front. Microbiology.* (2021) 12:687463. doi: 10.3389/fmicb.2021.687463

Ćurčić, Ž., Stepanović, J., **Zübert, C.**, ...**Kube, M.**, Duduk, B. Rubbery taproot disease of sugar beet in Serbia associated with 'Candidatus phytoplasma solani', *Plant Disease*, 2021, 105(2), pp. 255–263

## 2020:

Schneider B, Hüttel B, **Zübert C, Kube M.** Genetic variation, phylogenetic relationship and spatial distribution of 'Candidatus Phytoplasma ulmi' strains in Germany. *Sci Rep.* 2020 Dec 14;10(1):21864. PMID: 33318538

Ćurčić Ž, Mitrovic J, **Zübert C**, Taški Ajduković K, Kosovac A, Rekanovic E, **Kube M**, Duduk B. Rubbery Taproot Disease of Sugar Beet in Serbia Associated with 'Candidatus Phytoplasma solani'. *Plant Dis.* 2020 Oct 6. PMID: 33021915

Becker R, Ulrich K, Behrendt U, **Kube M**, Ulrich A. Analyzing Ash Leaf-Colonizing Fungal Communities for Their Biological Control of *Hymenoscyphus fraxineus*. *Frontiers in Microbiology*, 2020, 11, 590944. PMID: 30661070

Fernández FD, **Zübert C**, Huettel B, **Kube M**, Concia, L.R. Draft genome sequence of "Candidatus phytoplasma pruni" (X-Disease Group, Subgroup 16SrIII-B) strain ChTDIII from Argentina. *Microbiology Resource Announcements*, 2020, 9(38), e0079220

Ulrich K, Becker R, Behrendt U, **Kube M**, Ulrich A. A Comparative Analysis of Ash Leaf-Colonizing Bacterial Communities Identifies Putative Antagonists of *Hymenoscyphus fraxineus*. *Front. Microbiol.*, 29 May 2020. PMID: 32547506

Schneider B, Kätzel R, **Kube M.** Widespread occurrence of 'Candidatus Phytoplasma ulmi' in elm species in Germany. *BMC Microbiol.* 2020 Mar 31;20(1):74. PMID: 32234008

## 2019:

**Kube M**, Furch ACU. Symptomless phytoplasmosis of black alder (*Alnus glutinosa*): a model for host tolerance. *Plant Physiology Reports.* 2019; 24(1):550–554. Doi: 10.1007/s40502-019-00489-1

- Duduk B, Duduk N, Vico I, Stepanović J, Marković T, Rekanović E, **Kube M**, Radanović D. Chamomile Floricolous Downy Mildew Caused by *Peronospora radii*. *Phytopathology*. 2019 Nov;109(11):1900-1907. PMID: 31369362
- Kube M**, Duduk B, Oshima K: Genome Sequencing. *In: Genomics, Host Pathogen Interactions and Diagnosis*. *Phytoplasmas: Plant Pathogenic Bacteria, Volume III*. Edited by Bertaccini A, Oshima K, **Kube M**, Rao GP. Singapore: Springer Singapore; 2019: 1-16. Doi: 10.1007/978-981-13-9632-8
- Dermastia M, **Kube M**, Seruga-Music M: Transcriptomic and Proteomic Studies of Phytoplasma-Infected Plants. *In: Genomics, Host Pathogen Interactions and Diagnosis*. *Phytoplasmas: Plant Pathogenic Bacteria, Volume III*. Edited by Bertaccini A, Oshima K, **Kube M**, Rao GP. Singapore: Springer Singapore; 2019: 33-35. Doi: 10.1007/978-981-13-9632-8
- Toth R**, Seemüller E, **Kube M**. A universal PCR assay amplifying the unique malic enzyme of phytoplasmas. *Phytopathogenic Mollicutes*. 2019; 9(1):87-88. Doi: 10.5958/2249-4677.2019.00044.6
- Marjanovic M, Stepanovic J, Rekanovic E, **Kube M**, Duduk B. Alder yellows phytoplasmas in *Alnus* species in Serbia. *Phytopathogenic Mollicutes*. 2019; 9(1):57-58. Doi: 10.5958/2249-4677.2019.00029.X
- Schneider B, **Kube M**. Occurrence of 'Candidatus phytoplasma ulmi' in native elm trees in Germany. *Phytopathogenic Mollicutes*. 2019; 9(1):51-52. Doi: 10.5958/2249-4677.2019.00026.4
- Holz, S., **Kube M.**, Bartoszewski, G., Huettel, B., Büttner, C. Silicon-Initial Studies on Cucumber Transcriptome Analysis under Silicon Treatment. 2019, 11(5), pp. 2365–2369

## **2018 ...**

- Kube M**, Liesebach M. Resistenzforschung im Forst, in: *Gehölze in historischen Gärten im Klimawandel*, Hrsg. Norbert Kühn, Sten Gillner und Antje Schmidt-Wiegand: *Landschaftsentwicklung und Umweltforschung*, Bd. 131, Berlin 2017, S. 201-205.
- Kube M**. Analysen der genetischen Ausstattung von Vertretern aus der phytopathogenen 'Candidatus Phytoplasma'- Gruppe sowie verwandter *Acholeplasmataceae*" (2015). Berlin: Humboldt-Univ, 207 p, Berlin, Humboldt-Univ, Habil-Schr, 2016.
- Holz S, **Kube M**, Bartoszewski G, Hüttel B, Büttner C (2015) Initial studies on Cucumber Transcriptome Analysis under silicon treatment [online]. *Silicon: in press*, DOI:10.1007/s12633-015-9335-2
- Bennett GM, Abbà S, **Kube M**, Marzachi C. Complete genome sequences of the obligate symbionts "Candidatus Sulcia muelleri" and "Ca. Nasuia deltocephalinicola" from the pestiferous leafhopper *Macrosteles quadripunctulatus* (Hemiptera: *Cicadellidae*) [online]. *Genome Announcements*. 2016, 4(1):01604-15. PMID: 26798106
- Holz S, Duduk B, Büttner C, **Kube M**. Genetic variability of Alder yellows phytoplasma in *Alnus glutinosa* in its natural Spreewald habitat. *Forest Pathol*. 2016, 46(1):11-21.
- Zhu B, Ibrahim M, Cui Z, Xie G-L, Jin G, **Kube M**, Li B, Zhou X. Multi-omics analysis of niche specificity provides new insights into ecological adaptation in bacteria. *ISME J*. 2016, 10(8):2072-2075. PMID: 26859773
- Holz S, **Kube M**, Bartoszewski G, Büttner C (2015). The impact of silicon on transcripts related to Cucumber Mosaic Virus Infection in Cucumber. *Communications in Agricultural and Applied Sciences*. 80(3):411-20. PMID: 27141739
- Quaglino F, **Kube M**, Jawhari M, Abou-Jawdah Y, Siewert C, Choueira E, Sobh H, Casati P, Tedeschi R, Molino Lova M, Alma A, Bianco PA. 'Candidatus Phytoplasma phoenicium' associated with almond witches'-broom disease: from draft genome to genetic diversity among strain populations. *BMC Microbiol*. 2015, 15:148. PMID: 26223451

- Mitrovic J, Smiljkovic M., Seemüller E, Reinhardt R, Hüttel B, Büttner C, Bertaccini A, **Kube M**, Duduk B. Differentiation of '*Candidatus* Phytoplasma cynodontis' based on 16S rRNA and *groEL* genes and identification of a new subgroup, 16SrXIV-C. *Plant Dis.* 2015, 99(11):1578-1583.
- Siewert C, Hess WR, Duduk B, Huettel B, Reinhardt R, Büttner C, **Kube M**. Complete genome determination and analysis of *Acholeplasma oculi* strain 19L, highlighting the loss of basic genetic features in the *Acholeplasmataceae*. *BMC Genomics.* 2014 Oct 24;15:931. PMID: 25344468
- Luge T, **Kube M**, Freiwald A, Meierhofer D, Seemüller E, Sauer S. Transcriptomics assisted proteomic analysis of *Nicotiana occidentalis* infected by *Candidatus* Phytoplasma mali strain AT. *Proteomics.* 2014 Aug;14(16):1882-9. PMID: 24920314
- Li B, Ibrahim M, Ge M, Cui Z, Sun G, Xu F, **Kube M**. Transcriptome analysis of *Acidovorax avenae* subsp. *avenae* cultivated in vivo and co-culture with *Burkholderia seminalis*. *Sci Rep.* 2014 Jul 16;4:5698. PMID: 25027476
- Kube M**, Siewert C, Migdoll AM, Duduk B, Holz S, Rabus R, Seemüller E, Mitrovic J, Müller I, Büttner C, Reinhardt R. Analysis of the complete genomes of *Acholeplasma brassicae*, *A. palmae* and *A. laidlawii* and their comparison to the obligate parasites from '*Candidatus* Phytoplasma'. *J Mol Microbiol Biotechnol.* 2014;24(1):19-36. PMID: 24158107
- Mitrović J, Siewert C, Duduk B, Hecht J, Mölling K, Broecker F, Beyerlein P, Büttner C, Bertaccini A, **Kube M**. Generation and analysis of draft sequences of 'stolbur' phytoplasma from multiple displacement amplification templates. *J Mol Microbiol Biotechnol.* 2014;24(1):1-11. PMID: 24158016
- Siewert C, Luge T, Duduk B, Seemüller E, Büttner C, Sauer S, **Kube M**. Analysis of expressed genes of the bacterium '*Candidatus* Phytoplasma mali' highlights key features of virulence and metabolism. *PLoS One.* 2014 Apr 11;9(4):e94391. PMID: 24728201
- Kube M**, Siewert C, Migdoll AM, Duduk B, Mitrovic J, Holz S, Rabus R, Reinhardt R, Seemüller E, Büttner C. "Complete genomes and deduced metabolism of acholeplasmas in comparison to members of '*Candidatus* Phytoplasma'." In: *Phytoplasmas and phytoplasma disease management: how to reduce their economic impact*. Ed. A. Bertaccini. Bologna, Italy: IPWG - International Phytoplasmaologist Working Group, 2014. 263-71. [www.cost.eu/download/FAP\\_FA0807](http://www.cost.eu/download/FAP_FA0807).
- Contreras-Porcia L, Lopez-Cristoffanini C, Lovazzano C **et al**. Differential gene expression in *Pyropia columbina* (Bangiales, Rhodophyta) under natural hydration and desiccation conditions. *Latin American Journal of Aquatic Research.* 2013 Nov; 41(5):933-958.
- Lefèvre CT, Trubitsyn D, Abreu F, Kolinko S, Jogler C, de Almeida LG, de Vasconcelos AT, **Kube M**, Reinhardt R, Lins U, Pignol D, Schüler D, Bazylnski DA, Ginet N. Comparative genomic analysis of magnetotactic bacteria from the Deltaproteobacteria provides new insights into magnetite and greigite magnetosome genes required for magnetotaxis. *Environ Microbiol.* 2013 Oct;15(10):2712-35. PMID: 23607663
- Tingaud-Sequeira A, Lozano JJ, Zapater C, Otero D, **Kube M**, Reinhardt R, Cerdà J. A rapid transcriptome response is associated with desiccation resistance in aerially-exposed killifish embryos. *PLoS One.* 2013 May 31;8(5):e64410. PMID: 23741328
- Wöhlbrand L, Jacob JH, **Kube M**, Mussmann M, Jarling R, Beck A, Amann R, Wilkes H, Reinhardt R, Rabus R. Complete genome, catabolic sub-proteomes and key-metabolites of *Desulfobacula toluolica* Tol2, a marine, aromatic compound-degrading, sulfate-reducing bacterium. *Environ Microbiol.* 2013 May;15(5):1334-55. PMID: 23088741
- Finster KW, Kjeldsen KU, **Kube M**, Reinhardt R, Mussmann M, Amann R, Schreiber L. Complete genome sequence of *Desulfocapsa sulfexigens*, a marine Deltaproteobacterium specialized in disproportionating inorganic sulfur compounds. *Stand Genomic Sci.* 2013 Apr 15;8(1):58-68. PMID: 23961312
- Seemüller E, Sule S, **Kube M**, Jelkmann W, Schneider B. The AAA+ ATPases and HflB/FtsH proteases of '*Candidatus* Phytoplasma mali': phylogenetic diversity, membrane topology, and relationship to strain virulence. *Mol Plant Microbe Interact.* 2013 Mar;26(3):367-76. PMID: 23387471

- Broecker F, **Kube M**, Klumpp J, Schuppler M, Biedermann L, Hecht J, Hombach M, Keller PM, Rogler G, Moelling K. Analysis of the intestinal microbiome of a recovered *Clostridium difficile* patient after fecal transplantation. *Digestion*. 2013;88(4):243-51. PMID: 24335204
- Kube M**, Chernikova TN, Al-Ramahi Y, et. al. Genome sequence and functional genomic analysis of the oil-degrading bacterium *Oleispira antarctica*. *Nat Commun*. 2013;4:2156. PMID: 23877221
- Nübel U, Nachtnebel M, Falkenhorst G, Benzler J, Hecht J, **Kube M**, Bröcker F, Moelling K, Bühner C, Gastmeier P, Piening B, Behnke M, Dehnert M, Layer F, Witte W, Eckmanns T. MRSA transmission on a neonatal intensive care unit: epidemiological and genome-based phylogenetic analyses. *PLoS One*. 2013;8(1):e54898. PMID: 23382995
- Lenk S, Moraru C, Hahnke S, Arnds J, Richter M, **Kube M**, Reinhardt R, Brinkhoff T, Harder J, Amann R, Mußmann M. Roseobacter clade bacteria are abundant in coastal sediments and encode a novel combination of sulfur oxidation genes. *ISME J*. 2012 Dec;6(12):2178-87. PMID: 22739490
- Dam B, Dam S, **Kube M**, Reinhardt R, Liesack W. Complete genome sequence of *Methylocystis* sp. strain SC2, an aerobic methanotroph with high-affinity methane oxidation potential. *J Bacteriol*. 2012 Nov;194(21):6008-9. PMID: 23045511
- Li B, Shi Y, Ibrahim M, Liu H, Shan C, Wang Y, **Kube M**, Xie GL, Sun G. Genome sequence of the rice pathogen *Dickeya zeae* strain ZJU1202. *J Bacteriol*. 2012 Aug;194(16):4452-3. PMID: 22843587
- Lemak S, Tchigvintsev A, Petit P, Flick R, Singer AU, Brown G, Evdokimova E, Egorova O, Gonzalez CF, Chernikova TN, Yakimov MM, **Kube M**, Reinhardt R, Golyshev PN, Savchenko A, Yakunin AF. Structure and activity of the cold-active and anion-activated carboxyl esterase OLEI01171 from the oil-degrading marine bacterium *Oleispira antarctica*. *Biochem J*. 2012 Jul 15;445(2):193-203. PMID: 22519667
- Dam B, **Kube M**, Dam S, Reinhardt R, Liesack W. Complete sequence analysis of two methanotroph-specific repABC-containing plasmids from *Methylocystis* sp. strain SC2. *Appl Environ Microbiol*. 2012 Jun;78(12):4373-9. PMID: 22504811
- Lahme S, Eberlein C, Jarling R, **Kube M**, Boll M, Wilkes H, Reinhardt R, Rabus R. Anaerobic degradation of 4-methylbenzoate via a specific 4-methylbenzoyl-CoA pathway. *Environ Microbiol*. 2012 May;14(5):1118-32. PMID: 22264224
- Felder KM, Carranza PM, Gehrig PM, Roschitzki B, Barkow-Oesterreicher S, Hoelzle K, Riedel K, **Kube M**, Hoelzle LE. Insights into the gene expression profile of uncultivable hemotrophic *Mycoplasma suis* during acute infection, obtained using proteome analysis. *J Bacteriol*. 2012 Mar;194(6):1505-14. PMID: 22267506
- Ibrahim M, Shi Y, Qiu H, Li B, Jabeen A, Li L, Liu H, **Kube M**, Xie G, Wang Y, Sun G. Differential expression of *in vivo* and *in vitro* protein profile of outer membrane of *Acidovorax avenae* subsp. *avenae*. *PLoS One*. 2012;7(11):e49657. PMID: 23166741
- Clark MS, Denekamp NY, Thorne MA, Reinhardt R, Drungowski M, Albrecht MW, Klages S, Beck A, **Kube M**, Lubzens E. Long-term survival of hydrated resting eggs from *Brachionus plicatilis*. *PLoS One*. 2012;7(1):e29365. PMID: 22253713
- Kube M**, Mitrovic J, Duduk B, Rabus R, Seemüller E. Current view on phytoplasma genomes and encoded metabolism. *ScientificWorldJournal*. 2012; 2012:185942. Review. PMID: 22550465
- Struck TH, Paul C, Hill N, Hartmann S, Hösel C, **Kube M**, Lieb B, Meyer A, Tiedemann R, Purschke G, Bleidorn C. Phylogenomic analyses unravel annelid evolution. *Nature*. 2011 Mar 3;471(7336):95-8. PMID: 21368831
- Kube M**. Insights in host dependency encoded within phytoplasma genomes. *Bulletin of Insectology*. 2011; 64(S):S9-S11.
- Müller I, Lurz R, **Kube M**, Quedenau C, Jelkmann W, Geider K. Molecular and physiological properties of bacteriophages from North America and Germany affecting the fire blight pathogen *Erwinia amylovora*. *Microb Biotechnol*. 2011 Nov;4(6):735-45. PMID: 21791029
- Massa SI, Pearson GA, Aires T, **Kube M**, Olsen JL, Reinhardt R, Serrão EA, Arnaud-Haond S. Expressed sequence tags from heat-shocked seagrass *Zostera noltii* (Hornemann) from its southern distribution range. *Mar Genomics*. 2011 Sep;4(3):181-8. PMID: 21867970
- Jones AC, Monroe EA, Podell S, Hess WR, Klages S, Esquenazi E, Niessen S, Hoover H, Rothmann M, Lasken RS, Yates JR 3rd, Reinhardt R, **Kube M**, Burkart MD, Allen EE,

- Dorrestein PC, Gerwick WH, Gerwick L. Genomic insights into the physiology and ecology of the marine filamentous cyanobacterium *Lyngbya majuscula*. **Proc Natl Acad Sci U S A**. 2011 May 24;108(21):8815-20. PMID: 21555588
- Kube M**, Luge T, Seemüller E et al. First data obtained by shotgun proteomics from *Nicotiana occidentalis* infected by '*Candidatus* Phytoplasma mali'. *Bulletin of Insectology*. 2011; 64(S):S277-S278.
- Oehlerking J, **Kube M**, Felder KM, Matter D, Wittenbrink MM, Schwarzenbach S, Kramer MM, Hoelzle K, Hoelzle LE. Complete genome sequence of the hemotrophic *Mycoplasma suis* strain KI3806. *J Bacteriol*. 2011 May;193(9):2369-70. PMID: 21398558
- De Gregoris TB, Rupp O, Klages S, Knaust F, Bekel T, **Kube M**, Burgess JG, Arnone MI, Goesmann A, Reinhardt R, Clare AS. Deep sequencing of naupliar-, cyprid- and adult-specific normalised Expressed Sequence Tag (EST) libraries of the acorn barnacle *Balanus amphitrite*. *Biofouling*. 2011 Apr;27(4):367-74. PMID: 21526438
- Zedelius J, Rabus R, Grundmann O, Werner I, Brodkorb D, Schreiber F, Ehrenreich P, Behrends A, Wilkes H, **Kube M**, Reinhardt R, Widdel F. Alkane degradation under anoxic conditions by a nitrate-reducing bacterium with possible involvement of the electron acceptor in substrate activation. *Environ Microbiol Rep*. 2011 Feb;3(1):125-135. PMID: 21837252
- Müller I, **Kube M**, Reinhardt R, Jelkmann W, Geider K. Complete genome sequences of three *Erwinia amylovora* phages isolated in north america and a bacteriophage induced from an *Erwinia tasmaniensis* strain. *J Bacteriol*. 2011 Feb;193(3):795-6. PMID: 21097611
- Huntley S, Hamann N, Wegener-Feldbrügge S, Treuner-Lange A, **Kube M**, Reinhardt R, Klages S, Müller R, Ronning CM, Nierman WC, Søgaard-Andersen L. Comparative genomic analysis of fruiting body formation in Myxococcales. *Mol Biol Evol*. 2011 Feb;28(2):1083-97. PMID: 21037205
- Stolle E, Wilfert L, Schmid-Hempel R, Schmid-Hempel P, **Kube M**, Reinhardt R, Moritz RF. A second generation genetic map of the bumblebee *Bombus terrestris* (Linnaeus, 1758) reveals slow genome and chromosome evolution in the *Apidae*. *BMC Genomics*. 2011 Jan 19;12:48. PMID: 21247459
- Jogler C, Wanner G, Kolinko S, Niebler M, Amann R, Petersen N, **Kube M**, Reinhardt R, Schüler D. Conservation of proteobacterial magnetosome genes and structures in an uncultivated member of the deep-branching Nitrospira phylum. **Proc Natl Acad Sci U S A**. 2011 Jan 18;108(3):1134-9. PMID: 21191098
- Jogler C, Niebler M, Lin W, **Kube M**, Wanner G, Kolinko S, Stief P, Beck AJ, De Beer D, Petersen N, Pan Y, Amann R, Reinhardt R, Schüler D. Cultivation-independent characterization of '*Candidatus* Magnetobacterium bavaricum' via ultrastructural, geochemical, ecological and metagenomic methods. *Environ Microbiol*. 2010 Sep;12(9):2466-78. PMID: 20406295
- Kube M**, Migdoll AM, Gehring I, Heitmann K, Mayer Y, Kuhl H, Knaust F, Geider K, Reinhardt R. Genome comparison of the epiphytic bacteria *Erwinia billingiae* and *E. tasmaniensis* with the pear pathogen *E. pyrifoliae*. *BMC Genomics*. 2010 Jun 22;11:393. PMID: 20565991
- Glöckner J, **Kube M**, Shrestha PM, Weber M, Glöckner FO, Reinhardt R, Liesack W. Phylogenetic diversity and metagenomics of candidate division OP3. *Environ Microbiol*. 2010 May;12(5):1218-29. PMID: 20158507
- Denekamp NY, Reinhardt R, **Kube M**, Lubzens E. Late embryogenesis abundant (LEA) proteins in nondesiccated, encysted, and diapausing embryos of rotifers. *Biol Reprod*. 2010 Apr;82(4):714-24. PMID: 20018906
- Pearson GA, Hoarau G, Lago-Leston A, Coyer JA, **Kube M**, Reinhardt R, Henckel K, Serrão ET, Corre E, Olsen JL. An expressed sequence tag analysis of the intertidal brown seaweeds *Fucus serratus* (L.) and *F. vesiculosus* (L.) (Heterokontophyta, Phaeophyceae) in response to abiotic stressors. *Mar Biotechnol (NY)*. 2010 Apr;12(2):195-213. PMID: 19609612
- Jackson DJ, McDougall C, Woodcroft B, Moase P, Rose RA, **Kube M**, Reinhardt R, Rokhsar DS, Montagnani C, Joubert C, Piquemal D, Degnan BM. Parallel evolution of nacre building gene sets in molluscs. *Mol Biol Evol*. 2010 Mar;27(3):591-608. PMID: 19915030
- Sadd BM, **Kube M**, Klages S, Reinhardt R, Schmid-Hempel P. Analysis of a normalised expressed sequence tag (EST) library from a key pollinator, the bumblebee *Bombus terrestris*. *BMC Genomics*. 2010 Feb 15;11:110. PMID: 20156341

- Meyerdierks A, **Kube M**, Kostadinov I, Teeling H, Glöckner FO, Reinhardt R, Amann R. Metagenome and mRNA expression analyses of anaerobic methanotrophic archaea of the ANME-1 group. *Environ Microbiol.* 2010 Feb;12(2):422-39. PMID: 19878267
- Raabe CA, Sanchez CP, Randau G, Robeck T, Skryabin BV, Chinni SV, **Kube M**, Reinhardt R, Ng GH, Manickam R, Kuryshev VY, Lanzer M, Brosius J, Tang TH, Rozhddestvensky TS. A global view of the nonprotein-coding transcriptome in *Plasmodium falciparum*. **Nucleic Acids Res.** 2010 Jan;38(2):608-17. PMID: 19864253
- Roeding F, Borner J, **Kube M**, Klages S, Reinhardt R, Burmester T. A 454 sequencing approach for large scale phylogenomic analysis of the common emperor scorpion (*Pandinus imperator*). *Mol Phylogenet Evol.* 2009 Dec;53(3):826-34. PMID: 196953336.
- Jogler C, Lin W, Meyerdierks A, **Kube M**, Katzmann E, Flies C, Pan Y, Amann R, Reinhardt R, Schüler D. Toward cloning of the magnetotactic metagenome: identification of magnetosome island gene clusters in uncultivated magnetotactic bacteria from different aquatic sediments. *Appl Environ Microbiol.* 2009 Jun;75(12):3972-9. PMID: 19395570
- Denekamp NY, Thorne MA, Clark MS, **Kube M**, Reinhardt R, Lubzens E. Discovering genes associated with dormancy in the monogonont rotifer *Brachionus plicatilis*. *BMC Genomics.* 2009 Mar 13;10:108. PMID: 19284654
- Jogler C, **Kube M**, Schübbe S, Ullrich S, Teeling H, Bazylnski DA, Reinhardt R, Schüler D. Comparative analysis of magnetosome gene clusters in magnetotactic bacteria provides further evidence for horizontal gene transfer. *Environ Microbiol.* 2009 May;11(5):1267-77. PMID: 19220405
- Shrestha PM, **Kube M**, Reinhardt R, Liesack W. Transcriptional activity of paddy soil bacterial communities. *Environ Microbiol.* 2009 Apr;11(4):960-70. PMID: 19170728
- Musat F, Galushko A, Jacob J, Widdel F, **Kube M**, Reinhardt R, Wilkes H, Schink B, Rabus R. Anaerobic degradation of naphthalene and 2-methylnaphthalene by strains of marine sulfate-reducing bacteria. *Environ Microbiol.* 2009 Jan;11(1):209-19. PMID: 18811643
- Kolmakov NN, **Kube M**, Reinhardt R, Canario AV. Analysis of the goldfish *Carassius auratus* olfactory epithelium transcriptome reveals the presence of numerous non-olfactory GPCR and putative receptors for progesterin pheromones. *BMC Genomics.* 2008 Sep 20;9:429. PMID: 18803863
- Sauer S, Freiwald A, Maier T, **Kube M**, Reinhardt R, Kostrzewa M, Geider K. Classification and identification of bacteria by mass spectrometry and computational analysis. *PLoS One.* 2008 Jul 30;3(7):e2843. PMID: 18665227
- Kube M**, Schneider B, Kuhl H, Dandekar T, Heitmann K, Migdoll AM, Reinhardt R, Seemüller E. The linear chromosome of the plant-pathogenic mycoplasma '*Candidatus Phytoplasma mali*'. *BMC Genomics.* 2008 Jun 26;9:306. PMID: 18582369
- Warren WC, Hillier LW, Marshall Graves JA **et al.** Genome analysis of the platypus reveals unique signatures of evolution. **Nature.** 2008 May 8;453(7192):175-83. PMID: 18464734
- Kube M**, Migdoll AM, Müller I, Kuhl H, Beck A, Reinhardt R, Geider K. The genome of *Erwinia tasmaniensis* strain Et1/99, a non-pathogenic bacterium in the genus *Erwinia*. *Environ Microbiol.* 2008 Sep;10(9):2211-22. PMID: 18462403
- Choudhury K, Zander D, **Kube M**, Reinhardt R, Clos J. Identification of a *Leishmania infantum* gene mediating resistance to miltefosine and SbIII. *Int J Parasitol.* 2008 Oct;38(12):1411-23. PMID: 18457839
- STAR Consortium.** SNP and haplotype mapping for genetic analysis in the rat. **Nat Genet.** 2008 May;40(5):560-6. PMID: 18443594
- Tran-Nguyen LT, **Kube M**, Schneider B, Reinhardt R, Gibb KS. Comparative genome analysis of "*Candidatus Phytoplasma australiense*" (subgroup tuf-Australia I; rp-A) and "*Ca. Phytoplasma asteris*" Strains OY-M and AY-WB. *J Bacteriol.* 2008 Jun; 190(11):3 979-91. PMID: 18359806
- Reusch TB, Veron AS, Preuss C, Weiner J, Wissler L, Beck A, Klages S, **Kube M**, Reinhardt R, Bornberg-Bauer E. Comparative analysis of expressed sequence tag (EST) libraries in the seagrass *Zostera marina* subjected to temperature stress. *Mar Biotechnol (NY).* 2008 May-Jun;10(3):297-309. PMID: 18239962
- Clark MS, Thorne MA, Purać J, Grubor-Lajsić G, **Kube M**, Reinhardt R, Worland MR. Surviving extreme polar winters by desiccation: clues from Arctic springtail (*Onychiurus arcticus*) EST libraries. *BMC Genomics.* 2007 Dec 21;8:475. PMID: 18154659

- Tanguy A, Bierre N, Saavedra C **et al.** Increasing genomic information in bivalves through new EST collections in four species: development of new genetic markers for environmental studies and genome evolution. *Gene*. 2008 Jan 31;408(1-2):27-36. PMID: 18054177
- Roeding F, Hagner-Holler S, Ruhberg H, Ebersberger I, von Haeseler A, **Kube M**, Reinhardt R, Burmester T. EST sequencing of Onychophora and phylogenomic analysis of Metazoa. *Mol Phylogenet Evol*. 2007 Dec;45(3):942-51. PMID: 17933557
- Knaust F, **Kube M**, Reinhardt R, Rabus R. Analyses of the *vrl* gene cluster in *Desulfococcus multivorans*: homologous to the virulence-associated locus of the ovine footrot pathogen *Dichelobacter nodosus* strain A198. *J Mol Microbiol Biotechnol*. 2007;13(1-3):156-64. PMID: 17693723
- Richter M, **Kube M**, Bazylnski DA, Lombardot T, Glöckner FO, Reinhardt R, Schüler D. Comparative genome analysis of four magnetotactic bacteria reveals a complex set of group-specific genes implicated in magnetosome biomineralization and function. *J Bacteriol*. 2007 Jul;189(13):4899-910. PMID: 17449609
- Bauer M, **Kube M**, Teeling H **et al.** Whole genome analysis of the marine Bacteroidetes '*Gramella forsetii*' reveals adaptations to degradation of polymeric organic matter. *Environ Microbiol*. 2006 Dec;8(12):2201-13. PMID: 17107561
- Erkel C, **Kube M**, Reinhardt R, Liesack W. Genome of Rice Cluster I archaea--the key methane producers in the rice rhizosphere. **Science**. 2006 Jul 21;313(5785):370-2. PMID: 16857943
- Muzny DM, Scherer SE, Kaul R **et al.** The DNA sequence, annotation and analysis of human chromosome 3. **Nature**. 2006 Apr 27;440(7088):1194-8. PMID: 16641997
- Erkel C, Kemnitz D, **Kube M**, Ricke P, Chin KJ, Dedysch S, Reinhardt R, Conrad R, Liesack W. Retrieval of first genome data for rice cluster I methanogens by a combination of cultivation and molecular techniques. *FEMS Microbiol Ecol*. 2005 Jul 1;53(2):187-204. PMID: 16329940
- Meyerdierks A, **Kube M**, Lombardot T, Knittel K, Bauer M, Glöckner FO, Reinhardt R, Amann R. Insights into the genomes of archaea mediating the anaerobic oxidation of methane. *Environ Microbiol*. 2005 Dec;7(12):1937-51. PMID: 16309392
- Ricke P, **Kube M**, Nakagawa S, Erkel C, Reinhardt R, Liesack W. First genome data from uncultured upland soil cluster alpha methanotrophs provide further evidence for a close phylogenetic relationship to *Methylocapsa acidiphila* B2 and for high-affinity methanotrophy involving particulate methane monooxygenase. *Appl Environ Microbiol*. 2005 Nov;71(11):7472-82. PMID: 16269789
- Ullrich S, **Kube M**, Schübbe S, Reinhardt R, Schüler D. A hypervariable 130-kilobase genomic region of *Magnetospirillum gryphiswaldense* comprises a magnetosome island which undergoes frequent rearrangements during stationary growth. *J Bacteriol*. 2005 Nov;187(21):7176-84. PMID: 16237001
- Mussmann M, Richter M, Lombardot T, Meyerdierks A, Kuever J, **Kube M**, Glöckner FO, Amann R. Clustered genes related to sulfate respiration in uncultured prokaryotes support the theory of their concomitant horizontal transfer. *J Bacteriol*. 2005 Oct;187(20):7126-37. PMID: 16199583
- Gade D, Theiss D, Lange D, Mirgorodskaya E, Lombardot T, Glöckner FO, **Kube M**, Reinhardt R, Amann R, Lehrach H, Rabus R, Gobom J. Towards the proteome of the marine bacterium *Rhodospirillum rubrum*: mapping the soluble proteins. *Proteomics*. 2005; Sep;5(14):3654-71. PMID:16127728
- Kube M**, Beck A, Zinder SH, Kuhl H, Reinhardt R, Adrian L. Genome sequence of the chlorinated compound-respiring bacterium *Dehalococcoides* species strain CBDB1. **Nat Biotechnol**. 2005 Oct;23(10):1269-73. PMID: 16116419
- Ivens AC, Peacock CS, Worthey EA **et al.** The genome of the kinetoplastid parasite, *Leishmania major*. **Science**. 2005 Jul 15;309(5733):436-42. PMID: 16020728
- Kube M**, Beck A, Meyerdierks A, Amann R, Reinhardt R, Rabus R. A catabolic gene cluster for anaerobic benzoate degradation in methanotrophic microbial Black Sea mats. *Syst Appl Microbiol*. 2005 Jun;28(4):287-94. PMID: 15997700
- Kühner S, Wöhlbrand L, Fritz I, Wruck W, Hultschig C, Hufnagel P, **Kube M**, Reinhardt R, Rabus R. Substrate-dependent regulation of anaerobic degradation pathways for toluene and ethylbenzene in a denitrifying bacterium, strain EbN1. *J Bacteriol*. 2005 Feb;187(4):1493-503. PMID: 15687214

- Rabus R, **Kube M**, Heider J, Beck A, Heitmann K, Widdel F, Reinhardt R. The genome sequence of an anaerobic aromatic-degrading denitrifying bacterium, strain EbN1. *Arch Microbiol.* 2005 Jan;183(1):27-36. PMID: 15551059
- Schultheiss D, Kube M, Schüler D. Inactivation of the flagellin gene *flaA* in *Magnetospirillum gryphiswaldense* results in nonmagnetotactic mutants lacking flagellar filaments. *Appl Environ Microbiol.* 2004 Jun;70(6):3624-31. PMID: 15184166
- Watanabe H, Fujiyama A, Hattori M **et al.** DNA sequence and comparative analysis of chimpanzee chromosome 22. **Nature.** 2004 May 27;429(6990):382-8. PMID: 15164055
- Ricke P, Erkel C, **Kube M**, Reinhardt R, Liesack W. Comparative analysis of the conventional and novel *pmo* (particulate methane monooxygenase) operons from methylocystis strain SC2. *Appl Environ Microbiol.* 2004 May;70(5):3055-63. PMID: 15128567
- Grünberg K, Müller EC, Otto A, Reszka R, Linder D, **Kube M**, Reinhardt R, Schüler D. Biochemical and proteomic analysis of the magnetosome membrane in *Magnetospirillum gryphiswaldense*. *Appl Environ Microbiol.* 2004 Feb;70(2):1040-50. PMID: 14766587
- Kube M**, Heider J, Amann J, Hufnagel P, Kühner S, Beck A, Reinhardt R, Rabus R. Genes involved in the anaerobic degradation of toluene in a denitrifying bacterium, strain EbN1. *Arch Microbiol.* 2004 Mar;181(3):182-94. PMID: 14735297
- Sakaki Y, Watanabe H, Taylor T **et al.** Human versus chimpanzee chromosome-wide sequence comparison and its evolutionary implication. Chimpanzee Chromosome 22 Sequencing Consortium. *Cold Spring Harb Symp Quant Biol.* 2003;68:455-60.
- Krüger M, Meyerdierks A, Glöckner FO, Amann R, Widdel F, **Kube M**, Reinhardt R, Kahnt J, Böcher R, Thauer RK, Shima S. A conspicuous nickel protein in microbial mats that oxidize methane anaerobically. **Nature.** 2003 Dec 18;426(6968):878-81. PMID: 14685246
- Schübbe S, **Kube M**, Scheffel A, Wawer C, Heyen U, Meyerdierks A, Madkour MH, Mayer F, Reinhardt R, Schüler D. Characterization of a spontaneous nonmagnetic mutant of *Magnetospirillum gryphiswaldense* reveals a large deletion comprising a putative magnetosome island. *J Bacteriol.* 2003 Oct;185(19):5779-90. PMID: 13129949
- Glöckner FO, **Kube M**, Bauer M, Teeling H, Lombardot T, Ludwig W, Gade D, Beck A, Borzym K, Heitmann K, Rabus R, Schlesner H, Amann R, Reinhardt R. Complete genome sequence of the marine planctomycete *Pirellula* sp. strain 1. **Proc Natl Acad Sci U S A.** 2003 Jul 8;100(14):8298-303. PMID: 12835416
- Rabus R, **Kube M**, Beck A, Widdel F, Reinhardt R. Genes involved in the anaerobic degradation of ethylbenzene in a denitrifying bacterium, strain EbN1. *Arch Microbiol.* 2002 Dec;178(6):506-16. PMID: 12420173
- Rabus R, Gade D, Helbig R, Bauer M, Glöckner FO, **Kube M**, Schlesner H, Reinhardt R, Amann R. Analysis of N-acetylglucosamine metabolism in the marine bacterium *Pirellula* sp. strain 1 by a proteomic approach. *Proteomics.* 2002 Jun;2(6):649-55. PMID: 12112844
- Seo HC, **Kube M**, Edvardsen RB, Jensen MF, Beck A, Spriet E, Gorsky G, Thompson EM, Lehrach H, Reinhardt R, Chourrout D. Miniature genome in the marine chordate *Oikopleura dioica*. **Science.** 2001 Dec 21;294(5551):2506. PMID: 11752568d