

Biosketch

Univ.-Prof. Dr. Thomas Rattei

Position in CoE: Key Researcher

Personal Details

Place of birth	Dresden, Germany
Nationality	German
Children	–
Affiliation:	University of Vienna
E-Mail	thomas.rattei@univie.ac.at
Profile	ResearcherID: F-1366-2011
List of publications	ORCID: 0000-0002-0592-7791
Academic age	20 years since PhD



Academic Career and Positions Held

I studied Chemistry at the **Technical University of Dresden** and earned the Diploma degree in **1995**. I did my **PhD** at the same university in the Department of Biochemistry. In parallel, 1995, **I founded** and headed an **IT company**. Between 1999 and 2001, I expanded my company and sold it in 2001. I joined the novel field of bioinformatics and was appointed as PostDoc, later **assistant professor**, at the **Technical University Munich**. I also worked as a guest researcher at the Helmholtz Center Munich. I received my **habilitation** (*venia legendi*) in **2010**. I was appointed at the **University of Vienna** as a **full professor** heading CUBE, the Division of Computational Systems Biology, March **2010**. I am currently heading the Doctoral School Microbiology and Environmental Science and am **Vice-head** of the **Department of Microbiology and Ecosystem Science**.

Scientific Achievements and Scientific Contribution to the CoE

Scientific Achievements. My team maintains and develops internationally relevant **resources in computational biology**, such as the SIMAP database of protein sequence similarities and the web portal effectivedb.org predicting bacterial secreted proteins and secretion systems. I have been named **Highly Cited Researcher** (Clarivate) in multiple years, including 2021.

My team and I operate specialized **high-performance computing infrastructure** for bioinformatics and computational life science. The main difference to larger, generic computing facilities, such as the Vienna Scientific Cluster (VSC) is the equipment with a rich, flexible and up-to-date bioinformatics software repository and the availability of major biological databases on-site. This installation allows users of the CoE to analyse their data easily and efficiently, usually without any software installation, just by using the pre-installed tools and databases.

Scientific Contribution to the CoE. I will work on **computational genomics** problems in the CoE. These include the analysis and functional interpretation of multi-omics data, large-scale comparative and functional genomics, as well as the development of novel bioinformatic approaches for the prediction of microbe host interactions. Furthermore, I will also work on data management and data integration within the CoE.

10 Most Important Publications (*relevant for the CoE)

1. Maixner, F.; Sarhan, M. S.; (12 authors); **Rattei, T.**; Moritz, R. L.; Oegg, K.; Segata, N.; Zink, A.; Reschreiter, H.; Kowarik, K. Hallstatt Miners Consumed Blue Cheese and Beer during the Iron Age and Retained a Non-Westernized Gut Microbiome until the Baroque Period. *Current Biology* **2021**, *31* (23), 5149–5162.e6. <https://doi.org/10.1016/j.cub.2021.09.031>.
2. *Feldbauer, R.; Gosch, L.; Lüftinger, L.; Hyden, P.; Flexer, A.; **Rattei, T.** DeepNOG: Fast and Accurate Protein Orthologous Group Assignment. *Bioinformatics* **2021**, *36* (22–23), 5304–5312. <https://doi.org/10.1093/bioinformatics/btaa1051>.
3. *Huerta-Cepas, J.; Szklarczyk, D.; Heller, D.; Hernández-Plaza, A.; Forslund, S. K.; Cook, H.; Mende, D. R.; Letunic, I.; **Rattei, T.**; Jensen, L. J.; von Mering, C.; Bork, P. EggNOG 5.0: A Hierarchical, Functionally and Phylogenetically Annotated Orthology Resource Based on 5090 Organisms and 2502 Viruses. *Nucleic Acids Research* **2019**, *47* (D1), D309–D314. <https://doi.org/10.1093/nar/gky1085>.
4. Tett, A.; Huang, K. D.; (13 authors); **Rattei, T.**; Boulund, F.; Engstrand, L.; Zink, A.; Collado, M. C.; Littman, D. R.; Eibach, D.; Ercolini, D.; Rota-Stabelli, O.; Huttenhower, C.; Maixner, F.; Segata, N. The Prevotella Copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. *Cell Host & Microbe* **2019**, *26* (5), 666–679.e7. <https://doi.org/10.1016/j.chom.2019.08.018>.
5. Maixner, F.; Turaev, D.; (36 authors); **Rattei, T.**; Grimm, R.; Zink, A. The Iceman’s Last Meal Consisted of Fat, Wild Meat, and Cereals. *Current Biology* **2018**, *28* (14), 2348–2355.e9. <https://doi.org/10.1016/j.cub.2018.05.067>.
6. *Szczyrba, A.; Hofmann, P.; (62 authors); **Rattei, T.**; McHardy, A. C. Critical Assessment of Metagenome Interpretation—a Benchmark of Metagenomics Software. *Nat Methods* **2017**, *14* (11), 1063–1071. <https://doi.org/10.1038/nmeth.4458>.
7. *Maixner, F.; Krause-Kyora, B.; (19 authors); **Rattei, T.**; Zink, A. The 5300-Year-Old Helicobacter Pylori Genome of the Iceman. *Science* **2016**, *351* (6269), 162–165. <https://doi.org/10.1126/science.aad2545>.
8. *Daims, H.; Lebedeva, E. V.; Pjevac, P.; Han, P.; Herbold, C.; Albertsen, M.; Jehmlich, N.; Palatinszky, M.; Vierheilig, J.; Bulaev, A.; Kirkegaard, R. H.; von Bergen, M.; **Rattei, T.**; Bendinger, B.; Nielsen, P. H.; Wagner, M. Complete Nitrification by Nitrospira Bacteria. *Nature* **2015**, *528* (7583), 504–509. <https://doi.org/10.1038/nature16461>.
9. *Chapman, J. A.; Kirkness, E. F.; Simakov, O.; Hampson, S. E.; Mitros, T.; Weinmaier, T.; **Rattei, T.**; (67 authors). The Dynamic Genome of Hydra. *Nature* **2010**, *464* (7288), 592–596. <https://doi.org/10.1038/nature08830>.
10. *The International Brachypodium Initiative. Genome Sequencing and Analysis of the Model Grass Brachypodium Distachyon. *Nature* **2010**, *463* (7282), 763–768. <https://doi.org/10.1038/nature08747>.