Curriculum Vitae

Personal Data

Title	Prof. Dr.
First name	Stefan A.
Name	Rensing
Current position	Professor (W3)
Current institution(s)/site(s), country	University of Freiburg, Germany
Identifiers/ORCID	0000-0002-0225-873X

Qualifications and Career

Stages	Periods and Details
Degree programme	Biology (diploma), 1986-1993, University of Freiburg, Germany
Doctorate	1995, P. Sitte/U.-G. Maier, Molecular characterization of cryptomonads, University of Freiburg, Germany
Stages of academic/professional career	Since 2022, Prof. (W3) for data integration and systems modelling of eukaryotic model organisms / since 2021, Vice president for research and innovation, both at University of Freiburg 2019-2022 Prof. (W3) for Plant Cell Biology, University of Marburg 2018 Declined call to University College London, Quain Chair of Botany 2012-2019 Prof. (W2) for Plant Cell Biology, University of Marburg 2010-2012 Prof. (adj.) for Bioinformatics and Systems Biology, University of Freiburg 2007-2011 Lecturer Bioinformatics and Systems Biology, University of Freiburg (FRISYS) 2003-2007 Group leader Computational Biology, University of Freiburg 1995-2003 Postdoc positions in Bayreuth and Freiburg

Activities in the Research System

I have been a member of the faculty council at the University of Freiburg/Marburg for many years, have been vice dean and dean of my faculty at the University of Marburg, and currently serve the University of Freiburg as vice rector for research and innovation.

I am an associate editor for The Plant Journal and previously for BMC Plant Biology and Frontiers in Plant Science. Peer reviews: of grant proposals and papers for many agencies and journals, including e.g. the NSF/DFG/ANR/ERC, Science, Nature/Nature Plants, Cell, PNAS, Genome Biology, Plant Cell, Molecular Plant, New Phytologist.

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Member of Deutsche Botanische Gesellschaft (DBG), European Plant Science Organisation (EPSO), International Association of Bryologists (IAB), International Society of Endocytobiology (ISE), German Life Science Association (VBIO).

Coordinator (1. funding period) of the DFG Priority Programme 2237, MAdLand — Molecular Adaptation to Land: plant evolution to change; coordinator of the international *P. patens* flagship genome project (US DoE JGI). Member of many genome consortia as well as of the 1KP and 10KP projects. Coordinator of several national and international collaborative research projects.

Organization of meetings

2004	Organization of the international *Physcomitrella* meeting, MOSS 2004
2008 - 2010	Organization of the international *Physcomitrella* genome workshop
2010 - 2026	Organization of the non-seed plant workshop at PAG, San Diego
2011	Organization of the international *Physcomitrella* meeting, MOSS 2011
2015 - 2019	Organization of international Black Forest Summer Schools
2014	Organization of the Meeting of the International Society of Endocytobiology
2019	Organization of the Molecular Biology of Plants meeting (Dabringhausen)
2020 - 2023	Organization of the SPP 2237 MAdLand workshop and kickoff meeting

Supervision of Researchers in Early Career Phases

Number of theses supervised: Bachelor 29, master 14, diploma 18, PhD 16, Habilitation 2.

Scientific Results
Category A

Rensing, S.A., Lang, D., Zimmer, A.D. [65 co-authors] Grigoriev, I.V., Quatrano, R.S. and Boore, J.L. (2008) The *Physcomitrella* genome reveals evolutionary insights into the conquest of land by plants. Science, 319, 64-69; DOI: 10.1126/science.1150646.
Available from http://plantco.de/papers/Rensing_2008_Science_319-64.pdf

This is my “signature paper”: with the publication of “the moss genome” as the fourth plant genome (after Arabidopsis, rice and poplar) we laid the ground for comparative genomics to unravel plant trait evolution. The paper has been cited > 1,800 times so far. I was responsible for major parts of the analyses as well as writing.

Lang, D., Ullrich, K.K., Murat, F. [51 co-authors] Maumus, F., Salse, J., Schmutz, J. and **Rensing, S.A.** (2018) The *Physcomitrella patens* chromosome-scale assembly reveals moss genome structure and evolution. Plant J, 93, 515-533; DOI: 10.1111/tpj.13801. Open access.

An update of the “moss genome”: Awarded silver prize for the best Original Article in TPJ 2018; SEB-Wiley-TPJ award for outstanding papers published in TPJ in 2018; downloaded often enough to be a #Top20Article. Cited 275 times so far (Nov.22), i.e. ca. 70 times per year. I conceived of the study, acquired funding and supervised the parts carried out by my lab. I coordinated the collaborative project.

Rensing, S.A., Goffinet, B., Meyberg, R., Wu, S.Z. and Bezanilla, M. (2020) The Moss *Physcomitrium* (*Physcomitrella*) *patens*: A Model Organism for Non-Seed Plants. Plant Cell; DOI: 10.1105/tpc.19.00828. Open access.

An invited review on what we know about one of the most important non-seed plant models, *P. patens*, and how to make use of it.

Nishiyama, T., Sakayama, H., de Vries, J., [54 co-authors] Van Der Straeten, D., Gould, S.B. and **Rensing, S.A.** (2018) The *Chara* Genome: Secondary Complexity and Implications for Plant Terrestrialization. Cell, 174, 448-464 e424; DOI: 10.1016/j.cell.2018.06.033. Open access.

Another long-term genomics project: conceived of in 2008, published in Cell in 2018. Informing to a large extent our understanding of early land plant evolution. I conceived of the study, acquired funding and supervised the parts carried out by my lab. I coordinated the collaborative project. Cover contribution.

Rensing, S.A. (2018) Great moments in evolution: the conquest of land by plants. Curr Opin Plant Biol, 42, 49-54; DOI: 10.1016/j.pbi.2018.02.006.
Available from http://plantco.de/papers/Rensing_2018_CurrOpPlantBiol.pdf.

An invited review detailing what we knew (at the time) about early plant evolution, mainly derived from comparative genomics and evo-devo studies.

Wilhelmsson, P.K.I., Muhlich, C., Ullrich, K.K. and **Rensing, S.A.** (2017) Comprehensive Genome-Wide Classification Reveals That Many Plant-Specific Transcription Factors Evolved in Streptophyte Algae. Genome Biol Evol, 9, 3384-3397; DOI: 10.1093/gbe/evx258. Open access

One of the major topics that my lab pursues: evolution of transcription factors. Here we show, based on >120 plant and algal genomes, that many TF families previously thought to be land plant-specific indeed evolved in the common ancestor of plants and algae. I conceived of the study, acquired funding and supervised it.

Fernandez-Pozo, N., Haas, F.B., Meyberg, R., Ullrich, K.K., Hiss, M., Perroud, P.F., Hanke, S., Kratz, V., Powell, A.F., Vesty, E.F., Daum, C.G., Zane, M., Lipzen, A., Sreedasyam, A., Grimwood, J., Coates, J.C., Barry, K., Schmutz, J., Mueller, L.A. and **Rensing, S.A.** (2019) PEATmoss (Physcomitrella Expression Atlas Tool): a unified gene expression atlas for the model plant *Physcomitrella patens*. Plant J; DOI: 10.1111/tpj.14607. Open access.

My lab has developed a number of web-based community tools. PEATmoss unites the available expression profiling data for *P. patens* and makes it available to the public. It has since been expanded with more functions and more datasets (to be published soon in the framework of the PP 2437 “MAdLand” initiative). I conceived of the study, acquired funding and supervised it.

Hiss, M., Meyberg, R., Westermann, J., Haas, F.B., Schneider, L., Schallenberg-Rudinger, M., Ullrich, K.K. and **Rensing, S.A.** (2017) Sexual reproduction, sporophyte development and molecular variation in the model moss *Physcomitrella patens*: introducing the ecotype Reute. Plant J, 90, 606-620; DOI: 10.1111/tpj.13501. Open access.

My lab is interested in the evolution of sexual reproduction, and in particular how the plant alternation of generation evolved and is controlled. In this study we laid the methodological basis for such studies, since then used by several labs. I conceived of the study, acquired funding and supervised it. I coordinated the collaborative project.

Meyberg, R., Perroud, P.F., Haas, F.B., Schneider, L., Heimerl, T., Renzaglia, K.S. and **Rensing, S.A.** (2020) Characterization of evolutionarily conserved key players affecting eukaryotic flagellar motility and fertility using a moss model. New Phytol; DOI: 10.1111/nph.16486. Open access.

In this study on plant sexual reproduction we show that flagella of moss male sperm might be used as a model of human/animal disease and fertility studies. I conceived of the study, acquired funding and supervised it. Cover contribution.

Petroll, R., Varshney D., Hiltemann S., Finke H., Schreiber M., de Vries J., **Rensing S.A.** (2025). Enhanced sensitivity of TAPscan v4 enables comprehensive analysis of streptophyte transcription factor evolution. Plant J 121(1): e17184. DOI: 10.1111/tpj.17184. Open access.

With this paper, we made the code and underlying database for the TAPscan tool publicly available. The TAPscan tool has been developed by my lab since 2007 and is the most accurate and up to date tool for plant transcription factor family annotation. SEB-Wiley-TPJ award for outstanding papers with students as first authors published in TPJ in 2025. I conceived of the study, acquired funding and supervised it.

Category B

The landing page for the web-based community resources that my lab developed:
https://plantcode.cup.uni-freiburg.de/ including TAPscan, PEATmoss, GTP/ATP2, AetarDB.
Code for the TAPscan tool and the genome zoo database is publicly available from https://github.com/Rensing-Lab.

Technology transfer

1997 - 2003	CEO of dnaX, production of embedded DNA pendants
2006 - 2008	Scientific consultant of dnaX/Dr. Vogts Forschung
2008	Patent “Galactosyltransferase”, WO 2008/037490
2011 - 2021	CEO of evermoss, production of ornamental mosses
2020	Patent “Capsaicin”, submitted, EP 20190931.4
2026	Patent submission on novel substance for control of grapevine powdery mildew

Scientific communication

I am actively communicating via my Bluesky handle, @RensingStefan.
I regularly reach out via press releases and public discussion, including Pint of Science or podium discussions (e.g., https://tinyurl.com/p8z6fytx).

Academic Distinctions

Elected president of the international molecular moss science society (iMOSS), 2016-2022.
Honorary member of iMOSS and awarded the “golden spore” in 2021, “for his contribution to developing the *P. patens* genome, providing genomic tools and resources, and his tremendous efforts towards community building”.
Elected speaker of the section Plant Physiology and Molecular Plant Biology of the German Botanical Society (DBG) since 2019.