

## Short CV – Prof. Dr. Andreas Keller

Prof. Dr. Andreas Keller is Chair for Clinical Bioinformatics at Saarland University (Germany), leads the bioinformatics group at the Helmholtz Institute for Pharmaceutical Research (HIPS), and is guest professor at Stanford University in the department of Neurobiology and Neurology. At Saarland university, he is member of the Medical Faculty and the Saarland Informatics Campus since 2013. Keller studied computational biology at his alma mater. Likewise at Saarland University, Keller did his Ph.D in Computational Biology and qualified as a professor in Human Genetics. Before joining the university, Keller was VP for Biomarker Discovery at the Heidelberg-based company febit GmbH. From 2011 on, he was director for diagnostic innovation at the Siemens Healthineers Headquarter in Erlangen, Germany, where he was responsible for disruptive developments in molecular diagnosis and healthcare IT systems. In 2016, he co-founded the molecular diagnostic company Hummingbird Diagnostics, a company with focus on blood-borne non-coding RNA biomarkers for early-stage lung cancer, neurodegenerative disorders (Alzheimer's and Parkinson's Disease) as well as heart failure. Keller's Research focus is the development of novel multi-parametric diagnostic tests using machine learning and deep learning techniques. In particular, he aims at making complex test results understandable and explainable for clinicians and patients and to integrate genomic, transcriptomic, phenomic and radiomic data. In addition to the non-coding RNA research, Keller works on models to predict resistance against antibiotics in infectious diseases from next-generation sequencing data. Keller is co-author of 277 peer-reviewed research manuscripts that get cited over 2,500 times per year. He is also innovator on 82 patent filings and granted patents in the area of biomarkers and computational approaches for diagnosing diseases and predicting the therapy response.

### Personal data:

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27<sup>th</sup> June 1982, Saarbrücken (Germany), male  
married, one children  
Saarland University, Medical Faculty  
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### Education:

2006 Bachelor in Bioinformatics  
2006 Master in Bioinformatics (honors degree)  
2009 Ph. D. in Bioinformatics (summa cum laude)  
2012 Habilitation in Human Genetics

### Career:

2002	-	2006	Research Associate, Saarland University, Center for Bioinformatics
2006	-	2009	Ph.D. Student, Saarland University, Center for Bioinformatics
2010	-	2011	VP Biomarker Discovery, febit GmbH, Heidelberg
2011	-	2013	Director Diagnostic Information, Siemens Healthineers, Erlangen
<b>2013</b>	-	<b>present</b>	<b>Professor for Clinical Bioinformatics, Saarland University</b>
2013	-	present	Steering committee of the Centre of Bioinformatics, Saarland University
2016	-	present	Co-founder and Scientific Lead Hummingbird DX, Heidelberg, Boston
2018	-	2021	Speaker of the Center for Bioinformatics, Saarland University

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### **Miscellaneous:**

Associate Executive Editor in Chief, Genomics, Proteomics & Bioinformatics (6.6 IF)

Co-Author on 277 Publications, ~2,500 citations per year, H-index of 63

Inventor on 82 patents, thereof 38 granted patents

Germany – Land of Ideas Award 2017

Merck GFI Award 2015

Günther Hotz Medal, 2006

### **List of 10 relevant publications:**

Kern, F., Fehlmann, T., Violich, I., Alsop, E., Hutchins, E., Kahraman, M., Grammes, N., Guimarães, P., Backes, C., Poston, K., Casey, B., Balling, R., Geffers, L., Krüger, R., Galasko, D., Mollenhauer, B., Meese, E., Wyss-Coray, T., Craig, D., Van Keuren-Jensen, K., Keller, A. Deep sncRNA-seq of the PPMI cohort to study Parkinson's disease progression. *Nature Aging*. (2021)

Fehlmann T, Lehallier B, Schaum N, Hahn O, Kahraman M, Li Y, Grammes N, Geffers L, Backes C, Balling R, Kern F, Krüger R, Lammert F, Ludwig N, Meder B, Fromm B, Maetzler W, Berg D, Brockmann K, Deuschle C, von Thaler AK, Eschweiler GW, Milman S, Barzilai N, Reichert M, Wyss-Coray T, Meese E, Keller A. Common diseases alter the physiological age-related blood microRNA profile. *Nature Communications*. (2020)

Schaum, N., Lehallier, B., Hahn, O., Pálovics, R., Hosseinzadeh, S., Lee, SE., Sit, R., Lee, DP., Losada, PM., Zardeneta, ME., Fehlmann, T., Webber, JT., McGeever, A., Calcuttawala, K., Zhang, H., Berdnik, D., Mathur, V., Tan, W., Zee, A., Tan, M.; Tabula Muris Consortium, Pisco, AO., Karkani, J., Neff, NF., Keller, A., Darmanis, S., Quake, SR., Wyss-Coray, T. Ageing hallmarks exhibit organ-specific temporal signatures. *Nature*. (2020)

Fehlmann, T., Kahraman, M., Ludwig, N., Laufer, T., Backes, C., Galata, V., Keller, V., Geffers, G., Mercaldo, N., Roeske, A., Dueterloh, A., Hornung, D., Weis, T., Kayvanpour, E., Abu-Halima, M., Deuschle, C., Schulte, C., Suenkel, U., von Thaler, A., Maetzler, W., Herr, C., Faehndrich, S., Vogelmeier, C., Guimaraes, P., Hecksteden, A., Meyer, T., Metzger, F., Diener, C., Deutscher, S., Abdul-Khalik, H., Stehle, I., Haeusler, S., Meiser, A., Groesdonk, H., Volk, T., Lenhof, HP., Katus, H., Balling, R., Meder, B., Kruger, R., Huwer, H., Bals, R., Meese, E., Keller, A. Evaluating the Use of Circulating MicroRNA Profiles for Lung Cancer Detection in Symptomatic Patients. *Jama Oncology*. (2020)

Lehallier, B., Gate, D., Schaum, N., Nanasi, T., Lee, S., Yousef, H., Losada, PM., Berdnik, D., Keller, A., Verghese, J., Sathyan, S., Franceschi, C., Milman, S., Barzilai, N., Wyss-Coray, T. Undulating changes in human plasma proteome profiles across the lifespan. *Nature Medicine*. (2020)

Guimarães P, Keller A, Fehlmann T, Lammert F, Casper M. Deep-learning based detection of gastric precancerous conditions. *Gut*. (2019)

Alles, J., Fehlmann, T., Fischer, U., Backes, C., Galata, V., Minet, M., Hart, M., Abu-Halima, M., Grässer, FA., Lenhof, HP., Keller, A., Meese, E. An estimate of the total number of true human miRNAs. *Nucleic Acids Res*. 2019 Apr 23;47(7):3353-3364. doi: 10.1093/nar/gkz097 (2019)

Ludwig, N., Leidinger, P., Becker, K., Backes, C., Fehlmann, T., Pallasch, C., Rheinheimer, S., Meder, B., Stähler, C., Meese, E., Keller, A. Distribution of miRNA expression across human tissues. *Nucleic Acids Research*. (2016)

Keller, A., Graefen, A., Ball, M., Matzas, M., Boisguerin, V., Maixner, F., Leidinger, P., Backes, C., Khairat, R., Forster, M., Stade, B., Franke, A., Mayer, J., Spangler, J., McLaughlin, S., Shah, M., Lee, C., Harkins, T., Sartori, A., Moreno-Estrada, A., Henn, B., Sikora, M., Semino, O., Chiaroni, J., Rootsi, S., Myres, N., Cabrera, V., Underhill, P., Bustamante, C., Vigl E., Samadelli, M., Cipollini, G., Haas, J., Katus, H., O'Connor B., Carlson, M., Meder, B., Blin, N., Meese, E., Pusch, C., Zink, A. *New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing*. *Nature Communications*. (2011)

Keller, A., Leidinger, P., Bauer, A., ElSharawy, A., Haas, J., Backes, C., Wendschlag, A., Giese, N., Tjaden, C., Ott, K., Werner, J., Hackert, T., Ruprecht, K., Huwer, H., Huebers, J., Jacobs, G., Rosenstiel, P., Dommisch, H., Schaefer, A., Müller-Quernheim, J., Wullich, B., Keck, B., Graf, N., Reichrath, J., Vogel, B., Nebel, A., Jager, S., Staehler, P., Amarantos, I., Boisguerin, V., Staehler, C., Beier, M., Scheffler, M., Büchler, M., Wischhusen, J., Haeusler, S., Dietl, J., Hofmann, S., Lenhof, HP., Schreiber, S., Katus, H., Rottbauer, W., Meder, B., Hoheisel, J., Franke, A., Meese, E. *Towards discovering the blood-born miRNome of human diseases*. *Nature Methods*. (2011)