CURRICULUM VITAE

Personal Data

Title	Prof. Dr.
First name	Mario
Name	Looso
Current position	Group Leader Bioinformatics and IT Core Unit
Current institution(s)/site(s), country	Max Planck Institute for Heart and Lung Research, Bad Nauheim, Germany
Identifiers/ORCID	0000-0003-1495-9530

Qualifications and Career

Stages	**Periods and Details**
Degree programme	Diplom Bioinformatics, 2003 – 2006, University of Applied Sciences Mittelhessen, Germany
Doctorates	2006 – 2010, Prof. Dr. Thomas Braun, Max Planck Institute for Heart and Lung Research (Department of Cardiac Development and Remodelling), Bad Nauheim, Germany
Stages of academic/ professional career	2022 – date, Member of the Life Sciene Engineering section at the Promotionszentrum für Ingenieurswissenschaften, Forschungscampus Mittelhessen 2019 – date, Hub Leader, Translational Hub for Cardio-Pulmonary Systems Biology and Medicine, Cardio-Pulmonary Institute, Giessen, Germany 2018 – date, Honorary Professor at the University of Applied Sciences Mittelhessen 2010 – date, Group Leader, Bioinformatics Core Unit (BCU), Max Planck Institute for Heart and Lung Research, Bad Nauheim, Germany 2007 – date, Head IT department, Max Planck Institute for Heart and Lung Research, Bad Nauheim, Germany

Activities in the Research System

Since 2019	Lecture and Course “Angewandte Datenanalyse” for students of Systems-Biology and Bioinformatics (MSc), Justus Liebig University Gießen
Since 2012	Lecture “Biodatenanalyse” for students of Biotechnology and Biopharmaceutics Technology (BSc and MSc), University of Applied Sciences Mittelhessen
Since 2015	Ringvorlesung „Moderne Aspekte der Bioinformatik und Systembiologie“, Systemsbiology and Bioinformatics (MSc), Justus Liebig University Gießen

Scientific Results

Category A ($^{+}$ =Corresponding author, *= equal contribition, the contribution to the publication is outlined in brackets)

1. Cho H, Lai CC, Bonnavion R, Alnouri MW, Wang S, Roquid KA, Kawase H, Campos D, Chen M, Weinstein LS, Martínez A, **Looso M**, Sanda M, Offermanns S. (2025). ***Science***, Feb 7;387(6734):674-682. (Applied newly inhouse developed software to data)
2. Detleffsen J, Bruns B, Bentsen M, Kuenne C, and **Looso M^{+}** (2025). PEAKQC: periodicity evaluation in single-cell ATAC-seq data for quality assessment. ***Brief Bioinform***; 26(5). (Group software project, Supervision and Funding requisition)
3. Vega-Sendino M, Lüttmann FF, Olbrich T, Chen Y, Kuenne C, Stein P, Tillo D, Carey GI, Zhong J, Savy V, Radonova L, Lu T, Saykali B, Kim KP, Domingo CN, Schüler L, Günther S, Bentsen M, Bosnakovski D, Schöler H, Kyba M, Maity TK, Jenkins LM, **Looso M**, Williams CJ, Kim J, Ruiz S, (2024) The homeobox transcription factor DUXBL controls exit from totipotency. ***Nat Genet***. Apr;56(4):697-709 (Applied newly inhouse developed software to data, supervised FF Lüttmann together with J Kim as joined PhD student, Funding requisition)
4. Li X, Wu F, Günther S, **Looso M**, Kuenne C, Zhang T, Wiesnet M, Klatt S, Zukunft S, Fleming I, Poschet G, Wietelmann A, Atzberger A, Potente M, Yuan X, Braun T. (2023). Inhibition of fatty acid oxidation enables heart regeneration in adult mice. ***Nature*** Oct;622(7983):619-626 (Applied newly inhouse developed software to data)
5. Wu F, Li X, **Looso M**, Liu H, Ding D, Günther S, Kuenne C, Liu S, Weissmann N, Boettger T, Atzberger A, Kolahian S, Renz H, Offermanns S, Gärtner U, Potente M, Zhou Y, Yuan X, Braun T. (2023)Spurious transcription causing innate immune responses is prevented by 5-hydroxymethylcytosine. ***Nature Genet*** Jan;55(1):100-111. (Developed a new analysis pipeline for the given typ of data)
6. Bentsen M, Heger V, Schultheis H, Kuenne C, **Looso M^{+}** (2022). TF-COMB – discovering grammar of transcription factor binding sites. ***CSBJ***, 2022 Jul 21;20:4040-4051 (Software development project within my group, accepted and used within epigenetics community, Funding requisition)
7. Allanki S, Strilic B, Scheinberger L, Onderwater YL, Marks A, Günther S, Preussner J, Kikhi K, **Looso M**, Stainier DYR, Reischauer S. (2021). Interleukin-11 signaling promotes cellular reprogramming and limits fibrotic scarring during tissue regeneration. ***Sci Adv***, 10;7(37):eabg6497.
8. Bentsen M, Goymann P, Schultheis H, Klee K, Petrova A, Wiegandt R, Fust A, Preussner J, Kuenne C, Braun T, Kim J, **Looso M^{+}**. (2020). ATAC-seq footprinting unravels kinetics of transcription factor binding during zygotic genome activation. ***Nat Commun*** 11, 4267. (Software development project within my group, widely accepted and used within epigenetics community, Funding requisition)
9. Preussner, J.,Zhong, J., Sreenivasan, K., Gunther, S., Engleitner, T., Kunne, C., Glatzel, M., Rad, R., **Looso, M**., Braun, T., Kim, J. (2018). Oncogenic Amplification of Zygotic Dux Factors in Regenerating p53-Deficient Muscle Stem Cells Defines a Molecular Cancer Subtype. ***Cell Stem Cell*** 23, 794-805 e794. (Applied inhouse software to data, supervised J Preussner together with T Braun as joined PhD student, Funding requisition)
10. Kuenne, C., Preussner, J., Herzog, M., Braun, T. & **Looso, M^{+}**. (2014). MIRPIPE: quantification of microRNAs in niche model organisms. ***Bioinformatics*** 30, 3412-3413 (one of the first group software projects, used for small RNA projects until today, Funding requisition)

Further publications peer reviewed:

https://pubmed.ncbi.nlm.nih.gov/?term=Looso+M%5BAuthor%5D&sort=date&size=100