

Jonathan J. Froehlich

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Molecular biologist using functional genomics and computational tools to answer complex biological questions.

PROFESSIONAL EXPERIENCE

[\[LinkedIn\]](#)

01/2023–07/2026

Postdoctoral researcher

Max-Planck-Institute for Molecular Genetics, Berlin, DE, Systems Epigenetics, Dr. Edda Schulz. Third-party funding of the group, non-permanent.

- Identified gene programs and regulatory DNA from genomic dose-responses after quantitative CRISPRi perturbations of Oct4 in mouse embryonic stem cells.
- Established protocols and software workflows for scRNA-seq, ATAC-seq, and MPRAs to detect genomic regions that respond to different doses of a transcription factor, predict cis-regulatory elements, and test synthetic CRE libraries.

01/2014–12/2021

Doctoral researcher

Max-Delbrueck-Center for Molecular Medicine & Berlin Inst. for Medical Systems Biol., Berlin, DE, Systems Biology of Regulatory Elements, Prof. Nikolaus Rajewsky

- Pioneered an *in vivo*, parallelized CRISPR-Cas9 screening in *C. elegans* to test over 1,000 gene regulatory mutations, a 100-fold increase over previous approaches.
- Engineered a new kilobase-sized amplicon sequencing protocol and partnered with a computational colleague to create specialized analysis software.
- Discovered that adjacent microRNA binding sites in the *lin-41* 3'-UTR function independently and compensatory.

04/2012–09/2012

Master's student

Max Planck Institute of Immunobiology and Epigenetics, Freiburg, DE, Epigenetics, Prof. Thomas Jenuwein

- Used a microscopy-based screen with a kinase inhibitor library to demonstrate that the Pi3K signaling pathway promotes cellular heterochromatin condensation.

04/2012–09/2012

Research Intern

Ludwig Maximilian University, Munich, DE, Chromatin Dynamics and Nuclear Function, Prof. Peter Becker

- By purifying functional RNA-protein complexes I showed which regions of the non-coding RNAs RoX1/2 bind the helicase MLE, critical data which contributed to a publication.

08/2011–09/2011

Research Intern

Ludwig Maximilian University, Munich, DE, Epigenetics, Prof. Heinrich Leonhardt

- Tested protein interactions in live cells with the help of LacO-array-based foci.

11/2010–07/2011

Research Intern

Ludwig Maximilian University, Munich, DE, Epigenetic Gene Regulation – Prof. Gunnar Schotta

- Performed endogenous marker knock-ins in mouse embryonic stem cells pre-CRISPR, the results contributed to a publication.

01/2010–09/2010

Bachelor's student

Max Planck Institute of Immunobiology and Epigenetics, Freiburg, DE, Epigenetics, Prof. Thomas Jenuwein

- Developed a semi-automated microscopy screening platform and image analysis pipeline to quantify heterochromatin status in mouse fibroblast reporter cells.

07/2009–09/2009

Research Intern

Max Planck Institute of Immunobiology and Epigenetics, Freiburg, DE, Epigenetics, Prof. Thomas Jenuwein

- Tested if two proteins of interest translocated to the nucleus in response to cell stress, using imaging and western blotting.

07/2008–10/2008

Research Intern

Institute of Molecular Pathology, Vienna, AT, Synaptic and Circuit Mechanisms of Memory, Prof. Simon Rumpel

- Constructed a 3D mouse brain reference atlas, using slices of the Allens 2D atlas.

02/2007–06/2007

Research Intern

Leibniz Institute of Virology, Hamburg, DE, Somatic Stem Cell Genetics, PD Dr. Heinz Lother

- Assisted in cloning of shRNAs and got familiar with basic molecular biology.

07/2006–09/2006

Research Intern

Leibniz Institute of Virology, Hamburg, DE, Electronmicroscopy and Microtechnology, Prof. Heinrich Hohenberg

- Compared two staining protocols and tested a new visualization for scanned sample blocks.

EDUCATION

2014–2022	Dr. rer. nat., Molecular Biology , Humboldt University, Berlin, DE
2010–2012	MSc, Biology , Ludwig Maximilian University, Munich, DE
2007–2010	BSc, Molecular Biotechnology , FH Campus Vienna, Vienna, AT
2006	Abitur, Biology & Math , Gymnasium Rahlstedt, Hamburg, DE

PUBLICATIONS

[[Google Scholar](#)] [[Orcid](#)]

- 2025 Till Schwaemmle, Gemma Noviello, Eleni Kanata, **Jonathan J Froehlich**, Melissa Bothe, Aybuge Altay, Jade Scouarnec, Vivi-Yun Feng, Martin Vingron, Edda G Schulz, "Reporter CRISPR screens decipher cis-and trans-regulatory principles at the Xist locus", *Nature Struct Mol Biol*, [DOI].
- 2023 **Jonathan J Froehlich**, Nikolaus Rajewsky, "C. elegans gene regulatory alleles and reporter bashing studies", *Micropublication Biology*, [DOI].
- 2022 **Jonathan J Froehlich**, "Parallel Genetics of Gene Regulatory Sequences in *Caenorhabditis elegans*", Dissertation, Humboldt University Berlin, [DOI].
- 2021 **Jonathan J Froehlich***, Bora Uyar*, Margareta Herzog, Kathrin Theil, Petar Glažar, Altuna Akalin, Nikolaus Rajewsky, "Parallel genetics of regulatory sequences using scalable genome editing in vivo", *Cell Reports*, [DOI] [news] [software] *co-first
- 2021 **Jonathan J Froehlich**, Nikolaus Rajewsky, Collin Ewald, "Estimation of C. elegans cell- and tissue volumes", *Micropublication Biology*, [DOI].
- 2013 Sylvain Maenner, Marisa Müller, **Jonathan Froehlich**, Diana Langer, Peter B Becker, "ATP-dependent roX RNA remodeling by the helicase maleless enables specific association of MSL proteins", *Molecular Cell*, [DOI].
- 2012 Silvia Dambacher, Wen Deng, Matthias Hahn, Dennis Sadic, **Jonathan Froehlich**, Alexander Nuber, Christian Hoischen, Stephan Diekmann, Heinrich Leonhardt, Gunnar Schotta, "CENP-C facilitates the recruitment of M18BP1 to centromeric chromatin", *Nucleus*, [DOI].

ACTIVITIES

LEADERSHIP & ENGAGEMENT

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|------------------|---|
| 2023–2026 | Postdoc association representative |
| 2023–2026 | Maintainer of team's website |
| 2023–2026 | Leading one main- and collaborating on five side projects |
| 2015, 2023, 2025 | Co-organizer of 3 retreats with 15-30 participants |
| 2023 | Co-hosted a distinguished speaker at the institute |
| 2014–2023 | Contributed 17 biological diagrams to Wikipedia [Wikipedia contributions] |
| 2023 | Assistant at a conference, designed full program booklet |
| 2014–2022 | Led one main- and two side projects from conceptualization to publication |
| 2020–2021 | Coordinated weekly team meetings, established guidelines |
| 2020–2021 | Initiated a community gardening project on the institute's terrace |
| 2016–2021 | Coordinated monthly social event "After Hour" at the institute, MDC/BIMSB |
| 2014–2019 | Communicated science to public at 4 events "Long Night of Science Berlin" |

PERSONAL INTERESTS

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|--------------|---|
| 2016–present | Scuba diving including caverns |
| 2014–present | Different side projects, listed on my [personal website] |
| 2012–2013 | Worked with artists [B.Härter][F.Kiessling][E.Burlyga][Artitude][TV show] |
| 2012 | Bringing people together at event series "Johnny's lounge", Freiburg |

TEACHING

04/2024–09/2025	Supervised Master's student, CRISPRi lines and cis-regulatory DNA reporter
06/2018–07/2018	Supervised Master's student, knock-in C.elegans
02/2023	Instructor at university course on CRISPR, Free University, Berlin
03/2014	Instructor at university course on C.elegans, Humboldt University, Berlin

PRESENTATIONS

2023-2026	Internal progress reports, ~3-month intervals, Schulz group
2025	Internal talk, "Institute Seminar", Max Planck Institute for Molecular Genetics MPI-MG, Berlin, DE
2023	Poster, "Day of Science", Max Planck Institute for Molecular Genetics MPI-MG, Berlin, DE
2014-2022	Internal progress reports, ~5-month intervals, Rajewsky group
2019	Selected Talk, "22nd International C. elegans Conference", Genetics Society of America, UCLA, Los Angeles, USA
2015/2017/2019	Talks, "Student Seminar Series", Max Delbrueck Center for Molecular Medicine, MDC, Berlin, DE
2017	Selected Talk, "21st International C. elegans Conference", Genetics Society of America, UCLA, Los Angeles, USA
2015/2016/2017	Posters, "BIMSB Summer Meeting", Berlin Institute for Medical Systems Biology, MDC, Berlin, DE
2016	Poster, "Complex Life of mRNA", European Molecular Biology Organization, EMBL, Heidelberg, DE
2016	Poster, "European Worm Meeting", Group of Elegans New Investigators in Europe, MDC, Berlin, DE

RESEARCH INTERESTS

[Bluesky/Twitter] [Personal bibliography]

Comprehensive analyses, perturbations, or engineering of complex biological systems to find new rules, mechanisms, or uses. For example:

- How is signaling translated to cell and tissue function?
- How are cell properties and phenotype encoded in genomes?
- Which mechanisms control cell specification?
- Which rules act on gene regulatory sequences in vivo?
- What can cause and what can cure a specific disease?
- On the technical side: parallel reporter assays, CRISPR screens, mammalian cells/organoids, genetic circuits, multi-parameter microscopy, automation, single-cell/spatial, genomic profiling, advanced computational analysis.
- since 2014 I follow the literature broadly on systems-, synthetic biology and gene regulation.

TECHNICAL EXPERIENCE

LABORATORY

2023–present	tunable CRISPRi, ATAC-seq, scRNA-seq with sample multiplexing (PD)
2023–present	Cell culture of sensitive embryonic stem cells and differentiation (PD)
2015–present	Synthetic DNA construct design, cloning, delivery, line generation
2009–present	Operating various epi-, and confocal microscopes, flow cytometer
2007–present	Molecular biology of RNA, DNA, and proteins
2014–2022	Multiplexed CRISPR-Cas9 screening of non-coding DNA in <i>C.elegans</i> (PhD)
2014–2022	<i>C.elegans</i> handling and phenotype screening (PhD)
2017–2021	mRNA/DNA amplicon sequencing Illumina & Pacbio (PhD)
2010, 2012	96-well semi-automated microscopy-based molecule screening (BSc, MSc)
2011–2012	<i>D.melanogaster</i> handling and maintenance (intern)
2009–2011	Cell culture of fibroblast cell-lines and embryonic stem cells (intern, BSc)

COMPUTE

2024–present	ATAC-seq analysis, ChromBPNet seq2fun, TF motif grammar (PD)
2023–present	ScRNA-seq analysis with STARsolo/R Bioconductor (PD)
2022–present	Reproducible analysis of RT-qPCR, FACS, and other data with R
2014–present	Discussed data analysis in interdisciplinary wet- & dry-lab teams
2007–present	Standard day-to-day tools Microsoft suite, Adobe Illustrator/Photoshop, DNA plasmid design/analysis Geneious/Ape/Bioedit
2010, 2012	Automated image analysis with Cellprofiler, and CPAnalyst/SQL (BSc, MSc)
2008, 2020	3D imaging: Amira for segmentation, Blender to measure volumes (intern)

REFERENCES

Dr. Edda Schulz, Group Leader, Max Planck Institute for Molecular Genetics, Berlin, DE
2023-Present, supervisor of Postdoc, edda.schulz@molgen.mpg.de, +49 30 8413 1226

Prof. Nikolaus Rajewsky, Scientific Director, Berlin Institute for Medical Systems Biology,
Max Delbrueck Center for Molecular Medicine, Berlin, DE
2014-2021, supervisor of PhD, rajewsky@mdc-berlin.de, +49 30 9406 2999

Prof. Thomas Jenuwein, Director, MPI for Immunobiology and Epigenetics, Freiburg, DE
2012 & 2010, supervisor of BSc & MSc, jenuwein@immunbio.mpg.de, +49 76 15108 785

Additional references on request.