

# Max Frank

PhD Candidate

★ 26.02.1993, Vienna

✉ max.frank@embl.de

☎ +49 151 106 616 07

in /in/max-frank

📍 Heidelberg, Germany

👤 Max Frank

## SCIENTIFIC DEGREES

**2024:** PhD, EMBL & Heidelberg University (Defense May)

**2017:** Master's Degree in Systems Biology, ETH Zurich

**2016:** Bachelor's Degree in Biology, ETH Zurich

## SKILLS

Single-cell multi-omics data, Proteomics, Epigenomics

Probabilistic modeling, Statistics, Python and R

HPC cluster, Workflow management, Bash, Linux

Basic molecular biology skills

Data presentation, Scientific communication

## DOCTORAL STUDIES

10/2018 - 01/2024 **Group of Prof. Oliver Stegle**  
Joint Ph.D. Program of EMBL and Heidelberg University

Thesis Title **Modeling epigenetic heterogeneity across time and genome in single-cell multi-omics experiments**

Summary During my PhD., I developed modeling frameworks to study developmental processes using multimodal single-cell sequencing technologies. My approach leveraged the combination of pseudotime inference on transcriptomics data with base-pair resolution modeling of DNA methylation and chromatin accessibility. To model highly sparse single-cell epigenetic data accurately I developed a custom model utilizing Gaussian process regression, that dynamically shares information between cells and across the genome. This model allowed the study of gene-regulatory processes in mouse gastrulation with high temporal resolution.

Teaching

- EMBO Integrative analysis of multi-omics data: 2022 · Practical course
- EMBL Predoc Course: 2019, 2020, 2021 · Single-cell Practical for PhD students
- Single cell course at University of Heidelberg 2020, 2021, 2022 · Practical for University students
- Supervised Master students: 2022 Caroline Wandlinger

Conferences **Selected talks/posters/workshops:**

- Talk: Probabilistic Modeling in Genomics, Aussois, October 2019
- Poster: From functional Genomics to Systems Biology, Heidelberg 2022
- Workshop: Human Cell Atlas Jamboree, Boston, 2018
- Workshop: Gaussian Process Summer School, Sheffield, September 2019
- Workshop: Mathematical Frameworks for Integrative Analysis of Emerging Biological Data Types, BIRS, June 2020

Extracurricular **PhD Symposium 2019 – Organizer**  
Website Team Leader – phdsymposium-archive/2019/

## UNDERGRADUATE STUDIES

**9/2015 – 9/2017 MSc. System Biology** **ETH Zurich**  
ETH Zurich, Diploma: 5.91 (Scale: 6 highest, 1 lowest)  
Received ETH Medal for outstanding Master's theses 2017

9/2016 – 5/2017 Development of a proteogenomic strategy to assess splice- and sequence variant impact on protein complex assembly – Master Thesis **ETH Zurich**  
  
Group of Prof. Ruedi Aebersold · Supervisors: Dr. Isabell Bludau, Dr. Moritz Heusel  
Development of R-package · Algorithm development for differential protein complex detection  
• Establishing a proteogenomics pipeline

3/2016 – 7/2016 Assessing the impact of disease mutations on the quantitative proteome – 5 month MSc. Project **ETH Zurich**  
  
Laboratory of Prof. Dr. Ruedi Aebersold · Supervisor: Dr. Marija Buljan  
Integration of genomics and proteomics data · Genomic variant calling

<b>9/2012 – 9/2016</b>	<b>BSc. Biology</b> ETH Zurich, Diploma: Ø 5.26 (Scale: 6 highest, 1 lowest)	
2015	Exchange Semester on Stipend	<b>Princeton University</b>

## EXPERIENCE

1/2018 – 7/2018	<b>Computational Proteomics – Research assistant</b> Group of Prof. Hannes Röst Developed computational methods for diaPASEF, a strategy that enables proteomics experiments with low input amounts at high accuracy	<b>University of Toronto</b>
2014 – 2016	<b>Fundamentals of Computer Science – Teaching assistant</b> Recieved best Teaching assistant of the year award 2016	<b>ETH Zurich</b>

## LANGUAGES

**English** – fluent · **German** – native · **Italian** – basic

## INTERESTS

Rock climbing · Personal genomics · Skiing · Hiking · Cycling

## SELECTED PUBLICATIONS

2024	<b>GPmeth: Modeling continuous epigenetic changes based on single-cell multi-omics profiling</b> <u>Frank M.</u> , Stegle O.	<b>In preparation</b>
2021	<b>Systematic detection of functional proteoform groups from bottom-up proteomic datasets</b> Bludau I., <u>Frank M.</u> , Dörig C., Cai Y., Heusel M., Rosenberger G., Picotti P., Collins B., Röst H. , Aebersold R.	<b>Nature communications</b>
2020	<b>diaPASEF: parallel accumulation–serial fragmentation combined with data-independent acquisition</b> Meier F., Brunner A., <u>Frank M.</u> , Ha A., Bludau I., Voytik E., Kaspar-Schoenefeld S., Lubeck M., Raether O., Bache N., Aebersold R., Collins B., Röst H., Mann M.	<b>Nature methods</b>
2020	<b>Complex-centric proteome profiling by SEC-SWATH-MS for the parallel detection of hundreds of protein complexes</b> Bludau, I., Heusel, M., <u>Frank, M.</u> , Rosenberger G., Hafen R., Banaei-Esfahani A., van Drogen A., Collins B., Gstaiger M. , Aebersold, R.	<b>Nature protocols</b>
2019	<b>Multi-omic measurements of heterogeneity in HeLa cells across laboratories</b> Liu Y., Mi Y., Mueller T, Kreibich S., Williams E., Van Drogen A., Borel C., <u>Frank M.</u> , Germain P., Bludau I., Mehnert M., Seifert M., Emmenlauer M., Sorg I., Bezrukov F., Bena F., Zhou H., Dehio C., Testa G., Saez-Rodriguez J., Antonarakis S., Hardt W., Aebersold R.	<b>Nature biotechnology</b>
2019	<b>Complex-centric proteome profiling by SEC-SWATH-MS</b> Heusel M., Bludau, I., Rosenberger G., Hafen R., <u>Frank, M.</u> , Banaei-Esfahani A., van Drogen A., Collins B., Gstaiger M. , Aebersold, R.	<b>Molecular systems biology</b>

## REFERENCES

PhD supervisor  
**Prof. Oliver Stegle**  
o.stegle@dkfz.de

Supervisor during 6-month internship  
**Prof. Hannes Röst**  
hannes.rost@utoronto.ca

Supervisor MSc Thesis  
**Prof. Ruedi Aebersold**  
rudolfa@ethz.ch