

Jonas KOEPPPEL

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Academic Positions

09.2024 – present **Postdoctoral Scholar**
University of Washington & Seattle Hub for Synthetic Biology
Advisors: Prof. Jay Shendure and Dr. Sudarshan Pinglay. EMBO fellow.

Education

10.2019 – 02.2024 **Ph.D. in Genomics**
University of Cambridge & Wellcome Sanger Institute
Advisors: Dr. Leopold Parts and Dr. Peter Campbell. Thesis [\[LINK\]](#)

10.2016 – 08.2019 **M.Sc. in Molecular Bioscience, Major Cancer Biology**
Heidelberg University & German Cancer Research Center (Grade 1.0, best possible)

10.2013 – 09.2016 **B.Sc. in Biosciences**
Heidelberg University (Grade 1.2, “very good”)

Selected research projects

09.2024 – present **Postdoctoral research: Saturation deletion scanning of the human genome**
Shendure & Pinglay labs – [University of Washington](#), Seattle, US

- Mapping the dispensability of all sequences in the human genome by creating highly multiplexed deletions in human cell lines using transposons and CRISPR-Cas3.

06.2020 – 02.2024 **PhD project: Randomizing the human genome by engineering recombination between repeat elements**
Parts lab – [Wellcome Sanger Institute](#), Cambridge, UK

- Targeted high-copy-number elements with CRISPR prime editing to precisely insert hundreds of recombinase sites into a single human genome allowing for recombinase-mediated shuffling.
- Induced thousands of structural variants and mapped the selection pressures acting on them.
- Resulted in a first author publication in *Science* [\[LINK\]](#).

06.2020 – 02.2024 **PhD project: Resolution of a human super-enhancer by targeted genome randomization**
Parts lab – [Wellcome Sanger Institute](#), Cambridge, UK

- Engineered efficient prime editing cell lines and tiled regulatory regions with recombinase sites.
- Established targeted nanopore sequencing methods to read out structural variation.
- Discovered a novel enhancer cluster controlling the *OTX2* gene and experimentally assessed the impact of shuffling and deleting enhancers within the cluster.
- Manuscript preprinted [\[LINK\]](#) and in review at *Molecular Cell*.

06.2020 – 02.2023 **PhD project: Prediction of prime editing insertion efficiencies using sequence features and DNA repair determinants**
Parts lab – [Wellcome Sanger Institute](#), Cambridge, UK

- Characterized the efficiencies for thousands of small insertions with prime editing, uncovered the determinants governing the rates, and built a computational model to predict efficiencies.
- Discovered a novel repair pathway involved in prime editing.
- Resulted in a first author publication in *Nature Biotechnology* [\[LINK\]](#).

- 01.2018 – 11.2020 **Master's Thesis: Small-molecule induced polymerization triggers the degradation of BCL6**
Ebert lab – [Broad Institute of Harvard and MIT](#) / Dana Farber Cancer Institute, Harvard Medical School, MA, USA & Fröhling lab – [National Center for Tumor Diseases](#) / German Cancer Research Center, Heidelberg, BW, Germany
- Elucidated the mechanism of action of a small-molecule using CRISPR screens and biochemistry.
 - Discovered targeted protein polymerization followed by degradation as a novel drug modality.
 - Resulted in a US patent application and a shared first author publication in *Nature* [[LINK](#)].

Teaching experience

- 09.2024 – present **Mentorship/Supervision**
- ELEFThERIA BERES (First year PhD student in the Pinglay lab at the University of Washington)
 - CARINA BIAR (First year PhD student in the Shendure lab at the University of Washington)
 - SAMANTHA SGRIZZI (Rotation student in the MCB Graduate Program at the University of Washington)
 - PEIXI CHEN (Rotation student in the MCB Graduate Program at the University of Washington)
 - FAAIZ QUAISAR (Research assistant in the Pinglay lab at the University of Washington)
- 02.2022 – 12.2022 – MÉLANIE GOULEY (Master's thesis – European School of Biotechnology, Strasbourg). Now a PhD student at ETH Zürich in the lab of Randall Platt. The thesis project was graded with the best possible mark by independent examiners.
- VALENTIN REBERNING (Bachelor's thesis – University in Wiener Neustadt). Now a Master's student at Heidelberg University.
- 10.2020 – 07.2021 **Supervising University of Cambridge students in "Cell and Developmental Biology"**
Weekly supervisions in small groups (2-3 students). Discussing course material, assigning and grading essays, preparing mock exams, introducing students to relevant research.
- 04.2015 – 07.2016 **Teaching assistant for the practical laboratory course "Methods of Molecular Bioscience"**
- Demonstrated the experiments (genomic and plasmid DNA preparation, agarose gel electrophoresis, SDS-PAGE) and presented the theory in introductory lectures before each session.
 - Graded reports and prepared exam preparation tutorials.

Fellowships and Stipends

- 08.2025 – 07.2027 EMBO Postdoctoral Fellowship (€130,800 over two years; funds my Postdoctoral salary)
- 05.2023 Pembroke College Grant (£1,156 covering expenses for the Biology of Genomes conference)
- 04.2022 Keystone symposia scholarship (\$1,200 covering conference expenses)
- 10.2019 – 02.2024 Wellcome Sanger Institute stipend (£22,189/yr covering my PhD at the Wellcome Sanger Institute)
- 01.2018 – 05.2018 PROMOS stipend (€2,575. German Academic Exchange Service (DAAD))
- 10.2016 – 10.2018 Germany stipend (€7,200. Federal Government of Germany and Prof. Helmut Determann)

Extracurricular projects

- 02.2022 – 02.2024 **Entrepreneurship**
- Coordinated the filing of a patent on the genome randomization method developed in my PhD.
 - Established connections with partners from Hummingbird, Civilization Ventures, and Fifty Years for potential future commercialization routes.
- 10.2016 – 05.2018 **Mentor for the 'Jugend Forscht' high school science fair (2018)**
- Our team placed **3rd nationally** out of over 1200 participants in Biology.

10.2017 – 06.2018 **Organized a weekly ‘Data Analysis and Programming with R’ course**

- Initiated a self-study R course to complement the limited offerings of our master’s at the time.
- Contacted Data Camp who provided us with free licenses for courses on their platform.
- Gave a three-session workshop on the analysis of large screen and mutation data sets.

Skills

Experimental	Genome engineering: CRISPR Cas3; CRISPR prime editing and knockout; bridge recombinases; CRISPR-associated transposases. Functional genomics: Arrayed and pooled screens with proliferation or sorting-based readouts. Sequencing: Short-read (Illumina) and long-read (ONT) whole genome and targeted sequencing.
Computational	R, Bash, compute clusters (LSF). Analysis workflows: Whole-genome sequencing, ATAC-seq, RNA-seq, and CRISPR screens; from FASTQ processing and alignment (bwa-mem, minimap2, NGMLR) to SNV and SV calling (caveman, pindel, gridss, brass, sniffles2, nanomonsv, savana), genome assembly (flye), and variant classification.
Languages	German (native), Chinese (spoken: native, written HSK 4), English (IELTS 8.5/9)

Scientific contributions

First and shared first author publications

J Koepfel*, R Ferreira*, T Vanderstichele, LM Riedmayr, EM Peets, G Girling, J Weller, FG Liberante, T Ellis, GM Church, L Parts. (2025) **“Randomizing the human genome by engineering recombination between repeat elements”**. **Science**.

J Koepfel*, P Murat*, G Girling, EM Peets, M Gouley, V Reberning, A. Maheshwari, J Hepkema, J Weller, JHJ Jebaraj, R Crawford, FG Liberante, L Parts. (2024) **“Resolution of a human super-enhancer by targeted genome randomisation”**. **bioRxiv** (in review at Molecular Cell).

J Koepfel*, J Weller*, EM Peets*, A Pallaseni, I Kuzmin, U Raudvere, H Peterson, F Liberante, L Parts (2023). **“Prediction of prime editing insertion efficiencies using sequence features and DNA repair determinants”**. **Nature Biotechnology**.

M Stabicki*, H Yoon*, **J Koepfel***, L Nitsch, SR Burman, CAD Genua, KA Donovan, AS Sperling, M Hunkeler, JM Tsai, R Sharma, A Guirguis, C Zou, P Chudasama, JA Glasser, PG Miller, C Scholl, S Fröhling, RP Nowak, ES Fischer, BL Ebert (2020). **“Small molecule-induced polymerization triggers degradation of BCL6”**. **Nature**.

J Koepfel, J Weller, T Vanderstichele, L Parts (2024). **“Engineering structural variants to interrogate human genome function”** (review article). **Nature Genetics**.

Co-author publications

K Krupina, A Goginashvili, M W Baughn, S Moore, C D Steele, A T Nguyen, D L Zhang, J Koepfel, [...], D W Cleveland (2025). **“Chromothripsis and ecDNA initiated by N4BP2 nuclease fragmentation of cytoplasm-exposed chromosomes”**. **Science**.

J Weller, G Girling, EM Peets, **J Koepfel**, S Kitada, P Murat, F Liberante, Y Belattar, S Iwama, T Ellis, L Parts (2025). **“Generating long deletions across the genome with pooled paired prime editing screens”**. **bioRxiv** (In review at Nature Genetics).

LM Riedmayr, **J Koepfel**, GM Church, L Parts, R Ferreira (2025). **“Genome Structure Interrogation via Recombinase Shuffling of Multiplexed Prime Edits”** **In review at Nature Protocols**.

S Pinglay, JB Lallanne, RM Daza, **J Koepfel**, XY Li, DS Lee and J Shendure (2025). **“Multiplex generation and single cell analysis of structural variants in a mammalian genome”**. **Science**.

MA Mahlke, L Lumerman, P Nath, C Chittenden, S Hoyt, **J Koepfel**, [...], Y Nechemia-Arbely (2025). **“Evolution and instability of human centromeres are accelerated by heterochromatin boundary loss and CENP-A overexpression”**. **bioRxiv**.

M Coelho, M Strauss, A Watterson, S Cooper, S Bhosle, G Illuzzi, E Karakoc, C Dinçer, S F Vieira, M Sharma, M Moullet, D Conticelli, **J Koepfel**, [...], M Garnett (2024). **“Base editing screens define the genetic landscape of cancer drug resistance mechanisms”**. **Nature Genetics**.

T Vanderstichele, KL Burnham, N de Klein, M Tardaguila, B Howell, K Walter, K Kundu, **J Koepfel**, [...], E Davenport (2024) **Misexpression of inactive genes in whole blood is associated with nearby rare structural variants**. **AJHG**.

J Weller*, A Pallaseni*, **J Koepfel**, L Parts (2023). **“Predicting Mutations Generated by Cas9, Base Editing, and Prime Editing in Mammalian Cells”**. **The CRISPR Journal**. (Review Article)

M Stabicki*, Z Kozicka*, G Petzold*, YD Li, M Manojkumar, RD Bunker, KA Donovan, QL Sievers, **J Koepfel**, D Suchyta, AS Sperling, EC Fink, JA Gasser, LR Wang, SM Corsello, RS Sellar, M Jan, D Gillingham, C Scholl, S Frohling, TR Golub, ES Fischer, NH Thoma and BL Ebert (2020). **“The CDK inhibitor CR8 acts as a molecular glue degrader that depletes cyclin K”**. **Nature**.

A Pallaseni*, EM Peets*, **J Koepfel**, J Weller, T Vanderstichele, UL Ho, L Crepaldi, J Leeuwen, F Allen, L Parts (2022). "Predicting base editing outcomes using position-specific sequence determinants". **Nucleic acids research**.

L Nitsch*, P Jensen*, H Yoon, **J Koepfel**, SSR Burman, ES Fischer, C Scholl, S Fröhling, M Słabicki (2022). "BTB^{BCL6} dimers as building blocks for reversible drug-induced protein oligomerization". **Cell reports methods**.

JC Fowler*, C King, C Bryant, M Hall, R Sood, SH Ong, E Earp, D Fernandez-Antoran, **J Koepfel**, SC Dentre, D Shorthouse, A Durrani, K Fife, E Rytina, D Milne, A Roshan, K Mahububani, K Saeb-Parsy, BA Hall, M Gerstung, PH Jones (2020). "Selection of oncogenic mutant clones in normal human skin varies with body site". **Cancer Discovery**.

RS Sellar*, AS Sperling*, M Słabicki, JA Gasser, ME McConkey, KA Donovan, N Mageed, DN Adams, C Zou, PG Miller, RK Dutta, S Boettcher, AE Lin, B Sandoval, VA Quevedo Barrios, V Kovalcik, **J Koepfel**, EK Henderson, EC Fink, L Yang, A Chan, SP Pokharel, EJ Bergstrom, R Burt, ND Udeshi, SA Carr, ES Fischer, C Chen, BL Ebert (2022) "Degradation of GSPT1 causes TP53-independent cell death in leukemia while sparing normal hematopoietic stem cells". **The Journal of Clinical Investigation**.

J Wu*, S Ma*, R Sandhoff*, Y Ming, A Hotz-Wagenblatt, V Timmerman, N Bonello-Palot, B Schlotter-Weigel, M Auer-Grumbach, P Seeman, WN Loscher, M Reindl, F Weiss, E Mah, N Weisshaar, A Madi, K Mohr, T Schlimbach, RM Velasco Cardenas, **J Koepfel**, [...], G Cui (2019). "Loss of Neurological Disease HSN-I-Associated Gene SPTLC2 Impairs CD8(+) T Cell Responses to Infection by Inhibiting T Cell Metabolic Fitness". **Immunity**.

Inventions

L Parts, J Koepfel, T Ellis, R Ferreira, GM Church (2023) "Methods for modifying a cell genome". Provisional US Patent App.

B Ebert, M Słabicki, ES Fischer, H Yoon, J Koepfel (2022) "Chemically inducible polypeptide polymerization". US Patent App. 17/750,061

Oral presentations and posters

Contributed talk, Saturation deletion scanning of the human genome. Cascadia Advanced Genomics Technology (June 2025). Vancouver, Canada.

Contributed poster, Saturation deletion scanning of the human genome. Advances in Genomic Technology Development (AGTD) Annual Meeting (June 2025). St. Louis, US.

Invited talk, Randomizing the human genome by engineering recombination between repeat elements. Harvard Medical School – Marks lab journal club (2025). Virtual.

Invited talk, Randomizing the human genome by engineering recombination between repeat elements. University at Buffalo – Gokcumen Lab seminar series (2025). Virtual.

Contributed talk, Randomizing the human genome by engineering recombination between repeat elements. Keystone Symposia - Precision genome engineering conference (2024). Banff, Canada.

Invited talk, Engineering genomes with prime editing. MPI for Evolutionary Anthropology – Pääbo/Riesenberg department seminar (2023). Leipzig, Germany

Contributed poster, Randomizing the human genome by engineering recombination between repeat elements. Cold Spring Harbor Laboratories – Biology of Genomes conference (2023). Cold Spring Harbor, US.

Invited talk, Prediction of prime editing insertion efficiencies using sequence features and DNA repair determinants. Harvard Medical School – Genome Engineering Seminar Series (2023). Virtual.

Contributed talk, Randomizing gene regulatory regions using prime editing. Wellcome Connecting Science - Synthetic Biology for Future Health (2023). Cambridge, UK.

Contributed poster, Randomizing gene regulatory regions using prime editing. American Institute of Chemical Engineers - International Mammalian Synthetic Biology Workshop (2022). Edinburgh, UK.

Contributed talk, Predicting the efficiency of writing short sequences into the genome using prime editing. Keystone Symposia - Precision genome engineering conference. *Keystone Symposia scholarship awarded* (2022). Keystone, USA.

Contributed poster, Predicting the efficiency of writing short sequences into the genome using prime editing. Keystone Symposia - Precision genome engineering conference (2022). Keystone, USA.

Contributed talk, Determinants of efficiency for writing small sequences into the genome using prime editing. Wellcome Connecting Science - CRISPR and Beyond: Perturbations at Scale to Understand Genomes 2021 (2021). Cambridge, UK.

Invited talk, Determinants of efficiency for writing small sequences into the genome using prime editing. Atlas of Variant Effect Alliance - Variant effect seminar series (2021). Virtual. [[LINK](#)]

Invited talk, Chemically induced degradation of the oncogenic transcription factor BCL6. Boehringer Ingelheim webinar (2021). Virtual. [[LINK](#)].

Invited talk, Small-molecule-induced protein polymerization. Dana-Farber Cancer Institute - Targeted protein degradation seminar series (2020). Virtual. [[LINK](#)]

Contributed poster, Functional dissection of protein degradation. Broad Institute of MIT and Harvard – Cancer Program Poster Session (2019). Boston, USA

Peer review: Reviewer or review collaborator for manuscripts at Cell, Nature, Nature Biotechnology and Nature Communications, and Nature Protocols.