

# DAVID N.P. KOPPSTEIN

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## Education

Massachusetts Institute of Technology

Ph.D, Biology

CAMBRIDGE, MA

2015

Yale University

B.S., Molecular Biophysics and Biochemistry

NEW HAVEN, CT

2008

## Experience

DKTK Partner Site Düsseldorf/Essen

DÜSSELDORF, GERMANY

**Junior Group Leader, Cancer Bioinformatics and Multiomics**

June '23 – present

Investigating the role of spliceosomal mutations in SHH medulloblastoma using long reads. Studying mutations in transcriptional coactivators that promote BCP-ALL glucocorticoid resistance.

Bioinformatics Core, MPI for Immunobiology and Epigenetics

FREIBURG, GERMANY

**Staff Bioinformatician**

August '22 – April '23

Performed analysis of transcript isoforms and chromosomal conformation using long reads.

Nikolaus Rajewsky Lab, Max Delbrück Center for Molecular Medicine

BERLIN, GERMANY

**Postdoctoral Researcher**

June '18 – June '22

Used 10X Visium to analyze aberrant RNA isoforms in neuromuscular organoids models of ALS. Discovered role of vault RNAs in SARS-CoV-2 infection.

Viral Immunology Systems Program, Kirby Institute, UNSW

SYDNEY, AUSTRALIA

**Postdoctoral Researcher**

Apr '17 – April '18

Codeveloped VDJPuzzle, a computational method for analyzing single-cell transcriptomics data of immune cells. Used this method to analyze single-cell transcriptomes of rogue B cells in Sjögren's disease.

Juno Therapeutics (formerly AbViro)

SEATTLE, WA, USA

**Data Scientist**

Mar '15 – Mar '17

Principal architect of the immunosequencing bioinformatics pipeline. Codiscovered effective TCR binders for HPV E6 and E7. Served as interim manager of the data science team.

David Bartel Lab, MIT

BOSTON, MA, USA

**Graduate Student**

May '10 – Mar '15

Profiled influenza's cap-snatching repertoire using NGS, discovering that snRNAs are primary targets of this process. Used Poly(A) profiling to annotate APA events.

## Fellowships and Awards

- Juno CEO Award for Outstanding Performance, 2016
- NSF Graduate Research Fellowship Program, Honorable Mention, 2011

## Selected Publications

Alfonso-Gonzalez C, Legnini I, Holec S, Arrigioni L, Ozbulut HC, Mateos F, **Koppstein D**, Rybak-Wolf A, Bönisch U, Rajewsky N, Hilgers V. Sites of transcription initiation drive mRNA isoform selection. 2023. *Cell*. doi: 10.1016/j.cell.2023.04.012.

Wyller M, Mösbauer K, Franke F, Diag A, Gottula LT, Arsie R, Klironomos F, **Koppstein D**, ..., Rajewsky N, Drosten C, Landthaler M. Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. 2021. *iScience*. doi: 10.1016/j.isci.2021.102151.

Singh M, Jackson KJL, Wang JJ, Schofield P, Field MA, **Koppstein D**, ..., Luciani F, Gordon TP, Goodnow CC, Reed JH. Lymphoma driver mutations in the pathogenic evolution of an iconic human autoantibody. 2020. *Cell*. doi:10.1016/j.cell.2020.01.029.

Rizzetto S, **Koppstein D**, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. B-cell receptor reconstruction from single-cell RNA-seq with VDJPuzzle. 2018. *Bioinformatics*. doi:10.1093/bioinformatics/bty203.

**Koppstein D**, Ashour J, and Bartel DP. Sequencing the cap-snatching repertoire of H1N1 influenza provides insight into the mechanism of viral transcription initiation. 2015. *Nucleic Acids Research* 43(10), 5052-5064.

Hezroni H, **Koppstein D**, Schwartz M, Tabin CJ, Bartel DP, and Ulitsky I. 2015. Principles of long noncoding RNA evolution derived from direct comparison of transcriptomes in 14 vertebrates. *Cell Reports* 11(7), 1110-1122.