

# 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

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## Experience

Nikolaus Rajewsky Lab, Max Delbrück Center for Molecular Medicine <b>Postdoctoral Researcher</b> Investigating the function of alternative RNA isoforms during differentiation of neural lineages in the context of neurodegenerative disease. Mentoring one Masters student.	BERLIN, GERMANY June '18 – present
Viral Immunology Systems Program, Kirby Institute, UNSW <b>Postdoctoral Researcher</b> Developed computational methods for analyzing single-cell transcriptomics data of immune cells. Mentored two Ph.D students, a Masters student, and an Honors student.	SYDNEY, AUSTRALIA Apr '17 – April '18
Juno Therapeutics <b>Data Scientist</b> Analyzed and communicated immunosequencing analyses for internal projects and external academic collaborators. Conducted analyses for internal RNA-seq and vector integration profiling projects. Served as interim manager of the data science team.	SEATTLE, WA, USA Jan '16 – Mar '17
AbVitro <b>Data Scientist</b> Designed bioinformatics pipeline for single-cell immunosequencing. Mined receptor sequences from tumor-infiltrating lymphocytes and nominated candidates for screening. ( <i>Acquired by Juno Therapeutics</i> ).	BOSTON, MA, USA Mar '15 – Dec '15
David Bartel Lab, MIT <b>Graduate Student</b> Designed, implemented, and analyzed high-throughput sequencing experiments using the Illumina platform to investigate influenza's cap-snatching repertoire. Utilized 3P-seq to precisely examine alternative cleavage and polyadenylation in diverse genetic backgrounds and model organisms.	BOSTON, MA, USA May '10 – Mar '15
Joan Steitz Lab, Yale <b>Undergraduate Student</b> Investigated the function of Herpesvirus saimiri Small U RNAs (HSURs).	NEW HAVEN, CT, USA May '06 – Apr '08

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## Publications and Preprints

Wyler M, Mösbauer K, Franke F, Diag A, Gottula LT, Arsie R, Klironomos F, **Koppstein D**, ..., Rajewsky N, Drosten C, Landthaler M. Bulk and single-cell gene expression profiling of SARS-CoV-2 infected human cell lines identifies molecular targets for therapeutic intervention. 2020. *Accepted Mol. Cell.*

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.

Grüning B, Dale R, Sjödin A, Chapman BA, Rowe J, Tomkins-Tinch CH, Valieris R, Koster J, **The Bioconda Team**. Bioconda: sustainable and comprehensive software distribution for the life sciences. 2018. *Nature Methods* 15, 475-76.

Grigaityte K, Carter JA, Goldfless SJ, Jefferey EW, Hause RJ, Jiang Y, **Koppstein D**, Briggs AW, Church GM, Vigneault F, Atwal GS. Single-cell sequencing reveals  $\alpha\beta$  chain pairing shapes the T cell repertoire. 2017. *bioRxiv*.

Briggs AW, Goldfless SJ, Timberlake S, Belmont BJ, Clouser CR, **Koppstein D**, Sok D, Vander Heiden JA, Tamminen MV, Kleinstein SH, Burton DR, Church GM, Vigneault F. 2017. Tumor-infiltrating immune repertoires captured by single-cell barcoding in emulsion. *bioRxiv*.

**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.

Nam J-W, Rissland OS, **Koppstein D**, Abreu-Goodger C, Jan CH, Agarwal V, Yildirim, Rodriguez A, and Bartel DP. 2014. Global Analyses of the Effect of Different Cellular Contexts on MicroRNA Targeting. *Molecular Cell*. 53, 1031-1043.

Ulitsky I, Shkumatava A, Jan C, Subtelny AO, **Koppstein D**, Bell G, Sive H, and Bartel DP. 2012. Extensive alternative polyadenylation during zebrafish development. *Genome Research*. 22(10):2054-66.

Agarwal A\*, **Koppstein D\***, Rozowsky J, Sboner A, Habegger L, Hillier LW, Sasidharan R, Reinke V, Waterston RH, and Gerstein M. 2010. Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. *BMC Genomics*. 11:383.

Mukhopadhyay J, Das K, Ismail S, **Koppstein D**, Jang M, Hudson B, Sarafianos S, Tuske S, Patel J, Jansen R, Irschik H, Arnold E, and Ebright RH. 2008. Myxopyronin, Coralopyronin, and Ripostatin Inhibit Transcription by Binding to the RNA Polymerase Switch Region. *Cell*. 135:295-307.

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## Presentations and Posters

**Koppstein D**, Rizzetto S, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. VDJPuzzle: A computational method for BCR and TCR reconstruction from single-cell sequencing data. Australian Bioinformatics And Computational Biology Society. Oral presentation delivered in Adelaide, Australia, November 2017.

**Koppstein D** Rizzetto S, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. VDJPuzzle: A computational method for BCR and TCR reconstruction from single-cell sequencing data. Australian Cellular Panomics Consortium. Poster presentation delivered in Melbourne, Australia, November 2017.

**Koppstein D**, Rizzetto S, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. VDJPuzzle: A computational method for BCR and TCR reconstruction from single-cell sequencing data. Australian Society for Immunology. Oral presentation delivered in Bowral, Australia, November 2017.

**Koppstein D**, Ashour J, Bartel D. Quantitative assessment of influenza's cap-snatching repertoire by RNA sequencing. RNA Society. Poster presentation delivered in Quebec City, Canada, June 2014.

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## Skills

### Wet lab

Extensive experience with Illumina library preparation and custom design: 3P-Seq, SMART-seq, and standard RNA-seq. Experience running single-cell 10X Chromium. Experience with molecular cloning, tissue culture, Northern/Western blots, protein purification, PCR, and yeast genetics.

### Dry lab

Fluent in Python and R. Expertise with modern bioinformatics tools including samtools, STAR, featureCounts, edgeR, Picard, etc. Experience with analysing single-cell sequencing data using scater, Seurat, etc. Experience writing scalable computational pipelines using Snakemake. Experience with statistical methods and machine learning techniques. Experience managing a team of computational biologists using agile methods.

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## Fellowships and Awards

- Juno CEO Award for Outstanding Performance, 2016
- NSF Graduate Research Fellowship Program, Honorable Mention, 2011
- Yale STARS II Research Fellowship, 2007-8

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## Extracurricular

- Urban Cycling Skills and Safety Clinic Organizer, 2013-4
- Whitehead Partner for High School Science Teacher Outreach, 2012
- MIT Cycling Team Officer, 2012-2014

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\* Authors contributed equally to this publication.