

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

Nikolaus Rajewsky Lab, Max Delbrück Center for Molecular Medicine

BERLIN, GERMANY

Postdoctoral Researcher

June '18 – present

Investigating the function of alternative polyadenylation during differentiation of neural lineages in single cells. Investigating coupling between polyadenylation and splicing using long reads.

Viral Immunology Systems Program, Kirby Institute, UNSW

SYDNEY, AUSTRALIA

Postdoctoral Researcher

Apr '17 – April '18

Developed computational methods for analyzing single-cell transcriptomics data of immune cells.

Juno Therapeutics

SEATTLE, WA, USA

Data Scientist

Jan '16 – Mar '17

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.

AbVitro

BOSTON, MA, USA

Data Scientist

Mar '15 – Dec '15

Designed bioinformatics pipeline for single-cell immunosequencing. Mined receptor sequences from tumor-infiltrating lymphocytes and nominated candidates for screening. (*Acquired by Juno Therapeutics*).

David Bartel Lab, MIT

CAMBRIDGE, MA, USA

Graduate Student

May '10 – Mar '15

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.

Mark Gerstein Lab, Yale University

NEW HAVEN, CT, USA

Bioinformatics Researcher

June '08 – June '09

Designed and implemented bioinformatic methods to compare and calibrate RNA-seq and microarray data.

Joan Steitz Lab, Yale University

NEW HAVEN, CT, USA

Student Researcher

May '06 – Apr '08

Investigated the function of Herpesvirus saimiri Small U RNAs (HSURs).

Richard Ebright Lab, Rutgers University

PISCATAWAY, NEW JERSEY, USA

Student Researcher

May '04 – Aug '04

Mutagenized bacterial RNA polymerase and isolated mutants resistant to small molecules.

Teaching and Mentoring Experience

Viral Immunology Systems Program, Kirby Institute, UNSW

SYDNEY, AUSTRALIA

Student Supervisor

Apr '17 – Apr '18

Cosupervised two Ph.D students, one Masters student, and one Honors student. Held weekly meetings with other supervisors and provided daily feedback and advice on single-cell sequencing projects.

Genetics, 7.03, MIT

CAMBRIDGE, MA, USA

Teaching Assistant

Feb '12 – May '12

Led review sections and held office hours. Contributed to exam creation and graded exams.

Quantitative Biology for Graduate Students, 7.57, MIT

CAMBRIDGE, MA, USA

Teaching Assistant

Feb '10 – May '10

Responsible for computational lab component of course. Led computational labs, review sections, and held office hours. Created and graded exams and problem sets incorporating bioinformatic exercises.

Publications and Preprints

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 VDJ-Puzzle. 2018. *Bioinformatics*. doi:10.1093/bioinformatics/bty203.

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.

Presentations and Posters

Koppstein D, Rizzetto S, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. VDJ-Puzzle: 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. VDJ-Puzzle: 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. VDJ-Puzzle: 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.

Fellowships and Awards

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

Activities

- Whitehead Partner for High School Science Teacher Outreach, 2012
- Organic Chemistry and Biochemistry Tutor, 2006-2010
- Urban Cycling Skills and Safety Clinic Organizer, 2013-4
- MIT Cycling Team Officer, 2012-2014

References

References are available upon request.

* Authors contributed equally to this publication.