

## Curriculum Vitae Anat Kreimer, Ph.D.

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### CURRENT POSITION

*Assistant Professor*

Core Member of the Center for Advanced Biotechnology and Medicine (CABM)  
Department of Biochemistry and Molecular Biology, Robert Wood Johnson Medical School (RWJMS)  
Secondary appointment at the Department of Pediatrics, RWJMS  
Rutgers University

### POSTDOCTORAL TRAINING

2014 – 2020 *Postdoctoral Fellow, Computer Science and Computational Biology*  
UNIVERSITY OF CALIFORNIA BERKELEY, BERKELEY, CA, USA  
UNIVERSITY OF CALIFORNIA SAN FRANCISCO, SF, CA, USA

- Advisors: Professor of Computer Science Nir Yosef and Professor of Biology Nadav Ahituv.

### EDUCATION

2009 – 2014 *Ph.D. Biomedical Informatics*  
COLUMBIA UNIVERSITY, New York, NY, USA

- Thesis research advisor: Professor of Computer Science Itsik Pe'er.

2006 – 2008 *M.Sc. Applied Mathematics, Thesis in Bioinformatics*  
TEL-AVIV UNIVERSITY, Tel-Aviv, Israel

- Thesis research advisor: Professor of Computer Science and Medicine Eytan Ruppin.
- Completed thesis work *summa cum laude*.
- Graduated from School of Mathematical Sciences *magna cum laude*.

2002 – 2005 *B.Sc. Mathematics and Computer Sciences*  
TEL-AVIV UNIVERSITY, Tel-Aviv, Israel

### AWARDS & SCHOLARSHIPS

- **2018-2023: NIH K99/R00 Pathway to Independence Award.**
- 2019: Travel stipend to attend the 9th ILANIT/FISEB Conference at Eilat Israel.
- 2019: Koret-Berkeley-TAU Travel scholarship.
- 2016: Travel stipend to attend the Next Gen Immunology Conference in the Weizmann institute, Israel.
- 2009-2014: Predoctoral appointment - including full tuition scholarship, stipend and full medical insurance from the Department of Biomedical Informatics, Columbia University.
- 2005-2008: Full tuition Master's degree research scholarship and stipend from the School of Computer Science, Tel-Aviv University.
- 2007: Google Global Community Scholarship for the Grace Hopper Celebration of Women in Computing.

### PUBLICATIONS

\* Equal contribution. # Corresponding author.

1. **Anat Kreimer** and Nir Yosef. Evaluation of Davis et al.: Exploring Sequence of Determinants of Transcriptional Regulation - The Case of c-AMP Response Element. *Cell Systems*. (2020) <https://doi.org/10.1016/j.cels.2020.07.001>
2. Gracie Gordon, Fumitaka Inoue, Beth Martin, Max Schubach, Vikram Agarwal, Sean Whalen, Shiyun Feng, Jingjing Zhao, Tal Ashuach, Ryan Ziffra, **Anat Kreimer**, Ilias Georgakopoulos-Soares, Nir Yosef, Chun Ye, Katherine Pollard, Martin Kircher, Jay Shendure, Nadav Ahituv. *Nature Protocols* (2020). lentiMPRA & MPRAflow for high-throughput functional characterization of gene regulatory elements. doi: 10.1038/s41596-020-0333-5
3. Ryan S Ziffra, Chang N Kim, Amy Wilfert, Tychele N Turner, Maximilian Haeussler, Alex M Casella, Pawel F Przytycki, **Anat Kreimer**, Katherine S Pollard, Seth A Ament, Evan E Eichler, Nadav Ahituv,

- Tomasz J Nowakowski. *BioRxiv* (2020). Single cell epigenomic atlas of the developing human brain and organoids.
4. Fumitaka Inoue\*, **Anat Kreimer\***, Tal Ashuach, Nadav Ahituv, Nir Yosef. *Cell Stem Cell* (2019). Identification and Massively Parallel Characterization of Regulatory Elements Driving Neural Induction. doi:<https://doi.org/10.1016/j.stem.2019.09.010>
  5. **Anat Kreimer\***<sup>#</sup>, Zhongxia Yan\*, Nadav Ahituv, Nir Yosef<sup>#</sup>. *Human Mutation* (2019). Meta-analysis of massively parallel reporter assays enables prediction of regulatory function across cell types. doi:<https://doi.org/10.1002/humu.23820> **Top performing method for predicting functional variants in disease associated regulatory elements in the Critical Assessment of Genome Interpretation (CAGI5) challenge.**
  6. Tal Ashuach\*, David Sebastian Fischer\*, **Anat Kreimer**, Nadav Ahituv, Fabian J Theis, Nir Yosef. *Genome Biology* (2019). MPRAnalyze -A statistical framework for Massively Parallel Reporter Assays. Volume 20, Article number: 183. doi:10.1186/s13059-019-1787-z
  7. Dustin Shigaki, Orit Adato, Aashish Adhikar, Shengcheng Dong, Alex Hawkins-Hooker, Fumitaka Inoue, Henry Kenlay, Beth Martin, Ayoti Patra, Dmitry Penzar, Max Schubach, Chenling Xiong, Zhongxia Yan, Alan Boyle, **Anat Kreimer**, Ivan Kulakovskiy, John Reid, Ron Unger, Nir Yosef, Jay Shendure, Nadav Ahituv, Martin Kircher, Michael A Beer. *Human Mutation* (2019). Integration of Multiple Epigenomic Marks Improves Prediction of Variant Impact in Saturation Mutagenesis Reporter Assay. doi:<https://doi.org/10.1002/humu.23797>
  8. Ann H Ryu, Walter L Eckalbar, **Anat Kreimer**, Nir Yosef, Nadav Ahituv. *Scientific Reports* (2017). Use antibiotics in cell culture with caution: genome-wide identification of antibiotic-induced changes in gene expression and regulation. Volume 7, Article number: 7533. doi:10.1038/s41598-017-07757-w
  9. **Anat Kreimer\***<sup>#</sup>, Haoyang Zeng, Matthew D Edwards, Yuchun Guo, Kevin Tian, Sunyoung Shin, Rene Welch, Michael Wainberg, Rahul Mohan, Nicholas A Sinnott-Armstrong, Yue Li, Gökçen Eraslan, Talal Bin AMIN, Jonathan Goke, Nikola S Mueller, Manolis Kellis, Anshul Kundaje, Michael A Beer, Sunduz Keles, David K Gifford, Nir Yosef<sup>#</sup>. *Human Mutation* (2017). Predicting gene expression in massively parallel reporter assays: a comparative study. doi:10.1002/humu.23197
  10. Jonathan M Carlson, Victor Y Du, Nico Pfeifer, Anju Bansal, Vincent Y F Tan, Karen Power, Chanson J Brumme, **Anat Kreimer**, Charles E DeZiel, Nicolo Fusi, Malinda Schaefer, Mark A Brockman, Jill Gilmour, Matt A Price, William Kilembe, Richard Haubrich, Mina John, Simon Mallal, Roger Shapiro, John Frater, P Richard Harrigan, Thumbi Ndung'u, Susan Allen, David Heckerman, John Sidney, Todd M Allen, Philip J R Goulder, Zabrina L Brumme, Eric Hunter and Paul A Goepfert. *Nature Medicine* (2016). Impact of pre-adapted HIV transmission. 22 (6):606–613. doi:10.1038/nm.4100
  11. Roie Levy, Rogan Carr, **Anat Kreimer**, Shiri Freilich and Elhanan Borenstein. *BMC Bioinformatics* (2015). NetCooperate: a network-based tool for inferring host-microbe and microbe-microbe cooperation. 16:164 doi:10.1186/s12859-015-0588-y.
  12. **Anat Kreimer\***<sup>#</sup> and Itsik Pe'er. *PLOS Genetics* (2014). Co-regulated transcripts associated to cooperating eSNPs define bi-fan motifs in human gene networks. doi: 10.1371/journal.pgen.1004587.
  13. **Anat Kreimer\***<sup>#</sup> and Itsik Pe'er. Variants in exons and in transcription factors affect gene expression in trans. *Genome Biology* (2013), 14:R71. doi:10.1186/gb-2013-14-7-r71
  14. **Anat Kreimer\***<sup>#</sup>, Adi Doron-Faigenboim\*, Elhanan Borenstein and Shiri Freilich<sup>#</sup>. *Bioinformatics*, (2012). NetCmpt: a network-based tool for calculating the metabolic competition between bacterial species. 28 (16):2195-2197. doi:10.1093/bioinformatics/bts323
  15. **Anat Kreimer\***<sup>#</sup>, Oren Litvin, Ke Hao, Cliona Molony, Dana Pe'er and Itsik Pe'er. *Nucleic Acids Research* (2012). Inference of modules associated to eQTLs. doi: 10.1093/nar/gks269
  16. Shiri Freilich, **Anat Kreimer**, Isacc Meilijson, Uri Gophna, Roded Sharan & Eytan Ruppin. *Nucleic Acids Research* (2010). The large scale organization of the bacterial ecological-interaction network. doi:10.1093/nar/gkq118
  17. Shiri Freilich\*, **Anat Kreimer\***, Elhanan Borenstein, Uri Gophna, Roded Sharan, and Eytan Ruppin. *PLOS Computational biology* (2010). Decoupling Environment-Dependant and Independent Genetic Robustness across Bacterial Species. Volume: 6, Issue: 2.
  18. Shiri Freilich\*, **Anat Kreimer\***, Elhanan Borenstein, Nir Yosef, Uri Gophna, Roded Sharan, and Eytan Ruppin. *Genome Biology* (2009). Metabolic-network driven analysis of bacterial ecological strategies. 10(6):R61.

19. **Anat Kreimer\***, Elhanan Borenstein\*, Uri Gophna and Eytan Ruppim. *Proceedings of the National Academy of Sciences* (2008). The Evolution of Modularity in Bacterial Metabolic Networks. Volume: 105, No. 19, Pages: 6976–6981.

### **INVITED TALKS**

- 2020: “Identification and Massively Parallel Characterization of Regulatory Elements Driving Neural Induction”. Genomics of Brain Disorders, Wellcome Genome Campus, UK.

### **CONFERENCE ORAL PRESENTATIONS**

- 2020: “Massively parallel characterization of regulatory dynamics during neural induction”. The 9th ILANIT/FISEB Conference, Eilat Israel.
- 2019: “Massively parallel characterization of regulatory dynamics during neural induction”. American Society of Human Genetics Conference, Houston, TX USA.  
**ASHG is the largest human genetics meeting in the world.**
- 2019: “Massively parallel characterization of regulatory dynamics during neural induction”. Biology of Genomes Conference, Cold Spring Harbor, NY, USA.  
**Biology of Genomes is the number one genomics meeting in the world.**
- 2018: “Massively parallel characterization of regulatory dynamics during neural induction”. RECOMB/ISCB Conference on Regulatory and Systems Genomics, NY, NY, USA.
- 2018: “MPRAnalyze: A statistical framework for massively parallel reporter assay data“. ENCODE Consortium meeting. Palo Alto, CA, USA.
- 2016: “Assessment for the eQTL causal SNPs challenge”. Critical Assessment of Genome Interpretation (CAGI 4) conference, UCSF, San Francisco, CA USA.
- 2014: “Co-regulated transcripts associated to cooperating eSNPs define bi-fan motifs in human gene networks”. European Conference of Human Genetics, Milan Italy.
- 2013: “Finding co-regulated transcripts associated to cooperating SNPs”. Human Genome Variation Conference, Seoul, South Korea.
- 2012: “Variants in Exons and in Transcription Factors Affect Gene Expression in *Trans*”. American Society of Human Genetics Conference, San Francisco, CA USA.
- 2012: “Variants in Exons and in Transcription Factors Affect Gene Expression in *Trans*”. European Conference of Human Genetics, Nuremberg Germany.
- 2011: "The influence of genetic variations on regulatory modules in the liver". European Conference of Human Genetics, Amsterdam Holland.

### **POSTER PRESENTATIONS**

- 2018: “Comprehensive characterization of neural induction-associated enhancers by massively parallel reporter assays”. Global Regulation of Gene Expression Conference, Cold Spring Harbor, NY, USA and ENCODE Consortium meeting. Palo Alto, CA, USA (**won best poster award**).
- 2018: “MPRAnalyze: A statistical framework for massively parallel reporter assay data“. ENCODE Consortium meeting. Palo Alto, CA, USA.
- 2017: “Meta-analysis of massive parallel reporter assay enables functional regulatory elements prediction”. RECOMB/ISCB Conference on Regulatory and Systems Genomics, NY, NY, USA.
- 2017: “Leveraging massive parallel reporter assays for functional regulatory elements prediction”. Global Regulation of Gene Expression Conference, Biology of Genomes Conference, Cold Spring Harbor, NY, USA.
- 2016: “Deciphering the transcriptional landscape of immunological systems”. Next Gen Immunology Conference. Weizmann institute, Israel.
- 2015: “The regulatory landscape of early neural differentiation” ISMB 2015, Dublin Ireland.
- 2014: “Co-regulated transcripts associated to cooperating eSNPs define bi-fan motifs in human gene networks” Biology of Genomes Conference, Cold Spring Harbor, NY, USA.
- 2014: “Co-regulated transcripts associated to cooperating eSNPs define bi-fan motifs in human gene networks” Global Regulation of Gene Expression Conference, Cold Spring Harbor, NY, USA.
- 2013: “Finding co-regulated transcripts associated to cooperating SNPs” American Society of Human Genetics Conference, Boston, USA.
- 2011: “Inference of modules regulated by eQTLs” American Society of Human Genetics Conference, Montreal, Canada.

- 2010: "The Influence of Genetic Variations on Regulatory Modules in the Liver" Conference on Systems Biology, Regulatory Genomics, and Reverse Engineering Challenges, New York, USA.
- 2009: "Metabolic-network driven analysis of bacterial ecological strategies" The 12<sup>th</sup> Israeli Bioinformatics Symposium. Weizmann Institute of Science, Rehovot, Israel.

### **ADDITIONAL RESEARCH EXPERIENCE**

- 2012: eScience Research Group, Microsoft Research Los Angeles CA.

### **UNIVERSITY LEVEL TEACHING EXPERIENCE**

- 2011 – 2012 *Teaching Assistant*  
Columbia University Department of Computer Science, New York, USA  
Courses: Introduction to Biomedical Informatics and Methods in Computational Biology
- 2006 – 2007 *Teaching Assistant*  
TAU School of Mathematical Sciences, Tel-Aviv, Israel  
Courses: Mathematical foundations: e.g. Linear Algebra and Calculus

### **COMMUNITY SERVICE**

- 2009 – Present: Reviewer for Journals: Nature Biotechnology, Cell Systems, The American Journal of Human Genetics, Genome Research, Genome Biology, Bioinformatics, PLoS Genetics, PLoS Computational Biology, PLoS One.
- 2002 – 2004: Prepared underprivileged students for the matriculation exams in Mathematics.
- 1999: Prepared students for the Mathematics Olympiad under a special program of Ben-Gurion University.

### **MEMBERSHIP IN PROFESSIONAL SOCIETIES**

- 2010 – 2019: American Society of Human Genetics
- 2010 – 2014: European Society of Human Genetics
- 2011 – 2019: RECOMB/ISCB/ISMB

### **EMPLOYMENT EXPERIENCE**

- 2007 – 2009 *Software Engineer*, Sun Microsystems, Israel.
- Working in Engineering Services on porting Java ME to different OS and HW platforms.
  - Developing in C and Java.
  - Advising Sun customers in porting projects.
- 2004 – 2005 *Systems Maintenance Assistant*, SAP Labs, Developers Network Department, Israel.
- Edited videos of company presentation films.
- 2002 – 2004 *Teacher*, several private institutes, Israel.
- Tutored elementary and high school students in math, science, and grammar.

### **PROGRAMMING LANGUAGES**

Python, R, Matlab, Perl, C, C++, Java, Latex.

### **LANGUAGES**

Hebrew (mother tongue), English (fluent), Russian (spoken).

### **REFERENCES CONTACT INFORMATION**

- Nir Yosef, Department of Electrical Engineering and Computer Sciences, UCB, niryosef@berkeley.edu
- Nadav Ahituv, Department of Bioengineering and Therapeutic Sciences, UCSF, nadav.ahituv@ucsf.edu
- Stephan Sanders, Department of Psychiatry, UCSF, Stephan.Sanders@ucsf.edu
- Itsik Pe'er, Department of Computer Science, Columbia University, itsik@cs.columbia.edu
- Eytan Ruppín, National Cancer Institute (NCI), NIH, eytan.ruppín@nih.gov