

Curriculum Vitae - Oren Ram
Department of Biological Chemistry.
The Hebrew University of Jerusalem, 91904, Israel

Date of birth: 21.12.75,
Country of birth: Israel
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Higher Education:

- 2009 - 2015 Postdoctoral fellow.
Harvard Medical School and Broad Institute, Cambridge, MA, USA.
Prof. Bradley Bernstein.
Studying the combinatorial patterning of chromatin regulators
(i) Applying genome-wide location analysis (ChIP-seq) of chromatin regulators.
(ii) Developing a technology that will allow interrogating of both chromatin and RNA in single cells.
- 2003-2009 Direct track Ph.D.
Human Molecular Genetics and Biochemistry, Tel Aviv University, Israel.
Prof. Gil Ast.
My work focused on understanding the splicing mechanism leads to Alu exonization.
- 2000-2003 B.Sc. in Biology.
Tel Aviv University, Tel Aviv, Israel.

Appointments at the Hebrew University:

- October 2021 - Associate Professor. The Hebrew university of Jerusalem. Department of Biological Chemistry.
- October 2015 - Senior lecturer. The Hebrew university of Jerusalem. Department of Biological Chemistry.

Additional Functions/Tasks at the Hebrew University:

- 2021– 2022 Panel member: Israel Science Foundation (ISF). Molecular biology review committee.
- 2020– 2021 Amirim coordinator: The Hebrew University special program for outstanding students.
- 2019– 2020 Panel member: US-Israel Binational Science Foundation (BSF). Molecular biology and Genomic Research review committee.
- 2019– 2020 ISF young forum for biotechnology.
- 2016– 2019 Organizer of the Biological Chemistry departmental Seminar Series, Hebrew University of Jerusalem, Israel.
- 2018– Present The head of Wolfson Single Cell (SCA) Research Lab in the Hebrew University.
- 2021– Present Head committee of Life Sciences SMART prize.
- 2018– Present Committee member of Life Sciences SMART prize.

Service in other Academic and Research Institutions: NA

Other Activity:**Awards:**

2016-2017	Recipient of Golda Meir Fellowship.
2015-2017	Azrieli foundation, Faculty fellow award.
2009-2011	European molecular biology Organization (EMBO), long term fellowship for postdoctoral fellows.
2005	Joan and Jaime Constantiner Institute for Molecular Genetics Travel Scholarship.

Previous employments:

2021-2022	Consulting for Transition Bio Company. Their goal is to build a hypothesis-free drug discovery and diagnostics platform for human health care advancement and modern medicine based on droplet technology and biomolecular condensates.
2013-2014	Consulting for HiFiBiO Company. Based on our “microfluidics and epigenetic sequencing” patent, this company set up to develop application and commercialization of droplet microfluidic technology and related assay technologies for drug discovery and development.
1997-2003	Department of defense, airline security division (Air marshal).
1994-1997	Served in the Israel Defense Forces (Staff sergeant).

Research Grants:

- Azrieli foundation (Faculty fellow award) 9/2015-9/2017

Regulation and heterogeneity of epigenomic states in human cellular differentiation.

The goal is to study the role of heterogeneity and chromatin regulation in differentiation leveraging state-of-the-art microfluidics system for mapping chromatin at single cell resolution.

Role: Principal Investigator. \$210,000 (Annual direct: \$70,000)
- I-Core (RNA and Chromatin Gene Regulations) 7/2015-7/2019

Regulation and heterogeneity of epigenetic states in cancer.

The goal is to understand the epigenetic regulatory mechanisms and subpopulation structures underlying patient derived cancer cells.

Role: Principal Investigator. \$400,000 (Annual direct: \$80,000)
- Israel Science Foundation (ISF: Individual Research Grant) Ram (PI) 6/2016-6/2018

Regulation and heterogeneity of epigenomic states in neural cell differentiation.

The goal is to study chromatin regulation during neuronal induction.

Role: Principal Investigator. \$175,000 (Annual direct: \$55,000)
- ERC starting grant- SC-EpiCode 10/2017-10/2022

Decoding the epigenomic regulatory code by the use of single cell technologies.

The goal is to establish innovative technology for the studying of epigenomics.

Role: Principal Investigator. \$1,650,000 (Annual direct: \$330,000)
- Establishment of Single cell Research Labs in Israel by the Wolfson Foundation and Wolfson Family Charitable Trust

Role: Leader of the Single Cell group.
- MSCA ITN – a member at the EpiSystem project 3/2018-3/2021

Role: Principal Investigator. Covers PhD cost for three years.

7. Nofar-Israel innovation 5/2019-5/2020
Developing single-cell full-length transcriptional profiling.
Role: Co-Principal Investigator. Total of \$170,000 and \$85,000 to my lab (Annual direct: \$42,500)
8. Israel Science Foundation (ISF: Individual Research Grant) Ram (PI) 6/2019-6/2024
Cellular heterogeneity - study the impact of clonal cell origin on cell state determination.
Role: Principal Investigator. \$450,000 (Annual direct: \$90,000)
9. The ministry of science technology and space Harel and Ram (PIs) 1/2021-1/2024
Fish 'n' ChIP: Identifying spatiotemporal dynamics of vertebrate senescence in-vivo
Role: Co-Principal Investigator. Total of \$366,000 and \$183,000 to my lab (Annual direct: \$91,500)
10. ERC consolidator grant – CancerInDept.
Pre-decisional: Past to the interview stage B2 (25/01/2022)
Deciphering Cancer Clonal Heterogeneity using Single-Cell, Full-Length Profiling of Driver Mutation Landscapes.

Teaching at the Hebrew University:

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| 2020– 2021 | “Workshop for Amirim students” 76246, the Hebrew University of Jerusalem. |
| 2018– Present | “MSC joint seminar” 86840, the Hebrew University of Jerusalem. |
| 2016– Present | “Introduction to Molecular Biology” 72332, the Hebrew University of Jerusalem. |
| 2017 | “Advanced lab for ETGAR students” 72517, the Hebrew University of Jerusalem. |
| 2017– 2019 | “Selected topics in biochemistry” 92602, the Hebrew University of Jerusalem. |

List of publications:**Impact and Scholarly Contributions (08.11.21)**

27 publications in peer-reviewed journals with 10636 without self-citations (9531 cites is for article #9) according to ISI with h-index of 15. My h-index according to Google Scholar is 20.

Book Chapters:**Since joining HUJI:**

1. **Kozulin C^S and Ram O^{PI}**. *Single cell technological advancements*. Chapter in **Stem Cell Epigenetics**, Elsevier, Inc. 2020.

Review Articles:

1. **Ram O^S and Ast G^{PI}**. *SR proteins: a foot on the exon before the transition from intron to exon definition*. Review article **Trends Genet.** 2007. Impact factor: 9.729. #Cit=35.

Articles:

1. Goren A^{*S}, **Ram O^{*S}**, Amit M^S, Keren H^S, Lev-Maor G^{RA}, Vig I^{LM}, Pupko T^{PI} and Ast G^{PI}. *Comparative analysis identifies exonic splicing regulatory sequences - The complex definition of enhancers and silencers*. **Mol Cell.** 2006. Impact factor: 14.033. #Cit=237.
2. **Ram O^S**, Schwartz S^S and Ast G^{PI}. *Multifactorial interplay controls the splicing profile of Alu derived exons*. **Mol Cell Biol.** 2008. Impact factor: 5.942. #Cit=28.
3. Lev-Maor G^{*RA}, **Ram O^{*S}**, Kim E^S, Sela N^S, Goren A^S and Ast G^{PI}. *Intronic Alus influence alternative splicing*. **PLoS Genet.** 2008. Impact factor: 8.883. #Cit=102.

4. Gal-Mark N^S, Schwartz S^S, **Ram O^S**, Eyraş E^{CoPI}, Ast G^{PI}. *The pivotal roles of TIA proteins in 5' splice site selection of Alu exons and across evolution.* **PLoS Genet.** 2009. Impact factor: 9.532. #Cit=28.
5. Goren A^S, Kim E^S, Amit M^S, Vaknin K^S, Kfir N^S, **Ram O^S** and Ast G^{PI}. *Overlapping splicing regulatory motifs-combinatorial effects on splicing.* **Nucleic Acids Res.** 38(10):3318-27. 2010. Impact factor: 7.836. #Cit=11.
6. Schwartz S^{*S}, **Ram O^{*S}** and Ast G^{PI}. *Detection and removal of biases in the analysis of next-generation sequencing reads.* **PLoS One.** 2011. Impact factor: 4.092. #Cit=82.
7. **Ram O^{PD}**, Goren A^{PD}, Amit I^{PD}, Shores N^{RA}, Yosef N^{PD}, Ernst J^{PD}, Kellis M^{CoPI}, Gymrek M^S, Issner R^T, Coyne M^S, Durham T^S, Zhang X^S, Donaghey J^S, Epstein C.B^{RA}, Regev A^{PI} and Bernstein BE^{PI}. *Combinatorial patterning of chromatin regulators uncovered by genome-wide location analysis in human cells.* **Cell.** 2011. Impact factor: 32.403. #Cit=240.
8. Garber M^{PI}, Yosef N^{PD}, Goren A^{PD}, Raychowdhury R^S, Thielke A^S, Guttman M^{PD}, Robinson J^{PD}, Minie B^S, Chevrier N^S, Itzhaki Z^S, Blecher-Gonen R^S, Bornstein C^S, Amann-Zalcenstein D^S, Weiner A^S, Friedrich D^S, Meldrim J^{PD}, **Ram O^{PD}**, Cheng C^S, Gnirke A^{RA}, Fisher S^{PD}, Friedman N^{CoPI}, Wong B^{CoPI}, Bernstein BE^{CoPI}, Nusbaum C^{CoPI}, Hacohen N^{CoPI}, Regev A^{CoPI}, Amit I^{PI}. *A high-throughput chromatin immunoprecipitation approach reveals principles of dynamic gene regulation in mammals.* **Mol Cell.** 2012. Impact factor: 15.280. #Cit=260.
9. ENCODE Project Consortium, Dunham I^{PD}, Kundaje A^{PD}, Aldred SF^{PD}, ..., **Ram O^{PD}**, ..., Bernstein BE^{CoPI}, ..., Birney E^{PI}. *An integrated encyclopedia of DNA elements in the human genome.* **Nature.** 2012. Impact factor: 38.597. #Cit=11914.
10. Sebastián C^{PD}, Zwaans BM^{PD}, Silberman DM^{PD}, Gymrek M^S, Goren A^{PD}, Zhong L^S, **Ram O^{PD}**, Truelove J^S, Guimaraes AR^S, Toiber D^{PD}, Cosentino C^{PD}, Greenson JK^{PD}, MacDonald AI^{PD}, McGlynn L^{PD}, Maxwell F^{PD}, Edwards J^{PD}, Giacosa S^{PD}, Guccione E^{PD}, Weissleder R^{PD}, Bernstein BE^{CoPI}, Regev A^{CoPI}, Shiels PG^{CoPI}, Lombard DB^{PI}, Mostoslavsky R^{PI}. *The histone deacetylase SIRT6 is a tumor suppressor that controls cancer metabolism.* **Cell.** 2012. Impact factor: 31.957. #Cit=440.
11. Mendenhall EM^{PD}, W.K., Reyon D^S, Zou JY^S, **Ram O^{PD}**, Joung J^{PD}, Bernstein BE^{PI}, *Locus-specific editing of histone modifications at endogenous enhancers.* **Nat Biotechnol.** 2013. Impact factor: 39.080. #Cit=257.
12. Rotem A^{*PD}, **Ram O^{*PD}**, Sperling, RA^{PD}, Schnall-Levin Michael^{PD}, Shores N^{RA}, Zhang, H^{PD}, Basu, A^{PD}, Bernstein, BE^{PI}, and Weitz, DA^{PI}. *High-Throughput Single Cell Labeling (Hi-SCL) for RNA-Seq using drop-based microfluidics.* **PLoS One.** 2015. Impact factor: 3.057. #Cit=47.
13. Galen V P^{PD}, Viny AD^{PD}, **Ram O^{PD}**, Ryan J H R^{PD}, Cotton J M^T, Donohue L^S, Sievers C^{PD}, Drier Y^{PD}, Gillespie M S^T, Bernstein EB^{PI}. *A multiplexed system for quantitative comparisons of chromatin landscapes.* **Mol Cell.** 2015. Impact factor: 13.958. #Cit=56.
14. Rotem A^{*PD}, **Ram O^{*PD}**, Shores N^{*RA}, Sperling R^{PD}, A Goren^{PD}, Weitz AD^{PI} and Bernstein EB^{PI}. *Single-cell ChIP-seq reveals cell subpopulations defined by chromatin state.* **Nat Biotechnol.** 2015. Impact factor: 43.113. #Cit=420.
15. Yaacoby ES^{PD}, Jones D^{PD}, Shores N^{RA}, Donohue Laura^{PD}, **Ram O^{PD}**, Bernstein EB^{PI}. *Single-Molecule Decoding of Combinatorially Modified Nucleosomes.* **Science.** 2016. Impact factor: 37.205. #Cit=62.

Since joining HUJI:

16. Gutin J^S, Sadeh R^{RA}, Bodenheimer N^S, Strauss D^S, Klein-Brill A^S, Alajem A^{LM}, **Ram O^{CoPI}**, Friedman N^{PI}. *Fine-Resolution Mapping of TF Binding and Chromatin Interactions*. **Cell Rep**. 2018. Impact factor: 7.815. #Cit=19.

I advised on several aspects of the chromatin and sequencing and supervised Alajem A, my lab manager, during ChIP-seq experiments on mouse embryonic stem cells. Finally, I took a part in the writing process.

17. Diab A. M^S, Mor-Shaked H^S, Cohen E^S, Cohen-Hadad Y^S, **Ram O^{CoPI}**, Epsztejn-Litman S^S and Eiges R^{PI}. *The G-rich Repeats in FMR1 and C9orf72 Loci Are Hotspots for Local Unpairing of DNA*. **Genetics**. 2018. Impact factor: 3.564. #Cit=12.

I advised and processed the computational side of this project.

18. Benchetrit H^S, Jaber M^S, Zayat V^S, Sebban S^S, Pushett A^S, Makedonski K^S, Zakheim Z^S, Radwan A^S, Maoz N^{PD}, Lasry R^S, Renous N^S, Inbar M^S, **Ram O^{CoPI}**, Kaplan T^{CoPI}, Buganim Y^{PI}. *Direct Induction of the Three Pre-implantation Blastocyst Cell Types from Fibroblasts*. **Cell Stem Cell**. 2019. Impact factor: 20.860. #Cit=18.

My lab produced Histone marks and Esrrb ChIP-seq maps for this project. We were involved in the computational analysis of ChIP-seq maps. Finally I took a part in the writing process.

19. Goldshtein M^S, Mellul M^S, Deutch G^S, Imashimizu M^S, Takeuchi K^{CoPI}, Meshorer E^{CoPI}, **Ram O^{*}**^{PI}, Lukatsky DB^{*PI}. *Transcription Factor Binding in Embryonic Stem Cells Is Constrained by DNA Sequence Repeat Symmetry*. **Biophys J**. 2020. Impact factor: 4.033. #Cit=2.

My lab did the experimental work on this project. Based on a close and ongoing collaboration between the labs, Prof Lukatsky and I were both devised the biological and computational questions, instruct the students and wrote the manuscript. Our cover illustration was selected.

20. Tayri-Wilk T^S, Slavin M^S, Zamel J^S, Blass A^S, Cohen S^S, Motzik A^{PD}, Sun X^S, E Shalev D^S, **Ram O^{CoPI}**, Kalisman N^{PI}. *Mass spectrometry reveals the chemistry of formaldehyde cross-linking in structured proteins*. **Nat Commun**. 2020. Impact factor: 14.919. #Cit=14.

I have instructed Xue Sun, a PhD student in my lab, to be responsible for the tissue culturing needed for this project.

21. Aramin S^S, Fassler R^S, Chikne A^S, Goldenberg M^S, Arian T^S, Eliaz K.L^S, Rimon O, ^S **Ram O^{CoPI}**, Michaeli S^{CoPI}, Reichmann D^{PI}. *TrypOx, a Novel Eukaryotic Homolog of the Redox-Regulated Chaperone Hsp33 in Trypanosoma brucei*. **Front. Microbiol**. 2020. Impact factor: 5.640. #Cit=1.

I advised and processed some of the computational analysis of this project. Specifically, I analyzed genomic sequencing data to build bacteria dendrogram that allows evolutionary reconstruction of Chaperone Hsp33.

22. Alajem A^{LM}, Roth H^S, Ratgauzer S^S, Bavli D^{PD}, Motzik A^{PD}, Lahav S^S, Peled I^S, **Ram O^{PI}**. *DNA Methylation Patterns Expose Variations in Enhancer-Chromatin Modifications during Embryonic Stem Cell Differentiation*. **BioRxiv**: doi: <https://doi.org/10.1101/2020.11.25.39728>. **PLoS Genet**. 2021. Impact factor: 5.917. #Cit=1.

23. Brielle S^S, Bavli D^{PD}, Sun X^S, Kozulin C^S, Motzik A^{PD}, Kan-Tor Y^S, Avni B^{CoPI}, **Ram O^{*PI}**, Buxboim A^{*PI}. *Tropomyosin mediates matrix-directed differentiation of distinctive subpopulations of primary mesenchymal stem cells*. **BioRxiv**: <https://doi.org/10.1101/2020.11.23.394460>. **PNAS**. 2021. Impact factor: 11.205. #Cit=NA.

My lab was responsible for all of the single cell RNA-seq experiments in this project. I supervised the single cell RNA-seq computational analysis. Dr. Buxboim and I, devised the experimental approach, biological questions and the writing process.

24. Bavli D^{PD}, Sun X^S, Kozulin C^S, Ennis D^S, Motzik A^{PD}, Biran A^{PD}, Brielle S^S, Alajem A^{LB}, Meshorer E^{CoPI}, Buxboim A^{*PI}, **Ram O^{*PI}**. *CloneSeq: A Highly Sensitive Single-cell Analysis Platform for Comprehensive Characterization of Cells from 3D Culture*. **BioRxiv**:

- <https://doi.org/10.1101/2020.11.24.395541>. **Dev Cell**. 2021. Impact factor: 12.270. #Cit=NA. Our cover illustration was selected.
25. Rappaport Y^S, Achache H^{LM}, Falk R^S, Murik O^S, **Ram O**^{CoPI}, Tzur BY^{PI}. *Chromosome Integrity is required for the Initiation of Meiotic Sex Chromosome Inactivation in Caenorhabditis elegans*. **BioRxiv**: <https://doi.org/10.1101/2020.11.05.369132>. **Nat Commun**. 2021. Impact factor: 14.919. #Cit=NA. My lab was responsible for RNA-seq experiments and RNA-seq computational analysis.
 26. Masalha M^S, Ben-Dov I^S, **Ram O**^{CoPI}, Meninger T^S, Jacob-Hirsch J^S, Kassem R^S, Sidi Y^{PI}, Avni D^{PI}. *H3K27Ac modification and gene expression in psoriasis*. **Journal of Dermatological Science**. 2021. Impact factor: 4.563. #Cit=NA. My lab was responsible for ChIP-seq experiments and I supervised the ChIP-seq computational analysis.
 27. Sun X^{*S}, Bavli D^{*PD}, Kozulin C^{*S}, Motzik A^{PD}, Buxboim A^{CoPI}, **Ram O**^{*PI}. *CloneSeq - single-cell clonal 3D culture and analysis protocol*. **STAR protocols**. 2021. Impact factor: NA. #Cit=NA.
 28. Herchcovici LS^{*S}, Feldman S^{*S}, Arnon L^{*S}, Alajem A^{LM}, Bavli D^{PD}, Sun X^S, Buganim Y^{CoPI}, Ram O^{PI}. *Esrrb is a cell cycle dependent associated factor balancing between pluripotency and XEN differentiation*. **BioRxiv**: <https://www.biorxiv.org/content/10.1101/2020.08.03.234112v2.full.pdf>. **Stem Cell Rep**. 2021. Impact factor: 7.765. #Cit=NA.
 29. Meir Mellul^{*S}, Shlomit Zion Lahav^{*S}, David B. Lukatsky^{PI}, Oren Ram^{PI}. *DNA repeats apply negative design on gene expression in embryonic stem cells*. **Biophys J**. 2022. Impact factor: 4.033. #Cit=NA.

Participation in Scientific Conferences, Lectures, and Other Activity:

1. International Society for Stem Cell Research. ISSCR, March 28-31, Israel. 2022.
2. Microfluidics Solutions for Single-Cell Analysis & Sorting. Online conference. April 20-21, 2021.
3. Minerva-Gentner Symposium 2020, Single Cell Analysis: from Development to Disease. Israel 2020.
4. ICORE conference. Israel 2019.
5. Spring Hippocampal Research Conference. Taormina, Sicily. 2019.
6. 8th International Conference on Medical Education and Health Sciences. October 08-09, 2018. Osaka, Japan.
7. Istanbul Bioinformatics Workshop 2018.
8. Spetses Summer School on Chromatin and Metabolism 2018.
9. Genomics Symposium - One Cell at a Time. October 22, 2017. Tel Aviv University med-school, Tel Aviv, Israel.
10. HUJI Nano center annual conference. July 2, 2017. Dead Sea. Israel
11. ILANT 2017 FISEB. February 22, 2017. Eilat, Israel.
12. The 2nd genomics workshop of the center for Evolutionary genomics and medicine at BGU. December 13, 2016. Be'er Sheba, Israel.
13. Genetics Society of Israel Meeting. January 25, 2016. Jerusalem, Israel.
14. EMBO US Fellows Meeting. November 6, 2014. Salk Institute, La Jolla, USA.
15. Single Cell Genomics. October 1, 2013. Weizmann institute, Rehovot, Israel.
16. Boston Single-Cell Network symposium. September 17, 2013, Harvard med-school, Boston, USA.
17. Mapping chromatin in single cells with microfluidics. First annual Broad-Israel cell circuits symposium. June 21-23, 2013, Jerusalem, Israel.
18. Systematic screening of antibodies for 145 chromatin regulators by ChIP-string. Broad retreat, November 7-8, 2011, Boston, USA.
19. Combinatorial patterning of chromatin regulators uncovered by genome-wide location analysis in human cells. ENCODE and modENCODE Consortia Meeting, May 23-25, 2011, Washington DC, USA.

Patents:

- 2012 Methods for chromatin immuno-precipitations,
WO2012047726A1,
Inventors: Amit I^{PD}, Goren A^{PD}, **Ram O^{PD}**, Garber M^{RA}, Shores N^{RA}, Bernstein
BE^{PI}, Regev A^{PI}.
- 2016 Methods for Shearing and Tagging DNA for Chromatin Immunoprecipitation and
Sequencing,
US 2016/0208323 A1,
Inventors: Goren A^{PD}, **Ram O^{PD}**, Rotem A^{PD}, Tarjan D^S, XING J^S, Clarksville
MD^S, Nusbaum C^{PI}, Bernstein BE^{PI}, Weitz DA^{PI}, Regev A^{PI}.
- 2019 Methods for epigenetic sequencing,
EP 2 823 064 B1,
Inventors: Rotem A^{PD}, **Ram O^{PD}**, Bernstein BE^{PI}, Weitz DA^{PI}
- 2020 CloneSeq: 3D cell growing and Clone-level sequencing methods,
US provisional application,
Inventors: Bavli D^{PD}, Motzik A^{PD}, Buxboim A^{PI}, **Ram O^{PI}**.