

**Appointments**

- 2022-present **Bar-Ilan University**  
Associate Professor at the Department of Computer Science and Faculty of Life Sciences
- 2017-2022 **Ben-Gurion University of the Negev**  
Senior Lecturer at the School of Electrical and Computer Engineering
- 2014-2017 **Massachusetts Institute of Technology**  
Post-doctoral researcher in Computer Science. Advisor: Prof. Bonnie Berger  
Research: Computational modeling of protein-RNA interactions
- 2016 **University of California Berkeley**  
Research fellow, Simons Institute for the Theory of Computing

**Education**

- 2010-2014 **Tel-Aviv University**  
PhD in Computer Science. GPA: 96.7  
Thesis: Discovering Motifs Using High-Throughput in Vitro Data. Advisor: Prof. Ron Shamir
- 2007-2010 **Tel-Aviv University**  
MSc in Electrical Engineering. Summa Cum Laude. GPA: 95.87  
Thesis: Property Testing in Directed Graphs. Advisor: Prof. Dana Ron
- 2004-2008 **Tel-Aviv University**  
BSc in Electrical Engineering and Computer Science. Summa Cum Laude. GPA: 96.37

**Awards and Fellowships**

- 2025 Rector's award for scientific innovation
- 2018 Excellent teacher in Electrical and Computer Engineering
- 2017 Top 10 papers reading list in Regulatory and Systems Genomics
- 2017 RECOMB travel fellowship
- 2017 ILANIT/FISEB conference travel fellowship
- 2016 ISMB best paper award
- 2013, 2016 ISMB travel fellowship
- 2016 The Simons Institute for the Theory of Computing research fellowship
- 2014 Deutsch Prize for excellence in PhD research
- 2014 Best poster award, Edmond J. Safra Bioinformatics Retreat
- 2012-2014 In each year, enlisted among the top 100 teaching assistants at TAU
- 2010-2014 In each year, Safra fellowship for Ph.D. students in bioinformatics at TAU
- 2013 I-CORE: Israeli Center of Research Excellence fellowship
- 2012 Dan David fellowship for excellent research in the field of Genomics
- 2012 Excellent teaching assistant in Computer Science
- 2011 Best performer, DREAM 6 AML Patient Classification Challenge
- 2010 Best performer, DREAM 5 DNA-Motif Recognition Challenge
- 2009 Academic Excellence Award commemorating fallen Israeli soldiers, Engineering (M.Sc.)
- 2009 Wolf Foundation award for excellent M.Sc. research
- 2004-2008 The Adi Lautman Program for Outstanding Students, fellowship
- 2004-2008 Dean's list of excellent students in Engineering in all four years of B.Sc. studies
- 2004-2008 Dean's list of excellent students in Computer Science in each eligible year of B.Sc. studies
- 2007 Academic Excellence Award commemorating fallen Israeli soldiers, Computer Science (B.Sc.)
- 2007 Cisco Award for excellent students in Computer Science

## Grants

|           |                                                                                          |
|-----------|------------------------------------------------------------------------------------------|
| 2026-2030 | 264,000\$ United States-Israel Binational Science Foundation (BSF) (co-PI: S. Aviran)    |
| 2025-2027 | 67,000\$ Directorate of Defense Research & Development (MAFAT)                           |
| 2025-2027 | 140,000\$ Israel Ministry of Innovation, Science, and Technology (MOST) (co-PI: R. Amit) |
| 2024-2025 | 50,000\$ Israel Cancer Association (ICA)                                                 |
| 2023-2026 | 250,000\$ Helmholtz AI Project (co-PIs: F. Biedermann, P. Carloni)                       |
| 2022-2026 | 860,000\$ National Institute of Health (NIH) (co-PIs: E. Radisky, N. Papo, T. Caulfield) |
| 2022-2024 | 425,000\$ Israel Innovation Authority (IIA) (co-PI: R. Amit)                             |
| 2021-2025 | 337,000\$ Israel Science Foundation (ISF)                                                |
| 2021-2023 | 75,000\$ United States-Israel Binational Science Foundation (BSF) (co-PI: B. Berger)     |
| 2021-2022 | 22,500\$ Israel Cancer Association (ICA)                                                 |
| 2020-2023 | 290,000\$ Israel Innovation Authority (IIA) (CRISPRIL consortium)                        |

## Local Support

|           |                                                                                                 |
|-----------|-------------------------------------------------------------------------------------------------|
| 2026      | 20,000\$ BIU AI Convergence (co-PI: Z. Bar-Joseph)                                              |
| 2022      | 25,725\$ Israeli Council for Higher Education via Data Science Research Center, BGU             |
| 2021      | 12,000\$ BGU-NJIT seed grant (co-PI: Z. Wei)                                                    |
| 2021      | 9,350\$ Israeli Council for Higher Education via Data Science Research Center, BGU              |
| 2021      | 3,100\$ Israeli Council for Higher Education via Data Science Research Center, BGU              |
| 2021      | 27,300\$ Israeli Council for Higher Education via Data Science Research Center, BGU             |
| 2020-2021 | 20,000\$ MIT-Israel BGU Seed Fund (co-PI: B. Berger)                                            |
| 2020      | 14,670\$ Israeli Council for Higher Education via Data Science Research Center, BGU             |
| 2019      | 6,000\$ Engineering at BGU research support                                                     |
| 2019      | 20,000\$ Neuroscience at BGU collaboration grant (co-PI: R. Birnbaum)                           |
| 2019      | 20,000\$ Health-Engineering at BGU collaboration grant (co-PI: D. Levy)                         |
| 2019      | 4,000\$ Life Sciences at BGU multidisciplinary grant (co-PI: R. Birnbaum)                       |
| 2018      | 20,000\$ from Augmanity Nano Ltd. for consulting on computational analysis of SELEX data        |
| 2018      | 1,000\$ and computational resources from Intel Ltd. for teaching deep learning in comp. biology |

## Students

|                  |                                         |          |              |                                    |
|------------------|-----------------------------------------|----------|--------------|------------------------------------|
| MSc 2025-Present | Yehuda Dicker                           | PhD      | 2026-Present | Shay Sirek                         |
| 2025-Present     | Evyatar Komarovsky                      |          | 2023-Present | Noam Shimshoviz                    |
| 2023-2025        | Danielle Levy                           |          | 2023-Present | Ido Tziony (with MSc)              |
| 2023-2025        | Hagar Chen                              |          | 2023-Present | Jonathan Mandl (with MSc)          |
| 2023-2025        | Alon Luboshitz                          |          | 2023-Present | Reut Moshe                         |
| 2022-2024        | Karin Elimelech                         |          | 2020-2025    | Ofir Yaish (with MSc)              |
| 2022-2024        | Michal Rahimi                           |          |              |                                    |
| 2020-2023        | Reut Mosh (with Prof. Niv Papo)         | Visitors | 2023         | Marcus Bluestone, MIT              |
| 2020-2023        | Ori Feldman                             |          | 2023         | Joshua Brafman, Yeshiva University |
| 2020-2022        | Maor Turner                             |          | 2022         | Paul Schwerde-Klein, DKFZ          |
| 2019-2022        | Shai Elkayam                            |          | 2021         | Stephan Sinn, KIT                  |
| 2019-2022        | Sofia Aizenshtein                       |          | 2021         | Evelyn Peters, MIT                 |
| 2019-2021        | Maor Asif                               |          | 2020         | Alice Aubert, Polytechnique        |
| 2018-2021        | Yael Ben-Ari (with Prof. Ron Shamir)    |          | 2019         | Baris Ekim, MIT                    |
| 2018-2021        | Mira Barshai                            |          | 2019         | Tyler Shimko, Stanford             |
| 2018-2021        | Shaked Naor (with Prof. Michal Ziv)     |          |              |                                    |
| 2018-2020        | Eitamar Tripto (with Dr. Ilana Nisky)   |          |              |                                    |
| 2018-2020        | Yifat Dar (with Dr. Kobi Cohen)         |          |              |                                    |
| 2018-2020        | Yahel Salomon (with Dr. Ramon Birnbaum) |          |              |                                    |
| 2018-2019        | Ilia Golan                              |          |              |                                    |
| 2014-2018        | Maro Dan (with Prof. Ron Shamir)        |          |              |                                    |

## **Journal Reviews**

Bioinformatics, Briefings in Functional Genomics, Briefings in Bioinformatics, Nucleic Acids Research, PLoS Computational Biology, Frontiers in Genetics, Nature Biotechnology, Genome Biology, BMC Bioinformatics, IEEE Transactions on Computational Biology and Bioinformatics, Protein Science, RNA Biology, BMC Genomics, Journal of Computational Biology

## **Grant Reviews**

Israel Science Foundation (ISF), United States-Israel Binational Science Foundation (BSF), French National Research Agency – ANR, Biotechnology and Biological Science Research Council (BBSRC)

## **Program Committees**

2021-present Machine Learning in Computational Biology (MLCB)  
2021-present International Conference on Research in Computational Molecular Biology (RECOMB)  
2020-present Intelligent Systems for Molecular Biology (ISMB)  
2019-present European Conference on Computational Biology (ECCB)

## **Conference Reviews**

2017-present International Conference on Research in Computational Molecular Biology (RECOMB)  
2017-present Intelligent Systems for Molecular Biology (ISMB)

## **Review Editor**

2018-Present Frontiers in Genetics

## **Conference Organization**

2027 Israeli Bioinformatics Symposium, BIU – chair  
2026 MIND-IL Conference on Computational Biology, WIS – co-organizer  
2025 RECOMB-seq, Seoul – co-organizer  
2023 BIU Bioinformatics Day, BIU – co-organizer  
2022 RECOMB, San-Diego – poster track chair  
2022 AI and Big Data in Health and Medical Sciences, BGU – co-organizer

## **Teaching**

2023-present Lecturer, course on Algorithms for Computer Science students  
2018-present Lecturer, course on Deep Learning in Computational Biology  
2017-2022 Lecturer, course on Computer Architecture for Electrical and Computer Engineering students  
2011-2014 TA, courses on Computational Genomics for Computer Science students  
2010-2014 TA, courses on Data Structures for Computer Science students  
2010, 2013 TA, workshop in bioinformatics for Computer Science students  
2007-2010 TA, courses on Data Structures and Algorithms for Electrical Engineering students

## **Professional Experience**

2021 Bioinformatics consultant, BiomX, Israel  
2017 Bioinformatics consultant, Augmanity Nano, Israel  
2007-2010 Student position in IBM Haifa Research Labs, Israel  
2006-2007 Student position in wide-band firm-ware group, Intel Labs, Israel  
1999-2004 Worked in a technological unit of the Intelligence Corps, Israeli Defense Force

## **Academic Service**

2024-present Hiring Committee, Computer Science, BIU  
2022-present Admission, Hosting, Electronic Assets Committees, Life Sciences, BIU  
2018-2022 Newsletter, Seminar, Electronic Assets Committees, Electrical Engineering, BGU

**Journal Publications** [\* equal contribution, ^ equal correspondence]

1. A. Luboshitz\*, M. Rahimi\*, A. Hendel and **Y. Orenstein** (2026) EpiCRISPR: Improving CRISPR/Cas9 on- and off-target prediction by flanking sequences, epigenetic marks, and high-throughput datasets. To appear in *IEEE Transaction of Computational Biology and Bioinformatics*.
2. J. Mandl, M. Bluestone, S. Longwell, P. Fordyce and **Y. Orenstein** (2026) PrimerDesigner: Designing efficient primers for synthesizing large protein libraries without cross-hybridization. To appear in *Journal of Computational Biology*.
3. J. Mandl and **Y. Orenstein** (2026) ExoShorkie: Predicting RNA-seq coverage of exogenous genomes in yeast by transfer learning. *Bioinformatics* 42(Supplement\_2):bttag369
4. R. Meiri\*, O. Reuveni\*, M. Levi\*, E.S. Radisky^, N. Papo^ and **Y. Orenstein**^ (2026) Engineering selective amyloid precursor protein inhibitors by machine learning and deep mutational scanning. *Protein Science* 35(8):e70712
5. N. Tzuri, I. Kass, **Y. Orenstein**^ and N. Papo^ (2026) Machine-learning prediction of affinity and epistasis in the bovine pancreatic trypsin inhibitor–chymotrypsin complex. *Protein Science* 35(7):e70660
6. N. Shimshoviz, S. Butto and **Y. Orenstein** (2026) NBPBP: predicting binding preferences of uncharacterized nucleic-acid-binding proteins. *Bioinformatics* 42(Supplement\_1):bttag232
7. I. Tziony and **Y. Orenstein** (2026) CROP: a feature-independent context-aware method for CRISPR-Cas9 frameshift prediction. *Bioinformatics* 42(Supplement\_1):bttag210
8. D.S. Gozlan\*, R. Meiri\*, G. Shapira\*, M. Coban, E. Radisky^, **Y. Orenstein**^ and N. Papo^ (2026) Modifying inhibitor specificity for homologous enzymes by machine learning. *The FEBS Journal* febs.70249
9. S. Golan\*, I. Tziony\*, M. Kraus, **Y. Orenstein**^ and A. Shur^ (2025) GreedyMini: Generating low-density DNA minimizers. *Bioinformatics* 41(Supplemental\_1):i275-i284
10. O. Mizrahi, M. Corley, O. Feldman, T. Fröhlking, L. Sun, A. Ziesel, M. Antczak, M. Bernetti, S.I. Elhajjajy, W. Huang, G.G. Nguyen, S.S. Park, R.I. Perez Martell, L. Trinity, K. Xu, T. Zok, G. Bussi, H. Jabbari, **Y. Orenstein**, S. Aviran, M.M. Meyer and G. Yeo (2025) Evaluation of novel computational methods to identify RNA-binding protein footprints from structural data. *RNA* 31(8):1103-1124
11. S. Katchkovsky, R. Moshe, S. Lacham-Hartman, **Y. Orenstein**, N. Levaot and N. Papo (2025) Mapping the sclerostin-LRP4 binding interface: Identifying critical interaction hotspots in loops 1 and 3 of sclerostin. *FEBS Letters* 599(3):316-329. **Cover page.**
12. R. Meiri\*, S.L.A. Lotati\*, **Y. Orenstein**^ and N. Papo^ (2024) Deep neural networks for predicting the affinity landscape of protein-protein interactions. *iScience* 27(9)
13. S. Elkayam\*, I. Tziony\* and **Y. Orenstein** (2024) DeepCRISTL: deep transfer learning to predict CRISPR/Cas9 on-target editing efficiency in specific cellular contexts. *Bioinformatics* 40(8)
14. O. Yaish and **Y. Orenstein** (2024) Generating, modeling and evaluating a large-scale set of CRISPR/Cas9 off-target sites with bulges. *Nucleic Acids Research* gkae428
15. I. Vaknin, O. Willinger, J. Mandl, H. Heuberger, D. Ben-Ami, Y. Zeng, S. Goldberg, **Y. Orenstein** and R. Amit (2024) A universal system for boosting gene expression in eukaryotic cell-lines. *Nature Communications* 15(1):2394
16. O. Yaish, A. Malle, E. Cohen and **Y. Orenstein** (2024) SWOfffinder: Efficient and versatile search of CRISPR off-targets with bulges by Smith-Waterman alignment. *iScience* 27(1)
17. D. Pellow, L. Pu, B. Ekim, D. Kotlar, B. Berger, R. Shamir^ and **Y. Orenstein**^ (2023) Efficient minimizer orders for large values of k using minimum decycling sets. *Genome Research* 33(7):1154-1161
18. K. Elimelech-Zohar and **Y. Orenstein** (2023) An overview on nucleic-acid G-quadruplex prediction: from rule-based methods to deep neural networks. *Briefings in Bioinformatics* 24(4):bbad252
19. M. Barshai, B. Engel, I. Haim and **Y. Orenstein** (2023) G4mismatch: Deep neural networks to predict G-quadruplex propensity based on G4-seq data. *PLoS Computational Biology* 19(3):e1010948
20. R. Alatawneh, Y. Salomon, R. Eshel, **Y. Orenstein**^ and R. Birnbaum^ (2023) Deciphering transcription factors and their corresponding regulatory elements during inhibitory interneuron differentiation using deep neural networks. *Frontiers in Cell and Development* 22:1034604

21. S. Naor-Hoffmann\*, D. Svetlitsky\*, N. Sal-Man, **Y. Orenstein** and M. Ziv-Ukelson (2022) Predicting the pathogenicity of bacterial genomes using widely spread protein families. *BMC Bioinformatics* 23(1):1-18
22. M. Turner\*, Y.M. Danino\*, M. Barshai, N.S. Yacovzada, Y. Cohen, T. Olender, R. Rotkopf, D. Monchaud, E. Hornstein^ and **Y. Orenstein^** (2022) rG4detector, a novel RNA G-quadruplex predictor, uncovers their impact on stress granule formation. *Nucleic Acids Research*, gkac950
23. S. Aizenshtein-Gazit and **Y. Orenstein** (2022) DeepZF: improved DNA-binding prediction of C2H2-zinc-finger proteins by deep transfer learning. *Bioinformatics*, 38(Supplement\_2):ii62-ii67
24. O. Yaish, M. Barshai and **Y. Orenstein** (2022) A systematic evaluation of data processing and problem formulation of CRISPR off-target site prediction. *Briefings in Bioinformatics*, bbac157
25. O. Yaish and **Y. Orenstein** (2022) Computational modeling of mRNA degradation dynamics using deep neural networks. *Bioinformatics*, 38(4):1087-1101
26. E. Tripto and **Y. Orenstein** (2021) A comparative analysis of RNA-binding proteins binding models learned from RNAcompete, RNA Bind-n-Seq and eCLIP data. *Briefings in Bioinformatics*, bbab149
27. M. Barshai\*, A. Aubert\* and **Y. Orenstein** (2021) G4detector: Convolutional neural network to predict DNA G-quadruplexes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
28. N. Katz, E. Tripto, N. Granik, S. Goldberg, O. Atar, Z. Yakhini, **Y. Orenstein** and R. Amit (2021) Overcoming the design, build, test bottleneck for synthesis of nonrepetitive protein-RNA cassettes. *Nature Communications* 12(1):1:15
29. M. Asif and **Y. Orenstein** (2020) DeepSELEX: Inferring DNA-binding preferences from HT-SELEX data using multi-class CNNs. *Bioinformatics*, 36(Supplement\_2):i634-i642
30. M. Barshai, E. Tripto and **Y. Orenstein** (2020) Identifying regulatory elements via deep learning. *Annual Reviews of Biomedical Data Science*, 3:315-338
31. **Y. Orenstein** (2020) Reverse de Bruijn: Utilizing Reverse Peptide Synthesis to Cover All Amino Acid k-mers. *Journal of Computational Biology*, 27(3), 376-385
32. O. Adato, **Y. Orenstein**, J. Kopolovic, T. Juven-Gershon and R. Unger (2020) Quantitative Analysis of Differential Expression of HOX Genes in Multiple Cancers. *Cancers*, 12(6):1572
33. T.C. Shimko, P.M. Fordyce and **Y. Orenstein** (2020) DeCoDe: degenerate codon design for complete protein-coding DNA libraries. *Bioinformatics*, 35(11):3357-3364
34. S. Ray, D. Tillo, R.E. Boer, N. Assad, M. Barshai, G. Wu, **Y. Orenstein**, D. Yang, J.S. Schneekloth Jr and C. Vinson (2020) Custom DNA Microarrays Reveal Diverse Binding Preferences of Proteins and Small Molecules to Thousands of G-Quadruplexes. *ACS Chemical Biology*, 15(4),925-935
35. **Y. Orenstein**, Y.W. Yu and B. Berger (2018) Joker de Bruijn: covering k-mers using joker characters. *Journal of Computational Biology*, 25(11):1171-1178
36. I. Ben-Bassat, B. Chor and **Y. Orenstein** (2018) A deep neural network approach for learning intrinsic protein-RNA binding preferences. *Bioinformatics*, 34(17):i638-i646
37. D. Le, T. Shimko, A. Aditham, A. Keys, **Y. Orenstein** and P. Fordyce (2018) Comprehensive, high-resolution binding energy landscapes reveal context dependencies of transcription factor binding. *Proceedings of the National Academy of Sciences*, 201715888
38. **Y. Orenstein**, U. Ohler and B. Berger (2018) Finding RNA structure in the unstructured RBPome. *BMC Genomics*, 19(1):154
39. **Y. Orenstein\***, D. Pellow, G. Marcais, R. Shamir and C. Kingsford (2017) Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. *PLoS Computational Biology*, 13(10):e1005777
40. L. Yang\*, **Y. Orenstein\***, A. Jolma, Y. Yimeng, J. Taipale, R. Shamir and R. Rohs (2017) Transcription factor family-specific DNA shape readout revealed by quantitative specificity models. *Molecular Systems Biology*, 13(2):910. **Top 10 papers reading list in Regulatory and Systems Genomics**
41. G. Marcais, D. Pellow, D. Bork, **Y. Orenstein**, R. Shamir and C. Kingsford (2017) Improving the performance of minimizers and winnowing schemes. *Bioinformatics*, 33(14):i110-i117
42. **Y. Orenstein**, R. Puccinelli, R. Kim, P. Fordyce and B. Berger (2017) Optimized sequence library design for efficient in vitro interaction mapping. *Cell Systems*, 5(3):230-236

43. **Y. Orenstein** and R. Shamir (2016) Modeling protein-DNA binding via high throughput in vitro technologies. *Briefings in Functional Genomics*, elw030
44. D. Chen\*, **Y. Orenstein\***, R. Golodnitsky, M. Pellach, D. Avrahami, C. Wachtel, A. Ovadia-Shochat, H. Shir-Shapira, A. Kedmi, T. Juven-Gershon, R. Shamir and D. Gerber (2016) SELMAP - SELEX Affinity Landscape Mapping of transcription factor binding sites using integrated microfluidics. *Scientific Reports*, 6
45. **Y. Orenstein**, Y. Wang and B. Berger (2016) RCK: accurate and efficient inference of sequence and structure-based protein-RNA binding models from RNAcompete data. *Bioinformatics*, 32(12):i351-i359. **Best paper award**
46. **Y. Orenstein** and B. Berger (2015) Efficient design of compact unstructured RNA libraries covering all k-mers. *Journal of Computational Biology*, 23(2):67-79
47. Y. Glick\*, **Y. Orenstein\***, D. Chen, D. Avrahami, T. Zor, R. Shamir and D. Gerber (2015) Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities. *Nucleic Acid Research*, 44(6):e51
48. A. Sloutskin, Y. Danino, **Y. Orenstein**, Y. Zehavi, T. Doniger, R. Shamir and T. Juven-Gershon (2015) ElemeNT: A computational tool for detecting core promoter elements. *Transcription*, 6(3):41-50
49. A. Kedmi, Y. Zehavi, Y. Glick, **Y. Orenstein**, D. Ideses, C. Wachtel, T. Doniger, H. Waldman Ben-Asher, N. Muster, J. Thompson, S. Anderson, D. Avrahami, J.R. Yates, R. Shamir, D. Gerber and T. Juven-Gershon (2014) Drosophila TRF2 is a preferential core promoter regulator. *Genes and Development*, 28(19):2163-2174
50. **Y. Orenstein** and R. Shamir (2014) A comparative analysis of transcription factor binding models learned from PBM, HT-SELEX and ChIP data. *Nucleic Acid Research*, 42(8):e63
51. **Y. Orenstein** and R. Shamir (2013) Design of shortest double-stranded DNA sequences covering all k-mers with applications to protein-binding microarrays and synthetic enhancers. *Bioinformatics*, 29(13):i71-i79
52. **Y. Orenstein**, E. Mick and R. Shamir (2013) RAP: accurate and fast motif finding based on protein binding microarray data. *Journal of Computational Biology*, 20(5):375-382
53. MT. Weirauch, A. Cote, R. Norel *et al.* (**Y. Orenstein** as part of DREAM5 consortium) (2013) Evaluation of methods for modeling transcription factor sequence specificity. *Nature Biotechnology*, 31(2):126-134
54. **Y. Orenstein**, C. Linhart and R. Shamir (2012) Assessment of algorithms for inferring positional weight matrix motifs of transcription factor binding sites using protein binding microarray data. *PLoS One*, 7(9):e46145
55. **Y. Orenstein** and D. Ron (2011) Testing Eulerianity and connectivity in directed sparse graphs. *Theoretical Computer Science*, 412(45):6390-6408

#### Conference Proceedings [\* equal contribution, ^ equal correspondence]

1. A. Shur\*, I. Tziony\* and **Y. Orenstein^** (2026) Generating minimum-density minimizers. *Proceedings of the 24<sup>th</sup> International Symposium of String Processing and Information Retrieval (SPIRE)*
2. A. Shur, I. Tziony and **Y. Orenstein** (2026) 10-Minimizers: A promising class of constant-space minimizers. *Proceedings of the 26<sup>th</sup> Annual Workshop on Algorithms in Bioinformatics (WABI)*
3. D. Shrem and **Y. Orenstein** (2026) iMotifPredictor: i-motif prediction by multi-data integration. In *Proceedings of the 17th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*
4. A. Luboshitz, M. Rahimi, A. Hendel and **Y. Orenstein** (2025). EpiCRISPR: Improving CRISPR/Cas9 on-and off-target prediction by flanking sequences, epigenetic marks, and high-throughput datasets. In *Proceedings of the 16th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*
5. O. Yaish and **Y. Orenstein** (2025). F-MoDA: Efficient Fourier-based motif discovery in attribution maps. In *Machine Learning in Computational Biology (MLCB)*
6. I. Tziony\*, J. Mandl\*, K. Shapira, E. Eisenberg, E. Porat and **Y. Orenstein** (2024) FiSSC: Finding smallest sequence covers to sets of degenerate reads with applications to RNA editing. *Accepted to Proceedings of the 15<sup>th</sup> ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*
7. D. Pellow, L. Pu, B. Ekim, D. Kotlar, R. Shamir and **Y. Orenstein** (2023) Efficient minimizer orders for large values of k using minimum decycling sets. *Proceedings of the 27<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB)*

8. M. Turner, M. Barshai and **Y. Orenstein** (2022) rG4detector: convolutional neural network to predict RNA G-quadruplex propensity based on rG4-seq data. *The 13<sup>th</sup> ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*
9. Y. Ben-Ari, D. Flomin, L. Pu, **Y. Orenstein** and R. Shamir (2021) Improving the efficiency of de Bruijn graph construction using compact universal hitting sets. *The 12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*
10. J. Karin, H. Michel and **Y. Orenstein** (2021) MultiRBP: multi-task neural network for protein-RNA binding prediction. *The 12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*
11. B. Ekim, B. Berger and **Y. Orenstein** (2020) A randomized parallel algorithm for efficiently finding near-optimal universal hitting sets. *Proceedings of the 24<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB)*
12. M. Barshai and **Y. Orenstein** (2019) Predicting G-quadruplexes from DNA sequences using multi-kernel convolutional neural networks. *The 10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*
13. **Y. Orenstein** (2018) Reverse de Bruijn: utilizing reverse peptide synthesis to cover all amino acid k-mers. *Proceedings of the 22<sup>nd</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB)*
14. **Y. Orenstein**, R. Kim, P. Fordyce and B. Berger (2017) Joker de Bruijn: sequence libraries to cover all k-mers using joker characters. *Proceedings of the 21<sup>st</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB)*
15. **Y. Orenstein**, D. Pellow, G. Marcais, R. Shamir and C. Kingsford (2016) Compact universal k-mer hitting sets. *Proceedings of the 16<sup>th</sup> Annual Workshop on Algorithms in Bioinformatics (WABI)*
16. **Y. Orenstein** and B. Berger (2015) Efficient design of compact unstructured RNA libraries covering all k-mers. *Proceedings of the 15<sup>th</sup> Annual Workshop on Algorithms in Bioinformatics (WABI)*

## Book Chapters

1. **Y. Orenstein** (2021) Improved analysis of high-throughput sequencing data using small universal k-mer hitting sets. *Deep Sequencing Data Analysis*

## Refereed Conference Talks

- 10-minimizers: a promising class of constant-space minimizers, ISMB 2026, Washington DC, USA, July 2026
- ExoShorkie: Predicting RNA-seq coverage of exogenous genomes in yeast by transfer learning, ISMB 2026, Washington DC, USA, July 2026
- Machine Learning-Guided Engineering of Selective Protease Inhibitors by Deep Mutational Scanning, ISMB 2026, Washington DC, USA, July 2026
- CROP: A feature-independent context-aware method for CRISPR-Cas9 frameshift prediction, ISMB 2026, Washington DC, USA, July 2026
- NPBIP: Predicting Binding Preferences of Uncharacterized Nucleic-Acid-Binding Proteins, RECOMB-RSG, Thessaloniki, Greece, May 2026
- AutoFFinder: A Reconfigurable Hardware-Accelerated Platform for Multi-Guide CRISPR/Cas9 Off-Target Search, RECOMB-Arch, Thessaloniki, Greece, May 2026
- EpiCRISPR: Improving CRISPR/Cas9 on-target efficiency prediction by multiple epigenetic marks, high-throughput datasets, and flanking sequences, ISMB/ECCB 2025, Liverpool, UK, July 2025
- Mapping the affinity of protein-protein interactions with multiple amino acid mutations using deep neural networks, ISMB 2024, Montreal, Canada, July 2024
- CellRBP: Improving Protein-RNA Binding Prediction In Vivo Using Cell-Type-Specific Features, ISMB 2024, Montreal, Canada, July 2024
- G4mismatch: Deep neural networks to predict G-quadruplex propensity based onG4-seq data, ISMB/ECCB 2023, Lyon, France, July 2023
- Interpretability of deep neural networks in genomics. RSGDREAM 2022, Las Vegas, NV, November 2022

DeepSELEX: Inferring DNA-binding preferences from HT-SELEX data using multi-class CNNs, Protein-DNA binding meeting, Rehovot, Israel, October 2022

DeCoDe: degenerate codon design for complete protein-coding DNA libraries. ACM-BCB, Online, August 2020

Algorithms for universal, unbiased and compact DNA and amino acid libraries. The 2<sup>nd</sup> Israeli Synthetic Biology Meeting, Rehovot, Israel, March 2019

Reverse de Bruijn: utilizing reverse peptide synthesis to cover all amino acid k-mers. RECOMB, Paris, France, April 2018

Computational modeling of protein-RNA interactions. ACM-BCB, Boston, August 2017

Joker de Bruijn: sequence libraries to cover all k-mers using joker characters. RECOMB, Hong Kong, China, May 2017

Structure-based prediction of protein-RNA interactions on a transcriptome-wide scale. ILANIT, Eilat, Israel, February 2017

Structural analysis of the compendium of RNA-binding proteins. RECOMB-RSG, Phoenix, November 2016.

DNA shape readout specificities of different TF families. ISMB, Orlando, July 2016

RCK: accurate and efficient inference of sequence and structure-based protein-RNA binding models from RNAcompete data. ISMB, Orlando, July 2016

Efficient design of compact unstructured RNA libraries covering all k-mers. WABI, Atlanta, September 2015

The use of HT-SELEX to infer TF binding models: comparison to PBM and an improved algorithm. ISMB, Boston, July 2014

Design of shortest double-stranded DNA sequences covering all k-mers with applications to protein binding microarrays and synthetic enhancers. ISMB, Berlin, Germany, July 2013

RAP: accurate and fast motif finding based on protein binding microarray data. RECOMB Regulatory Genomics, San Francisco, November 2012

Identifying TFBS motifs and predicting probe binding intensities from protein binding microarray data. RECOMB DREAM, New York, November 2010

### **Non-refereed Conference Talks**

NPBIP: Predicting Binding Preferences of Uncharacterized Nucleic-Acid-Binding Proteins, Workshop on Protein-DNA Binding, ECCB, Geneva, Switzerland, September 2026

Designing Synthetic Universal Promoters, EPD Community Day, ECCB, Geneva, Switzerland, September 2026

Computational challenges in CRISPR/Cas9 genome editing, Israeli Bioinformatics Symposium, Herzliya, Israel, April 2025

Predicting protein-RNA binding based on in vivo and in vitro data, Dagstuhl meeting, Germany, December 2024

Designing Synthetic Universal Promoters, SCOJEN Institute Day, Reichman University, Herzliya, Israel, November 2024

On-target prediction utilizing epigenetics, CRISPR meeting, Rehovot, Israel, April 2023

rG4detector: convolutional neural network to predict RNA G-quadruplex propensity based on rG4-seq data, Ilanit, Eilat, Israel, February 2023

G-quadruplex prediction by deep neural networks, AIweek, Virtual, February 2022

Interpretability of deep neural networks in genomics. 2<sup>nd</sup> Summer School on Machine Learning in Bioinformatics, Virtual, August 2021

Convolutional neural networks for protein-DNA/RNA binding. 1<sup>st</sup> Summer School on Machine Learning in Bioinformatics, Virtual, August 2020

Deep learning for protein-RNA interactions. Rules of Protein-DNA Recognition: Computational and Experimental Advances, Oxaca, Mexico, June 2018

Utilizing de Bruijn graphs in universal sequence design for discovery of regulatory elements. Regulatory Genomics and Epigenomics workshop, Simons Institute, UC Berkeley, March 2016

Introduction to regulatory genomics and epigenomics: motif finding. Algorithmic Challenges in Genomics Boot Camp, Simons Institute, UC Berkeley, January 2016

Computational inference of binding site models from high-throughput SELEX data. Rules of Protein-DNA Recognition: Computational and Experimental Advances, Oxaca, Mexico, June 2015

Inferring binding site motifs from high-throughput in vitro data. Edmond J. Safra Bioinformatics Retreat, Kinneret, Israel, May 2014

Design of shortest double-stranded DNA sequence covering all k-mers. Workshop on Interdisciplinary Applications of Graph Theory, Combinatorics and Algorithms, Haifa, Israel, May 2013

Inferring binding site motifs from protein binding microarray data. Students Conference in Genetics, Genomics and Evolution, Beer-Sheva, Israel, September 2012

### **Conference Poster Presentations**

GreedyMini: generating low-density minimizer orders. ISMB/ECCB 2025, Liverpool, UK, July 2025

GreedyMini: generating low-density minimizer orders. RECOMB-seq, Seoul, South Korea, April 2025

A deep learning approach for predicting protein-RNA binding. Seventh Broad – Israel Science Foundation (ISF) Symposium, Jerusalem, July 2019

A deep learning approach for predicting protein-RNA binding. RECOMB, Paris, April 2018

A deep learning approach for predicting protein-RNA binding. Frontiers in Genetics XI, Tel-Aviv, February 2018

Sequence libraries to cover all k-mers using degenerate characters. Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, March 2017

Structure-based prediction of RNA-protein interactions on a transcriptome-wide scale. Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, March 2017

Transcription factor family-specific DNA shape readout revealed by quantitative specificity models. Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, March 2017

DNA shape readout specificities of different TF families. RECOMB-RSG, Phoenix, November 2016

Sequence libraries to cover all k-mers using degenerate characters. RECOMB-RSG, Phoenix, November 2016

Compact universal k-mer hitting sets. High-Throughput Sequencing Algorithms and Application Special Interest Group, Orlando, July 2016

Inferring binding site motifs from HT-SELEX data. Safra Retreat, Kinneret, Israel, May 2014

A comparative analysis of TF binding models learned from PBM, HT-SELEX and ChIP data. RECOMB/ISCB Regulatory and Systems Genomics, Toronto, Canada, November 2013

Inferring binding site motifs from high-throughput in vitro data. EMS Autumn School on Computational Aspects of Gene Regulation, Bedlewo, Poland, October 2013

Inferring binding site motifs from high-throughput technologies. Regulatory Genomics Special Interest Group, Berlin, Germany, July 2013

Inferring binding site motifs from high-throughput in vitro data. Israel Bioinformatics Symposium, Beer-Sheva, Israel, June 2013

Inferring binding site motifs from high-throughput technologies. DNA@60 conference, Haifa, Israel, May 2013

Inferring binding site motifs from high-throughput technologies. Safra Retreat, Kfar Giladi, Israel, May 2013

Accurate and user-friendly tools for discovering transcription factor microRNA binding sites. Frontiers in Genetics, Haifa, Israel, January 2013

RAP: accurate prediction of cis-regulatory motifs from protein binding microarrays. Safra Retreat, Ginosar, Israel, May 2012

RAP: accurate prediction of cis-regulatory motifs from protein binding microarrays. Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, March 2012

Accurate and user-friendly tools for discovering transcription factor and microRNA binding sites. Frontiers in Genetics, Rehovot, Israel, February 2011

Amadeus-PBM: fast and accurate motif discovery from protein binding microarray data. RECOMB Regulatory Genomics, Barcelona, Spain, October 2011

Regression based classification of AML flow cytometry profiles. RECOMB DREAM, Barcelona, Spain, October 2011

Discovering transcription factor binding site motifs from protein binding microarrays. Safra Retreat, Kibbutz Hagoshrim, Israel, May 2011

Accurate and user-friendly tools for discovering transcription factor and microRNA binding sites. ILANIT/FISEB conference, Eilat, Israel, February 2011

Identifying TFBS motifs and predicting probe binding intensities from protein binding microarray data. RECOMB DREAM, New York, November 2010