

Publications

A. Books and Edited Works

1. R. Shamir. "On the complexity of the Simplex method", Ph.D. dissertation, College of Engineering, University of California, Berkeley, 1984.
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7. R. Shamir, Editor. Selected papers from RECOMB 2000. Special issue of *Journal of Computational Biology*, Vol 7 issues 3/4, 2000.
8. M. Li, P. Pevzner, R. Shamir, Guest editors. *Journal of Computer and System Sciences*, Special issue on Computational Biology, Volume 65, No. 3, November 2002.
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10. S. Istrail, P. Pevzner, R. Shamir, Editors. Computational Molecular Biology *Topics in Discrete Mathematics*, Volume 12, North-Holland, Amsterdam 2003. Reprinted from *Discrete Applied Mathematics*, Volume 127, number 1, April 2003.
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12. R. M. Karp, M. Li, P. Pevzner, R. Shamir, Guest editors. *Journal of Computer and System Sciences*, 2nd special issue on Computational Biology, Volume 70, No. 3, May 2005.
13. S. Istrail, P. Pevzner, R. Shamir, Editors. *Discrete Applied Mathematics*, Fifth Special Issue in the Computational Molecular Biology Series, Volume 155, issues 6-7, April 2007.
14. R. M. Karp, M. Li, P. Pevzner, R. Shamir, Guest editors. *Journal of Computer and System Sciences*, 3rd special issue on Computational Biology, Volume 73, No. 7, November 2007.
15. S. Istrail, P. Pevzner, R. Shamir. F. Sun, Guest editors. *Communication in Information and Systems*, Special issues dedicated to Michael Waterman on the occasion of his 67th birthday. Vol 9 3-4 2009 and Vol 10 1-2 2010.
16. P. A. Pevzner, R. Shamir, Editors. Selected papers from the 2nd RECOMB satellite meeting on Bioinformatics Education (RECOMB-BE). *Journal of Computational Biology*, 18 (7), 2011.
17. P. A. Pevzner, R. Shamir, Editors. *Bioinformatics for Biologists*. Cambridge University Press, 2011.

B. Chapters in Books

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19. I. Adler, R. Shamir. “Greedy solvable transportation networks and edge-guided vertex elimination”. *Network Optimization Problems: Algorithms, Complexity and Applications*, D.-Z. Du and P. M. Pardalos, Editors, pp. 1–22, World Scientific Press, Singapore, 1993.
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23. A. Tanay, R. Sharan, R. Shamir. “Biclustering algorithms: A survey” *Handbook of Computational Molecular Biology*, S. Aluru, Editor, pp 26-1 – 26-17, Chapman and Hall/CRC Press, 2006.
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25. C. Linhart and R. Shamir. “Degenerate Primer Design: Theoretical Analysis and the HYDEN program”. *PCR primer design*, A. Yuryev, Editor. *Methods in Molecular Biology* 402: 221–44 , Humana Press, 2007.

C. Journal Articles

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E. Submitted for Publication

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270. D. Amar, R. Shamir, D. Yekutieli. “Extracting replicable associations across multiple studies: algorithms for controlling false discovery rate.

271. “A blood-based gene signature characterizing idiopathic Parkinson’s disease”. Ron Shamir, Christine Klein, David Amar, Eva-Juliane Vollstedt, Michael Bonin, Marija Usenovic, Yvette C Wong, Ale Maver, Andre Troiano, Sven Poths, Hershel Safer, Jean-Christophe Corvol, Suzanne Lesage, Ofer Lavi, Gnther Deuschl, Gregor Kuhlenbaeumer, Heike Pawlack, Igor Ulitsky, Meike Kasten, Olaf Riess, Alexis Brice, Borut Peterlin, Dimitri Krainc. “A blood-based gene signature characterizing idiopathic Parkinson’s disease”.

F. Titles in Preparation.

272. D. Amar, R. Shamir. “Multi-class analysis of blood biomarkers”.

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G. Software

- G. Mayraz, R. Shamir, “An algorithm for constructing physical maps from oligo fingerprints data”
- E. Hartuv, R. Shamir, “HCS: A new clustering algorithm”
- R. M. Karp, R. Shamir, I. Pe’er, “A practical algorithm for optical mapping”
- A. Ben-Dor, R. Shamir, Z. Yakhini, “CAST: Methods and system for partitioning data into subsets of related data”
- R. Sharan, R. Shamir, “CLICK: CLuster Identification via Connectivity Krenels”. A program for rapid clustering of large scale expression and other data.
- I. Pe’er, N. Arbili, R. Shamir. “Spectrum Alignment: Efficient resequencing by hybridization”
- A. Tanay, R. Shamir. “GENESYS: Genetic Expansion of NETwork SYstem”
- N. Orlev, R. Shamir, Y. Shiloh. “PIVOT: Protein Interactions VisualizatiOn Tool”
- C. Linhart, R. Elkon, Y. Shiloh, R. Shamir. “PRIMA: PRomoter Integration in Microarray Analysis” A program for finding transcription factors) whose binding sites are enriched in a given set of promoters.
- A. Maron-Katz, R. Sharan, A. Tanay, I. Ulitsky, C. Linhard, T. Hait, R. Elkon, Y. Shiloh, R. Shamir “EXPANDER: EXpression ANalyzer and DisplayER”. An integrative analysis tool for analysis of gene expression data.
- C. Linhart, R. Shamir. “HYDEN: Software for designing highly degenerate primers”.

- G. Kimmel, R. Shamir. “GERBIL: GEnotype Resolution and Block Identification using Likelihood”. A software for simultaneously phasing genotypes into haplotypes and block partitioning.
- T. Barzuza, I. Pe’er, J. Beckman, R. Shamir. “GREAL: Software for the Graph Realization Problem” A program for constructing a tree from a set of its edge-labeled paths.
- I. Gat-Viks, A. Tanay, D. Rajzman, R. Shamir. “MetaReg: Modeling and analysis of heterogeneous regulation in biological networks”. A modeling and analysis tool for biological networks, including algorithms for learning model parameters from experimental data.
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- S. Bruckner, F. Hueffner, R. M. Karp, R. Shamir, R. Sharan. “TORQUE: topology querying of protein interaction networks”
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- G. Karlebach, R. Shamir “ModEnt” - A tool that reconstructs gene regulatory networks from high throughput experimental data.
- I. Ulitsky, A. Krishnamurthy, R. M. Karp, R. Shamir, “DEGAS” - a tool for de novo discovery of dysregulated pathways in human diseases.
- M. Gutkin, G. Dror, R. Shamir, “SlimPLS” - a method for feature selection in gene expression-based disease classification.
- C. Linhart, Y. Halperin, R. Shamir, “AMADEUS” - A software tool for de novo transcription factor and microRNA motif discovery.
- M. Ozery-Flato, C. Linhart, L. Trakhtenbrot, S. Izraeli, R. Shamir, “STACK” - A portal for large-scale analysis of chromosomal aberrations in cancer karyotypes.
- M. Bansal, G. Banay, P. Gogarten, R. Shamir, “HIDE” - Software for detecting highways of horizontal gene transfer.
- Y. Orenstein, E. Mick, R. Shamir, “RAP” - Accurate and fast motif finding based on protein microarray data.

- D. Amar, H. Safer, R. Shamir, “DICER” - A tool for advanced analysis of differential co-expression case-control gene expression data.
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- R. Rozov, E. Halperin, R. Shamir. “MGMR” - An algorithm that leverages RNA-Seq population data to optimize expression estimation.
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H. Patents

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169. “Computational analysis of gene regulation, disease classification and protein networks”. Simon Fraser University, March 25, 2011.
170. “A systematic assessment of associations among chromosomal aberrations in cancer karyotypes” Oral presentation, RECOMB Computational Cancer Biology Satellite, Vancouver, BC, Canada, March 26-27 2011.
171. “Large-scale analysis of chromosomal aberrations in cancer karyotypes reveals two distinct paths to aneuploidy” Oral presentation, Meeting in celebration of 30 years since the establishment of the Cancer Biology Research Center, September 14-17, 2011. Safed, Israel.
172. “Computational Analysis of Gene Regulation, Disease Classification and Protein Networks”. Distinguished lecture series, Bioinformatics center, Saarbrucken University, Germany, February 8, 2012.
173. “Computational methods in analysis of gene regulation and protein interactions”. Lecture in Houry, W.A. (ed.), Protein Homeostasis: , The Biomedical and Life Sciences Collection, Henry Stewart Talks Ltd, London, 2012. (online at <http://hstalks.com/?t=BL1423117-Shamir>)
174. “Functional genomics and networks”. Epigenetics meets Sysmtes Biology - an EpigeneSys course and symposium, Weizmann Institute, Rehovot, Israel, June 3 2012.
175. “Dissecting dysregulated pathways and chromosomal aberrations in cancer”. I-CORE meeting Gene Regulation in Complex Disease Bar Ilan University October 11, 2012.
176. “Cancer, chromosomes and computing”. Department of Genetics, Hebrew University, December 12, 2012.
177. “Cancer, chromosomes and computing”. Department of Cell Research and Immunology, Tel Aviv University, March 5, 2013.
178. “On the relation of gene function and organization in normal and cancer cells”. National University of Singapore, 12 April 2013.
179. Trakhtenbrot, S. Izraeli. “On chromosomal aneuploidy in cancer and the functional linkage between chromosomes”. 2013 Meeting of the Cancer Society Research Center, Tel Aviv University. Safed, Israel June 19-21, 2013.
180. “Chromosome organization and gene function in normal and tumor cells”, Seminar of the Faculty of Life Sciences, Bar Ilan University 18 December 2013.
181. “Joint analysis of two biological networks using module maps”. Computer Science Colloquium, The Technion, April 29 2014.
182. “Understanding gene regulation using high throughput in vitro methods”. I-CORE Meeting: Cancer Tel Aviv University, October 6, 2014.
183. “Computations can help in understanding cancer: some examples”. Advances in Cell Biology and Cancer Research, a conference honoring Prof. Yoel Kloog. Tel Aviv University, 7 October 2014.
184. “Understanding gene regulation using high throughput in vitro methods”. Department of Molecular and Computational Biology, University of Southern California November 10, 2014.
185. “Pathway-based biomarkers specifically and robustly classify diverse multiple diseases”. Oral presentation, RECOMB/ISCB Conference on Regulatory and Systems Genomics, San Diego, California, November 9-14 2014.

186. “Improved disease classification using Big Expression Data”. The first TAU-AGAUR Biomed Symposium on Gene Regulation, Genomics and Stem Cells in Disease. Tel Aviv University, January 18, 2015.
187. “Using gene expression to understand and distinguish diseases”. Invited talk, Conference on Computational Modeling of Gene Expression and its Evolution. Tel Aviv University, October 13-16 2015.
188. “Understanding the signals of gene regulation”. Bioinformatics undergraduate seminar, May 12, 2015, Tel Aviv University.
189. “Supple algorithms for better dissection of cancer and brain data”. Stanford University, April 28, 2016.
190. “Network querying and copy number triplet problems - ILP to the rescue”. Simons workshop on Integer Linear Programming in Computational Biology. Simons Institute for the Theory of Computing, Berkeley, CA, USA May 9, 2016.
191. “Utilizing diverse omic data from many cancer studies: proof of concept and applications”. TAU-University of Toronto joint workshop on Big-data and Health, Tel Aviv University, Tel Aviv, Israel, November 1-2 2016.
192. “Chips, pains and computers”, Guest talk, Gentle Introduction to Programming Tel Aviv University, September 11, 2016.

Presentation of my work by others (last five years only)

- A. Paz, E. David, Y. Ber, S. Bialik, Z. Brownstein, D. Sagir, R. Elkon, I. Ulitsky, K. B. Avraham, A Kimchi, Y. Shiloh, R. Shamir. “SPIKE: A signaling pathways resource for DNA damage, apoptosis and the auditory system”. Poster presentation, 6th FISEB (Ilanit) meeting, Eilat, Israel, 7-10 February 2011.
- Y. Orenstein, C. Linhart, Y. Halperin, I. Ulitsky, R. Shamir. “Accurate and user-friendly tools for discovering transcription factor and microRNA binding sites” Poster presentation, 6th FISEB (Ilanit) meeting, Eilat, Israel, 7-10 February 2011.
- O. Tzfidia, A. Ma’ayan, L. Bradbury, R. Shamir, E. Wurtzel. “A systems biology approach for revealing the provitamin A carotenoid biosynthesis transcriptional regulation network” Poster presentation, International Society of Oncology and Biomarker (ISOBM) 2012 Congress, October, 13 - 17, 2012, Jerusalem, Israel.
- Y. Orenstein, E. Mick, C. Linhart and R. Shamir. “Inferring binding site motifs from high-throughput technologies”. Poster presentation, DNA @ 60: The 60th Anniversary of the Discovery of the DNA Double Helix, The Technion, Haifa, May 26 - 29, 2013.
- D. Amar, R. Shamir. “Discovery of structure in pairs of biological networks: application to disease dysregulation and genetic interactions”. Poster presentation, DNA @ 60: The 60th Anniversary of the Discovery of the DNA Double Helix, The Technion, Haifa, May 26 - 29, 2013.
- R. Rozov, E. Halperin, R. Shamir. “Graph based reference-free encoding and compression of sequencing reads”. Poster presentation, The 15th Israeli Bioinformatics Symposium, Ben-Gurion University of the Negev, June 27, 2013.
- D. Netanel, R. Shamir. “Identification of Breast Cancer Subtypes Based on RNA-Seq Data”. Poster presentation, The 15th Israeli Bioinformatics Symposium, Ben-Gurion University of the Negev, June 27, 2013.
- D. Amar, R. Shamir. “Algorithms for mapping modules in pairs of biological networks”. Poster presentation, The 15th Israeli Bioinformatics Symposium, Ben-Gurion University of the Negev, June 27, 2013.

- [Y. Orenstein](#), R. Shamir. “Inferring binding site motifs from high-throughput in vitro data”. Poster presentation, The 15th Israeli Bioinformatics Symposium, Ben-Gurion University of the Negev, June 27, 2013.
- [A. Maron-Katz](#), R. Elkon, I. Ulitsky, C. Linhart, D. Amar, A. Tanay, R. Sharan, E. David, T. Hait, D. Sagir, H. Safer, Y. Shiloh, R. Shamir. “EXPANDER: A platform for dissecting networks and functions using expression profiles”. Poster presentation, The 15th Israeli Bioinformatics Symposium, Ben-Gurion University of the Negev, June 27, 2013.
- [D. Amar](#), R. Shamir. “Algorithms for mapping modules in pairs of biological networks”. Oral presentation, Network Biology SIG meeting, ISMB/ECCB 2013 meeting, Berlin, Germany, July 19, 2013.
- [A. Thevenin](#), L. Ein-Dor, M. Ozery-Flato, R. Shamir. “Organization of functional gene groups”. Poster presentation, Conference on Models and Algorithms for Genome Evolution, Montreal, Canada, August 23–26, 2013.
- [A. Thevenin](#), L. Ein-Dor, M. Ozery-Flato, R. Shamir. “Organization of functional gene groups”. Poster presentation, Workshop on Algorithms in Bioinformatics (WABI), Sophia Antipolis, France, September 2–4, 2013.
- [A. Thevenin](#), L. Ein-Dor, M. Ozery-Flato, R. Shamir. “Functional gene groups are concentrated within chromosomes, among chromosomes and in the nuclear space of the human genome” Poster presentation, Recomb Comparative Genomics Conference, Lyon, France, 17-19 Oct. 2013.
- [Y. Orenstein](#), R. Shamir. “A comparative analysis of TF binding models learned from PBM, HT-SELEX and ChIP data”. Poster presentation, RECOMB/ISCB Conference on Regulatory and System Genomics, Toronto, November 2013.
- [Y. Orenstein](#), R. Shamir. “Inferring binding sites motifs from high-throughput in vitro data”. Poster presentation, EMS Autumn School on Computational Aspects of Gene Regulation, Bedlewo, Poland, October 2013.
- [Y. Orenstein](#), R. Shamir. “Transcription factor binding site motif reconstruction based on HT-SELEX data”. Gene Regulation in Complex Human Disease I-CORE Annual Conference Hadassah Medical Center, Hebrew University Jerusalem, Jan. 23, 2014.
- [D. Netanel](#), R. Shamir. “Identification of breast cancer sub-types using rna-seq data”. Poster Presentation, the 7th Congress of the Federation of the Israel Societies for Experimental Biology, Eilat, February 10-13, 2014.
- [D. Amar](#), C. Klein, D. Krainc, B. Peterlin, A. Brice, O. Reiss and R. Shamir. “The GenePark project: predicting Parkinson’s disease using blood expression profiles”. Poster Presentation, the 7th Congress of the Federation of the Israel Societies for Experimental Biology, Eilat, February 10-13, 2014.
- [K. Perl](#), Y. Bhonker, O. Yizhar-Barnea, S. Shvatzki, K. Ushakov, Y. Pozniak, O. Yaron, R. Shamir, N. Shomron, T. Geiger and K.B. Avraham. “Understanding the developmental and physiological conditions of the inner ear using transcriptome and proteome analysis”. Poster Presentation, the 7th Congress of the Federation of the Israel Societies for Experimental Biology, Eilat, February 10-13, 2014.
- [R. Rozov](#), R. Shamir, E. Halperin “Fast lossless compression via cascading Bloom filters”. Poster presentation, RECOMB 2014 conference, Pittsburgh, PA April 2-5 2014.
- [T. Hait](#), D. Amar and R. Shamir. “Pathway as robust biomarkers for cancer classification: the power of big expression data”. Poster presentation, Sixth Annual meeting of the Israeli Society for Cancer Research, ISCR 14, Faculty of Medicine, Technion, May 22, 2014.

- D. Amar, R. Shamir. “Constructing module maps for integrated analysis of heterogeneous biological networks”. oral presentation, highlights track, ISMB 2014 Boston, MA July 11-15, 2014.
- A. Maron-Katz, S. Vaisvaser, T. Lin, R. Shamir and T. Hendler. “Depicting network dynamic patterns related to prior affective state using a data driven approach”. Poster presentation, Organization for Human Brain Mapping (OHBM) conference 2014, Hamburg, Germany, June 8-12, 2014.
- Y. Orenstein, R. Shamir The use of HT-SELEX to infer TF binding models: comparison to PBM and an improved algorithm Oral presentation, RegGen SIG meeting, Boston, MA ISMB 2014, July 12,
- D. Amar, T. Hait, R. Shamir. “Pathways as robust biomarkers for cancer classification: the power of big expression data”. Oral presentation, Network Biology SIG meeting, Boston, MA ISMB 2014, July 11.
- D. Amar. “Computational Analysis of Genomewide Expression Data in XDP”. Invited talk, XDP Workshop, Luebeck, Germany, June 13-15, 2014
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- D. Amar, T. Hait, S. Izraeli, and R. Shamir. “Harnessing the power of large-scale heterogeneous expression profile collections to diagnose disease and propose treatment”. Poster presentation, the first TAU-AGAUR Biomed Symposium on Gene Regulation, Genomics and Stem Cells in Disease, Tel Aviv University, January 18th, 2015.
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- D. Netanely, A. Avraham, E. Evron, R. Shamir. ”Identification of breast cancer subtypes using high-throughput genomic data”. Poster presentation, Frontiers in Genetics IX, The Genetic Society of Israel, Weizmann Institute of Science, Rehovot, Israel, February 23, 2015.

- R. Eitan, and R. Shamir. "Reconstructing cancer karyotypes". Poster presentation, Frontiers in Genetics IX, The Genetic Society of Israel, Weizmann Institute of Science, Rehovot, Israel, February 23, 2015.
- D. Amar, T. Hait, S. Izraeli, and R. Shamir. "Integrated analysis of expression data across many diseases produces specific, robust biomarkers and suggests treatments". Poster presentation, Frontiers in Genetics IX, The Genetic Society of Israel, Weizmann Institute of Science, Rehovot, Israel, February 23, 2015.
- R. Rozov, R. Shamir, E. Halperin. "Fast lossless compression via cascading Bloom filters". Poster presentation, Frontiers in Genetics IX, The Genetic Society of Israel, Weizmann Institute of Science, Rehovot, Israel, February 23, 2015.
- A. Maron-Katz, T. Hait, R. Elkon, D. Netanel, R. Sharan, I. Ulitsky, C. Linhart, D. Sagir, H. Safer, D. Amar, Y. Shiloh, R. Shamir. "EXPANDER: A platform for dissecting networks and functions using RNA-Seq and microarray expression profiles". Poster presentation, Frontiers in Genetics IX, The Genetic Society of Israel, Weizmann Institute of Science, Rehovot, Israel, February 23, 2015.
- D. Netanel, A. Avraham, E. Evron and R. Shamir. "Identification of breast cancer subtypes using high-throughput genomic data". Poster presentation, The 17th Israeli Bioinformatics Symposium - IBS 2015, Tel Aviv University, May 26, 2015.
- T. Hait, D. Amar, S. Izraeli and R. Shamir. "Harnessing the power of myriad heterogeneous expression profiles to classify diseases and propose drug targets". Poster presentation, The 17th Israeli Bioinformatics Symposium - IBS 2015, Tel Aviv University, May 26, 2015.
- D. Amar, D. Yekutieli, A. Maron-Katz, T. Hendler and R. Shamir. "A hierarchical Bayesian model for flexible module discovery in three-way time series data". Poster presentation, The 17th Israeli Bioinformatics Symposium - IBS 2015, Tel Aviv University, May 26, 2015.
- D. Amar, D. Yekutieli, A. Maron-Katz, T. Hendler and R. Shamir. "A hierarchical Bayesian model for flexible module discovery in three-way time series data" Poster presentation, The 10th Annual Retreat of the Edmond J. Safra Center for Bioinformatics, Maagan, Sea of Galilee, Israel, May 31 - June 1, 2015.
- D. Netanel, A. Avraham, E. Evron and R. Shamir. "Identification of breast cancer subtypes using high-throughput genomic data" Poster presentation, The 10th Annual Retreat of the Edmond J. Safra Center for Bioinformatics, Maagan, Sea of Galilee, Israel, May 31 - June 1, 2015.
- R. Rozov, E. Halperin and R. Shamir. "Fast and low memory identification of critical nodes for de novo assembly" Poster presentation, The 10th Annual Retreat of the Edmond J. Safra Center for Bioinformatics, Maagan, Sea of Galilee, Israel, May 31 - June 1, 2015.
- M. Dan, Y. Orenstein and R. Shamir. "Discovery of RNA regulatory elements by multiple sequence and structure alignment" Poster presentation, The 10th Annual Retreat of the Edmond J. Safra Center for Bioinformatics, Maagan, Sea of Galilee, Israel, May 31 - June 1, 2015.
- K. Perl, Y. Bhonker, O. Yizhar-Barnea, S. Shivatzki, K. Ushakov, Y. Pozniak, O. Yaron, N. Shomron, T. Geiger, K.B. Avraham and R. Shamir. "Gene expression shows higher diversity than protein expression in mammalian tissues: observations and hypo" Poster presentation, The 10th Annual Retreat of the Edmond J. Safra Center for Bioinformatics, Maagan, Sea of Galilee, Israel, May 31 - June 1, 2015.
- R. Zeira, R. Shamir. "Sorting by cuts, joins and whole chromosome duplications". Oral presentation, the 15th Haifa Workshop on Interdisciplinary Applications of Graph Theory, Combinatorics, and Algorithms. Haifa, Israeli, June 22 - 25, 2015.

- A. Domingo, A. Westenberger, D. Amar, L. Lee, R. Rosales, R. D. Jamora, E. dela Paz, K. Lohmann, R. Shamir, C. Klein. “Genome-wide expression profiling identifies potential molecular pathways involved in X-linked dystonia-parkinsonism (XDP, DYT3)”. Late breaking abstract presentation, 19th International Parkinsons Disease and Movement Disorders Conference, San Diego, CA USA, June 14-18 2015.
- Y. Orenstein, R. Shamir. “Computational inference of binding site models from high-throughput SELEX data”. BIRS meeting on Rules of Protein-DNA Recognition: Computational and Experimental Advances Oaxaca, Mexico, June 21 to 26 2015.
- A. Sloutskin, Y. M. Danino, Y. Zehavi, Y. Orenstein, T. Doniger, R. Shamir, T. Juven-Gershon. “ElemenT: A computational tool for detecting core promoter elements”. Poster presentation, European Drosophila Research Conference, Heidelberg, Germany, September 2015.
- D. Amar, “Extracting reliable information from Big Expression Data” Oral presentation, Conference on Computational Modeling of Gene Expression and its Evolution, Tel Aviv University, October 13-16 2015.
- D. Amar, T. Hait, S. Izraeli and R. Shamir. “Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets”. Poster Presentation. CSBio, Bangkok, Thailand. November 22-25 2015
- I. Nurick, M. Ozery-Flato, L. Ein-Dor, R. Shamir. “3-D chromosomal domains and their relation to genomic function”. Poster presentation, Frontiers in Genetics X, The Hebrew University of Jerusalem, January 25, 2016.
- M. Zehavi, R. Zeira, R. Shamir. “The Copy Number Transformation Problem”. Workshop on Computational Cancer Biology, Simons Institute for Theoretical Computer Science, UC Berkeley February 2 2016, Berkeley, CA, USA.
- D. Amar, S. Izraeli, R. Shamir. “Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets”. Highlights presentation, RECOMB satellite conference on Computational Cancer Biology, April 16, 2016, Los Angeles, CA USA.
- A. Sloutskin, Y. M. Danino, Y. Zehavi, Y. Orenstein, T. Doniger, R. Shamir, T. Juven-Gershon. “ElemenT: A computational tool for detecting core promoter elements”. Poster presentation, The 18th Israeli Symposium on Bioinformatics (IBS 2016), May 18, 2016, Haifa University, Israel.
- T. A. Hait, R. Elkon and R. Shamir. “Enhancer RNAs as markers of active enhancers”. Poster presentation, The eleventh Retreat of the Edmond J. Safra Center for Bioinformatics at Tel Aviv University, Maagan, See of Galilee, Israel, May 29-30, 2016.
- R. Rozov, A. Brown Kav, D. Bogumil, E. Halperin, I. Mizrahi and R. Shamir. “Recycler : an algorithm for detecting plasmids from de novo assembly graphs”. Poster presentation, The eleventh Retreat of the Edmond J. Safra Center for Bioinformatics at Tel Aviv University, Maagan, See of Galilee, Israel, May 29-30, 2016.
- K. Perl, K. Ushakov, Y. Pozniak, O. Yizhar-Barnea, Y. Bhonker, S. Shivatzki, T. Geiger, K. B. Avraham and R. Shamir. “Changes in transcription levels across non-proliferating tissues are buffered on the protein level”. Poster presentation, The eleventh Retreat of the Edmond J. Safra Center for Bioinformatics at Tel Aviv University, Maagan, See of Galilee, Israel, May 29-30, 2016.
- R. Zeira, M. Zehavi and R. Shamir. “On copy number transformation problems”. Poster presentation, The eleventh Retreat of the Edmond J. Safra Center for Bioinformatics at Tel Aviv University, Maagan, See of Galilee, Israel, May 29-30, 2016.
- I. Nurick, M. Ozery-Flato, L. Ein-Dor and R. Shamir. “3-D chromosomal domains and their relation to genomic function”. Poster presentation, The eleventh Retreat of the Edmond J. Safra Center for Bioinformatics at Tel Aviv University, Maagan, See of Galilee, Israel, May 29-30, 2016.

- D. Netanel, A. Avraham, A. Ben-Baruch, E. Evron and R. Shamir. "Identification of breast cancer subtypes using high-throughput genomic data". Poster presentation, The eleventh Retreat of the Edmond J. Safra Center for Bioinformatics at Tel Aviv University, Maagan, See of Galilee, Israel, May 29-30, 2016.
- D. Amar, S. Izraeli and R. Shamir. "Cancer subtype classification using somatic mutation data alone and its applications". Poster presentation, The eleventh Retreat of the Edmond J. Safra Center for Bioinformatics at Tel Aviv University, Maagan, See of Galilee, Israel, May 29-30, 2016.
- D. Pellow and R. Shamir. "Clustering optical map intensity profiles for metagenomics applications". Poster presentation, The eleventh Retreat of the Edmond J. Safra Center for Bioinformatics at Tel Aviv University, Maagan, See of Galilee, Israel, May 29-30, 2016.
- Y. Orenstein, D. Pellow, G. Marcais, R. Shamir, C. Kingsford. "Compact universal k-mer hitting sets" Poster presentation, HiTseq16 conference, Orlando, Florida July 8-9 2016.
- Y. Orenstein, L. Yang, A. Jolma, J. Taipale, R. Rohs, R. Shamir. "DNA Shape Readout Specificities of Different TF Families". Oral presentation, RegGen ISMB SIG meeting, Orlando, Florida, USA, July 2016.
- D. Amar. "Novel methods for integrative analysis of heterogeneous large scale biomedical data". Biocomputing seminar. Ghent University, September 27, 2016.
- K. B. Avraham, K. Perl, K. Ushakov, Y. Pozniak, O. Yizhar-Barnea, Y. Bhonker, S. Shivatzki, T. Geiger, R. Shamir. "Transcriptomic and proteomic expression profiles of non-proliferating tissues reveal changes in protein levels are reduced relative to mRNA". Human Genome Meeting, From Genomics to therapy, Barcelona, Spain, February 5-7, 2017.