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Flatiron Institute
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&
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EDUCATION

2003	Ph.D. Biomedical Informatics Stanford University, Stanford, CA
1999	B.S. Computer Science and Biology, with Honors, *Summa Cum Laude,* Phi Beta Kappa University of Richmond, Richmond, VA

HONORS AND AWARDS

2020	FELLOW, Association for Computing Machinery
2017	FELLOW, International Society of Computational Biology
2014	IRA HERSKOWITZ AWARD, Genetic Society of America, Yeast Genetics Meeting Awarded bi-annually “for outstanding contributions in the field of yeast research in the last 20 years. This award is usually given to scientists under 50.“
2011	THE OVERTON PRIZE, International Society of Computational Biology Awarded annually “for outstanding accomplishment” by an early to mid career scientist who “has already made significant contribution to the field of computational biology”
2011	BLAVATNIK AWARD FOR YOUNG SCIENTISTS (FINALIST AWARD)
2009-2020	SENIOR FELLOW, CANADIAN INSTITUTE FOR ADVANCED RESEARCH
2011	THE 35TH ANNUAL CARL F. SCHMIDT HONORARY LECTURE, UNIVERSITY OF PENNSYLVANIA MEDICAL SCHOOL
2008	PHI BETA KAPPA TEACHING AWARD, PRINCETON UNIVERSITY
2008	MYRA SAMUELS MEMORIAL LECTURE, DEPARTMENT OF STATISTICS, PURDUE UNIVERSITY
2006	HOWARD WENTZ FACULTY AWARD, PRINCETON UNIVERSITY
2006	NSF CAREER AWARD
2005	SLOAN RESEARCH FELLOWSHIP
2004	MIT TECHNOLOGY REVIEW MAGAZINE TR35 AWARD List of top technology innovators in the world under the age of 35

RESEARCH/ADMINISTRATIVE EXPERIENCE

7/20-	**Associate Director, Lewis-Sigler Institute for Integrative Genomics, Princeton University, NJ**
11/16-	**Deputy Director for Genomics, CCB, Flatiron Institute, Simons Foundation, NY**
09/14-11/16	**Deputy Director for Genomics, Simons Center for Data Analysis, Simons Foundation, NY**
2/13-	**Professor, Princeton University, NJ** Department of Computer Science & Lewis-Sigler Institute for Integrative Genomics

10/13-08/14	**Consultant, Simons Center for Data Analysis, NY**
7/09-1/13	**Associate Professor, Princeton University, NJ** Department of Computer Science & Lewis-Sigler Institute for Integrative Genomics
6/10-6/12	**Visiting Associate Professor, Tromso University, Norway**
9/03-6/09	**Assistant Professor, Princeton University, NJ** Department of Computer Science & Lewis-Sigler Institute for Integrative Genomics
9/99-8/03	**Doctoral Student, Stanford University, CA** Dissertation: "Improving the Specificity of Biological Signal Detection from Microarray Data".
5/99-9/99	**Research Fellow, University of Haifa, Israel** Department of Computer Science and Genome Diversity Center
Sum '97&'98	**Summer Fellow, The Institute for Genomic Research (TIGR), MD**

TEACHING EXPERIENCE

Since 09/04	**COS 231/COS 232 An integrated, quantitative intro to natural sciences** Development and teaching of computer science component of the novel integrated 1st year curriculum that integrates computer science, physics, chemistry and biology
Spring 2004	**COS 554 Computational analysis of biological networks** Graduate course on analysis and modeling of biological networks from static and dynamic perspectives
10/03-10/05	**Cold Spring Harbor Laboratory Advanced Bioinformatics course** Teaching the microarray analysis component of the Advanced Bioinformatics course
09/03-5/15	**COS 557 Visualization and analysis of large-scale genomics data sets** Upper-level undergraduate and graduate course on analysis of genomic data from computational perspective
7/02-8/02	**Advanced Bioinformatics, California State University, Hayward, CA** Lecture and laboratory course on analysis of microarray datasets

PROFESSIONAL SERVICE, BOARD, AND COMMITTEE MEMBERSHIP (SELECTED)

Since 2020	National Advisory Council for Human Genome Research (appointment pending)
2019	AI Scientific Advisory Board, UCB CellTech
Since 2018	Scientific Advisory Board, Caris Life Sciences
Since 2018	Scientific Advisory Board, Computational analysis, Goldfinch Bio
Since 2017	Board of Scientific Counselors, The Jackson Laboratory
Since 2017	Selection committee of Schmidt Science Fellows, Schmidt Futures and the Rhodes Trust
2017	Advisory Committee, Harvard Department of Biostatistics, University of Pennsylvania Bioinformatics PhD Program, Dartmouth Computational Biology PhD Program
Since 2015	co-organizer of the Winter QBio conference, Hawaii, 2017
2016	Scientific Advisory Board, Interactome project
2016	American Heart Association's Strategic Planning Task Force for the new AHA Institute for Precision Cardiovascular Medicine
2015	co-Chair, Systems and Structural Biology track, Probabilistic Modeling in Genomics CSHL meeting 2015

2015	co-Chair, NIH workshop on "Phenotypes across species"
2014	Mining Biological Data Track co-Chair, CSHL Biological Data Science meeting 2014.
2012-2016	Chair, Scientific Advisory Group, GenomeSpace consortium
2012	co-Chair, NHGRI workshop "Integrating Functional Data for Connecting Genotype to Phenotype"
2012	Chair, Late Breaking Research Track, Intelligent Systems for Molecular Biology (ISMB) 2012
2011	Steering Committee, ISMB/ECCB 2011 conference Chair, Late Breaking Research Track, ISMB/ECCB 2011 conference
Since 2010	ENCODE/modENCODE External Consultants Panel
2010	Conference Chair, ISMB 2010 Conference Advisory Committee, AMIA Summit on Translational Bioinformatics 2011 Program Committee, Yeast Genetics and Molecualr Biology Meeting, 2010
Since 2010	Scientific Advisory Board, The Gene Ontology Consortium, GenomeSpace Consortium (SAG Chair since 8/2012)
2009	Program Committee, RECOMB 2009 Track Chair, 2009 Summit on Translational Bioinformatics
2008	Track co-Chair, Transcriptomics, ISMB 2008 Program Committee, Yeast Genetics and Molecular Biology Meeting, 2008 Track Chair, 2008 Summit on Translational Bioinformatics Program Committee, RECOMB Systems Biology
2007	Organizing Committee member, IPAM Workshop: Search and Knowledge Building for Biological Datasets PC co-Chair, Transcriptomics, ISMB and European Conference on Computational Biology (ECCB) 2007 PC member, Computational Systems Bioinformatics Conference (CSB) 2007 PC member, 7th Workshop on Algorithms in Bioinformatics (WABI) 2007
Since 2006	Board of Directors member, International Society for Computational Biology (ISCB)
2006	PC co-Chair, Proteomics, ISMB 2006 PC member, CSB 2006 PC member, WABI 2006 Organizer, NYAS Computational Biology and Bioinformatics Discussion Group Meetings
2005	PC member, IEEE CSB 2005 PC member, ISMB 2005.
2004	PC member, ISMB 2004
Since 2003	Member, Center for Discrete Mathematics and Theoretical Computer Science
2000	Founding co-chairwoman, Biomedical Computation @ Stanford conference.

EDITORIAL AND REVIEWING EXPERIENCES (SELECTED)

Since 2012	Series Editor (with A. Dress, M. Linial, and M. Vingron), Computational Biology series, Springer.
2006-2014	Associate Editor, *Bioinformatics*
Since 2006	ISCB Editor, *PLOS Computational Biology*
Since 09	Panels member, European Commission FP7 Systems Biology evaluations
1/06, 1/07	EU-Siemens Health-e-Child Project reviewer

Since 2005	Editorial boards, *Cell Systems*, *Genome Research*, *Journal of Biomedical Informatics, Journal of Biomedical Informatics, Bioinformatics, Biology Direct* (variable timing)
Since 2005	Various NIH and NSF study sections (variable timing)
Since 2001	Reviewer: *Science, Nature*, *Nature Genetics, Nature Oncogene, Nature Biotechnology, Cell, Bioinformatics, Protein Science, Pacific Symposium on Biocomputing, Nucleic Acids Research, BioMed Central Bioinformatics, Journal of Biomedical Informatics, Genome Research.*

RESEARCH GRANTS

9/19-8/24	NCI: Center for Synthetic Immunology: Tools to Reprogram the Immune System to Combat Cancer (**Princeton PI** with PI Wendell Lim, UCSF)
7/19-6/22	Chan Zuckerberg Initiative: A comprehensive single cell atlas of the human kidney (**Princeton PI** with PI Anna Greka, Broad Institute)
7/18-6/23	NIH/NIA: Functional networks in microglia and astrocytes regulating neuropathology of Alzheimer's Disease (**Princeton PI** with PI Greengard, Rockefeller)
4/05-3/23	NIH NIGMS RO1: Integration and Visualization of Diverse Biological Data (**PI**)
7/17-6/22	NIH/NIA: Generation of Human iPSC-derived Entorhinal Cortex Neurons for Probing Selective Neuronal Vulnerability in Alzheimer's Disease (**Princeton PI** with PI Greengard, Rockefeller)
7/17-6/22	NIH/NIDDK: Central Hub for Kidney Precision Medicine (**Princeton PI** with PI Himmelfarb, Univ of Washington)
7/17-6/22	NIH/NCATS: Microphysiological System for Kidney Disease Modeling and Drug Efficacy Testing (**Princeton PI** with PI Himmelfarb, Univ of Washington)
7/17-6/22	NIH/NIDDK: PREcision Medicine through IntErrogation of Rna in the kidney (Princeton PI with PI Kretzler, Univ of Michigan)
9/15-8/18	Simons Foundation: Methodologies for tissue- and cell-lineage specific analysis of complex functional genomic data (**PI**)
8/12-5/17	NIH NHLBI U54: Personalization of Therapeutic Efficacy and Risk (**co-PI and Director** of the Systems, Modeling, and Computation Core and of the Centralized PENTACON database, PI is Garret FitzGerald at the University of Pennsylvania School of Medicine)
11/12-11/13	2 Million Dogs Foundation: Molecular Study of Canine Mammary Tumor Development and Progression: from Genome To Clinical Outcome (**PI**)
4/05-1/16	NIH NIGMS RO1: Integration and Visualization of Diverse Biological Data (**PI**, co-PI Matthias Kretzler at the University of Michigan at Ann Harbor School of Medicine).
1/11-1/14	NIH NHGRI RO1: Context-Sensitive Search of Human Expression Compendia (**PI**, co-PI Kai Li)
12/10-12/11	Google Research Award: Social Systems for Complex Information Processing (**PI**, w. Sep Kamvar)
9/10-9/15	NIH NIAID: Modeling Immunity for Biodefense (PI: Stuart Sealfon, Mount Sinai Medical School)
8/07-5/12	NIH NCI RO1: Predicting and testing gene function in the human cell division cycle (co-PI, PI is Michael Whitfield, Dartmouth Medical School)
12/09-12/11	Project X, Princeton University Benign or Malignant: A Predictive Molecular Model of Breast Cancer Progression (**PI**)
1/07-1/08	Google Research Award. Context-sensitive search engine for cancer micro array data. (**PI**)
6/06-6/11	NSF CAREER award: An Integrated Approach to the Study of Biological Process Specific Networks. (**PI**)
9/05-8/07	Alfred P. Sloan Foundation Research Fellowship: Computational Functional Genomics is *S. cerevisiae*. (**PI**)

8/05-8/08	NSF Science and Engineering Informatics (BIO): Integrated analysis of heterogeneous genomic data for accurate prediction of gene function and interactions between proteins. (**PI**, co-PI Robert Schapire).
2/05-2/09	CSR-PDOS-Content-Searchable Storage for Feature-Rich Data. (co-PI along with Moses Charikar, Perry Cook, PI is Kai Li).
4/04-4/08	NGS: Software Tools for New-Generation, Display-Centric Applications. (co-PI along with Thomas Funkhouser, Szymon Rusinkiewicz, PI is Kai Li).

SOFTWARE RELEASED

2020	DeepSEA and ExPECTO in HumanBase: prediction of biochemical and expression effects of regulatory variants in the human genome
2020	FENRIR: associating distal regulatory regions with disease in a tissue-specific manner
2019	Selene: open source libraray for deep learning for biological sequence data
2019	URSA-HD - A Computational Framework for Genome-wide Characterization of the Human Disease Landscape
2018	YETI – analysis of individual omics experiments in the context of big data in biology
2018	DiseaseQUEST – an integrative framework for the study of human disease genes utilizing model organism experiments
2017	**HumanBase.io** – a one-stop resource of data-driven predictions about human molecular biology
2015	NetWAS – prioritization of novel disease-gene associations integrating quantitative genetics and functional networks
2015	GIANT – a web-based interactive system for analysis of tissue-specific protein function and interactions, providing functional networks in 144 tissues and cell types, and enabling analysis of tissue-specific rewiring
2015	IMP 2.0 - a web-based system for multi-species prediction of functional relationship networks, gene function and disease associations
2014	SEEK – a “google-like” search system for thousands of human gene expression datasets across >50 microarray and sequencing technology platforms
2013	nano.princeton.edu – a web server for predicting tissue- and cell-lineage-specific gene expression from large collections of expression compendia that are not necessarily resolved for that tissue
2012	IMP – a web-based system for multi-species prediction of functional relationship networks and function, using functional-knowledge based annotation transfer
2011	PILGRM – a web-based system enabling advanced machine learning analysis of large expression compendia by expert biologists
2011	Network Homologs server – a web-based system for identifying functional analogs of genes across model organisms
2010	ARAGraphle – a web-based system for tissue- and development- specific investigation of functional networks in the plant *Arabidopsis thaliana*.
2009	HEFalMp – a web-based system for interactive visualization and investigation of human functional maps in a process and disease-specific way
2008	Sleipnir – a library for very large-scale data integration and analysis
2008	MouseNET – a system for integration and analysis of biological networks in mouse
2008	HIDRA - visualization and analyis framework for simultaneously exploring multiple microarray datasets

2008	Software for analysis of cellular growth rate based on microarray data
2007	SPELL – a context-sensitive search system for very large microarray compendia
2006	MEFIT – a web-based system for microarray data integration and functional analysis
2006	GOLEM – a system for Gene Ontology navigation and analysis
2006	GRIFN – a general framework for evaluation and analysis of functional genomics data
2006	bioPIXIE – a general web-based system for data storage, integration, and methodology for prediction, visualization, and functional coherence analysis of biological pathways
2005	GeneVAND – software for visualization-based statistical analysis of microarray datasets
2005	ChARMView – software for visualization-based genome-scale discovery of aneuploidies
2004	ChARM – software for identification of chromosomal abnormalities from microarray data
2001	KNNimpute – software for missing value estimation for microarray datasets

PUBLICATIONS: Articles published in refereed journals & published review articles

***=co-corresponding authors**

1. Zhang Z, Park CY, Theesfeld CL, **Troyanskaya OG**. An automated framework for efficiently designing deep convolutional neural networks in genomics. ***Nature Machine Intelligence***. 2021.
2. Park CY, Zhou J, Wong AK, Chen KM, Theesfeld CL, Darnell RB, **Troyanskaya OG**. Genome-wide landscape of RNA-binding protein target site dysregulation reveals a major impact on psychiatric disorder risk. ***Nature Genetics***. 2021.
3. Graim K, Gorenshteyn D, Robinson DG, Carriero NJ, Cahill JA, Chakrabarti R, Goldschmidt MH, Durham AC, Funk J, Storey J, Kristensen VN, Theesfeld CL*, Sorenmo KU*, **Troyanskaya OG***. Modeling molecular development of breast cancer in canine mammary tumors. ***Genome Research***. 2020 Dec 23:gr.256388.119. doi: 10.1101/gr.256388.119. Epub ahead of print. PMID: 33361113.
4. Letizia AG, Ramos I, Obla A, Goforth C, Weir DL, Ge Y, Bamman MM, Dutta J, Ellis E, Estrella L, George MC, Gonzalez-Reiche AS, Graham WD, van de Guchte A, Gutierrez R, Jones F, Kalomoiri A, Lizewski R, Lizewski S, Marayag J, Marjanovic N, Millar EV, Nair VD, Nudelman G, Nunez E, Pike BL, Porter C, Regeimbal J, Rirak S, Santa Ana E, Sealfon RSG, Sebra R, Simons MP, Soares-Schanoski A, Sugiharto V, Termini M, Vangeti S, Williams C, **Troyanskaya OG**, van Bakel H, Sealfon SC. SARS-CoV-2 Transmission among Marine Recruits during Quarantine. ***New England Journal of Medicine***. 2020 Dec 17;383(25):2407-2416. doi: 10.1056/NEJMoa2029717. Epub 2020 Nov 11. PMID: 33176093; PMCID: PMC7675690.
5. Menon R, Otto EA, Sealfon R, Nair V, Wong AK, Theesfeld CL, Chen X, Wang Y, Boppana AS, Luo J, Yang Y, Kasson PM, Schaub JA, Berthier CC, Eddy S, Lienczewski CC, Godfrey B, Dagenais SL, Sohaney R, Hartman J, Fermin D, Subramanian L, Looker HC, Harder JL, Mariani LH, Hodgin JB, Sexton JZ, Wobus CE, Naik AS, Nelson RG, Troyanskaya OG*, Kretzler M*. SARS-CoV-2 receptor networks in diabetic and COVID-19-associated kidney disease. ***Kidney International***. 2020 Dec;98(6):1502-1518. doi: 10.1016/j.kint.2020.09.015. Epub 2020 Oct 8. PMID: 33038424; PMCID: PMC7543950.
6. Iserman C, Roden CA, Boerneke MA, Sealfon RSG, McLaughlin GA, Jungreis I, Fritch EJ, Hou YJ, Ekena J, Weidmann CA, Theesfeld CL, Kellis M, **Troyanskaya OG**, Baric RS, Sheahan TP, Weeks KM, Gladfelter AS. Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. ***Molecular Cell***. 2020 Dec 17;80(6):1078-1091.e6. doi: 10.1016/j.molcel.2020.11.041. Epub 2020 Nov 27. PMID: 33290746; PMCID: PMC7691212.
7. El-Achkar TM, Eadon MT, Menon R, Lake BB, Sigdel TK, Alexandrov T, Parikh S, Zhang G, Dobib D, Dunn KW, Otto EA, Anderton CR, Carson JM, Luo J, Park C, Hamidi H, Zhou J, Hoover P, Schroeder A, Joanes M, Azeloglu EU, Sealfon R, Winfree S, Steck B, He Y, D'Agati VD, Iyengar R,

Troyanskaya OG, Barisoni L, Gaut J, Zhang K, Laszik Z, Rovin B, Dagher PC, Sharma K, Sarwal M, Hodgin JB, Alpers CE, Kretzer M, Jain S, The Kidney Precision Medicine Project F. A Multimodal and Integrated Approach to Interrogate Human Kidney Biopsies with Rigor and Reproducibility: Guidelines from the Kidney Precision Medicine Project. ***Physiol Genomics***. 2020 Nov 16. doi: 10.1152/physiolgenomics.00104.2020. Epub ahead of print. PMID: 33197228.

8. Dannenfelser R, Allen GM, VanderSluis B, Koegel AK, Levinson S, Stark SR, Yao V, Tadych A, **Troyanskaya OG***, Lim WA*. Discriminatory Power of Combinatorial Antigen Recognition in Cancer T Cell Therapies. ***Cell Systems***. 2020 Sep 23;11(3):215-228.e5. doi: 10.1016/j.cels.2020.08.002. Epub 2020 Sep 10. PMID: 32916097.
9. Ledo JH, Zhang R, Mesin L, Mourão-Sá D, Azevedo EP, **Troyanskaya OG**, Bustos V, Greengard P. Lack of a site-specific phosphorylation of Presenilin 1 disrupts microglial gene networks and progenitors during development. ***PLoS One***. 2020 Aug 21;15(8):e0237773. doi: 10.1371/journal.pone.0237773. PMID: 32822378; PMCID: PMC7444478.
10. Ledo JH, Liebmann T, Zhang R, Chang JC, Azevedo EP, Wong E, Silva HM, **Troyanskaya OG**, Bustos V, Greengard P. Presenilin 1 phosphorylation regulates amyloid-β degradation by microglia. ***Molecular Psychiatry***. 2020 Aug 13. doi:10.1038/s41380-020-0856-8. Epub ahead of print. PMID: 32792660.
11. Orange DE, Yao V, Sawicka K, Fak J, Frank MO, Parveen S, Blachere NE, Hale C, Zhang F, Raychaudhuri S, **Troyanskaya OG**, Darnell RB. RNA Identification of PRIME Cells Predicting Rheumatoid Arthritis Flares. ***New England Jounral of Medicine***. 2020 Jul 16;383(3):218-228. doi: 10.1056/NEJMoa2004114. PMID: 32668112; PMCID: PMC7546156.
12. Sealfon RSG, Mariani LH, Kretzler M, **Troyanskaya OG**. Machine learning, the kidney, and genotype-phenotype analysis. ***Kidney International***. 2020 Jun;97(6):1141-1149. doi: 10.1016/j.kint.2020.02.028. Epub 2020 Apr 1. PMID: 32359808.
13. Richter F†, Morton SU†, Kim SW†, Kitaygorodsky A†, Wasson L†, Chen KM†, Zhou J, Qi H, Patel N, DePalma S, Parfenov M, Homsy J, Gorham JM, Manheimer KB, Velinder M, Farrell A, Marth G, Schadt EE, Kaltman JR, Newburger JW, Giardini A, Goldmuntz E, Brueckner M, Kim R, Porter GA, Bernstein D, Chung WK, Srivastava D*, Tristani-Firouzi M*, **Troyanskaya OG***, Dickel DE*, Sheng Y*, Seidman JG*, Seidman CE*, Gelb BD*. Role of noncoding de novo variants in congenital heart disease. ***Nature Genetics***. 2020; 52 (8): 769-777.
14. Menon R, Otto EA, Hoover P, Eddy S, Mariani L, Godfrey B, Berthier CC, Eichinger F, Subramanian L, Harder J, Ju W, Nair V, Larkina M, Naik AS, Luo J, Jain S, Sealfon R, **Troyanskaya O**, Hacohen N, Hodgin JB, Kretzler M, Kpmp KPMP; Nephrotic Syndrome Study Network (NEPTUNE). Single cell transcriptomics identifies focal segmental glomerulosclerosis remission endothelial biomarker. ***JCI Insight***. 2020 Mar 26;5(6):e133267. doi: 10.1172/jci.insight.133267. PMID: 32107344; PMCID: PMC7213795.
15. Roussarie JP, Yao V, Rodriguez-Rodriguez P, Oughtred R, Rust J, Plautz Z, Kasturia S, Albornoz C, Wang W, Schmidt EF, Dannenfelser R, Tadych A, Brichta L, Barnea-Cramer A, Heintz N, Hof PR, Heiman M, Dolinski K, Flajolet M, **Troyanskaya OG***, Greengard P*. Selective Neuronal Vulnerability in Alzheimer's Disease: A Network-Based Analysis. ***Neuron***. 2020 Sep 9;107(5):821-835.e12. doi:10.1016/j.neuron.2020.06.010. Epub 2020 Jun 29. PMID: 32603655; PMCID: PMC7580783.
16. Zhou J, Schor IE, Yao V, Theesfeld CL, Marco-Ferreres R, Tadych A, FurlongEEM*, **Troyanskaya OG***. Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development. ***PLoS Genetics***. 2019 Sep 25;15(9):e1008382.
17. Anikeeva P, Boyden E, Brangwynne C, Cissé II, Fiehn O, Fromme P, Gingras AC, Greene CS, Heard E, Hell SW, Hillman E, Jensen GJ, Karchin R, Kiessling LL, Kleinstiver BP, Knight R, Kukura P, Lancaster MA, Loman N, Looger L, Lundberg E, Luo Q, Miyawaki A, Myers EW Jr, Nolan GP, Picotti P, Reik W, Sauer M, Shalek AK, Shendure J, Slavov N, Tanay A, **Troyanskaya O**, van Valen D, Wang

HW, Yi C, Yin P, Zernicka-Goetz M, Zhuang X. Voices in methods development. ***Nature Methods***. 2019 Oct;16(10):945-951.

18. Zhu Q, Tekpli X, **Troyanskaya OG***, Kristensen VN*. Subtype-specific transcriptional regulators in breast tumors subjected to genetic and epigenetic alterations. ***Bioinformatics***. 2020 Feb 15;36(4):994-999
19. Sargin D, Chottekalapanda RU, Perit KE, Yao V, Chu D, Sparks DW, Kalik S, Power SK, **Troyanskaya OG**, Schmidt EF, Greengard P, Lambe EK. Mapping the physiological and molecular markers of stress and SSRI antidepressant treatment in S100a10 corticostriatal neurons. ***Mol Psychiatry***. 2019 Aug 20.
20. Zhou J, Park CY, Theesfeld CL, Wong AK, Yuan Y, Scheckel C, Fak JJ, Funk J, Yao K, Tajima Y, Packer A, Darnell RB, **Troyanskaya OG**. Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. ***Nature Genetics***. 2019 Jun;51(6):973-980.
21. Bradley PH, Gibney PA, Botstein D, **Troyanskaya OG**, Rabinowitz JD. Minor Isozymes Tailor Yeast Metabolism to Carbon Availability. ***mSystems***. 2019
22. Chen KM, Cofer EM, Zhou J, **Troyanskaya OG**. Selene: a PyTorch-based deep learning library for sequence data. ***Nature Methods***. 2019 Apr;16(4):315-318.
23. Shrine N, Guyatt AL, Erzurumluoglu AM, Jackson VE, Hobbs BD, Melbourne CA, … **Troyanskaya OG**, …Wain LV; Understanding Society Scientific Group. New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. ***Nature Genetics***. 2019 Mar;51(3):481-493.
24. Lee YS, Krishnan A, Oughtred R, Rust J, Chang CS, Ryu J, Kristensen VN, Dolinski K, Theesfeld CL, **Troyanskaya OG**. A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. ***Cell Systems***. 2019 Jan 14.
25. Lee YS, Wong AK, Tadych A, Hartmann BM, Park CY, DeJesus VA, Ramos I, Zaslavsky E, Sealfon* SC, **Troyanskaya OG***. Interpretation of an individual functional genomics experiment guided by massive public data. ***Nature Methods.*** 2018 Dec 15.
26. Yao V, Kaletsky R, Keyes W, Mor DE, Wong AK, Sohrabi S, Murphy CT*, **Troyanskaya OG***. An integrative tissue-network approach to identify and test human disease genes. ***Nature Biotechnology.*** 2018 Oct 22.
27. Menon R, Otto EA, Kokoruda A, Zhou J, Zhang Z, Yoon E, Chen YC, **Troyanskaya O**, Spence JR, Kretzler M, Cebrián C. Single-cell analysis of progenitor cell dynamics and lineage specification in the human fetal kidney. ***Development.*** 2018 Aug 30.
28. Jabeen S, Zucknick M, Nome M, Dannenfelser R, Fleischer T, Kumar S, Lüders T, von der Lippe Gythfeldt H, **Troyanskaya O**, Kyte JA, Børresen-Dale AL, Naume B, Tekpli X, Engebraaten O, Kristensen V. Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. ***Oncoimmunology.*** 2018 Aug 6.
29. Kaletsky R*, Yao V*, Williams A, Runnels AM, Tadych A, Zhou S, **Troyanskaya OG***, Murphy CT*. Transcriptome analysis of adult Caenorhabditis elegans cells reveals tissue-specific gene and isoform expression. ***PLoS Genetics.*** 2018 Aug.
30. Zhou J, Theesfeld CL, Yao K, Chen KM, Wong AK, **Troyanskaya OG**. Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk. ***Nature Genetics.*** 2018 Jul 16.
31. Yao V, Wong AK, **Troyanskaya OG**. Enabling Precision Medicine through Integrative Network Models. ***Journal of Molecular Biology.*** 2018 Jul 9.
32. Wong AK, Krishnan A, Troyanskaya OG. GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. ***Nucleic Acids Research.*** 2018 May 25.
33. Rangan AV, McGrouther CC, Kelsoe, Schork, Stahl, Zhu Q, Krishnan A, Yao V, **Troyanskaya O**, Bilaloglu, Raghavan, Bergen, Jureus, Landen. A loop-counting method for covariate-corrected low-rank

biclustering of gene-expression and genome-wide association study data. ***PLoS computational biology*** 14 (5), e1006105. 2018

34. T Clancy, R Dannenfelser, **O Troyanskaya**, KJ Malmberg, E Hovig, V Kristensen. Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. ***Current pharmaceutical design*** 23 (32), 4716-4725. 2018.
35. Dannenfelser R, Nome M, Tahiri A, Ursini-Siegel J, Vollan HKM, Haakensen VD, Helland A, Naume B, Caldas C, Borresen-Dale AL, Kristensen VN, **Troyanskaya OG**. Data-driven analysis of immune infiltrate in a large cohort of breast cancer and its association with disease progression, ER activity, and genomic complexity. ***Oncotarget.*** 2017;8(34):57121-33. doi: 10.18632/oncotarget.19078. PubMed PMID: 28915659; PMCID: PMC5593630.
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