

Olga G Troyanskaya

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5113145/olga-g-troyanskaya-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

96

papers

6,738

citations

36

h-index

82

g-index

107

ext. papers

9,070

ext. citations

15

avg, IF

6.18

L-index

#	Paper	IF	Citations
96	Predicting effects of noncoding variants with deep learning-based sequence model. <i>Nature Methods</i> , 2015 , 12, 931-4	21.6	1057
95	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016 , 353,	33.3	626
94	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015 , 47, 569-76	36.3	473
93	A Bayesian framework for combining heterogeneous data sources for gene function prediction (in <i>Saccharomyces cerevisiae</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 8348-53	11.5	431
92	Hierarchical multi-label prediction of gene function. <i>Bioinformatics</i> , 2006 , 22, 830-6	7.2	341
91	Nonparametric methods for identifying differentially expressed genes in microarray data. <i>Bioinformatics</i> , 2002 , 18, 1454-61	7.2	245
90	Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder. <i>Nature Neuroscience</i> , 2016 , 19, 1454-1462	25.5	214
89	Exploring the functional landscape of gene expression: directed search of large microarray compendia. <i>Bioinformatics</i> , 2007 , 23, 2692-9	7.2	202
88	Discovery of biological networks from diverse functional genomic data. <i>Genome Biology</i> , 2005 , 6, R114	18.3	162
87	Exploring the human genome with functional maps. <i>Genome Research</i> , 2009 , 19, 1093-106	9.7	159
86	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019 , 51, 481-493	36.3	156
85	Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk. <i>Nature Genetics</i> , 2018 , 50, 1171-1179	36.3	155
84	Finding function: evaluation methods for functional genomic data. <i>BMC Genomics</i> , 2006 , 7, 187	4.5	154
83	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. <i>Nature Genetics</i> , 2019 , 51, 973-980	36.3	122
82	Tissue-specific functional networks for prioritizing phenotype and disease genes. <i>PLoS Computational Biology</i> , 2012 , 8, e1002694	5	114
81	IFN γ Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. <i>Cell</i> , 2017 , 170, 127-141.e15	56.2	104
80	A scalable method for integration and functional analysis of multiple microarray datasets. <i>Bioinformatics</i> , 2006 , 22, 2890-7	7.2	101

79	Accurate detection of aneuploidies in array CGH and gene expression microarray data. <i>Bioinformatics</i> , 2004 , 20, 3533-43	7.2	100
78	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020 , 80, 1078-1091.e6	17.6	98
77	A genomewide functional network for the laboratory mouse. <i>PLoS Computational Biology</i> , 2008 , 4, e1000165	9	94
76	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. <i>Nature Methods</i> , 2015 , 12, 211-4, 3 p following 214	21.6	92
75	Context-sensitive data integration and prediction of biological networks. <i>Bioinformatics</i> , 2007 , 23, 2322-30	7	91
74	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , 2012 , 40, W484-90	20.1	76
73	Global prediction of tissue-specific gene expression and context-dependent gene networks in <i>Caenorhabditis elegans</i> . <i>PLoS Computational Biology</i> , 2009 , 5, e1000417	5	71
72	Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms. <i>Bioinformatics</i> , 2015 , 31, 1093-101	7.2	63
71	SynNotch-CAR T cells overcome challenges of specificity, heterogeneity, and persistence in treating glioblastoma. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	61
70	The Sleipnir library for computational functional genomics. <i>Bioinformatics</i> , 2008 , 24, 1559-61	7.2	59
69	Putting microarrays in a context: integrated analysis of diverse biological data. <i>Briefings in Bioinformatics</i> , 2005 , 6, 34-43	13.4	55
68	Single cell transcriptomics identifies focal segmental glomerulosclerosis remission endothelial biomarker. <i>JCI Insight</i> , 2020 , 5,	9.9	52
67	Metabolic network rewiring of propionate flux compensates vitamin B12 deficiency in <i>C. elegans</i> . <i>ELife</i> , 2016 , 5,	8.9	51
66	Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type TP53. <i>Molecular Cancer Research</i> , 2015 , 13, 493-501	6.6	48
65	Selene: a PyTorch-based deep learning library for sequence data. <i>Nature Methods</i> , 2019 , 16, 315-318	21.6	47
64	Functional genomics complements quantitative genetics in identifying disease-gene associations. <i>PLoS Computational Biology</i> , 2010 , 6, e1000991	5	46
63	IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , 2015 , 43, W128-33	20.1	44
62	Functional knowledge transfer for high-accuracy prediction of under-studied biological processes. <i>PLoS Computational Biology</i> , 2013 , 9, e1002957	5	44

61	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. <i>Immunity</i> , 2015 , 43, 605-14	32.3	41
60	Selective Neuronal Vulnerability in Alzheimer's Disease: A Network-Based Analysis. <i>Neuron</i> , 2020 , 107, 821-835.e12	13.9	35
59	Genomic analyses implicate noncoding de novo variants in congenital heart disease. <i>Nature Genetics</i> , 2020 , 52, 769-777	36.3	33
58	SARS-CoV-2 receptor networks in diabetic and COVID-19-associated kidney disease. <i>Kidney International</i> , 2020 , 98, 1502-1518	9.9	33
57	GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. <i>Nucleic Acids Research</i> , 2018 , 46, W65-W70	20.1	33
56	Directing experimental biology: a case study in mitochondrial biogenesis. <i>PLoS Computational Biology</i> , 2009 , 5, e1000322	5	31
55	An integrative tissue-network approach to identify and test human disease genes. <i>Nature Biotechnology</i> , 2018 ,	44.5	31
54	Implications of Big Data for cell biology. <i>Molecular Biology of the Cell</i> , 2015 , 26, 2575-8	3.5	30
53	Specific viral RNA drives the SARS CoV-2 nucleocapsid to phase separate 2020 ,		28
52	Global quantitative modeling of chromatin factor interactions. <i>PLoS Computational Biology</i> , 2014 , 10, e1003525	5	26
51	Discriminatory Power of Combinatorial Antigen Recognition in Cancer T Cell Therapies. <i>Cell Systems</i> , 2020 , 11, 215-228.e5	10.6	26
50	Accurate quantification of functional analogy among close homologs. <i>PLoS Computational Biology</i> , 2011 , 7, e1001074	5	25
49	Data-driven analysis of immune infiltrate in a large cohort of breast cancer and its association with disease progression, ER activity, and genomic complexity. <i>Oncotarget</i> , 2017 , 8, 57121-57133	3.3	24
48	Ontology-aware classification of tissue and cell-type signals in gene expression profiles across platforms and technologies. <i>Bioinformatics</i> , 2013 , 29, 3036-44	7.2	21
47	Mapping dynamic histone acetylation patterns to gene expression in nanog-depleted murine embryonic stem cells. <i>PLoS Computational Biology</i> , 2010 , 6, e1001034	5	20
46	Accurate evaluation and analysis of functional genomics data and methods. <i>Annals of the New York Academy of Sciences</i> , 2012 , 1260, 95-100	6.5	19
45	Simultaneous genome-wide inference of physical, genetic, regulatory, and functional pathway components. <i>PLoS Computational Biology</i> , 2010 , 6, e1001009	5	17
44	FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , 2015 , 43, W182-7	20.1	16

43	Discovering biological networks from diverse functional genomic data. <i>Methods in Molecular Biology</i> , 2009 , 563, 157-75	1.4	16
42	Low-variance RNAs identify Parkinson's disease molecular signature in blood. <i>Movement Disorders</i> , 2015 , 30, 813-21	7	14
41	Graphle: Interactive exploration of large, dense graphs. <i>BMC Bioinformatics</i> , 2009 , 10, 417	3.6	14
40	Probabilistic modelling of chromatin code landscape reveals functional diversity of enhancer-like chromatin states. <i>Nature Communications</i> , 2016 , 7, 10528	17.4	13
39	Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. <i>Oncolmmunology</i> , 2018 , 7, e1457598	7.2	13
38	Enabling Precision Medicine through Integrative Network Models. <i>Journal of Molecular Biology</i> , 2018 , 430, 2913-2923	6.5	11
37	A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. <i>Cell Systems</i> , 2019 , 8, 152-162.e6	10.6	10
36	Genome-wide landscape of RNA-binding protein target site dysregulation reveals a major impact on psychiatric disorder risk. <i>Nature Genetics</i> , 2021 , 53, 166-173	36.3	10
35	Artificial intelligence and cancer.. <i>Nature Cancer</i> , 2020 , 1, 149-152	15.4	9
34	BAYESIAN DATA INTEGRATION: A FUNCTIONAL PERSPECTIVE 2006 ,		9
33	Machine learning, the kidney, and genotype-phenotype analysis. <i>Kidney International</i> , 2020 , 97, 1141-1149	9	8
32	Single nucleus multi-omics regulatory landscape of the murine pituitary. <i>Nature Communications</i> , 2021 , 12, 2677	17.4	8
31	Spatial transcriptional mapping of the human nephrogenic program. <i>Developmental Cell</i> , 2021 , 56, 2381-2398.e6	23.98	8
30	Presenilin 1 phosphorylation regulates amyloid- β degradation by microglia. <i>Molecular Psychiatry</i> , 2020 ,	15.1	7
29	An automated framework for efficiently designing deep convolutional neural networks in genomics. <i>Nature Machine Intelligence</i> , 2021 , 3, 392-400	22.5	7
28	CROTON: an automated and variant-aware deep learning framework for predicting CRISPR/Cas9 editing outcomes. <i>Bioinformatics</i> , 2021 , 37, i342-i348	7.2	7
27	Decoding disease: from genomes to networks to phenotypes. <i>Nature Reviews Genetics</i> , 2021 , 22, 774-790	10.1	7
26	Minor Isozymes Tailor Yeast Metabolism to Carbon Availability. <i>MSystems</i> , 2019 , 4,	7.6	6

25	Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. <i>Current Pharmaceutical Design</i> , 2017 , 23, 4716-4725	3.3	6
24	Tissue-specific enhancer functional networks for associating distal regulatory regions to disease. <i>Cell Systems</i> , 2021 , 12, 353-362.e6	10.6	6
23	Mapping the physiological and molecular markers of stress and SSRI antidepressant treatment in S100a10 corticostriatal neurons. <i>Molecular Psychiatry</i> , 2020 , 25, 1112-1129	15.1	6
22	Lack of a site-specific phosphorylation of Presenilin 1 disrupts microglial gene networks and progenitors during development. <i>PLoS ONE</i> , 2020 , 15, e0237773	3.7	5
21	Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development. <i>PLoS Genetics</i> , 2019 , 15, e1008382	6	4
20	Viable virus shedding during SARS-CoV-2 reinfection. <i>Lancet Respiratory Medicine</i> , 2021 , 9, e56-e57	35.1	3
19	GIANT API: an application programming interface for functional genomics. <i>Nucleic Acids Research</i> , 2016 , 44, W587-92	20.1	2
18	Genome-wide characterization of genetic and functional dysregulation in autism spectrum disorder		2
17	Modeling transcriptional regulation of model species with deep learning. <i>Genome Research</i> , 2021 , 31, 1097-1105	9.7	2
16	Interpretation of an individual functional genomics experiment guided by massive public data. <i>Nature Methods</i> , 2018 , 15, 1049-1052	21.6	2
15	A sequence-based global map of regulatory activity for deciphering human genetics		2
14	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. <i>Cancer Cell</i> , 2022 , 40, 524-544.e5	24.3	2
13	Selene: a PyTorch-based deep learning library for biological sequence-level data		1
12	An analytical framework for interpretable and generalizable single-cell data analysis. <i>Nature Methods</i> , 2021 , 18, 1317-1321	21.6	1
11	DeepArk: modeling cis-regulatory codes of model species with deep learning		1
10	Single nucleus multi-omics regulatory atlas of the murine pituitary		1
9	An automated framework for efficiently designing deep convolutional neural networks in genomics		1
8	Single nucleus pituitary transcriptomic and epigenetic landscape reveals human stem cell heterogeneity with diverse regulatory mechanisms		1

7	AMBIENT: Accelerated Convolutional Neural Network Architecture Search for Regulatory Genomics		1
6	A loop-counting method for covariate-corrected low-rank biclustering of gene-expression and genome-wide association study data. <i>PLoS Computational Biology</i> , 2018 , 14, e1006105	5	1
5	Single nucleus transcriptome and chromatin accessibility of postmortem human pituitaries reveal diverse stem cell regulatory mechanisms.. <i>Cell Reports</i> , 2022 , 38, 110467	10.6	1
4	Asymptomatic SARS-CoV-2 Infection Is Associated With Higher Levels of Serum IL-17C, Matrix Metalloproteinase 10 and Fibroblast Growth Factors Than Mild Symptomatic COVID-19.. <i>Frontiers in Immunology</i> , 2022 , 13, 821730	8.4	1
3	Machine learning methods to model multicellular complexity and tissue specificity. <i>Nature Reviews Materials</i> , 2021 , 6, 717-729	73.3	0
2	"Getting started in...": a series not to miss. <i>PLoS Computational Biology</i> , 2007 , 3, 1841	5	
1	Unsupervised Machine Learning to Support Functional Characterization of Genes: Emphasis on Cluster Description and Class Discovery 2005 , 175-192		