

Olga G Troyanskaya

List of Publications by Year in Descending Order

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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	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
95	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
94	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
93	An analytical framework for interpretable and generalizable single-cell data analysis. <i>Nature Methods</i> , 2021 , 18, 1317-1321	21.6	1
92	An automated framework for efficiently designing deep convolutional neural networks in genomics. <i>Nature Machine Intelligence</i> , 2021 , 3, 392-400	22.5	7
91	Tissue-specific enhancer functional networks for associating distal regulatory regions to disease. <i>Cell Systems</i> , 2021 , 12, 353-362.e6	10.6	6
90	Modeling transcriptional regulation of model species with deep learning. <i>Genome Research</i> , 2021 , 31, 1097-1105	9.7	2
89	SynNotch-CAR T cells overcome challenges of specificity, heterogeneity, and persistence in treating glioblastoma. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	61
88	Viable virus shedding during SARS-CoV-2 reinfection. <i>Lancet Respiratory Medicine</i> , 2021 , 9, e56-e57	35.1	3
87	Single nucleus multi-omics regulatory landscape of the murine pituitary. <i>Nature Communications</i> , 2021 , 12, 2677	17.4	8
86	Machine learning methods to model multicellular complexity and tissue specificity. <i>Nature Reviews Materials</i> , 2021 , 6, 717-729	73.3	0
85	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
84	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
83	Spatial transcriptional mapping of the human nephrogenic program. <i>Developmental Cell</i> , 2021 , 56, 2381-2398.e6	23.8	6
82	Decoding disease: from genomes to networks to phenotypes. <i>Nature Reviews Genetics</i> , 2021 , 22, 774-790.e1	30.1	7
81	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020 , 80, 1078-1091.e6	17.6	98
80	Selective Neuronal Vulnerability in Alzheimer's Disease: A Network-Based Analysis. <i>Neuron</i> , 2020 , 107, 821-835.e12	13.9	35

79	Genomic analyses implicate noncoding de novo variants in congenital heart disease. <i>Nature Genetics</i> , 2020 , 52, 769-777	36.3	33
78	Artificial intelligence and cancer.. <i>Nature Cancer</i> , 2020 , 1, 149-152	15.4	9
77	Machine learning, the kidney, and genotype-phenotype analysis. <i>Kidney International</i> , 2020 , 97, 1141-1149	9.9	8
76	Single cell transcriptomics identifies focal segmental glomerulosclerosis remission endothelial biomarker. <i>JCI Insight</i> , 2020 , 5,	9.9	52
75	Specific viral RNA drives the SARS CoV-2 nucleocapsid to phase separate 2020 ,		28
74	Discriminatory Power of Combinatorial Antigen Recognition in Cancer T Cell Therapies. <i>Cell Systems</i> , 2020 , 11, 215-228.e5	10.6	26
73	SARS-CoV-2 receptor networks in diabetic and COVID-19-associated kidney disease. <i>Kidney International</i> , 2020 , 98, 1502-1518	9.9	33
72	Presenilin 1 phosphorylation regulates amyloid- β degradation by microglia. <i>Molecular Psychiatry</i> , 2020 ,	15.1	7
71	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
70	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
69	Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development. <i>PLoS Genetics</i> , 2019 , 15, e1008382	6	4
68	A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. <i>Cell Systems</i> , 2019 , 8, 152-162.e6	10.6	10
67	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. <i>Nature Genetics</i> , 2019 , 51, 973-980	36.3	122
66	Selene: a PyTorch-based deep learning library for sequence data. <i>Nature Methods</i> , 2019 , 16, 315-318	21.6	47
65	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
64	Minor Isozymes Tailor Yeast Metabolism to Carbon Availability. <i>MSystems</i> , 2019 , 4,	7.6	6
63	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
62	Enabling Precision Medicine through Integrative Network Models. <i>Journal of Molecular Biology</i> , 2018 , 430, 2913-2923	6.5	11

61	Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. <i>Oncotarget</i> , 2018 , 7, e1457598	7.2	13
60	Interpretation of an individual functional genomics experiment guided by massive public data. <i>Nature Methods</i> , 2018 , 15, 1049-1052	21.6	2
59	An integrative tissue-network approach to identify and test human disease genes. <i>Nature Biotechnology</i> , 2018 ,	44.5	31
58	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
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	IFN γ -Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. <i>Cell</i> , 2017 , 170, 127-141.e15	56.2	104
55	Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. <i>Current Pharmaceutical Design</i> , 2017 , 23, 4716-4725	3.3	6
54	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
53	GIANT API: an application programming interface for functional genomics. <i>Nucleic Acids Research</i> , 2016 , 44, W587-92	20.1	2
52	Probabilistic modelling of chromatin code landscape reveals functional diversity of enhancer-like chromatin states. <i>Nature Communications</i> , 2016 , 7, 10528	17.4	13
51	Metabolic network rewiring of propionate flux compensates vitamin B12 deficiency in <i>C. elegans</i> . <i>ELife</i> , 2016 , 5,	8.9	51
50	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016 , 353,	33.3	626
49	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
48	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
47	Implications of Big Data for cell biology. <i>Molecular Biology of the Cell</i> , 2015 , 26, 2575-8	3.5	30
46	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015 , 47, 569-76	36.3	473
45	Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms. <i>Bioinformatics</i> , 2015 , 31, 1093-101	7.2	63
44	Low-variance RNAs identify Parkinson's disease molecular signature in blood. <i>Movement Disorders</i> , 2015 , 30, 813-21	7	14

43	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
42	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
41	Predicting effects of noncoding variants with deep learning-based sequence model. <i>Nature Methods</i> , 2015 , 12, 931-4	21.6	1057
40	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. <i>Immunity</i> , 2015 , 43, 605-14	32.3	41
39	FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , 2015 , 43, W182-7	20.1	16
38	Global quantitative modeling of chromatin factor interactions. <i>PLoS Computational Biology</i> , 2014 , 10, e1003525	5	26
37	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
36	Functional knowledge transfer for high-accuracy prediction of under-studied biological processes. <i>PLoS Computational Biology</i> , 2013 , 9, e1002957	5	44
35	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
34	Tissue-specific functional networks for prioritizing phenotype and disease genes. <i>PLoS Computational Biology</i> , 2012 , 8, e1002694	5	114
33	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
32	Accurate quantification of functional analogy among close homologs. <i>PLoS Computational Biology</i> , 2011 , 7, e1001074	5	25
31	Simultaneous genome-wide inference of physical, genetic, regulatory, and functional pathway components. <i>PLoS Computational Biology</i> , 2010 , 6, e1001009	5	17
30	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
29	Functional genomics complements quantitative genetics in identifying disease-gene associations. <i>PLoS Computational Biology</i> , 2010 , 6, e1000991	5	46
28	Directing experimental biology: a case study in mitochondrial biogenesis. <i>PLoS Computational Biology</i> , 2009 , 5, e1000322	5	31
27	Exploring the human genome with functional maps. <i>Genome Research</i> , 2009 , 19, 1093-106	9.7	159
26	Graphle: Interactive exploration of large, dense graphs. <i>BMC Bioinformatics</i> , 2009 , 10, 417	3.6	14

25	Discovering biological networks from diverse functional genomic data. <i>Methods in Molecular Biology</i> , 2009 , 563, 157-75	1.4	16
24	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
23	A genomewide functional network for the laboratory mouse. <i>PLoS Computational Biology</i> , 2008 , 4, e1000165	9	94
22	The Sleipnir library for computational functional genomics. <i>Bioinformatics</i> , 2008 , 24, 1559-61	7.2	59
21	"Getting started in...": a series not to miss. <i>PLoS Computational Biology</i> , 2007 , 3, 1841	5	
20	Exploring the functional landscape of gene expression: directed search of large microarray compendia. <i>Bioinformatics</i> , 2007 , 23, 2692-9	7.2	202
19	Context-sensitive data integration and prediction of biological networks. <i>Bioinformatics</i> , 2007 , 23, 2322-30	7	91
18	Finding function: evaluation methods for functional genomic data. <i>BMC Genomics</i> , 2006 , 7, 187	4.5	154
17	A scalable method for integration and functional analysis of multiple microarray datasets. <i>Bioinformatics</i> , 2006 , 22, 2890-7	7.2	101
16	Hierarchical multi-label prediction of gene function. <i>Bioinformatics</i> , 2006 , 22, 830-6	7.2	341
15	BAYESIAN DATA INTEGRATION: A FUNCTIONAL PERSPECTIVE 2006 ,		9
14	Putting microarrays in a context: integrated analysis of diverse biological data. <i>Briefings in Bioinformatics</i> , 2005 , 6, 34-43	13.4	55
13	Discovery of biological networks from diverse functional genomic data. <i>Genome Biology</i> , 2005 , 6, R114	18.3	162
12	Unsupervised Machine Learning to Support Functional Characterization of Genes: Emphasis on Cluster Description and Class Discovery 2005 , 175-192		
11	Accurate detection of aneuploidies in array CGH and gene expression microarray data. <i>Bioinformatics</i> , 2004 , 20, 3533-43	7.2	100
10	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
9	Nonparametric methods for identifying differentially expressed genes in microarray data. <i>Bioinformatics</i> , 2002 , 18, 1454-61	7.2	245
8	Selene: a PyTorch-based deep learning library for biological sequence-level data		1

7	DeepArk: modeling cis-regulatory codes of model species with deep learning	1
6	Single nucleus multi-omics regulatory atlas of the murine pituitary	1
5	An automated framework for efficiently designing deep convolutional neural networks in genomics	1
4	Genome-wide characterization of genetic and functional dysregulation in autism spectrum disorder	2
3	Single nucleus pituitary transcriptomic and epigenetic landscape reveals human stem cell heterogeneity with diverse regulatory mechanisms	1
2	AMBIENT: Accelerated Convolutional Neural Network Architecture Search for Regulatory Genomics	1
1	A sequence-based global map of regulatory activity for deciphering human genetics	2