

Olga G Troyanskaya

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

10,614
citations

71102

41
h-index

45317

90
g-index

107
all docs

107
docs citations

107
times ranked

15595
citing authors

#	ARTICLE	IF	CITATIONS
1	Single nucleus transcriptome and chromatin accessibility of postmortem human pituitaries reveal diverse stem cell regulatory mechanisms. <i>Cell Reports</i> , 2022, 38, 110467.	6.4	27
2	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.	4.8	21
3	Molecular Characterization of Membranous Nephropathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 1208-1221.	6.1	12
4	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. <i>Cancer Cell</i> , 2022, 40, 524-544.e5.	16.8	23
5	A reference tissue atlas for the human kidney. <i>Science Advances</i> , 2022, 8, .	10.3	67
6	A sequence-based global map of regulatory activity for deciphering human genetics. <i>Nature Genetics</i> , 2022, 54, 940-949.	21.4	71
7	Presenilin 1 phosphorylation regulates amyloid- β^2 degradation by microglia. <i>Molecular Psychiatry</i> , 2021, 26, 5620-5635.	7.9	17
8	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.	21.4	49
9	An automated framework for efficiently designing deep convolutional neural networks in genomics. <i>Nature Machine Intelligence</i> , 2021, 3, 392-400.	16.0	29
10	Tissue-specific enhancer functional networks for associating distal regulatory regions to disease. <i>Cell Systems</i> , 2021, 12, 353-362.e6.	6.2	24
11	Modeling transcriptional regulation of model species with deep learning. <i>Genome Research</i> , 2021, 31, 1097-1105.	5.5	5
12	SynNotch-CAR T cells overcome challenges of specificity, heterogeneity, and persistence in treating glioblastoma. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	215
13	Viable virus shedding during SARS-CoV-2 reinfection. <i>Lancet Respiratory Medicine</i> , 2021, 9, e56-e57.	10.7	11
14	Single nucleus multi-omics regulatory landscape of the murine pituitary. <i>Nature Communications</i> , 2021, 12, 2677.	12.8	38
15	Machine learning methods to model multicellular complexity and tissue specificity. <i>Nature Reviews Materials</i> , 2021, 6, 717-729.	48.7	13
16	CROTON: an automated and variant-aware deep learning framework for predicting CRISPR/Cas9 editing outcomes. <i>Bioinformatics</i> , 2021, 37, i342-i348.	4.1	17
17	Spatial transcriptional mapping of the human nephrogenic program. <i>Developmental Cell</i> , 2021, 56, 2381-2398.e6.	7.0	44
18	Decoding disease: from genomes to networks to phenotypes. <i>Nature Reviews Genetics</i> , 2021, 22, 774-790.	16.3	46

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19	An analytical framework for interpretable and generalizable single-cell data analysis. <i>Nature Methods</i> , 2021, 18, 1317-1321.	19.0	9
20	Mapping the physiological and molecular markers of stress and SSRI antidepressant treatment in S100a10 corticostriatal neurons. <i>Molecular Psychiatry</i> , 2020, 25, 1112-1129.	7.9	18
21	Discriminatory Power of Combinatorial Antigen Recognition in Cancer T Cell Therapies. <i>Cell Systems</i> , 2020, 11, 215-228.e5.	6.2	52
22	SARS-CoV-2 receptor networks in diabetic and COVID-19-associated kidney disease. <i>Kidney International</i> , 2020, 98, 1502-1518.	5.2	64
23	Lack of a site-specific phosphorylation of Presenilin 1 disrupts microglial gene networks and progenitors during development. <i>PLoS ONE</i> , 2020, 15, e0237773.	2.5	11
24	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020, 80, 1078-1091.e6.	9.7	255
25	Selective Neuronal Vulnerability in Alzheimer's Disease: A Network-Based Analysis. <i>Neuron</i> , 2020, 107, 821-835.e12.	8.1	99
26	Genomic analyses implicate noncoding de novo variants in congenital heart disease. <i>Nature Genetics</i> , 2020, 52, 769-777.	21.4	97
27	Artificial intelligence and cancer. <i>Nature Cancer</i> , 2020, 1, 149-152.	13.2	26
28	Machine learning, the kidney, and genotype-phenotype analysis. <i>Kidney International</i> , 2020, 97, 1141-1149.	5.2	23
29	Single cell transcriptomics identifies focal segmental glomerulosclerosis remission endothelial biomarker. <i>JCI Insight</i> , 2020, 5, .	5.0	108
30	Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development. <i>PLoS Genetics</i> , 2019, 15, e1008382.	3.5	9
31	A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. <i>Cell Systems</i> , 2019, 8, 152-162.e6.	6.2	19
32	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. <i>Nature Genetics</i> , 2019, 51, 973-980.	21.4	216
33	Selene: a PyTorch-based deep learning library for sequence data. <i>Nature Methods</i> , 2019, 16, 315-318.	19.0	98
34	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.	21.4	350
35	Minor Isozymes Tailor Yeast Metabolism to Carbon Availability. <i>MSystems</i> , 2019, 4, .	3.8	14
36	Voices in methods development. <i>Nature Methods</i> , 2019, 16, 945-951.	19.0	5

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37	Interpretation of an individual functional genomics experiment guided by massive public data. <i>Nature Methods</i> , 2018, 15, 1049-1052.	19.0	5
38	An integrative tissue-network approach to identify and test human disease genes. <i>Nature Biotechnology</i> , 2018, 36, 1091-1099.	17.5	54
39	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.	3.2	3
40	GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. <i>Nucleic Acids Research</i> , 2018, 46, W65-W70.	14.5	59
41	Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk. <i>Nature Genetics</i> , 2018, 50, 1171-1179.	21.4	375
42	Enabling Precision Medicine through Integrative Network Models. <i>Journal of Molecular Biology</i> , 2018, 430, 2913-2923.	4.2	15
43	Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. <i>Oncotarget</i> , 2018, 9, e1457598.	4.6	18
44	IFN β -Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. <i>Cell</i> , 2017, 170, 127-141.e15.	28.9	140
45	Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. <i>Current Pharmaceutical Design</i> , 2017, 23, 4716-4725.	1.9	11
46	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.	1.8	31
47	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	12.6	979
48	Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder. <i>Nature Neuroscience</i> , 2016, 19, 1454-1462.	14.8	359
49	GIANT API: an application programming interface for functional genomics. <i>Nucleic Acids Research</i> , 2016, 44, W587-W592.	14.5	2
50	Probabilistic modelling of chromatin code landscape reveals functional diversity of enhancer-like chromatin states. <i>Nature Communications</i> , 2016, 7, 10528.	12.8	18
51	Metabolic network rewiring of propionate flux compensates vitamin B12 deficiency in <i>C. elegans</i> . <i>ELife</i> , 2016, 5, .	6.0	96
52	FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , 2015, 43, W182-W187.	14.5	25
53	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. <i>Nature Methods</i> , 2015, 12, 211-214.	19.0	137
54	Implications of Big Data for cell biology. <i>Molecular Biology of the Cell</i> , 2015, 26, 2575-2578.	2.1	42

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55	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015, 47, 569-576.	21.4	738
56	Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms. <i>Bioinformatics</i> , 2015, 31, 1093-1101.	4.1	99
57	Low-variance RNAs identify Parkinson's disease molecular signature in blood. <i>Movement Disorders</i> , 2015, 30, 813-821.	3.9	18
58	Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type <i>TP53</i> . <i>Molecular Cancer Research</i> , 2015, 13, 493-501.	3.4	53
59	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-W133.	14.5	60
60	Predicting effects of noncoding variants with deep learning-based sequence model. <i>Nature Methods</i> , 2015, 12, 931-934.	19.0	1,714
61	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. <i>Immunity</i> , 2015, 43, 605-614.	14.3	49
62	Global Quantitative Modeling of Chromatin Factor Interactions. <i>PLoS Computational Biology</i> , 2014, 10, e1003525.	3.2	32
63	Ontology-aware classification of tissue and cell-type signals in gene expression profiles across platforms and technologies. <i>Bioinformatics</i> , 2013, 29, 3036-3044.	4.1	27
64	Functional Knowledge Transfer for High-accuracy Prediction of Under-studied Biological Processes. <i>PLoS Computational Biology</i> , 2013, 9, e1002957.	3.2	62
65	Tissue-Specific Functional Networks for Prioritizing Phenotype and Disease Genes. <i>PLoS Computational Biology</i> , 2012, 8, e1002694.	3.2	137
66	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-W490.	14.5	105
67	Accurate evaluation and analysis of functional genomics data and methods. <i>Annals of the New York Academy of Sciences</i> , 2012, 1260, 95-100.	3.8	20
68	Accurate Quantification of Functional Analogy among Close Homologs. <i>PLoS Computational Biology</i> , 2011, 7, e1001074.	3.2	34
69	Simultaneous Genome-Wide Inference of Physical, Genetic, Regulatory, and Functional Pathway Components. <i>PLoS Computational Biology</i> , 2010, 6, e1001009.	3.2	20
70	Mapping Dynamic Histone Acetylation Patterns to Gene Expression in Nanog-Depleted Murine Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2010, 6, e1001034.	3.2	23
71	Functional Genomics Complements Quantitative Genetics in Identifying Disease-Gene Associations. <i>PLoS Computational Biology</i> , 2010, 6, e1000991.	3.2	55
72	Directing Experimental Biology: A Case Study in Mitochondrial Biogenesis. <i>PLoS Computational Biology</i> , 2009, 5, e1000322.	3.2	35

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73	Exploring the human genome with functional maps. <i>Genome Research</i> , 2009, 19, 1093-1106.	5.5	196
74	Graphlet: Interactive exploration of large, dense graphs. <i>BMC Bioinformatics</i> , 2009, 10, 417.	2.6	15
75	Discovering Biological Networks from Diverse Functional Genomic Data. <i>Methods in Molecular Biology</i> , 2009, 563, 157-175.	0.9	18
76	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.	3.2	84
77	A Genomewide Functional Network for the Laboratory Mouse. <i>PLoS Computational Biology</i> , 2008, 4, e1000165.	3.2	103
78	The Sleipnir library for computational functional genomics. <i>Bioinformatics</i> , 2008, 24, 1559-1561.	4.1	68
79	â€œGetting Started Inâ€¦ A Series Not to Miss. <i>PLoS Computational Biology</i> , 2007, 3, e224.	3.2	0
80	Exploring the functional landscape of gene expression: directed search of large microarray compendia. <i>Bioinformatics</i> , 2007, 23, 2692-2699.	4.1	243
81	Context-sensitive data integration and prediction of biological networks. <i>Bioinformatics</i> , 2007, 23, 2322-2330.	4.1	101
82	Finding function: evaluation methods for functional genomic data. <i>BMC Genomics</i> , 2006, 7, 187.	2.8	189
83	A scalable method for integration and functional analysis of multiple microarray datasets. <i>Bioinformatics</i> , 2006, 22, 2890-2897.	4.1	127
84	Hierarchical multi-label prediction of gene function. <i>Bioinformatics</i> , 2006, 22, 830-836.	4.1	422
85	BAYESIAN DATA INTEGRATION: A FUNCTIONAL PERSPECTIVE. , 2006, , .		12
86	Unsupervised Machine Learning to Support Functional Characterization of Genes: Emphasis on Cluster Description and Class Discovery. , 2005, , 175-192.		0
87	Putting microarrays in a context: Integrated analysis of diverse biological data. <i>Briefings in Bioinformatics</i> , 2005, 6, 34-43.	6.5	60
88	Discovery of biological networks from diverse functional genomic data. <i>Genome Biology</i> , 2005, 6, R114.	9.6	183
89	Accurate detection of aneuploidies in array CGH and gene expression microarray data. <i>Bioinformatics</i> , 2004, 20, 3533-3543.	4.1	109
90	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, 8348-8353.	7.1	491

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91	Nonparametric methods for identifying differentially expressed genes in microarray data. <i>Bioinformatics</i> , 2002, 18, 1454-1461.	4.1	276