Olga G Troyanskaya

List of Publications by Year
in descending order

91	10,614	71102 41	45317 90
papers	citations	h-index	g-index

107	107	107	15595
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Predicting effects of noncoding variants with deep learningâ€“based sequence model. Nature Methods, 2015, 12, 931-934.	19.0	1,714
2	A global genetic interaction network maps a wiring diagram of cellular function. Science, 2016, 353, .	12.6	979
3	Understanding multicellular function and disease with human tissue-specific networks. Nature Genetics, 2015, 47, 569-576.	21.4	738
4	A Bayesian framework for combining heterogeneous data sources for gene function prediction (inSaccharomyces cerevisiae). Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8348-8353.	7.1	491
5	Hierarchical multi-label prediction of gene function. Bioinformatics, 2006, 22, 830-836.	4.1	422
6	Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk. Nature Genetics, 2018, 50, 1171-1179.	21.4	375
7	Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder. Nature Neuroscience, 2016, 19, 1454-1462.	14.8	359
8	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	21.4	350
9	Nonparametric methods for identifying differentially expressed genes in microarray data. Bioinformatics, 2002, 18, 1454-1461.	4.1	276
10	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. Molecular Cell, 2020, 80, 1078-1091.e6.	9.7	255
11	Exploring the functional landscape of gene expression: directed search of large microarray compendia. Bioinformatics, 2007, 23, 2692-2699.	4.1	243
12	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. Nature Genetics, 2019, 51, 973-980.	21.4	216
13	SynNotch-CAR T cells overcome challenges of specificity, heterogeneity, and persistence in treating glioblastoma. Science Translational Medicine, 2021, 13, .	12.4	215
14	Exploring the human genome with functional maps. Genome Research, 2009, 19, 1093-1106.	5.5	196
15	Finding function: evaluation methods for functional genomic data. BMC Genomics, 2006, 7, 187.	2.8	189
16	Discovery of biological networks from diverse functional genomic data. Genome Biology, 2005, 6, R114.	9.6	183
17	IFNÎ³-Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. Cell, 2017, 170, 127-141.e15.	28.9	140
18	Tissue-Specific Functional Networks for Prioritizing Phenotype and Disease Genes. PLoS Computational Biology, 2012, 8, e1002694.	3.2	137

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19	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. Nature Methods, 2015, 12, 211-214.	19.0	137
20	A scalable method for integration and functional analysis of multiple microarray datasets. Bioinformatics, 2006, 22, 2890-2897.	4.1	127
21	Accurate detection of aneuploidies in array CGH and gene expression microarray data. Bioinformatics, 2004, 20, 3533-3543.	4.1	109
22	Single cell transcriptomics identifies focal segmental glomerulosclerosis remission endothelial biomarker. JCI Insight, 2020, 5, .	5.0	108
23	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Research, 2012, 40, W484-W490.	14.5	105
24	A Genomewide Functional Network for the Laboratory Mouse. PLoS Computational Biology, 2008, 4, e1000165.	3.2	103
25	Context-sensitive data integration and prediction of biological networks. Bioinformatics, 2007, 23, 2322-2330.	4.1	101
26	Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms. Bioinformatics, 2015, 31, 1093-1101.	4.1	99
27	Selective Neuronal Vulnerability in Alzheimerâ€™s Disease: A Network-Based Analysis. Neuron, 2020, 107, 821-835.e12.	8.1	99
28	Selene: a PyTorch-based deep learning library for sequence data. Nature Methods, 2019, 16, 315-318.	19.0	98
29	Genomic analyses implicate noncoding de novo variants in congenital heart disease. Nature Genetics, 2020, 52, 769-777.	21.4	97
30	Metabolic network rewiring of propionate flux compensates vitamin B12 deficiency in C. elegans. ELife, 2016, 5, .	6.0	96
31	Global Prediction of Tissue-Specific Gene Expression and Context-Dependent Gene Networks in Caenorhabditis elegans. PLoS Computational Biology, 2009, 5, e1000417.	3.2	84
32	A sequence-based global map of regulatory activity for deciphering human genetics. Nature Genetics, 2022, 54, 940-949.	21.4	71
33	The Sleipnir library for computational functional genomics. Bioinformatics, 2008, 24, 1559-1561.	4.1	68
34	A reference tissue atlas for the human kidney. Science Advances, 2022, 8, .	10.3	67
35	SARS-CoV-2 receptor networks in diabetic and COVID-19â€“associated kidney disease. Kidney International, 2020, 98, 1502-1518.	5.2	64
36	Functional Knowledge Transfer for High-accuracy Prediction of Under-studied Biological Processes. PLoS Computational Biology, 2013, 9, e1002957.	3.2	62

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37	Putting microarrays in a context: Integrated analysis of diverse biological data. Briefings in Bioinformatics, 2005, 6, 34-43.	6.5	60
38	IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Research, 2015, 43, W128-W133.	14.5	60
39	GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. Nucleic Acids Research, 2018, 46, W65-W70.	14.5	59
40	Functional Genomics Complements Quantitative Genetics in Identifying Disease-Gene Associations. PLoS Computational Biology, 2010, 6, e1000991.	3.2	55
41	An integrative tissue-network approach to identify and test human disease genes. Nature Biotechnology, 2018, 36, 1091-1099.	17.5	54
42	Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type TP53. Molecular Cancer Research, 2015, 13, 493-501.	3.4	53
43	Discriminatory Power of Combinatorial Antigen Recognition in Cancer T Cell Therapies. Cell Systems, 2020, 11, 215-228.e5.	6.2	52
44	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. Immunity, 2015, 43, 605-614.	14.3	49
45	Genome-wide landscape of RNA-binding protein target site dysregulation reveals a major impact on psychiatric disorder risk. Nature Genetics, 2021, 53, 166-173.	21.4	49
46	Decoding disease: from genomes to networks to phenotypes. Nature Reviews Genetics, 2021, 22, 774-790.	16.3	46
47	Spatial transcriptional mapping of the human nephrogenic program. Developmental Cell, 2021, 56, 2381-2398.e6.	7.0	44
48	Implications of Big Data for cell biology. Molecular Biology of the Cell, 2015, 26, 2575-2578.	2.1	42
49	Single nucleus multi-omics regulatory landscape of the murine pituitary. Nature Communications, 2021, 12, 2677.	12.8	38
50	Directing Experimental Biology: A Case Study in Mitochondrial Biogenesis. PLoS Computational Biology, 2009, 5, e1000322.	3.2	35
51	Accurate Quantification of Functional Analogy among Close Homologs. PLoS Computational Biology, 2011, 7, e1001074.	3.2	34
52	Global Quantitative Modeling of Chromatin Factor Interactions. PLoS Computational Biology, 2014, 10, e1003525.	3.2	32
53	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, 57121-57133.	1.8	31
54	An automated framework for efficiently designing deep convolutional neural networks in genomics. Nature Machine Intelligence, 2021, 3, 392-400.	16.0	29

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55	Ontology-aware classification of tissue and cell-type signals in gene expression profiles across platforms and technologies. Bioinformatics, 2013, 29, 3036-3044.	4.1	27
56	Single nucleus transcriptome and chromatin accessibility of postmortem human pituitaries reveal diverse stem cell regulatory mechanisms. Cell Reports, 2022, 38, 110467.	6.4	27
57	Artificial intelligence and cancer. Nature Cancer, 2020, 1, 149-152.	13.2	26
58	FNTM: a server for predicting functional networks of tissues in mouse. Nucleic Acids Research, 2015, 43, W182-W187.	14.5	25
59	Tissue-specific enhancer functional networks for associating distal regulatory regions to disease. Cell Systems, 2021, 12, 353-362.e6.	6.2	24
60	Mapping Dynamic Histone Acetylation Patterns to Gene Expression in Nanog-Depleted Murine Embryonic Stem Cells. PLoS Computational Biology, 2010, 6, e1001034.	3.2	23
61	Machine learning, the kidney, and genotypeâ€“phenotype analysis. Kidney International, 2020, 97, 1141-1149.	5.2	23
62	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. Cancer Cell, 2022, 40, 524-544.e5.	16.8	23
63	Asymptomatic SARS-CoV-2 Infection Is Associated With Higher Levels of Serum IL-17C, Matrix Metalloproteinase 10 andÂFibroblast Growth Factors Than Mild Symptomatic COVID-19. Frontiers in Immunology, 2022, 13, 821730.	4.8	21
64	Simultaneous Genome-Wide Inference of Physical, Genetic, Regulatory, and Functional Pathway Components. PLoS Computational Biology, 2010, 6, e1001009.	3.2	20
65	Accurate evaluation and analysis of functional genomics data and methods. Annals of the New York Academy of Sciences, 2012, 1260, 95-100.	3.8	20
66	A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. Cell Systems, 2019, 8, 152-162.e6.	6.2	19
67	Discovering Biological Networks from Diverse Functional Genomic Data. Methods in Molecular Biology, 2009, 563, 157-175.	0.9	18
68	Lowâ€variance RNAs identify Parkinson's disease molecular signature in blood. Movement Disorders, 2015, 30, 813-821.	3.9	18
69	Probabilistic modelling of chromatin code landscape reveals functional diversity of enhancer-like chromatin states. Nature Communications, 2016, 7, 10528.	12.8	18
70	Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. OncoImmunology, 2018, 7, e1457598.	4.6	18
71	Mapping the physiological and molecular markers of stress and SSRI antidepressant treatment in S100a10 corticostriatal neurons. Molecular Psychiatry, 2020, 25, 1112-1129.	7.9	18
72	Presenilin 1 phosphorylation regulates amyloid-Î² degradation by microglia. Molecular Psychiatry, 2021, 26, 5620-5635.	7.9	17

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73	CROTON: an automated and variant-aware deep learning framework for predicting CRISPR/Cas9 editing outcomes. Bioinformatics, 2021, 37, i342-i348.	4.1	17
74	Graphle: Interactive exploration of large, dense graphs. BMC Bioinformatics, 2009, 10, 417.	2.6	15
75	Enabling Precision Medicine through Integrative Network Models. Journal of Molecular Biology, 2018, 430, 2913-2923.	4.2	15
76	Minor Isozymes Tailor Yeast Metabolism to Carbon Availability. MSystems, 2019, 4, .	3.8	14
77	Machine learning methods to model multicellular complexity and tissue specificity. Nature Reviews Materials, 2021, 6, 717-729.	48.7	13
78	BAYESIAN DATA INTEGRATION: A FUNCTIONAL PERSPECTIVE. , 2006, , .		12
79	Molecular Characterization of Membranous Nephropathy. Journal of the American Society of Nephrology: JASN, 2022, 33, 1208-1221.	6.1	12
80	Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. Current Pharmaceutical Design, 2017, 23, 4716-4725.	1.9	11
81	Lack of a site-specific phosphorylation of Presenilin 1 disrupts microglial gene networks and progenitors during development. PLoS ONE, 2020, 15, e0237773.	2.5	11
82	Viable virus shedding during SARS-CoV-2 reinfection. Lancet Respiratory Medicine,the, 2021, 9, e56-e57.	10.7	11
83	Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development. PLoS Genetics, 2019, 15, e1008382.	3.5	9
84	An analytical framework for interpretable and generalizable single-cell data analysis. Nature Methods, 2021, 18, 1317-1321.	19.0	9
85	Interpretation of an individual functional genomics experiment guided by massive public data. Nature Methods, 2018, 15, 1049-1052.	19.0	5
86	Voices in methods development. Nature Methods, 2019, 16, 945-951.	19.0	5
87	Modeling transcriptional regulation of model species with deep learning. Genome Research, 2021, 31, 1097-1105.	5.5	5
88	A loop-counting method for covariate-corrected low-rank biclustering of gene-expression and genome-wide association study data. PLoS Computational Biology, 2018, 14, e1006105.	3.2	3
89	GIANT API: an application programming interface for functional genomics. Nucleic Acids Research, 2016, 44, W587-W592.	14.5	2
90	Unsupervised Machine Learning to Support Functional Characterization of Genes: Emphasis on Cluster Description and Class Discovery. , 2005, , 175-192.		0

#	Article	IF	Citations
91	â€œGetting Started Inâ€¦â€: A Series Not to Miss. PLoS Computational Biology, 2007, 3, e224.	3.2	0