Irit Gat-Viks

List of Publications by Year
in descending order

45 papers	3,002 citations	394421 19 h-index	254184 43 g-index
48 all docs	48 docs citations	48 times ranked	7037 citing authors

#	Article	IF	Citations
1	Regenerating the Injured Spinal Cord at the Chronic Phase by Engineered iPSCs‐Derived 3D Neuronal Networks. Advanced Science, 2022, 9, e2105694.	11.2	23
2	An integrative model of cardiometabolic traits identifies two types of metabolic syndrome. ELife, 2021, 10, .	6.0	4
3	Leveraging the cell lineage to predict cell-type specificity of regulatory variation from bulk genomics. Genetics, 2021, 217, .	2.9	1
4	Predicting brain metastasis in early stage non-small cell lung cancer patients by gene expression profiling. Translational Lung Cancer Research, 2020, 9, 682-692.	2.8	14
5	Exploring Neural Networks and Related Visualization Techniques in Gene Expression Data. Frontiers in Genetics, 2020, 11, 402.	2.3	3
6	Inferring cellular heterogeneity of associations from single cell genomics. Bioinformatics, 2020, 36, 3466-3473.	4.1	1
7	Anemia measurements to distinguish between viral and bacterial infections in the emergency department. European Journal of Clinical Microbiology and Infectious Diseases, 2019, 38, 2331-2339.	2.9	4
8	Predicting Phenotypic Diversity from Molecular and Genetic Data. Genetics, 2019, 213, 297-311.	2.9	3
9	Linking Cell Dynamics With Gene Coexpression Networks to Characterize Key Events in Chronic Virus Infections. Frontiers in Immunology, 2019, 10, 1002.	4.8	7
10	Cell composition analysis of bulk genomics using single-cell data. Nature Methods, 2019, 16, 327-332.	19.0	94
11	Personalized Tissue Implants: Personalized Hydrogels for Engineering Diverse Fully Autologous Tissue Implants (Adv. Mater. 1/2019). Advanced Materials, 2019, 31, 1970007.	21.0	4
12	Personalized Hydrogels for Engineering Diverse Fully Autologous Tissue Implants. Advanced Materials, 2019, 31, e1803895.	21.0	85
13	Mapping novel genetic loci associated with female liver weight variations using Collaborative Cross mice. Animal Models and Experimental Medicine, 2018, 1, 212-220.	3.3	6
14	Significant common environmental effects on leukocyte subpopulations. PLoS ONE, 2018, 13, e0196193.	2.5	0
15	Dissection of Influenza Infection InÂVivo by Single-Cell RNA Sequencing. Cell Systems, 2018, 6, 679-691.e4.	6.2	165
16	Reconstructing the Molecular Function of Genetic Variation in Regulatory Networks. Genetics, 2017, 207, 1699-1709.	2.9	0
17	POEM: Identifying Joint Additive Effects on Regulatory Circuits. Frontiers in Genetics, 2016, 7, 48.	2.3	1
18	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. Frontiers in Genetics, 2016, 7, 172.	2.3	12

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19	Extracellular Matrix Proteolysis by MT1-MMP Contributes to Influenza-Related Tissue Damage and Mortality. Cell Host and Microbe, 2016, 20, 458-470.	11.0	82
20	Mapping liver fat female-dependent quantitative trait loci in collaborative cross mice. Mammalian Genome, 2016, 27, 565-573.	2.2	20
21	ImmQuant: a user-friendly tool for inferring immune cell-type composition from gene-expression data. Bioinformatics, 2016, 32, 3842-3843.	4.1	51
22	Exploiting Gene-Expression Deconvolution to Probe the Genetics of the Immune System. PLoS Computational Biology, 2016, 12, e1004856.	3.2	8
23	CoD: inferring immune-cell quantities related to disease states. Bioinformatics, 2015, 31, 3961-3969.	4.1	10
24	A statistical framework for revealing signaling pathways perturbed by DNA variants. Nucleic Acids Research, 2015, 43, e74-e74.	14.5	6
25	Analysing human neural stem cell ontogeny by consecutive isolation of Notch active neural progenitors. Nature Communications, 2015, 6, 6500.	12.8	73
26	Proteomics–level analysis of myelin formation and regeneration in a mouse model for Vanishing White Matter disease. Journal of Neurochemistry, 2015, 134, 513-526.	3.9	25
27	Linking traits based on their shared molecular mechanisms. ELife, 2015, 4, .	6.0	9
28	Dissecting Dynamic Genetic Variation That Controls Temporal Gene Response in Yeast. PLoS Computational Biology, 2014, 10, e1003984.	3.2	2
29	Digital cell quantification identifies global immune cell dynamics during influenza infection. Molecular Systems Biology, 2014, 10, 720.	7.2	103
30	A minimum-labeling approach for reconstructing protein networks across multiple conditions. Algorithms for Molecular Biology, 2014, 9, 1.	1.2	29
31	Elucidating Influenza Inhibition Pathways via Network Reconstruction. Journal of Computational Biology, 2014, 21, 394-404.	1.6	1
32	Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. Nature Genetics, 2013, 45, 299-303.	21.4	237
33	Deciphering molecular circuits from genetic variation underlying transcriptional responsiveness to stimuli. Nature Biotechnology, 2013, 31, 342-349.	17.5	41
34	Systematic Discovery of TLR Signaling Components Delineates Viral-Sensing Circuits. Cell, 2011, 147, 853-867.	28.9	177
35	Understanding Gene Sequence Variation in the Context of Transcription Regulation in Yeast. PLoS Genetics, 2010, 6, e1000800.	3.5	10
36	A Faster Algorithm for Simultaneous Alignment and Folding of RNA. Journal of Computational Biology, 2010, 17, 1051-1065.	1.6	9

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37	Elucidating regulatory mechanisms downstream of a signaling pathway using informative experiments. Molecular Systems Biology, 2009, 5, 287.	7.2	26
38	Evidence for Gene-Specific Rather Than Transcription Rate–Dependent Histone H3 Exchange in Yeast Coding Regions. PLoS Computational Biology, 2009, 5, e1000282.	3.2	13
39	SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. Nature Genetics, 2009, 41, 1238-1242.	21.4	862
40	A Physical and Regulatory Map of Host-Influenza Interactions Reveals Pathways in H1N1 Infection. Cell, 2009, 139, 1255-1267.	28.9	593
41	MetaReg: A platform for modeling, analysis and visualization of biological systems using large-scale experimental data. Genome Biology, 2008, 9, R1.	9.6	18
42	Refinement and expansion of signaling pathways: The osmotic response network in yeast. Genome Research, 2007, 17, 358-367.	5.5	54
43	A Probabilistic Methodology for Integrating Knowledge and Experiments on Biological Networks. Journal of Computational Biology, 2006, 13, 165-181.	1.6	63
44	A Global View of the Selection Forces in the Evolution of Yeast Cis-Regulation. Genome Research, 2004, 14, 829-834.	5.5	27
45	Modeling and Analysis of Heterogeneous Regulation in Biological Networks. Journal of Computational Biology, 2004, 11, 1034-1049.	1.6	26