Irit Gat-Viks

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. Nature Genetics, 2009, 41, 1238-1242.	21.4	862
2	A Physical and Regulatory Map of Host-Influenza Interactions Reveals Pathways in H1N1 Infection. Cell, 2009, 139, 1255-1267.	28.9	593
3	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
4	Systematic Discovery of TLR Signaling Components Delineates Viral-Sensing Circuits. Cell, 2011, 147, 853-867.	28.9	177
5	Dissection of Influenza Infection InÂVivo by Single-Cell RNA Sequencing. Cell Systems, 2018, 6, 679-691.e4.	6.2	165
6	Digital cell quantification identifies global immune cell dynamics during influenza infection. Molecular Systems Biology, 2014, 10, 720.	7.2	103
7	Cell composition analysis of bulk genomics using single-cell data. Nature Methods, 2019, 16, 327-332.	19.0	94
8	Personalized Hydrogels for Engineering Diverse Fully Autologous Tissue Implants. Advanced Materials, 2019, 31, e1803895.	21.0	85
9	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
10	Analysing human neural stem cell ontogeny by consecutive isolation of Notch active neural progenitors. Nature Communications, 2015, 6, 6500.	12.8	73
11	A Probabilistic Methodology for Integrating Knowledge and Experiments on Biological Networks. Journal of Computational Biology, 2006, 13, 165-181.	1.6	63
12	Refinement and expansion of signaling pathways: The osmotic response network in yeast. Genome Research, 2007, 17, 358-367.	5.5	54
13	ImmQuant: a user-friendly tool for inferring immune cell-type composition from gene-expression data. Bioinformatics, 2016, 32, 3842-3843.	4.1	51
14	Deciphering molecular circuits from genetic variation underlying transcriptional responsiveness to stimuli. Nature Biotechnology, 2013, 31, 342-349.	17.5	41
15	A minimum-labeling approach for reconstructing protein networks across multiple conditions. Algorithms for Molecular Biology, 2014, 9, 1.	1.2	29
16	A Global View of the Selection Forces in the Evolution of Yeast Cis-Regulation. Genome Research, 2004, 14, 829-834.	5.5	27
17	Modeling and Analysis of Heterogeneous Regulation in Biological Networks. Journal of Computational Biology, 2004, 11, 1034-1049.	1.6	26
18	Elucidating regulatory mechanisms downstream of a signaling pathway using informative experiments. Molecular Systems Biology, 2009, 5, 287.	7.2	26

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19	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
20	Regenerating the Injured Spinal Cord at the Chronic Phase by Engineered iPSCs–Derived 3D Neuronal Networks. Advanced Science, 2022, 9, e2105694.	11.2	23
21	Mapping liver fat female-dependent quantitative trait loci in collaborative cross mice. Mammalian Genome, 2016, 27, 565-573.	2.2	20
22	MetaReg: A platform for modeling, analysis and visualization of biological systems using large-scale experimental data. Genome Biology, 2008, 9, R1.	9.6	18
23	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
24	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
25	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
26	Understanding Gene Sequence Variation in the Context of Transcription Regulation in Yeast. PLoS Genetics, 2010, 6, e1000800.	3.5	10
27	CoD: inferring immune-cell quantities related to disease states. Bioinformatics, 2015, 31, 3961-3969.	4.1	10
28	A Faster Algorithm for Simultaneous Alignment and Folding of RNA. Journal of Computational Biology, 2010, 17, 1051-1065.	1.6	9
29	Linking traits based on their shared molecular mechanisms. ELife, 2015, 4, .	6.0	9
30	Exploiting Gene-Expression Deconvolution to Probe the Genetics of the Immune System. PLoS Computational Biology, 2016, 12, e1004856.	3.2	8
31	Linking Cell Dynamics With Gene Coexpression Networks to Characterize Key Events in Chronic Virus Infections. Frontiers in Immunology, 2019, 10, 1002.	4.8	7
32	A statistical framework for revealing signaling pathways perturbed by DNA variants. Nucleic Acids Research, 2015, 43, e74-e74.	14.5	6
33	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
34	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
35	Personalized Tissue Implants: Personalized Hydrogels for Engineering Diverse Fully Autologous Tissue Implants (Adv. Mater. 1/2019). Advanced Materials, 2019, 31, 1970007.	21.0	4
36	An integrative model of cardiometabolic traits identifies two types of metabolic syndrome. ELife, 2021, 10, .	6.0	4

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37	Predicting Phenotypic Diversity from Molecular and Genetic Data. Genetics, 2019, 213, 297-311.	2.9	3
38	Exploring Neural Networks and Related Visualization Techniques in Gene Expression Data. Frontiers in Genetics, 2020, 11, 402.	2.3	3
39	Dissecting Dynamic Genetic Variation That Controls Temporal Gene Response in Yeast. PLoS Computational Biology, 2014, 10, e1003984.	3.2	2
40	Elucidating Influenza Inhibition Pathways via Network Reconstruction. Journal of Computational Biology, 2014, 21, 394-404.	1.6	1
41	POEM: Identifying Joint Additive Effects on Regulatory Circuits. Frontiers in Genetics, 2016, 7, 48.	2.3	1
42	Inferring cellular heterogeneity of associations from single cell genomics. Bioinformatics, 2020, 36, 3466-3473.	4.1	1
43	Leveraging the cell lineage to predict cell-type specificity of regulatory variation from bulk genomics. Genetics, 2021, 217, .	2.9	1
44	Reconstructing the Molecular Function of Genetic Variation in Regulatory Networks. Genetics, 2017, 207, 1699-1709.	2.9	0
45	Significant common environmental effects on leukocyte subpopulations. PLoS ONE, 2018, 13, e0196193.	2.5	0