Itai Yanai

List of Publications by Year
in descending order

79 papers	9,718 citations	94433 37 h-index	66911 78 g-index
100 all docs	100 docs citations	100 times ranked	15496 citing authors

#	Article	IF	Citations
1	Improvisational science. Genome Biology, 2022, 23, 4.	8.8	14
2	Quantifying gene duplication. Nature Reviews Genetics, 2022, 23, 196-197.	16.3	2
3	New adventures in spatial transcriptomics. Developmental Cell, 2022, 57, 1209-1210.	7.0	6
4	A molecular handbook for human development. Nature, 2021, 590, 43-44.	27.8	0
5	The data-hypothesis conversation. Genome Biology, 2021, 22, 58.	8.8	5
6	Novel predictions arise from contradictions. Genome Biology, 2021, 22, 153.	8.8	17
7	Exploring tissue architecture using spatial transcriptomics. Nature, 2021, 596, 211-220.	27.8	593
8	Gene expression levels modulate germline mutation rates through the compound effects of transcription-coupled repair and damage. Human Genetics, 2021, , 1.	3.8	8
9	Cooperation between melanoma cell states promotes metastasis through heterotypic cluster formation. Developmental Cell, 2021, 56, 2808-2825.e10.	7.0	37
10	Cancer cell states and emergent properties of the dynamic tumor system. Genome Research, 2021, 31, 1719-1727.	5.5	12
11	Single cell biology—a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
12	Spatially resolved transcriptomics reveals the architecture of the tumor-microenvironment interface. Nature Communications, 2021, 12, 6278.	12.8	112
13	Iterations of evolution A (Very) Short History of Life on Earth <i>Henry Gee</i> St. Martin's Press, 2021. 288 pp.. Science, 2021, 374, 828-828.	12.6	2
14	The Stress-Like Cancer Cell State Is a Consistent Component of Tumorigenesis. Cell Systems, 2020, 11, 536-546.e7.	6.2	65
15	A hypothesis is a liability. Genome Biology, 2020, 21, 231.	8.8	45
16	Gene expression dynamics are a proxy for selective pressures on alternatively polyadenylated isoforms. Nucleic Acids Research, 2020, 48, 5926-5938.	14.5	11
17	The two languages of science. Genome Biology, 2020, 21, 147.	8.8	26
18	Renaissance minds in 21st century science. Genome Biology, 2020, 21, 67.	8.8	10

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19	Integrating microarray-based spatial transcriptomics and single-cell RNA-seq reveals tissue architecture in pancreatic ductal adenocarcinomas. Nature Biotechnology, 2020, 38, 333-342.	17.5	517
20	Widespread Transcriptional Scanning in the Testis Modulates Gene Evolution Rates. Cell, 2020, 180, 248-262.e21.	28.9	111
21	Signatures of medical student applicants and academic success. PLoS ONE, 2020, 15, e0227108.	2.5	11
22	Phylogenetic debugging of a complete human biosynthetic pathway transplanted into yeast. Nucleic Acids Research, 2020, 48, 486-499.	14.5	11
23	A periodic table of cell types. Development (Cambridge), 2019, 146, .	2.5	54
24	Plasticity and Clonality of Cancer Cell States. Trends in Cancer, 2019, 5, 655-656.	7.4	15
25	Night science. Genome Biology, 2019, 20, 179.	8.8	32
26	CEL-Seq2â€"Single-Cell RNA Sequencing by Multiplexed Linear Amplification. Methods in Molecular Biology, 2019, 1979, 45-56.	0.9	15
27	What is the question?. Genome Biology, 2019, 20, 289.	8.8	9
28	The gene regulatory program of <i>Acrobeloides nanus</i> reveals conservation of phylum-specific expression. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4459-4464.	7.1	20
29	Bimodal Evolutionary Developmental miRNA Program in Animal Embryogenesis. Molecular Biology and Evolution, 2018, 35, 646-654.	8.9	8
30	Development and Evolution through the Lens of Global Gene Regulation. Trends in Genetics, 2018, 34, 11-20.	6.7	20
31	Spatiotemporal Gene Expression Analysis of the Caenorhabditis elegans Germline Uncovers a Syncytial Expression Switch. Genetics, 2018, 210, 587-605.	2.9	45
32	Developmental constraints shape the evolution of the nematode mid-developmental transition. Nature Ecology and Evolution, 2017, 1, 113.	7.8	67
33	It's about time: studying gene regulatory programs across serial organs. Genome Biology, 2017, 18, 30.	8.8	0
34	New skin for the old RNA-Seq ceremony: the age of single-cell multi-omics. Genome Biology, 2017, 18, 159.	8.8	10
35	scDual-Seq: mapping the gene regulatory program of Salmonella infection by host and pathogen single-cell RNA-sequencing. Genome Biology, 2017, 18, 200.	8.8	82
36	Computational biologists: moving to the driver's seat. Genome Biology, 2017, 18, 223.	8.8	12

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37	A Distinct Gene Module for Dysfunction Uncoupled from Activation in Tumor-Infiltrating T Cells. Cell, 2016, 166, 1500-1511.e9.	28.9	315
38	A Single-Cell Transcriptomic Map of the Human and Mouse Pancreas Reveals Inter- and Intra-cell Population Structure. Cell Systems, 2016, 3, 346-360.e4.	6.2	1,098
39	Forty years of The Selfish Gene are not enough. Genome Biology, 2016, 17, 39.	8.8	3
40	CEL-Seq2: sensitive highly-multiplexed single-cell RNA-Seq. Genome Biology, 2016, 17, 77.	8.8	900
41	The mid-developmental transition and the evolution of animal body plans. Nature, 2016, 531, 637-641.	27.8	231
42	Remarkably Divergent Regions Punctuate the Genome Assembly of the *Caenorhabditis elegans* Hawaiian Strain CB4856. Genetics, 2015, 200, 975-989.	2.9	136
43	Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity. Molecular Biology and Evolution, 2015, 32, 2367-2382.	8.9	66
44	Spatiotemporal transcriptomics reveals the evolutionary history of the endoderm germ layer. Nature, 2015, 519, 219-222.	27.8	160
45	BLIND ordering of large-scale transcriptomic developmental timecourses. Development (Cambridge), 2014, 141, 1161-1166.	2.5	51
46	Seeing is believing: new methods for in situ single-cell transcriptomics. Genome Biology, 2014, 15, 110.	9.6	16
47	Gene length and expression level shape genomic novelties. Genome Research, 2014, 24, 1497-1503.	5.5	73
48	Natural RNA interference directs a heritable response to the environment. Scientific Reports, 2014, 4, 7387.	3.3	81
49	ELOPER: elongation of paired-end reads as a pre-processing tool for improved *de novo* genome assembly. Bioinformatics, 2013, 29, 1455-1457.	4.1	6
50	The genomic determinants of genotype Ã— environment interactions in gene expression. Trends in Genetics, 2013, 29, 479-487.	6.7	82
51	Spatial localization of co-regulated genes exceeds genomic gene clustering in the Saccharomyces cerevisiae genome. Nucleic Acids Research, 2013, 41, 2191-2201.	14.5	50
52	A novel lineage of myoviruses infecting cyanobacteria is widespread in the oceans. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2037-2042.	7.1	105
53	A genomic bias for genotypeâ€"environment interactions in *C. elegans*. Molecular Systems Biology, 2012, 8, 587.	7.2	94
54	CEL-Seq: Single-Cell RNA-Seq by Multiplexed Linear Amplification. Cell Reports, 2012, 2, 666-673.	6.4	1,071

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55	Identifying functional links between genes by evolutionary transcriptomics. Molecular BioSystems, 2012, 8, 2585.	2.9	3
56	Developmental Milestones Punctuate Gene Expression in the Caenorhabditis Embryo. Developmental Cell, 2012, 22, 1101-1108.	7.0	207
57	Toward an unbiased evolutionary platform for unraveling *Xenopus* developmental gene networks. Genesis, 2012, 50, 186-191.	1.6	1
58	Mapping Gene Expression in Two Xenopus Species: Evolutionary Constraints and Developmental Flexibility. Developmental Cell, 2011, 20, 483-496.	7.0	187
59	Core promoter T-blocks correlate with gene expression levels in *C. elegans*. Genome Research, 2011, 21, 707-717.	5.5	36
60	Revealing developmental networks by comparative transcriptomics. Transcription, 2010, 1, 154-158.	3.1	9
61	Comparison of diverse developmental transcriptomes reveals that coexpression of gene neighbors is not evolutionarily conserved. Genome Research, 2009, 19, 2214-2220.	5.5	56
62	Getting Started in Gene Expression Microarray Analysis. PLoS Computational Biology, 2009, 5, e1000543.	3.2	127
63	Pairing of competitive and topologically distinct regulatory modules enhances patterned gene expression. Molecular Systems Biology, 2008, 4, 163.	7.2	28
64	Similar gene expression profiles do not imply similar tissue functions. Trends in Genetics, 2006, 22, 132-138.	6.7	59
65	Widespread ectopic expression of olfactory receptor genes. BMC Genomics, 2006, 7, 121.	2.8	216
66	Neutrality and Selection in the Evolution of Gene Families. , 2006, , 226-235.		0
67	Alternative splicing and gene duplication are inversely correlated evolutionary mechanisms. Nature Genetics, 2005, 37, 588-589.	21.4	139
68	Modular genes with metazoan-specific domains have increased tissue specificity. Trends in Genetics, 2005, 21, 210-213.	6.7	21
69	Rewiring of the Yeast Transcriptional Network Through the Evolution of Motif Usage. Science, 2005, 309, 938-940.	12.6	268
70	Genome-wide midrange transcription profiles reveal expression level relationships in human tissue specification. Bioinformatics, 2005, 21, 650-659.	4.1	971
71	An avidin-like domain that does not bind biotin is adopted for oligomerization by the extracellular mosaic protein fibropellin. Protein Science, 2005, 14, 417-423.	7.6	10
72	Incongruent Expression Profiles between Human and Mouse Orthologous Genes Suggest Widespread Neutral Evolution of Transcription Control. OMICS A Journal of Integrative Biology, 2004, 8, 15-24.	2.0	124

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73	New type of polyubiquitin-like genes with intein-like autoprocessing domains. Trends in Genetics, 2004, 20, 538-542.	6.7	22
74	GeneAnnot: Interfacing GeneCards with high-throughput gene expression compendia. Briefings in Bioinformatics, 2003, 4, 349-360.	6.5	17
75	Predictome: a database of putative functional links between proteins. Nucleic Acids Research, 2002, 30, 306-309.	14.5	129
76	The society of genes: networks of functional links between genes from comparative genomics. Genome Biology, 2002, 3, research0064.1.	9.6	34
77	Evolution of gene fusions: horizontal transfer versus independent events. Genome Biology, 2002, 3, research0024.1.	9.6	78
78	Identifying functional links between genes using conserved chromosomal proximity. Trends in Genetics, 2002, 18, 176-179.	6.7	67
79	Predictions of Gene Family Distributions in Microbial Genomes: Evolution by Gene Duplication and Modification. Physical Review Letters, 2000, 85, 2641-2644.	7.8	84