

# Itai Yanai

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

9,718  
citations

94269

37  
h-index

66788

78  
g-index

100  
all docs

100  
docs citations

100  
times ranked

15496  
citing authors

#	ARTICLE	IF	CITATIONS
1	Improvisational science. <i>Genome Biology</i> , 2022, 23, 4.	3.8	14
2	Quantifying gene duplication. <i>Nature Reviews Genetics</i> , 2022, 23, 196-197.	7.7	2
3	New adventures in spatial transcriptomics. <i>Developmental Cell</i> , 2022, 57, 1209-1210.	3.1	6
4	A molecular handbook for human development. <i>Nature</i> , 2021, 590, 43-44.	13.7	0
5	The data-hypothesis conversation. <i>Genome Biology</i> , 2021, 22, 58.	3.8	5
6	Novel predictions arise from contradictions. <i>Genome Biology</i> , 2021, 22, 153.	3.8	17
7	Exploring tissue architecture using spatial transcriptomics. <i>Nature</i> , 2021, 596, 211-220.	13.7	593
8	Gene expression levels modulate germline mutation rates through the compound effects of transcription-coupled repair and damage. <i>Human Genetics</i> , 2021, , 1.	1.8	8
9	Cooperation between melanoma cell states promotes metastasis through heterotypic cluster formation. <i>Developmental Cell</i> , 2021, 56, 2808-2825.e10.	3.1	37
10	Cancer cell states and emergent properties of the dynamic tumor system. <i>Genome Research</i> , 2021, 31, 1719-1727.	2.4	12
11	Single cell biologyâ€™a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 74-97.	1.8	3
12	Spatially resolved transcriptomics reveals the architecture of the tumor-microenvironment interface. <i>Nature Communications</i> , 2021, 12, 6278.	5.8	112
13	Iterations of evolution <b>A (Very) Short History of Life on Earth</b> <i>Henry Gee</i> St. Martinâ€™s Press, 2021. 288 pp.. <i>Science</i> , 2021, 374, 828-828.	6.0	2
14	The Stress-Like Cancer Cell State Is a Consistent Component of Tumorigenesis. <i>Cell Systems</i> , 2020, 11, 536-546.e7.	2.9	65
15	A hypothesis is a liability. <i>Genome Biology</i> , 2020, 21, 231.	3.8	45
16	Gene expression dynamics are a proxy for selective pressures on alternatively polyadenylated isoforms. <i>Nucleic Acids Research</i> , 2020, 48, 5926-5938.	6.5	11
17	The two languages of science. <i>Genome Biology</i> , 2020, 21, 147.	3.8	26
18	Renaissance minds in 21st century science. <i>Genome Biology</i> , 2020, 21, 67.	3.8	10

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19	Integrating microarray-based spatial transcriptomics and single-cell RNA-seq reveals tissue architecture in pancreatic ductal adenocarcinomas. <i>Nature Biotechnology</i> , 2020, 38, 333-342.	9.4	517
20	Widespread Transcriptional Scanning in the Testis Modulates Gene Evolution Rates. <i>Cell</i> , 2020, 180, 248-262.e21.	13.5	111
21	Signatures of medical student applicants and academic success. <i>PLoS ONE</i> , 2020, 15, e0227108.	1.1	11
22	Phylogenetic debugging of a complete human biosynthetic pathway transplanted into yeast. <i>Nucleic Acids Research</i> , 2020, 48, 486-499.	6.5	11
23	A periodic table of cell types. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	54
24	Plasticity and Clonality of Cancer Cell States. <i>Trends in Cancer</i> , 2019, 5, 655-656.	3.8	15
25	Night science. <i>Genome Biology</i> , 2019, 20, 179.	3.8	32
26	CEL-Seq2—Single-Cell RNA Sequencing by Multiplexed Linear Amplification. <i>Methods in Molecular Biology</i> , 2019, 1979, 45-56.	0.4	15
27	What is the question?. <i>Genome Biology</i> , 2019, 20, 289.	3.8	9
28	The gene regulatory program of <i>Acroboloides nanus</i> reveals conservation of phylum-specific expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4459-4464.	3.3	20
29	Bimodal Evolutionary Developmental miRNA Program in Animal Embryogenesis. <i>Molecular Biology and Evolution</i> , 2018, 35, 646-654.	3.5	8
30	Development and Evolution through the Lens of Global Gene Regulation. <i>Trends in Genetics</i> , 2018, 34, 11-20.	2.9	20
31	Spatiotemporal Gene Expression Analysis of the <i>Caenorhabditis elegans</i> Germline Uncovers a Syncytial Expression Switch. <i>Genetics</i> , 2018, 210, 587-605.	1.2	45
32	Developmental constraints shape the evolution of the nematode mid-developmental transition. <i>Nature Ecology and Evolution</i> , 2017, 1, 113.	3.4	67
33	It's about time: studying gene regulatory programs across serial organs. <i>Genome Biology</i> , 2017, 18, 30.	3.8	0
34	New skin for the old RNA-Seq ceremony: the age of single-cell multi-omics. <i>Genome Biology</i> , 2017, 18, 159.	3.8	10
35	scDual-Seq: mapping the gene regulatory program of <i>Salmonella</i> infection by host and pathogen single-cell RNA-sequencing. <i>Genome Biology</i> , 2017, 18, 200.	3.8	82
36	Computational biologists: moving to the driver's seat. <i>Genome Biology</i> , 2017, 18, 223.	3.8	12

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37	A Distinct Gene Module for Dysfunction Uncoupled from Activation in Tumor-Infiltrating T Cells. <i>Cell</i> , 2016, 166, 1500-1511.e9.	13.5	315
38	A Single-Cell Transcriptomic Map of the Human and Mouse Pancreas Reveals Inter- and Intra-cell Population Structure. <i>Cell Systems</i> , 2016, 3, 346-360.e4.	2.9	1,098
39	Forty years of <i>The Selfish Gene</i> are not enough. <i>Genome Biology</i> , 2016, 17, 39.	3.8	3
40	CEL-Seq2: sensitive highly-multiplexed single-cell RNA-Seq. <i>Genome Biology</i> , 2016, 17, 77.	3.8	900
41	The mid-developmental transition and the evolution of animal body plans. <i>Nature</i> , 2016, 531, 637-641.	13.7	231
42	Remarkably Divergent Regions Punctuate the Genome Assembly of the <i>Caenorhabditis elegans</i> Hawaiian Strain CB4856. <i>Genetics</i> , 2015, 200, 975-989.	1.2	136
43	Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity. <i>Molecular Biology and Evolution</i> , 2015, 32, 2367-2382.	3.5	66
44	Spatiotemporal transcriptomics reveals the evolutionary history of the endoderm germ layer. <i>Nature</i> , 2015, 519, 219-222.	13.7	160
45	BLIND ordering of large-scale transcriptomic developmental timecourses. <i>Development (Cambridge)</i> , 2014, 141, 1161-1166.	1.2	51
46	Seeing is believing: new methods for in situ single-cell transcriptomics. <i>Genome Biology</i> , 2014, 15, 110.	13.9	16
47	Gene length and expression level shape genomic novelties. <i>Genome Research</i> , 2014, 24, 1497-1503.	2.4	73
48	Natural RNA interference directs a heritable response to the environment. <i>Scientific Reports</i> , 2014, 4, 7387.	1.6	81
49	ELOPER: elongation of paired-end reads as a pre-processing tool for improved <i>de novo</i> genome assembly. <i>Bioinformatics</i> , 2013, 29, 1455-1457.	1.8	6
50	The genomic determinants of genotype–environment interactions in gene expression. <i>Trends in Genetics</i> , 2013, 29, 479-487.	2.9	82
51	Spatial localization of co-regulated genes exceeds genomic gene clustering in the <i>Saccharomyces cerevisiae</i> genome. <i>Nucleic Acids Research</i> , 2013, 41, 2191-2201.	6.5	50
52	A novel lineage of myoviruses infecting cyanobacteria is widespread in the oceans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2037-2042.	3.3	105
53	A genomic bias for genotype–environment interactions in <i>C. elegans</i> . <i>Molecular Systems Biology</i> , 2012, 8, 587.	3.2	94
54	CEL-Seq: Single-Cell RNA-Seq by Multiplexed Linear Amplification. <i>Cell Reports</i> , 2012, 2, 666-673.	2.9	1,071

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55	Identifying functional links between genes by evolutionary transcriptomics. <i>Molecular BioSystems</i> , 2012, 8, 2585.	2.9	3
56	Developmental Milestones Punctuate Gene Expression in the <i>Caenorhabditis</i> Embryo. <i>Developmental Cell</i> , 2012, 22, 1101-1108.	3.1	207
57	Toward an unbiased evolutionary platform for unraveling <i>Xenopus</i> developmental gene networks. <i>Genesis</i> , 2012, 50, 186-191.	0.8	1
58	Mapping Gene Expression in Two <i>Xenopus</i> Species: Evolutionary Constraints and Developmental Flexibility. <i>Developmental Cell</i> , 2011, 20, 483-496.	3.1	187
59	Core promoter T-blocks correlate with gene expression levels in <i>C. elegans</i> . <i>Genome Research</i> , 2011, 21, 707-717.	2.4	36
60	Revealing developmental networks by comparative transcriptomics. <i>Transcription</i> , 2010, 1, 154-158.	1.7	9
61	Comparison of diverse developmental transcriptomes reveals that coexpression of gene neighbors is not evolutionarily conserved. <i>Genome Research</i> , 2009, 19, 2214-2220.	2.4	56
62	Getting Started in Gene Expression Microarray Analysis. <i>PLoS Computational Biology</i> , 2009, 5, e1000543.	1.5	127
63	Pairing of competitive and topologically distinct regulatory modules enhances patterned gene expression. <i>Molecular Systems Biology</i> , 2008, 4, 163.	3.2	28
64	Similar gene expression profiles do not imply similar tissue functions. <i>Trends in Genetics</i> , 2006, 22, 132-138.	2.9	59
65	Widespread ectopic expression of olfactory receptor genes. <i>BMC Genomics</i> , 2006, 7, 121.	1.2	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. <i>Nature Genetics</i> , 2005, 37, 588-589.	9.4	139
68	Modular genes with metazoan-specific domains have increased tissue specificity. <i>Trends in Genetics</i> , 2005, 21, 210-213.	2.9	21
69	Rewiring of the Yeast Transcriptional Network Through the Evolution of Motif Usage. <i>Science</i> , 2005, 309, 938-940.	6.0	268
70	Genome-wide midrange transcription profiles reveal expression level relationships in human tissue specification. <i>Bioinformatics</i> , 2005, 21, 650-659.	1.8	971
71	An avidin-like domain that does not bind biotin is adopted for oligomerization by the extracellular mosaic protein fibropellin. <i>Protein Science</i> , 2005, 14, 417-423.	3.1	10
72	Incongruent Expression Profiles between Human and Mouse Orthologous Genes Suggest Widespread Neutral Evolution of Transcription Control. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 15-24.	1.0	124

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73	New type of polyubiquitin-like genes with intein-like autoprocessing domains. Trends in Genetics, 2004, 20, 538-542.	2.9	22
74	GeneAnnot: Interfacing GeneCards with high-throughput gene expression compendia. Briefings in Bioinformatics, 2003, 4, 349-360.	3.2	17
75	Predictome: a database of putative functional links between proteins. Nucleic Acids Research, 2002, 30, 306-309.	6.5	129
76	The society of genes: networks of functional links between genes from comparative genomics. Genome Biology, 2002, 3, research0064.1.	13.9	34
77	Evolution of gene fusions: horizontal transfer versus independent events. Genome Biology, 2002, 3, research0024.1.	13.9	78
78	Identifying functional links between genes using conserved chromosomal proximity. Trends in Genetics, 2002, 18, 176-179.	2.9	67
79	Predictions of Gene Family Distributions in Microbial Genomes: Evolution by Gene Duplication and Modification. Physical Review Letters, 2000, 85, 2641-2644.	2.9	84