

Yoav Gilad

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

19,100
citations

17440

63
h-index

18130

120
g-index

154
all docs

154
docs citations

154
times ranked

28696
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. <i>Genome Research</i> , 2008, 18, 1509-1517.	5.5	2,393
2	Understanding mechanisms underlying human gene expression variation with RNA sequencing. <i>Nature</i> , 2010, 464, 768-772.	27.8	1,200
3	Sex-specific genetic architecture of human disease. <i>Nature Reviews Genetics</i> , 2008, 9, 911-922.	16.3	623
4	DNase- χ l sensitivity QTLs are a major determinant of human expression variation. <i>Nature</i> , 2012, 482, 390-394.	27.8	608
5	RNA splicing is a primary link between genetic variation and disease. <i>Science</i> , 2016, 352, 600-604.	12.6	574
6	High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. <i>PLoS Genetics</i> , 2008, 4, e1000214.	3.5	510
7	Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data. <i>Genome Research</i> , 2011, 21, 447-455.	5.5	501
8	WASP: allele-specific software for robust molecular quantitative trait locus discovery. <i>Nature Methods</i> , 2015, 12, 1061-1063.	19.0	474
9	Revealing the architecture of gene regulation: the promise of eQTL studies. <i>Trends in Genetics</i> , 2008, 24, 408-415.	6.7	463
10	Identification of Genetic Variants That Affect Histone Modifications in Human Cells. <i>Science</i> , 2013, 342, 747-749.	12.6	429
11	Comparative studies of gene expression and the evolution of gene regulation. <i>Nature Reviews Genetics</i> , 2012, 13, 505-516.	16.3	399
12	Impact of regulatory variation from RNA to protein. <i>Science</i> , 2015, 347, 664-667.	12.6	399
13	RNA-seq: impact of RNA degradation on transcript quantification. <i>BMC Biology</i> , 2014, 12, 42.	3.8	366
14	Expression profiling in primates reveals a rapid evolution of human transcription factors. <i>Nature</i> , 2006, 440, 242-245.	27.8	283
15	Batch effects and the effective design of single-cell gene expression studies. <i>Scientific Reports</i> , 2017, 7, 39921.	3.3	275
16	Taxonomic Classification of Bacterial 16S rRNA Genes Using Short Sequencing Reads: Evaluation of Effective Study Designs. <i>PLoS ONE</i> , 2013, 8, e53608.	2.5	273
17	Social environment is associated with gene regulatory variation in the rhesus macaque immune system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6490-6495.	7.1	257
18	Controls of Nucleosome Positioning in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1003036.	3.5	255

#	ARTICLE	IF	CITATIONS
19	Methylation QTLs Are Associated with Coordinated Changes in Transcription Factor Binding, Histone Modifications, and Gene Expression Levels. <i>PLoS Genetics</i> , 2014, 10, e1004663.	3.5	255
20	Noisy Splicing Drives mRNA Isoform Diversity in Human Cells. <i>PLoS Genetics</i> , 2010, 6, e1001236.	3.5	254
21	Seasonal Variation in Human Gut Microbiome Composition. <i>PLoS ONE</i> , 2014, 9, e90731.	2.5	246
22	Human specific loss of olfactory receptor genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3324-3327.	7.1	245
23	ENCODE explained. <i>Nature</i> , 2012, 489, 52-54.	27.8	245
24	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	5.5	239
25	Deciphering the genetic architecture of variation in the immune response to <i>Mycobacterium tuberculosis</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1204-1209.	7.1	238
26	Genome-Wide Association Studies of the Human Gut Microbiota. <i>PLoS ONE</i> , 2015, 10, e0140301.	2.5	228
27	Different noses for different people. <i>Nature Genetics</i> , 2003, 34, 143-144.	21.4	217
28	Primate Transcript and Protein Expression Levels Evolve Under Compensatory Selection Pressures. <i>Science</i> , 2013, 342, 1100-1104.	12.6	215
29	Mechanisms for Evolving Hypervariability: The Case of Conopeptides. <i>Molecular Biology and Evolution</i> , 2001, 18, 120-131.	8.9	210
30	A Genome-Wide Study of DNA Methylation Patterns and Gene Expression Levels in Multiple Human and Chimpanzee Tissues. <i>PLoS Genetics</i> , 2011, 7, e1001316.	3.5	196
31	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015, 25, 1801-1811.	5.5	195
32	Natural selection on gene expression. <i>Trends in Genetics</i> , 2006, 22, 456-461.	6.7	187
33	The Functional Consequences of Variation in Transcription Factor Binding. <i>PLoS Genetics</i> , 2014, 10, e1004226.	3.5	187
34	Where Are the Disease-Associated eQTLs?. <i>Trends in Genetics</i> , 2021, 37, 109-124.	6.7	163
35	Multi-species microarrays reveal the effect of sequence divergence on gene expression profiles. <i>Genome Research</i> , 2005, 15, 674-680.	5.5	155
36	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. <i>Genome Research</i> , 2012, 22, 602-610.	5.5	145

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37	Prediction of the odorant binding site of olfactory receptor proteins by human-mouse comparisons. <i>Protein Science</i> , 2004, 13, 240-254.	7.6	143
38	Gene Regulation in Primates Evolves under Tissue-Specific Selection Pressures. <i>PLoS Genetics</i> , 2008, 4, e1000271.	3.5	143
39	The Genetic and Mechanistic Basis for Variation in Gene Regulation. <i>PLoS Genetics</i> , 2015, 11, e1004857.	3.5	142
40	Dynamic genetic regulation of gene expression during cellular differentiation. <i>Science</i> , 2019, 364, 1287-1290.	12.6	142
41	Natural Selection on the Olfactory Receptor Gene Family in Humans and Chimpanzees. <i>American Journal of Human Genetics</i> , 2003, 73, 489-501.	6.2	137
42	Genomic-scale capture and sequencing of endogenous DNA from feces. <i>Molecular Ecology</i> , 2010, 19, 5332-5344.	3.9	127
43	The effects of EBV transformation on gene expression levels and methylation profiles. <i>Human Molecular Genetics</i> , 2011, 20, 1643-1652.	2.9	124
44	Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. <i>ELife</i> , 2016, 5, .	6.0	122
45	A comparison of the human and chimpanzee olfactory receptor gene repertoires. <i>Genome Research</i> , 2005, 15, 224-230.	5.5	120
46	Evolution of Bitter Taste Receptors in Humans and Apes. <i>Molecular Biology and Evolution</i> , 2005, 22, 432-436.	8.9	117
47	Characterizing natural variation using next-generation sequencing technologies. <i>Trends in Genetics</i> , 2009, 25, 463-471.	6.7	116
48	A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. <i>ELife</i> , 2015, 4, e07103.	6.0	114
49	Impact of regulatory variation across human iPSCs and differentiated cells. <i>Genome Research</i> , 2018, 28, 122-131.	5.5	114
50	Absence of the TAP2 Human Recombination Hotspot in Chimpanzees. <i>PLoS Biology</i> , 2004, 2, e155.	5.6	112
51	Genetic Variation, Not Cell Type of Origin, Underlies the Majority of Identifiable Regulatory Differences in iPSCs. <i>PLoS Genetics</i> , 2016, 12, e1005793.	3.5	111
52	Metastasis Suppressors Regulate the Tumor Microenvironment by Blocking Recruitment of Prometastatic Tumor-Associated Macrophages. <i>Cancer Research</i> , 2015, 75, 4063-4073.	0.9	100
53	The genetic architecture of gene expression levels in wild baboons. <i>ELife</i> , 2015, 4, .	6.0	99
54	Functional Comparison of Innate Immune Signaling Pathways in Primates. <i>PLoS Genetics</i> , 2010, 6, e1001249.	3.5	94

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55	Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. <i>ELife</i> , 2018, 7, .	6.0	94
56	Dichotomy of single-nucleotide polymorphism haplotypes in olfactory receptor genes and pseudogenes. <i>Nature Genetics</i> , 2000, 26, 221-224.	21.4	92
57	A comparison of gene expression and DNA methylation patterns across tissues and species. <i>Genome Research</i> , 2020, 30, 250-262.	5.5	91
58	A reanalysis of mouse ENCODE comparative gene expression data. <i>F1000Research</i> , 2015, 4, 121.	1.6	91
59	Evidence for positive selection and population structure at the human MAO-A gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 862-867.	7.1	90
60	Population Differences in the Human Functional Olfactory Repertoire. <i>Molecular Biology and Evolution</i> , 2003, 20, 307-314.	8.9	90
61	Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. <i>Genetics</i> , 2011, 187, 1225-1234.	2.9	89
62	The human olfactory transcriptome. <i>BMC Genomics</i> , 2016, 17, 619.	2.8	87
63	An Evolutionarily Conserved Sexual Signature in the Primate Brain. <i>PLoS Genetics</i> , 2008, 4, e1000100.	3.5	81
64	Systematic Comparison of High-throughput Single-Cell and Single-Nucleus Transcriptomes during Cardiomyocyte Differentiation. <i>Scientific Reports</i> , 2020, 10, 1535.	3.3	74
65	Epigenetic modifications are associated with inter-species gene expression variation in primates. <i>Genome Biology</i> , 2014, 15, 547.	8.8	72
66	Reorganization of 3D genome structure may contribute to gene regulatory evolution in primates. <i>PLoS Genetics</i> , 2019, 15, e1008278.	3.5	71
67	Co-binding by YY1 identifies the transcriptionally active, highly conserved set of CTCF-bound regions in primate genomes. <i>Genome Biology</i> , 2013, 14, R148.	9.6	68
68	Host Genetic Variation Influences Gene Expression Response to Rhinovirus Infection. <i>PLoS Genetics</i> , 2015, 11, e1005111.	3.5	67
69	Mycobacterial infection induces a specific human innate immune response. <i>Scientific Reports</i> , 2015, 5, 16882.	3.3	63
70	Characterizing and inferring quantitative cell cycle phase in single-cell RNA-seq data analysis. <i>Genome Research</i> , 2020, 30, 611-621.	5.5	63
71	Copy Number Variation of CCL3-like Genes Affects Rate of Progression to Simian-AIDS in Rhesus Macaques (<i>Macaca mulatta</i>). <i>PLoS Genetics</i> , 2009, 5, e1000346.	3.5	61
72	Host genetic variation in mucosal immunity pathways influences the upper airway microbiome. <i>Microbiome</i> , 2017, 5, 16.	11.1	61

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73	A Signature of Evolutionary Constraint on a Subset of Ectopically Expressed Olfactory Receptor Genes. <i>Molecular Biology and Evolution</i> , 2008, 26, 491-494.	8.9	59
74	A Genome Sequence Resource for the Aye-Aye (<i>Daubentonia madagascariensis</i>), a Nocturnal Lemur from Madagascar. <i>Genome Biology and Evolution</i> , 2012, 4, 126-135.	2.5	59
75	A Comparative Assessment of Human and Chimpanzee iPSC-derived Cardiomyocytes with Primary Heart Tissues. <i>Scientific Reports</i> , 2018, 8, 15312.	3.3	57
76	Discovery and characterization of variance QTLs in human induced pluripotent stem cells. <i>PLoS Genetics</i> , 2019, 15, e1008045.	3.5	56
77	Reducing mitochondrial reads in ATAC-seq using CRISPR/Cas9. <i>Scientific Reports</i> , 2017, 7, 2451.	3.3	51
78	General Olfactory Sensitivity Database (GOSdb): Candidate Genes and their Genomic Variations. <i>Human Mutation</i> , 2013, 34, 32-41.	2.5	47
79	The combination of a genome-wide association study of lymphocyte count and analysis of gene expression data reveals novel asthma candidate genes. <i>Human Molecular Genetics</i> , 2012, 21, 2111-2123.	2.9	46
80	Expression quantitative trait loci detected in cell lines are often present in primary tissues. <i>Human Molecular Genetics</i> , 2009, 18, 4296-4303.	2.9	45
81	Alternative polyadenylation mediates genetic regulation of gene expression. <i>ELife</i> , 2020, 9, .	6.0	45
82	Using DNA microarrays to study natural variation. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 553-558.	3.3	43
83	Social environmental effects on gene regulation. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 4323-4339.	5.4	42
84	Dynamic effects of genetic variation on gene expression revealed following hypoxic stress in cardiomyocytes. <i>ELife</i> , 2021, 10, .	6.0	41
85	Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions. <i>ELife</i> , 2021, 10, .	6.0	41
86	A Combination of Genomic Approaches Reveals the Role of FOXO1a in Regulating an Oxidative Stress Response Pathway. <i>PLoS ONE</i> , 2008, 3, e1670.	2.5	41
87	A TAD Skeptic: Is 3D Genome Topology Conserved?. <i>Trends in Genetics</i> , 2021, 37, 216-223.	6.7	40
88	Regulatory element copy number differences shape primate expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12656-12661.	7.1	37
89	msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding. <i>PLoS ONE</i> , 2015, 10, e0138030.	2.5	37
90	Population differences in haplotype structure within a human olfactory receptor gene cluster. <i>Human Molecular Genetics</i> , 2002, 11, 1381-1390.	2.9	35

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91	A generally conserved response to hypoxia in iPSC-derived cardiomyocytes from humans and chimpanzees. <i>ELife</i> , 2019, 8, .	6.0	35
92	Mouseâ€“Human Orthology Relationships in an Olfactory Receptor Gene Cluster. <i>Genomics</i> , 2001, 71, 296-306.	2.9	33
93	Gene expression variability in human and chimpanzee populations share common determinants. <i>ELife</i> , 2020, 9, .	6.0	33
94	A comparative study of endoderm differentiation in humans and chimpanzees. <i>Genome Biology</i> , 2018, 19, 162.	8.8	32
95	Identification and characterization of coding single-nucleotide polymorphisms within a human olfactory receptor gene cluster. <i>Gene</i> , 2000, 260, 87-94.	2.2	30
96	Reprogramming LCLs to iPSCs Results in Recovery of Donor-Specific Gene Expression Signature. <i>PLoS Genetics</i> , 2015, 11, e1005216.	3.5	29
97	Single-cell sequencing reveals lineage-specific dynamic genetic regulation of gene expression during human cardiomyocyte differentiation. <i>PLoS Genetics</i> , 2022, 18, e1009666.	3.5	28
98	Silencing of transposable elements may not be a major driver of regulatory evolution in primate iPSCs. <i>ELife</i> , 2018, 7, .	6.0	27
99	Segmental Duplications Contribute to Gene Expression Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2009, 182, 627-630.	2.9	26
100	The Effect of Freeze-Thaw Cycles on Gene Expression Levels in Lymphoblastoid Cell Lines. <i>PLoS ONE</i> , 2014, 9, e107166.	2.5	25
101	Comparative metabolomics in primates reveals the effects of diet and gene regulatory variation on metabolic divergence. <i>Scientific Reports</i> , 2015, 4, 5809.	3.3	24
102	Benchmarking sequencing methods and tools that facilitate the study of alternative polyadenylation. <i>Genome Biology</i> , 2021, 22, 291.	8.8	23
103	Exon-Specific QTLs Skew the Inferred Distribution of Expression QTLs Detected Using Gene Expression Array Data. <i>PLoS ONE</i> , 2012, 7, e30629.	2.5	18
104	Integrated analyses of gene expression and genetic association studies in a founder population. <i>Human Molecular Genetics</i> , 2016, 25, 2104-2112.	2.9	18
105	Cracking the regulatory code. <i>Nature</i> , 2017, 550, 190-191.	27.8	18
106	Prime time for primate functional genomics. <i>Current Opinion in Genetics and Development</i> , 2020, 62, 1-7.	3.3	18
107	Using Reporter Gene Assays to Identify cis Regulatory Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2007, 176, 2069-2076.	2.9	15
108	A Framework for Exploring Functional Variability in Olfactory Receptor Genes. <i>PLoS ONE</i> , 2007, 2, e682.	2.5	15

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109	Comparative studies of gene regulatory mechanisms. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 68-74.	3.3	14
110	Gene expression in local stroma reflects breast tumor states and predicts patient outcome. <i>Scientific Reports</i> , 2016, 6, 39240.	3.3	11
111	Divergence in alternative polyadenylation contributes to gene regulatory differences between humans and chimpanzees. <i>ELife</i> , 2021, 10, .	6.0	11
112	Evolutionary insights into primate skeletal gene regulation using a comparative cell culture model. <i>PLoS Genetics</i> , 2022, 18, e1010073.	3.5	10
113	Effective study design for comparative functional genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 385-386.	16.3	9
114	Does a unique olfactory genome imply a unique olfactory world?. <i>Nature Neuroscience</i> , 2014, 17, 6-8.	14.8	8
115	Predicting susceptibility to tuberculosis based on gene expression profiling in dendritic cells. <i>Scientific Reports</i> , 2017, 7, 5702.	3.3	8
116	Human embryoid bodies as a novel system for genomic studies of functionally diverse cell types. <i>ELife</i> , 2022, 11, .	6.0	7
117	Using Genomic Tools to Study Regulatory Evolution. <i>Methods in Molecular Biology</i> , 2012, 856, 335-361.	0.9	6
118	Time-dependent transcriptional profiling links gene expression to mitogen-activated protein kinase kinase 4 (MKK4)-mediated suppression of omental metastatic colonization. <i>Clinical and Experimental Metastasis</i> , 2012, 29, 397-408.	3.3	4
119	A Methodological Assessment and Characterization of Genetically-Driven Variation in Three Human Phosphoproteomes. <i>Scientific Reports</i> , 2018, 8, 12106.	3.3	2
120	Characterizing gene expression in an <i>in vitro</i> biomechanical strain model of joint health. <i>F1000Research</i> , 0, 11, 296.	1.6	1