

Yoav Gilad

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1573801/publications.pdf>

Version: 2024-02-01

120
papers

19,100
citations

20036

63
h-index

20625

120
g-index

154
all docs

154
docs citations

154
times ranked

32331
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell sequencing reveals lineage-specific dynamic genetic regulation of gene expression during human cardiomyocyte differentiation. PLoS Genetics, 2022, 18, e1009666.	1.5	28
2	Human embryoid bodies as a novel system for genomic studies of functionally diverse cell types. ELife, 2022, 11, .	2.8	7
3	Evolutionary insights into primate skeletal gene regulation using a comparative cell culture model. PLoS Genetics, 2022, 18, e1010073.	1.5	10
4	Where Are the Disease-Associated eQTLs?. Trends in Genetics, 2021, 37, 109-124.	2.9	163
5	A TAD Skeptic: Is 3D Genome Topology Conserved?. Trends in Genetics, 2021, 37, 216-223.	2.9	40
6	Divergence in alternative polyadenylation contributes to gene regulatory differences between humans and chimpanzees. ELife, 2021, 10, .	2.8	11
7	Dynamic effects of genetic variation on gene expression revealed following hypoxic stress in cardiomyocytes. ELife, 2021, 10, .	2.8	41
8	Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions. ELife, 2021, 10, .	2.8	41
9	Benchmarking sequencing methods and tools that facilitate the study of alternative polyadenylation. Genome Biology, 2021, 22, 291.	3.8	23
10	Prime time for primate functional genomics. Current Opinion in Genetics and Development, 2020, 62, 1-7.	1.5	18
11	A comparison of gene expression and DNA methylation patterns across tissues and species. Genome Research, 2020, 30, 250-262.	2.4	91
12	Systematic Comparison of High-throughput Single-Cell and Single-Nucleus Transcriptomes during Cardiomyocyte Differentiation. Scientific Reports, 2020, 10, 1535.	1.6	74
13	Effective study design for comparative functional genomics. Nature Reviews Genetics, 2020, 21, 385-386.	7.7	9
14	Characterizing and inferring quantitative cell cycle phase in single-cell RNA-seq data analysis. Genome Research, 2020, 30, 611-621.	2.4	63
15	Alternative polyadenylation mediates genetic regulation of gene expression. ELife, 2020, 9, .	2.8	45
16	Gene expression variability in human and chimpanzee populations share common determinants. ELife, 2020, 9, .	2.8	33
17	Reorganization of 3D genome structure may contribute to gene regulatory evolution in primates. PLoS Genetics, 2019, 15, e1008278.	1.5	71
18	Dynamic genetic regulation of gene expression during cellular differentiation. Science, 2019, 364, 1287-1290.	6.0	142

#	ARTICLE	IF	CITATIONS
19	Discovery and characterization of variance QTLs in human induced pluripotent stem cells. PLoS Genetics, 2019, 15, e1008045.	1.5	56
20	A generally conserved response to hypoxia in iPSC-derived cardiomyocytes from humans and chimpanzees. ELife, 2019, 8, .	2.8	35
21	Impact of regulatory variation across human iPSCs and differentiated cells. Genome Research, 2018, 28, 122-131.	2.4	114
22	A comparative study of endoderm differentiation in humans and chimpanzees. Genome Biology, 2018, 19, 162.	3.8	32
23	A Comparative Assessment of Human and Chimpanzee iPSC-derived Cardiomyocytes with Primary Heart Tissues. Scientific Reports, 2018, 8, 15312.	1.6	57
24	Silencing of transposable elements may not be a major driver of regulatory evolution in primate iPSCs. ELife, 2018, 7, .	2.8	27
25	Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. ELife, 2018, 7, .	2.8	94
26	A Methodological Assessment and Characterization of Genetically-Driven Variation in Three Human Phosphoproteomes. Scientific Reports, 2018, 8, 12106.	1.6	2
27	Host genetic variation in mucosal immunity pathways influences the upper airway microbiome. Microbiome, 2017, 5, 16.	4.9	61
28	Reducing mitochondrial reads in ATAC-seq using CRISPR/Cas9. Scientific Reports, 2017, 7, 2451.	1.6	51
29	Batch effects and the effective design of single-cell gene expression studies. Scientific Reports, 2017, 7, 39921.	1.6	275
30	Cracking the regulatory code. Nature, 2017, 550, 190-191.	13.7	18
31	Predicting susceptibility to tuberculosis based on gene expression profiling in dendritic cells. Scientific Reports, 2017, 7, 5702.	1.6	8
32	Genetic Variation, Not Cell Type of Origin, Underlies the Majority of Identifiable Regulatory Differences in iPSCs. PLoS Genetics, 2016, 12, e1005793.	1.5	111
33	Gene expression in local stroma reflects breast tumor states and predicts patient outcome. Scientific Reports, 2016, 6, 39240.	1.6	11
34	Integrated analyses of gene expression and genetic association studies in a founder population. Human Molecular Genetics, 2016, 25, 2104-2112.	1.4	18
35	RNA splicing is a primary link between genetic variation and disease. Science, 2016, 352, 600-604.	6.0	574
36	The human olfactory transcriptome. BMC Genomics, 2016, 17, 619.	1.2	87

#	ARTICLE	IF	CITATIONS
37	Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. <i>ELife</i> , 2016, 5, .	2.8	122
38	Mycobacterial infection induces a specific human innate immune response. <i>Scientific Reports</i> , 2015, 5, 16882.	1.6	63
39	A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. <i>ELife</i> , 2015, 4, e07103.	2.8	114
40	Metastasis Suppressors Regulate the Tumor Microenvironment by Blocking Recruitment of Prometastatic Tumor-Associated Macrophages. <i>Cancer Research</i> , 2015, 75, 4063-4073.	0.4	100
41	Host Genetic Variation Influences Gene Expression Response to Rhinovirus Infection. <i>PLoS Genetics</i> , 2015, 11, e1005111.	1.5	67
42	Reprogramming LCLs to iPSCs Results in Recovery of Donor-Specific Gene Expression Signature. <i>PLoS Genetics</i> , 2015, 11, e1005216.	1.5	29
43	The Genetic and Mechanistic Basis for Variation in Gene Regulation. <i>PLoS Genetics</i> , 2015, 11, e1004857.	1.5	142
44	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015, 25, 1801-1811.	2.4	195
45	WASP: allele-specific software for robust molecular quantitative trait locus discovery. <i>Nature Methods</i> , 2015, 12, 1061-1063.	9.0	474
46	Impact of regulatory variation from RNA to protein. <i>Science</i> , 2015, 347, 664-667.	6.0	399
47	Comparative metabolomics in primates reveals the effects of diet and gene regulatory variation on metabolic divergence. <i>Scientific Reports</i> , 2015, 4, 5809.	1.6	24
48	A reanalysis of mouse ENCODE comparative gene expression data. <i>F1000Research</i> , 2015, 4, 121.	0.8	91
49	msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding. <i>PLoS ONE</i> , 2015, 10, e0138030.	1.1	37
50	Genome-Wide Association Studies of the Human Gut Microbiota. <i>PLoS ONE</i> , 2015, 10, e0140301.	1.1	228
51	The genetic architecture of gene expression levels in wild baboons. <i>ELife</i> , 2015, 4, .	2.8	99
52	Seasonal Variation in Human Gut Microbiome Composition. <i>PLoS ONE</i> , 2014, 9, e90731.	1.1	246
53	The Effect of Freeze-Thaw Cycles on Gene Expression Levels in Lymphoblastoid Cell Lines. <i>PLoS ONE</i> , 2014, 9, e107166.	1.1	25
54	The Functional Consequences of Variation in Transcription Factor Binding. <i>PLoS Genetics</i> , 2014, 10, e1004226.	1.5	187

#	ARTICLE	IF	CITATIONS
55	Methylation QTLs Are Associated with Coordinated Changes in Transcription Factor Binding, Histone Modifications, and Gene Expression Levels. <i>PLoS Genetics</i> , 2014, 10, e1004663.	1.5	255
56	RNA-seq: impact of RNA degradation on transcript quantification. <i>BMC Biology</i> , 2014, 12, 42.	1.7	366
57	Epigenetic modifications are associated with inter-species gene expression variation in primates. <i>Genome Biology</i> , 2014, 15, 547.	3.8	72
58	Does a unique olfactory genome imply a unique olfactory world?. <i>Nature Neuroscience</i> , 2014, 17, 6-8.	7.1	8
59	Comparative studies of gene regulatory mechanisms. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 68-74.	1.5	14
60	Social environmental effects on gene regulation. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 4323-4339.	2.4	42
61	Identification of Genetic Variants That Affect Histone Modifications in Human Cells. <i>Science</i> , 2013, 342, 747-749.	6.0	429
62	Primate Transcript and Protein Expression Levels Evolve Under Compensatory Selection Pressures. <i>Science</i> , 2013, 342, 1100-1104.	6.0	215
63	General Olfactory Sensitivity Database (GOSdb): Candidate Genes and their Genomic Variations. <i>Human Mutation</i> , 2013, 34, 32-41.	1.1	47
64	Taxonomic Classification of Bacterial 16S rRNA Genes Using Short Sequencing Reads: Evaluation of Effective Study Designs. <i>PLoS ONE</i> , 2013, 8, e53608.	1.1	273
65	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.	13.9	68
66	Controls of Nucleosome Positioning in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1003036.	1.5	255
67	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.	3.3	238
68	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.	1.1	59
69	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. <i>Genome Research</i> , 2012, 22, 602-610.	2.4	145
70	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.	3.3	257
71	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.	1.4	46
72	DNase-seq sensitivity QTLs are a major determinant of human expression variation. <i>Nature</i> , 2012, 482, 390-394.	13.7	608

#	ARTICLE	IF	CITATIONS
73	ENCODE explained. <i>Nature</i> , 2012, 489, 52-54.	13.7	245
74	Using Genomic Tools to Study Regulatory Evolution. <i>Methods in Molecular Biology</i> , 2012, 856, 335-361.	0.4	6
75	Exon-Specific QTLs Skew the Inferred Distribution of Expression QTLs Detected Using Gene Expression Array Data. <i>PLoS ONE</i> , 2012, 7, e30629.	1.1	18
76	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.	3.3	37
77	Comparative studies of gene expression and the evolution of gene regulation. <i>Nature Reviews Genetics</i> , 2012, 13, 505-516.	7.7	399
78	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.	1.7	4
79	The effects of EBV transformation on gene expression levels and methylation profiles. <i>Human Molecular Genetics</i> , 2011, 20, 1643-1652.	1.4	124
80	Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. <i>Genetics</i> , 2011, 187, 1225-1234.	1.2	89
81	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.	1.5	196
82	Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data. <i>Genome Research</i> , 2011, 21, 447-455.	2.4	501
83	Genomic-scale capture and sequencing of endogenous DNA from feces. <i>Molecular Ecology</i> , 2010, 19, 5332-5344.	2.0	127
84	Understanding mechanisms underlying human gene expression variation with RNA sequencing. <i>Nature</i> , 2010, 464, 768-772.	13.7	1,200
85	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	2.4	239
86	Noisy Splicing Drives mRNA Isoform Diversity in Human Cells. <i>PLoS Genetics</i> , 2010, 6, e1001236.	1.5	254
87	Functional Comparison of Innate Immune Signaling Pathways in Primates. <i>PLoS Genetics</i> , 2010, 6, e1001249.	1.5	94
88	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.	1.5	61
89	Segmental Duplications Contribute to Gene Expression Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2009, 182, 627-630.	1.2	26
90	Expression quantitative trait loci detected in cell lines are often present in primary tissues. <i>Human Molecular Genetics</i> , 2009, 18, 4296-4303.	1.4	45

#	ARTICLE	IF	CITATIONS
91	Characterizing natural variation using next-generation sequencing technologies. <i>Trends in Genetics</i> , 2009, 25, 463-471.	2.9	116
92	Sex-specific genetic architecture of human disease. <i>Nature Reviews Genetics</i> , 2008, 9, 911-922.	7.7	623
93	Revealing the architecture of gene regulation: the promise of eQTL studies. <i>Trends in Genetics</i> , 2008, 24, 408-415.	2.9	463
94	RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. <i>Genome Research</i> , 2008, 18, 1509-1517.	2.4	2,393
95	A Signature of Evolutionary Constraint on a Subset of Ectopically Expressed Olfactory Receptor Genes. <i>Molecular Biology and Evolution</i> , 2008, 26, 491-494.	3.5	59
96	Gene Regulation in Primates Evolves under Tissue-Specific Selection Pressures. <i>PLoS Genetics</i> , 2008, 4, e1000271.	1.5	143
97	High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. <i>PLoS Genetics</i> , 2008, 4, e1000214.	1.5	510
98	An Evolutionarily Conserved Sexual Signature in the Primate Brain. <i>PLoS Genetics</i> , 2008, 4, e1000100.	1.5	81
99	A Combination of Genomic Approaches Reveals the Role of FOXO1a in Regulating an Oxidative Stress Response Pathway. <i>PLoS ONE</i> , 2008, 3, e1670.	1.1	41
100	Using Reporter Gene Assays to Identify cis Regulatory Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2007, 176, 2069-2076.	1.2	15
101	A Framework for Exploring Functional Variability in Olfactory Receptor Genes. <i>PLoS ONE</i> , 2007, 2, e682.	1.1	15
102	Using DNA microarrays to study natural variation. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 553-558.	1.5	43
103	Expression profiling in primates reveals a rapid evolution of human transcription factors. <i>Nature</i> , 2006, 440, 242-245.	13.7	283
104	Natural selection on gene expression. <i>Trends in Genetics</i> , 2006, 22, 456-461.	2.9	187
105	Multi-species microarrays reveal the effect of sequence divergence on gene expression profiles. <i>Genome Research</i> , 2005, 15, 674-680.	2.4	155
106	Evolution of Bitter Taste Receptors in Humans and Apes. <i>Molecular Biology and Evolution</i> , 2005, 22, 432-436.	3.5	117
107	A comparison of the human and chimpanzee olfactory receptor gene repertoires. <i>Genome Research</i> , 2005, 15, 224-230.	2.4	120
108	Absence of the TAP2 Human Recombination Hotspot in Chimpanzees. <i>PLoS Biology</i> , 2004, 2, e155.	2.6	112

#	ARTICLE	IF	CITATIONS
109	Prediction of the odorant binding site of olfactory receptor proteins by human-mouse comparisons. <i>Protein Science</i> , 2004, 13, 240-254.	3.1	143
110	Different noses for different people. <i>Nature Genetics</i> , 2003, 34, 143-144.	9.4	217
111	Natural Selection on the Olfactory Receptor Gene Family in Humans and Chimpanzees. <i>American Journal of Human Genetics</i> , 2003, 73, 489-501.	2.6	137
112	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.	3.3	245
113	Population Differences in the Human Functional Olfactory Repertoire. <i>Molecular Biology and Evolution</i> , 2003, 20, 307-314.	3.5	90
114	Population differences in haplotype structure within a human olfactory receptor gene cluster. <i>Human Molecular Genetics</i> , 2002, 11, 1381-1390.	1.4	35
115	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.	3.3	90
116	Mouse-Human Orthology Relationships in an Olfactory Receptor Gene Cluster. <i>Genomics</i> , 2001, 71, 296-306.	1.3	33
117	Mechanisms for Evolving Hypervariability: The Case of Conopeptides. <i>Molecular Biology and Evolution</i> , 2001, 18, 120-131.	3.5	210
118	Dichotomy of single-nucleotide polymorphism haplotypes in olfactory receptor genes and pseudogenes. <i>Nature Genetics</i> , 2000, 26, 221-224.	9.4	92
119	Identification and characterization of coding single-nucleotide polymorphisms within a human olfactory receptor gene cluster. <i>Gene</i> , 2000, 260, 87-94.	1.0	30
120	Characterizing gene expression in an <i>in vitro</i> biomechanical strain model of joint health. <i>F1000Research</i> , 0, 11, 296.	0.8	1