

Thomas R Gingeras

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

130
papers

72,979
citations

76
h-index

137
g-index

137
ext. papers

93,354
ext. citations

19.5
avg, IF

8.45
L-index

#	Paper	IF	Citations
130	STAR: ultrafast universal RNA-seq aligner. <i>Bioinformatics</i> , 2013 , 29, 15-21	7.2	18121
129	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
128	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
127	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
126	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012 , 22, 1775-89	9.7	3408
125	CD127 expression inversely correlates with FoxP3 and suppressive function of human CD4+ T reg cells. <i>Journal of Experimental Medicine</i> , 2006 , 203, 1701-11	16.6	1963
124	RNA maps reveal new RNA classes and a possible function for pervasive transcription. <i>Science</i> , 2007 , 316, 1484-8	33.3	1903
123	High density synthetic oligonucleotide arrays. <i>Nature Genetics</i> , 1999 , 21, 20-4	36.3	1872
122	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004 , 306, 636-40	33.3	1692
121	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
120	Genomic maps and comparative analysis of histone modifications in human and mouse. <i>Cell</i> , 2005 , 120, 169-81	56.2	1198
119	Genome-wide analysis of estrogen receptor binding sites. <i>Nature Genetics</i> , 2006 , 38, 1289-97	36.3	1115
118	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011 , 471, 473-9	50.4	1094
117	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
116	Transcriptional maps of 10 human chromosomes at 5-nucleotide resolution. <i>Science</i> , 2005 , 308, 1149-54	33.3	967
115	Unbiased mapping of transcription factor binding sites along human chromosomes 21 and 22 points to widespread regulation of noncoding RNAs. <i>Cell</i> , 2004 , 116, 499-509	56.2	948
114	Identification of functional elements and regulatory circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010 , 330, 1787-97	33.3	892

113	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , 2012 , 148, 84-98	56.2	882
112	Large-scale transcriptional activity in chromosomes 21 and 22. <i>Science</i> , 2002 , 296, 916-9	33.3	711
111	Genome-wide transcription and the implications for genomic organization. <i>Nature Reviews Genetics</i> , 2007 , 8, 413-23	30.1	570
110	Global transcription in pluripotent embryonic stem cells. <i>Cell Stem Cell</i> , 2008 , 2, 437-47	18	503
109	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6131-8	11.5	490
108	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013 , 10, 1177-84	21.6	477
107	Extensive polymorphisms observed in HIV-1 clade B protease gene using high-density oligonucleotide arrays. <i>Nature Medicine</i> , 1996 , 2, 753-9	50.5	471
106	Mapping RNA-seq Reads with STAR. <i>Current Protocols in Bioinformatics</i> , 2015 , 51, 11.14.1-11.14.19	24.2	446
105	Synthetic spike-in standards for RNA-seq experiments. <i>Genome Research</i> , 2011 , 21, 1543-51	9.7	437
104	Diversity and dynamics of the Drosophila transcriptome. <i>Nature</i> , 2014 , 512, 393-9	50.4	418
103	Novel RNAs identified from an in-depth analysis of the transcriptome of human chromosomes 21 and 22. <i>Genome Research</i> , 2004 , 14, 331-42	9.7	410
102	Reprogramming of the macrophage transcriptome in response to interferon-gamma and Mycobacterium tuberculosis: signaling roles of nitric oxide synthase-2 and phagocyte oxidase. <i>Journal of Experimental Medicine</i> , 2001 , 194, 1123-40	16.6	394
101	Cellular gene expression altered by human cytomegalovirus: global monitoring with oligonucleotide arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 14470-5	11.5	380
100	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013 , 10, 1185-91.6	21.6	371
99	Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse. <i>Nature Genetics</i> , 2000 , 24, 381-6	36.3	371
98	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-713	30.4	360
97	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012 , 13, 418	18.3	340
96	The reality of pervasive transcription. <i>PLoS Biology</i> , 2011 , 9, e1000625; discussion e1001102	9.7	325

95	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs. <i>Genome Research</i> , 2012 , 22, 1616-25	9.7	317
94	Expression of the lacZ gene from two methanol-regulated promoters in <i>Pichia pastoris</i> . <i>Nucleic Acids Research</i> , 1987 , 15, 3859-76	20.1	298
93	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. <i>Blood</i> , 2009 , 113, 2526-34	2.2	271
92	Considerations when investigating lncRNA function in vivo. <i>ELife</i> , 2014 , 3, e03058	8.9	252
91	Microarray-based DNA methylation profiling: technology and applications. <i>Nucleic Acids Research</i> , 2006 , 34, 528-42	20.1	241
90	Comparison of the transcriptional landscapes between human and mouse tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17224-9	11.5	239
89	Examples of the complex architecture of the human transcriptome revealed by RACE and high-density tiling arrays. <i>Genome Research</i> , 2005 , 15, 987-97	9.7	236
88	Relationships between p63 binding, DNA sequence, transcription activity, and biological function in human cells. <i>Molecular Cell</i> , 2006 , 24, 593-602	17.6	227
87	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays. <i>Genome Research</i> , 1998 , 8, 435-48	9.7	219
86	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207
85	Evidence for compensatory upregulation of expressed X-linked genes in mammals, <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2011 , 43, 1179-85	36.3	206
84	Genome-wide antisense transcription drives mRNA processing in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20172-7	11.5	191
83	EGASP: the human ENCODE Genome Annotation Assessment Project. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S2.1-31	18.3	187
82	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012 , 13, R53	18.3	182
81	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2011 , 21, 301-14	9.7	171
80	Implications of chimaeric non-co-linear transcripts. <i>Nature</i> , 2009 , 461, 206-11	50.4	168
79	The isolation and characterization of the <i>Escherichia coli</i> DNA adenine methylase (dam) gene. <i>Nucleic Acids Research</i> , 1983 , 11, 837-51	20.1	165
78	Moving AHEAD with an international human epigenome project. <i>Nature</i> , 2008 , 454, 711-5	50.4	158

77	Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007 , 17, 839-51	9.7	158
76	Prominent use of distal 5Stranscription start sites and discovery of a large number of additional exons in ENCODE regions. <i>Genome Research</i> , 2007 , 17, 746-59	9.7	156
75	Biological function of unannotated transcription during the early development of <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2006 , 38, 1151-8	36.3	155
74	Origin of phenotypes: genes and transcripts. <i>Genome Research</i> , 2007 , 17, 682-90	9.7	141
73	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. <i>Nature Genetics</i> , 2017 , 49, 1731-1740	36.3	140
72	Reduced HIV-1 infectability of CD4+ lymphocytes from exposed-uninfected individuals: association with low expression of CCR5 and high production of beta-chemokines. <i>Virology</i> , 1998 , 244, 66-73	3.6	138
71	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , 2013 , 23, 169-80	9.7	133
70	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
69	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007 , 17, 852-64	9.7	131
68	The transcriptional responses of respiratory epithelial cells to <i>Bordetella pertussis</i> reveal host defensive and pathogen counter-defensive strategies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 13847-52	11.5	130
67	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010 , 7, 528-34	21.6	123
66	TUF love for "junk" DNA. <i>Cell</i> , 2006 , 125, 1215-20	56.2	119
65	MyD88 primes macrophages for full-scale activation by interferon-gamma yet mediates few responses to <i>Mycobacterium tuberculosis</i> . <i>Journal of Experimental Medicine</i> , 2003 , 198, 987-97	16.6	118
64	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008 , 18, 393-403	9.7	111
63	Comparative transcriptomics in human and mouse. <i>Nature Reviews Genetics</i> , 2017 , 18, 425-440	30.1	99
62	Temporal profile of replication of human chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 6419-24	11.5	97
61	Optimizing RNA-Seq Mapping with STAR. <i>Methods in Molecular Biology</i> , 2016 , 1415, 245-62	1.4	90
60	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017 , 4, 170112	8.2	88

59	Temporal Gene Regulation During HIV-1 Infection of Human CD4+ T Cells. <i>Genome Research</i> , 2001 , 11, 1198-1204	9.7	86
58	High resolution transcriptome maps for wild-type and nonsense-mediated decay-defective <i>Caenorhabditis elegans</i> . <i>Genome Biology</i> , 2009 , 10, R101	18.3	83
57	Nucleotide sequence of the PaeR7 restriction/modification system and partial characterization of its protein products. <i>Nucleic Acids Research</i> , 1985 , 13, 8441-61	20.1	83
56	STAR-Fusion: Fast and Accurate Fusion Transcript Detection from RNA-Seq		80
55	Whole-genome maps of USF1 and USF2 binding and histone H3 acetylation reveal new aspects of promoter structure and candidate genes for common human disorders. <i>Genome Research</i> , 2008 , 18, 380-92	9.7	72
54	ScrFI: a new sequence-specific endonuclease from <i>Streptococcus cremoris</i> . <i>Nucleic Acids Research</i> , 1982 , 10, 8171-9	20.1	72
53	A computer assisted method for the determination of restriction enzyme recognition sites. <i>Nucleic Acids Research</i> , 1978 , 5, 4105-27	20.1	72
52	Flexible use of high-density oligonucleotide arrays for single-nucleotide polymorphism discovery and validation. <i>Genome Research</i> , 2001 , 11, 1418-24	9.7	61
51	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
50	An effort to make sense of antisense transcription in bacteria. <i>RNA Biology</i> , 2012 , 9, 1039-44	4.8	57
49	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015 , 6, 5903	17.4	56
48	A genome-wide survey of sexually dimorphic expression of <i>Drosophila</i> miRNAs identifies the steroid hormone-induced miRNA let-7 as a regulator of sexual identity. <i>Genetics</i> , 2014 , 198, 647-68	4	55
47	Hybridization properties of immobilized nucleic acids. <i>Nucleic Acids Research</i> , 1987 , 15, 5373-90	20.1	54
46	Evidence for transcript networks composed of chimeric RNAs in human cells. <i>PLoS ONE</i> , 2012 , 7, e28213	3.7	51
45	Fifty years of molecular (DNA/RNA) diagnostics. <i>Clinical Chemistry</i> , 2005 , 51, 661-71	5.5	51
44	Extracellular vesicle-mediated transfer of processed and functional RNY5 RNA. <i>Rna</i> , 2015 , 21, 1966-79	5.8	47
43	De novo DNA demethylation and noncoding transcription define active intergenic regulatory elements. <i>Genome Research</i> , 2013 , 23, 1601-14	9.7	44
42	RAMPAGE: promoter activity profiling by paired-end sequencing of 5Scomplete cDNAs. <i>Current Protocols in Molecular Biology</i> , 2013 , 104, Unit 25B.11	2.9	44

41	Gene-specific patterns of expression variation across organs and species. <i>Genome Biology</i> , 2016 , 17, 151-183	44
40	Single-cell RNA sequencing of developing maize ears facilitates functional analysis and trait candidate gene discovery. <i>Developmental Cell</i> , 2021 , 56, 557-568.e6	10.2 39
39	Genome-wide mapping indicates that p73 and p63 co-occupy target sites and have similar dna-binding profiles in vivo. <i>PLoS ONE</i> , 2010 , 5, e11572	3.7 38
38	Blunt-end and single-strand ligations by Escherichia coli ligase: influence on an in vitro amplification scheme. <i>Gene</i> , 1990 , 89, 117-22	3.8 36
37	Efficient targeted transcript discovery via array-based normalization of RACE libraries. <i>Nature Methods</i> , 2008 , 5, 629-35	21.6 35
36	Emergence of dual resistance to zidovudine and lamivudine in HIV-1-infected patients treated with zidovudine plus lamivudine as initial therapy. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2000 , 23, 26-34	3.1 32
35	Genome-wide analysis of polymerase III-transcribed elements suggests cell-type-specific enhancer function. <i>Genome Research</i> , 2019 , 29, 1402-1414	9.7 31
34	Beyond expression profiling: next generation uses of high density oligonucleotide arrays. <i>Briefings in Functional Genomics & Proteomics</i> , 2003 , 2, 47-56	26
33	HIV-1 infectability of CD4+ lymphocytes with relation to beta-chemokines and the CCR5 coreceptor. <i>Immunology Letters</i> , 1999 , 66, 71-5	4.1 26
32	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E3366	11.5 22
31	Non-polyadenylated transcription in embryonic stem cells reveals novel non-coding RNA related to pluripotency and differentiation. <i>Nucleic Acids Research</i> , 2013 , 41, 6300-15	20.1 22
30	The DART classification of unannotated transcription within the ENCODE regions: associating transcription with known and novel loci. <i>Genome Research</i> , 2007 , 17, 732-45	9.7 21
29	Microarrays and genetic epidemiology: a multipurpose tool for a multifaceted field. <i>Genetic Epidemiology</i> , 2002 , 23, 4-20	2.6 19
28	A semi-automated method for the reading of nucleic acid sequencing gels. <i>Nucleic Acids Research</i> , 1982 , 10, 103-14	20.1 19
27	Processing by RNase 1 forms tRNA halves and distinct Y RNA fragments in the extracellular environment. <i>Nucleic Acids Research</i> , 2020 , 48, 8035-8049	20.1 15
26	Introduction and expression of the bacterial PaeR7 methylase gene in mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986 , 83, 7713-7	11.5 15
25	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020 , 30, 1047-1059	9.7 15
24	The fractured landscape of RNA-seq alignment: the default in our STARS. <i>Nucleic Acids Research</i> , 2018 , 46, 5125-5138	20.1 10

23	HIV regulation of the IL-7R: a viral mechanism for enhancing HIV-1 replication in human macrophages in vitro. <i>Journal of Leukocyte Biology</i> , 2006 , 79, 1328-38	6.5	10
22	Transcriptional landscape of the human and fly genomes: nonlinear and multifunctional modular model of transcriptomes. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2006 , 71, 101-10	3.9	10
21	Dynamics of microRNA expression during mouse prenatal development. <i>Genome Research</i> , 2019 , 29, 1900-1909	9.7	9
20	Rank-statistics based enrichment-site prediction algorithm developed for chromatin immunoprecipitation on chip experiments. <i>BMC Bioinformatics</i> , 2006 , 7, 434	3.6	9
19	Selective time-dependent changes in activity and cell-specific gene expression in human postmortem brain. <i>Scientific Reports</i> , 2021 , 11, 6078	4.9	9
18	Novel transcribed regions in the human genome. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2006 , 71, 111-6	3.9	7
17	Emergence of Dual Resistance to Zidovudine and Lamivudine in HIV-1 Infected Patients Treated With Zidovudine Plus Lamivudine as Initial Therapy. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2000 , 23, 26-34	3.1	7
16	Conserved noncoding transcription and core promoter regulatory code in early development. <i>ELife</i> , 2017 , 6,	8.9	6
15	Missing links in the transcriptome. <i>Nature Biotechnology</i> , 2009 , 27, 346-7	44.5	6
14	Differential analysis for high density tiling microarray data. <i>BMC Bioinformatics</i> , 2007 , 8, 359	3.6	6
13	Characteristics of oligonucleotide tiling arrays measured by hybridizing full-length cDNA clones: causes of signal variation and false positive signals. <i>Genomics</i> , 2007 , 89, 541-51	4.3	5
12	Ground tissue circuitry regulates organ complexity in maize and. <i>Science</i> , 2021 , 374, 1247-1252	33.3	5
11	RNA reference materials for gene expression studies. Difficult first steps. <i>Clinical Chemistry</i> , 2004 , 50, 1289-90	5.5	4
10	Detection of Deleted Genomic DNA Using a Semiautomated Computational Analysis of GeneChip Data. <i>Genome Research</i> , 2000 , 10, 2044-2054	9.7	4
9	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. <i>Frontiers in Plant Science</i> , 2020 , 11, 289	6.2	3
8	High-throughput annotation of full-length long noncoding RNAs with Capture Long-Read Sequencing		3
7	A limited set of transcriptional programs define major cell types		3
6	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021 , 12, 3297	17.4	3

5	Pan-genome Analysis in Sorghum Highlights the Extent of Genomic Variation and Sugarcane Aphid Resistance Genes		3
4	Variation in novel exons (RACEfrags) of the MECP2 gene in Rett syndrome patients and controls. <i>Human Mutation</i> , 2009 , 30, E866-79	4-7	1
3	The fractured landscape of RNA-seq alignment: The default in our STARS		1
2	Deciphering Molecular Circuitry Using High-Density DNA Arrays 1998 , 85-108		1
1	The Use of Transcription-based Amplification Systems in the Diagnosis of HIV-1 Infections 1994 , 33-58		