Thomas R Gingeras

List of Publications by Year in Descending Order

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130	72,979	76	137
papers	citations	h-index	g-index
137	93,354	19.5	8.45
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
130	Ground tissue circuitry regulates organ complexity in maize and. *Science*, **2021**, 374, 1247-1252	33.3	5
129	Selective time-dependent changes in activity and cell-specific gene expression in human postmortem brain. *Scientific Reports*, **2021**, 11, 6078	4.9	9
128	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. *Nature Communications*, **2021**, 12, 3297	17.4	3
127	Single-cell RNA sequencing of developing maize ears facilitates functional analysis and trait candidate gene discovery. *Developmental Cell*, **2021**, 56, 557-568.e6	10.2	39
126	Processing by RNase 1 forms tRNA halves and distinct Y RNA fragments in the extracellular environment. *Nucleic Acids Research*, **2020**, 48, 8035-8049	20.1	15
125	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. *Frontiers in Plant Science*, **2020**, 11, 289	6.2	3
124	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
123	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	50.4	360
122	A limited set of transcriptional programs define major cell types. *Genome Research*, **2020**, 30, 1047-1059	9.7	15
121	Dynamics of microRNA expression during mouse prenatal development. *Genome Research*, **2019**, 29, 1900-1909	9.7	9
120	Genome-wide analysis of polymerase III-transcribed elements suggests cell-type-specific enhancer function. *Genome Research*, **2019**, 29, 1402-1414	9.7	31
119	The fractured landscape of RNA-seq alignment: the default in our STARs. *Nucleic Acids Research*, **2018**, 46, 5125-5138	20.1	10
118	Comparative transcriptomics in human and mouse. *Nature Reviews Genetics*, **2017**, 18, 425-440	30.1	99
117	FANTOM5 CAGE profiles of human and mouse samples. *Scientific Data*, **2017**, 4, 170112	8.2	88
116	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. *Nature Genetics*, **2017**, 49, 1731-1740	36.3	140
115	Conserved noncoding transcription and core promoter regulatory code in early development. *ELife*, **2017**, 6,	8.9	6
114	Gene-specific patterns of expression variation across organs and species. *Genome Biology*, **2016**, 17, 151	18.3	44

(2013-2016)

113	Optimizing RNA-Seq Mapping with STAR. *Methods in Molecular Biology*, **2016**, 1415, 245-62	1.4	90
112	Extracellular vesicle-mediated transfer of processed and functional RNY5 RNA. *Rna*, **2015**, 21, 1966-79	5.8	47
111	Mapping RNA-seq Reads with STAR. *Current Protocols in Bioinformatics*, **2015**, 51, 11.14.1-11.14.19	24.2	446
110	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. *Nature Communications*, **2015**, 6, 5903	17.4	56
109	A promoter-level mammalian expression atlas. *Nature*, **2014**, 507, 462-70	50.4	1301
108	Diversity and dynamics of the Drosophila transcriptome. *Nature*, **2014**, 512, 393-9	50.4	418
107	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
106	Comparative analysis of the transcriptome across distant species. *Nature*, **2014**, 512, 445-8	50.4	207
105	A genome-wide survey of sexually dimorphic expression of Drosophila miRNAs identifies the steroid hormone-induced miRNA let-7 as a regulator of sexual identity. *Genetics*, **2014**, 198, 647-68	4	55
104	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E3366	11.5	22
103	Considerations when investigating lncRNA function in vivo. *ELife*, **2014**, 3, e03058	8.9	252
102	Defining functional DNA elements in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6131-8	11.5	490
101	Comparison of the transcriptional landscapes between human and mouse tissues. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 17224-9	11.5	239
100	Assessment of transcript reconstruction methods for RNA-seq. *Nature Methods*, **2013**, 10, 1177-84	21.6	477
99	Systematic evaluation of spliced alignment programs for RNA-seq data. *Nature Methods*, **2013**, 10, 1185-91	21.6	371
98	De novo DNA demethylation and noncoding transcription define active intergenic regulatory elements. *Genome Research*, **2013**, 23, 1601-14	9.7	44
97	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. *Genome Research*, **2013**, 23, 169-80	9.7	133
96	STAR: ultrafast universal RNA-seq aligner. *Bioinformatics*, **2013**, 29, 15-21	7.2	18121

95	Non-polyadenylated transcription in embryonic stem cells reveals novel non-coding RNA related to pluripotency and differentiation. *Nucleic Acids Research*, **2013**, 41, 6300-15	20.1	22
94	RAMPAGE: promoter activity profiling by paired-end sequencing of 5Scomplete cDNAs. *Current Protocols in Molecular Biology*, **2013**, 104, Unit 25B.11	2.9	44
93	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
92	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs. *Genome Research*, **2012**, 22, 1616-25	9.7	317
91	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. *Genome Research*, **2012**, 22, 1775-89	9.7	3408
90	Modeling gene expression using chromatin features in various cellular contexts. *Genome Biology*, **2012**, 13, R53	18.3	182
89	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. *Cell*, **2012**, 148, 84-98	56.2	882
88	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome Research*, **2012**, 22, 1658-67	9.7	133
87	Landscape of transcription in human cells. *Nature*, **2012**, 489, 101-8	50.4	3544
86	Evidence for transcript networks composed of chimeric RNAs in human cells. *PLoS ONE*, **2012**, 7, e28213	3.7	51
85	An effort to make sense of antisense transcription in bacteria. *RNA Biology*, **2012**, 9, 1039-44	4.8	57
84	An encyclopedia of mouse DNA elements (Mouse ENCODE). *Genome Biology*, **2012**, 13, 418	18.3	340
83	Synthetic spike-in standards for RNA-seq experiments. *Genome Research*, **2011**, 21, 1543-51	9.7	437
82	The developmental transcriptome of Drosophila melanogaster. *Nature*, **2011**, 471, 473-9	50.4	1094
81	Genome-wide antisense transcription drives mRNA processing in bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 20172-7	11.5	191
80	Evidence for compensatory upregulation of expressed X-linked genes in mammals, Caenorhabditis elegans and Drosophila melanogaster. *Nature Genetics*, **2011**, 43, 1179-85	36.3	206
79	The reality of pervasive transcription. *PLoS Biology*, **2011**, 9, e1000625; discussion e1001102	9.7	325
78	The transcriptional diversity of 25 Drosophila cell lines. *Genome Research*, **2011**, 21, 301-14	9.7	171

77	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. *Nature Methods*, **2010**, 7, 528-34	21.6	123
76	Genome-wide mapping indicates that p73 and p63 co-occupy target sites and have similar dna-binding profiles in vivo. *PLoS ONE*, **2010**, 5, e11572	3.7	38
75	Identification of functional elements and regulatory circuits by Drosophila modENCODE. *Science*, **2010**, 330, 1787-97	33.3	892
74	Variation in novel exons (RACEfrags) of the MECP2 gene in Rett syndrome patients and controls. *Human Mutation*, **2009**, 30, E866-79	4.7	1
73	Implications of chimaeric non-co-linear transcripts. *Nature*, **2009**, 461, 206-11	50.4	168
72	Missing lincs in the transcriptome. *Nature Biotechnology*, **2009**, 27, 346-7	44.5	6
71	High resolution transcriptome maps for wild-type and nonsense-mediated decay-defective Caenorhabditis elegans. *Genome Biology*, **2009**, 10, R101	18.3	83
70	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. *Blood*, **2009**, 113, 2526-34	2.2	271
69	Moving AHEAD with an international human epigenome project. *Nature*, **2008**, 454, 711-5	50.4	158
68	Efficient targeted transcript discovery via array-based normalization of RACE libraries. *Nature Methods*, **2008**, 5, 629-35	21.6	35
67	Global transcription in pluripotent embryonic stem cells. *Cell Stem Cell*, **2008**, 2, 437-47	18	503
66	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. *Genome Research*, **2008**, 18, 380-92	9.7	72
65	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. *Genome Research*, **2008**, 18, 393-403	9.7	111
64	Genome-wide transcription and the implications for genomic organization. *Nature Reviews Genetics*, **2007**, 8, 413-23	30.1	570
63	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
62	Differential analysis for high density tiling microarray data. *BMC Bioinformatics*, **2007**, 8, 359	3.6	6
61	Prominent use of distal 5Stranscription start sites and discovery of a large number of additional exons in ENCODE regions. *Genome Research*, **2007**, 17, 746-59	9.7	156
60	The DART classification of unannotated transcription within the ENCODE regions: associating transcription with known and novel loci. *Genome Research*, **2007**, 17, 732-45	9.7	21

59	Structured RNAs in the ENCODE selected regions of the human genome. *Genome Research*, **2007**, 17, 852-64	9.7	131
58	Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. *Genome Research*, **2007**, 17, 839-51	9.7	158
57	Characteristics of oligonucleotide tiling arrays measured by hybridizing full-length cDNA clones: causes of signal variation and false positive signals. *Genomics*, **2007**, 89, 541-51	4.3	5
56	RNA maps reveal new RNA classes and a possible function for pervasive transcription. *Science*, **2007**, 316, 1484-8	33.3	1903
55	Origin of phenotypes: genes and transcripts. *Genome Research*, **2007**, 17, 682-90	9.7	141
54	Rank-statistics based enrichment-site prediction algorithm developed for chromatin immunoprecipitation on chip experiments. *BMC Bioinformatics*, **2006**, 7, 434	3.6	9
53	Microarray-based DNA methylation profiling: technology and applications. *Nucleic Acids Research*, **2006**, 34, 528-42	20.1	241
52	HIV regulation of the IL-7R: a viral mechanism for enhancing HIV-1 replication in human macrophages in vitro. *Journal of Leukocyte Biology*, **2006**, 79, 1328-38	6.5	10
51	EGASP: the human ENCODE Genome Annotation Assessment Project. *Genome Biology*, **2006**, 7 Suppl 1, S2.1-31	18.3	187
50	TUF love for "junk" DNA. *Cell*, **2006**, 125, 1215-20	56.2	119
49	CD127 expression inversely correlates with FoxP3 and suppressive function of human CD4+ T reg cells. *Journal of Experimental Medicine*, **2006**, 203, 1701-11	16.6	1963
48	Relationships between p63 binding, DNA sequence, transcription activity, and biological function in human cells. *Molecular Cell*, **2006**, 24, 593-602	17.6	227
47	Novel transcribed regions in the human genome. *Cold Spring Harbor Symposia on Quantitative Biology*, **2006**, 71, 111-6	3.9	7
46	Transcriptional landscape of the human and fly genomes: nonlinear and multifunctional modular model of transcriptomes. *Cold Spring Harbor Symposia on Quantitative Biology*, **2006**, 71, 101-10	3.9	10
45	Biological function of unannotated transcription during the early development of Drosophila melanogaster. *Nature Genetics*, **2006**, 38, 1151-8	36.3	155
44	Genome-wide analysis of estrogen receptor binding sites. *Nature Genetics*, **2006**, 38, 1289-97	36.3	1115
43	Temporal profile of replication of human chromosomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 6419-24	11.5	97
42	Genomic maps and comparative analysis of histone modifications in human and mouse. *Cell*, **2005**, 120, 169-81	56.2	1198

(2000-2005)

41	Transcriptional maps of 10 human chromosomes at 5-nucleotide resolution. *Science*, **2005**, 308, 1149-54	33.3	967
40	Fifty years of molecular (DNA/RNA) diagnostics. *Clinical Chemistry*, **2005**, 51, 661-71	5.5	51
39	Examples of the complex architecture of the human transcriptome revealed by RACE and high-density tiling arrays. *Genome Research*, **2005**, 15, 987-97	9.7	236
38	RNA reference materials for gene expression studies. Difficult first steps. *Clinical Chemistry*, **2004**, 50, 1289-90	5.5	4
37	Novel RNAs identified from an in-depth analysis of the transcriptome of human chromosomes 21 and 22. *Genome Research*, **2004**, 14, 331-42	9.7	410
36	The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science*, **2004**, 306, 636-40	33.3	1692
35	Unbiased mapping of transcription factor binding sites along human chromosomes 21 and 22 points to widespread regulation of noncoding RNAs. *Cell*, **2004**, 116, 499-509	56.2	948
34	MyD88 primes macrophages for full-scale activation by interferon-gamma yet mediates few responses to Mycobacterium tuberculosis. *Journal of Experimental Medicine*, **2003**, 198, 987-97	16.6	118
33	Beyond expression profiling: next generation uses of high density oligonucleotide arrays. *Briefings in Functional Genomics & Proteomics*, **2003**, 2, 47-56		26
32	Microarrays and genetic epidemiology: a multipurpose tool for a multifaceted field. *Genetic Epidemiology*, **2002**, 23, 4-20	2.6	19
31	Large-scale transcriptional activity in chromosomes 21 and 22. *Science*, **2002**, 296, 916-9	33.3	711
30	Flexible use of high-density oligonucleotide arrays for single-nucleotide polymorphism discovery and validation. *Genome Research*, **2001**, 11, 1418-24	9.7	61
29	Reprogramming of the macrophage transcriptome in response to interferon-gamma and Mycobacterium tuberculosis: signaling roles of nitric oxide synthase-2 and phagocyte oxidase. *Journal of Experimental Medicine*, **2001**, 194, 1123-40	16.6	394
28	Temporal Gene Regulation During HIV-1 Infection of Human CD4+ T Cells. *Genome Research*, **2001**, 11, 1198-1204	9.7	86
27	Emergence of Dual Resistance to Zidovudine and Lamivudine in HIV-1Infected Patients Treated With Zidovudine Plus Lamivudine as Initial Therapy. *Journal of Acquired Immune Deficiency Syndromes (1999)*, **2000**, 23, 26-34	3.1	7
26	Emergence of dual resistance to zidovudine and lamivudine in HIV-1-infected patients treated with zidovudine plus lamivudine as initial therapy. *Journal of Acquired Immune Deficiency Syndromes (1999)*, **2000**, 23, 26-34	3.1	32
25	Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse. *Nature Genetics*, **2000**, 24, 381-6	36.3	371
24	The transcriptional responses of respiratory epithelial cells to Bordetella pertussis reveal host defensive and pathogen counter-defensive strategies. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 13847-52	11.5	130

23	Detection of Deleted Genomic DNA Using a Semiautomated Computational Analysis of GeneChip Data. *Genome Research*, **2000**, 10, 2044-2054	9.7	4
22	HIV-1 infectability of CD4+ lymphocytes with relation to beta-chemokines and the CCR5 coreceptor. *Immunology Letters*, **1999**, 66, 71-5	4.1	26
21	High density synthetic oligonucleotide arrays. *Nature Genetics*, **1999**, 21, 20-4	36.3	1872
20	Reduced HIV-1 infectability of CD4+ lymphocytes from exposed-uninfected individuals: association with low expression of CCR5 and high production of beta-chemokines. *Virology*, **1998**, 244, 66-73	3.6	138
19	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays. *Genome Research*, **1998**, 8, 435-48	9.7	219
18	Cellular gene expression altered by human cytomegalovirus: global monitoring with oligonucleotide arrays. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 14470-5	11.5	380
17	Deciphering Molecular Circuitry Using High-Density DNA Arrays **1998**, 85-108		1
16	Extensive polymorphisms observed in HIV-1 clade B protease gene using high-density oligonucleotide arrays. *Nature Medicine*, **1996**, 2, 753-9	50.5	471
15	The Use of Transcription-based Amplification Systems in the Diagnosis of HIV-1 Infections **1994**, 33-58		
14	Blunt-end and single-strand ligations by Escherichia coli ligase: influence on an in vitro amplification scheme. *Gene*, **1990**, 89, 117-22	3.8	36
13	Hybridization properties of immobilized nucleic acids. *Nucleic Acids Research*, **1987**, 15, 5373-90	20.1	54
12	Expression of the lacZ gene from two methanol-regulated promoters in Pichia pastoris. *Nucleic Acids Research*, **1987**, 15, 3859-76	20.1	298
11	Introduction and expression of the bacterial PaeR7 methylase gene in mammalian cells. *Proceedings of the National Academy of Sciences of the United States of America*, **1986**, 83, 7713-7	11.5	15
10	Nucleotide sequence of the PaeR7 restriction/modification system and partial characterization of its protein products. *Nucleic Acids Research*, **1985**, 13, 8441-61	20.1	83
9	The isolation and characterization of the Escherichia coli DNA adenine methylase (dam) gene. *Nucleic Acids Research*, **1983**, 11, 837-51	20.1	165
8	A semi-automated method for the reading of nucleic acid sequencing gels. *Nucleic Acids Research*, **1982**, 10, 103-14	20.1	19
7	ScrFI: a new sequence-specific endonuclease from Streptococcus cremoris. *Nucleic Acids Research*, **1982**, 10, 8171-9	20.1	72
6	A computer assisted method for the determination of restriction enzyme recognifion sites. *Nucleic Acids Research*, **1978**, 5, 4105-27	20.1	72

List of Publications

5	The fractured landscape of RNA-seq alignment: The default in our STARs	1
4	High-throughput annotation of full-length long noncoding RNAs with Capture Long-Read Sequencing	3
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2	A limited set of transcriptional programs define major cell types	3
1	Pan-genome Analysis in Sorghum Highlights the Extent of Genomic Variation and Sugarcane Aphid Resistance Genes	3