

Thomas R Gingeras

List of Publications by Year in descending order

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128
papers

105,281
citations

7069

78
h-index

15218

126
g-index

137
all docs

137
docs citations

137
times ranked

130902
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.1	129
2	Selective time-dependent changes in activity and cell-specific gene expression in human postmortem brain. <i>Scientific Reports</i> , 2021, 11, 6078.	1.6	39
3	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
4	Ground tissue circuitry regulates organ complexity in maize and <i>Setaria</i> . <i>Science</i> , 2021, 374, 1247-1252.	6.0	55
5	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
6	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
7	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020, 30, 1047-1059.	2.4	32
8	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.	6.5	41
9	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. <i>Frontiers in Plant Science</i> , 2020, 11, 289.	1.7	4
10	Genome-wide analysis of polymerase III-transcribed <i>Alu</i> elements suggests cell-type-specific enhancer function. <i>Genome Research</i> , 2019, 29, 1402-1414.	2.4	69
11	Dynamics of microRNA expression during mouse prenatal development. <i>Genome Research</i> , 2019, 29, 1900-1909.	2.4	21
12	The fractured landscape of RNA-seq alignment: the default in our STARs. <i>Nucleic Acids Research</i> , 2018, 46, 5125-5138.	6.5	17
13	Comparative transcriptomics in human and mouse. <i>Nature Reviews Genetics</i> , 2017, 18, 425-440.	7.7	168
14	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	2.4	195
15	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. <i>Nature Genetics</i> , 2017, 49, 1731-1740.	9.4	227
16	Conserved noncoding transcription and core promoter regulatory code in early <i>Drosophila</i> development. <i>ELife</i> , 2017, 6, .	2.8	10
17	Gene-specific patterns of expression variation across organs and species. <i>Genome Biology</i> , 2016, 17, 151.	3.8	89
18	Optimizing RNA-Seq Mapping with STAR. <i>Methods in Molecular Biology</i> , 2016, 1415, 245-262.	0.4	178

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19	Mapping RNA-seq Reads with STAR. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 11.14.1-11.14.19.	25.8	858
20	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015, 6, 5903.	5.8	73
21	Extracellular vesicle-mediated transfer of processed and functional RNY5 RNA. <i>Rna</i> , 2015, 21, 1966-1979.	1.6	66
22	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, 6131-6138.	3.3	635
23	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, 17224-17229.	3.3	337
24	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
25	Diversity and dynamics of the <i>Drosophila</i> transcriptome. <i>Nature</i> , 2014, 512, 393-399.	13.7	647
26	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
27	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	13.7	289
28	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, 647-668.	1.2	68
29	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.	3.3	25
30	Considerations when investigating lncRNA function in vivo. <i>ELife</i> , 2014, 3, e03058.	2.8	309
31	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	9.0	679
32	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	9.0	467
33	De novo DNA demethylation and noncoding transcription define active intergenic regulatory elements. <i>Genome Research</i> , 2013, 23, 1601-1614.	2.4	58
34	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , 2013, 23, 169-180.	2.4	176
35	STAR: ultrafast universal RNA-seq aligner. <i>Bioinformatics</i> , 2013, 29, 15-21.	1.8	35,376
36	Non-polyadenylated transcription in embryonic stem cells reveals novel non-coding RNA related to pluripotency and differentiation. <i>Nucleic Acids Research</i> , 2013, 41, 6300-6315.	6.5	28

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37	RAMPAGE: Promoter Activity Profiling by Paired-End Sequencing of 5' Complete cDNAs. <i>Current Protocols in Molecular Biology</i> , 2013, 104, Unit 25B.11.	2.9	58
38	An effort to make sense of antisense transcription in bacteria. <i>RNA Biology</i> , 2012, 9, 1039-1044.	1.5	65
39	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	13.9	410
40	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
41	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, 1616-1625.	2.4	401
42	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012, 22, 1775-1789.	2.4	4,428
43	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	13.9	231
44	RNA discrimination. <i>Nature</i> , 2012, 482, 310-311.	13.7	104
45	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98.	13.5	1,096
46	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	2.4	166
47	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
48	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. <i>PLoS ONE</i> , 2012, 7, e28213.	1.1	61
49	Synthetic spike-in standards for RNA-seq experiments. <i>Genome Research</i> , 2011, 21, 1543-1551.	2.4	588
50	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 473-479.	13.7	1,379
51	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, 20172-20177.	3.3	231
52	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, 1179-1185.	9.4	260
53	The Reality of Pervasive Transcription. <i>PLoS Biology</i> , 2011, 9, e1000625.	2.6	380
54	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2011, 21, 301-314.	2.4	235

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55	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	9.0	152
56	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.	1.1	42
57	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	6.0	1,124
58	Variation in novel exons (RACEfrags) of the MECP2 gene in Rett syndrome patients and controls. <i>Human Mutation</i> , 2009, 30, E866-E879.	1.1	1
59	Implications of chimaeric non-co-linear transcripts. <i>Nature</i> , 2009, 461, 206-211.	13.7	195
60	Missing lincs in the transcriptome. <i>Nature Biotechnology</i> , 2009, 27, 346-347.	9.4	7
61	High resolution transcriptome maps for wild-type and nonsense-mediated decay-defective <i>Caenorhabditis elegans</i> . <i>Genome Biology</i> , 2009, 10, R101.	13.9	91
62	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. <i>Blood</i> , 2009, 113, 2526-2534.	0.6	330
63	Moving AHEAD with an international human epigenome project. <i>Nature</i> , 2008, 454, 711-715.	13.7	177
64	Mapping the strand-specific transcriptome of fission yeast. <i>Nature Genetics</i> , 2008, 40, 935-936.	9.4	1
65	Efficient targeted transcript discovery via array-based normalization of RACE libraries. <i>Nature Methods</i> , 2008, 5, 629-635.	9.0	41
66	Global Transcription in Pluripotent Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2008, 2, 437-447.	5.2	603
67	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, 380-392.	2.4	85
68	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	2.4	117
69	Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. <i>Genome Research</i> , 2007, 17, 746-759.	2.4	173
70	The DART classification of unannotated transcription within the ENCODE regions: Associating transcription with known and novel loci. <i>Genome Research</i> , 2007, 17, 732-745.	2.4	25
71	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	2.4	150
72	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007, 17, 839-851.	2.4	191

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73	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, 541-551.	1.3	5
74	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. <i>Science</i> , 2007, 316, 1484-1488.	6.0	2,250
75	Origin of phenotypes: Genes and transcripts. <i>Genome Research</i> , 2007, 17, 682-690.	2.4	167
76	Genome-wide transcription and the implications for genomic organization. <i>Nature Reviews Genetics</i> , 2007, 8, 413-423.	7.7	652
77	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
78	Differential analysis for high density tiling microarray data. <i>BMC Bioinformatics</i> , 2007, 8, 359.	1.2	6
79	EGASP: the human ENCODE Genome Annotation Assessment Project. <i>Genome Biology</i> , 2006, 7, S2.	13.9	228
80	TUF Love for "Junk" DNA. <i>Cell</i> , 2006, 125, 1215-1220.	13.5	139
81	CD127 expression inversely correlates with FoxP3 and suppressive function of human CD4+ T reg cells. <i>Journal of Experimental Medicine</i> , 2006, 203, 1701-1711.	4.2	2,292
82	Relationships between p63 Binding, DNA Sequence, Transcription Activity, and Biological Function in Human Cells. <i>Molecular Cell</i> , 2006, 24, 593-602.	4.5	248
83	Novel Transcribed Regions in the Human Genome. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2006, 71, 111-116.	2.0	8
84	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, 101-110.	2.0	15
85	The multitasking genome. <i>Nature Genetics</i> , 2006, 38, 608-609.	9.4	12
86	Biological function of unannotated transcription during the early development of <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2006, 38, 1151-1158.	9.4	168
87	Genome-wide analysis of estrogen receptor binding sites. <i>Nature Genetics</i> , 2006, 38, 1289-1297.	9.4	1,227
88	Rank-statistics based enrichment-site prediction algorithm developed for chromatin immunoprecipitation on chip experiments. <i>BMC Bioinformatics</i> , 2006, 7, 434.	1.2	9
89	Microarray-based DNA methylation profiling: technology and applications. <i>Nucleic Acids Research</i> , 2006, 34, 528-542.	6.5	271
90	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, 1328-1338.	1.5	13

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91	Fifty Years of Molecular (DNA/RNA) Diagnostics. <i>Clinical Chemistry</i> , 2005, 51, 661-671.	1.5	58
92	Examples of the complex architecture of the human transcriptome revealed by RACE and high-density tiling arrays. <i>Genome Research</i> , 2005, 15, 987-997.	2.4	263
93	Temporal profile of replication of human chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6419-6424.	3.3	105
94	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. <i>Cell</i> , 2005, 120, 169-181.	13.5	1,348
95	Transcriptional Maps of 10 Human Chromosomes at 5-Nucleotide Resolution. <i>Science</i> , 2005, 308, 1149-1154.	6.0	1,073
96	RNA Reference Materials for Gene Expression Studies. <i>Clinical Chemistry</i> , 2004, 50, 1289-1290.	1.5	4
97	Novel RNAs Identified From an In-Depth Analysis of the Transcriptome of Human Chromosomes 21 and 22. <i>Genome Research</i> , 2004, 14, 331-342.	2.4	460
98	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004, 306, 636-640.	6.0	2,121
99	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.	13.5	1,047
100	MyD88 Primes Macrophages for Full-Scale Activation by Interferon- β yet Mediates Few Responses to <i>Mycobacterium tuberculosis</i> . <i>Journal of Experimental Medicine</i> , 2003, 198, 987-997.	4.2	133
101	Beyond expression profiling: Next generation uses of high density oligonucleotide arrays. <i>Briefings in Functional Genomics & Proteomics</i> , 2003, 2, 47-56.	3.8	30
102	Large-Scale Transcriptional Activity in Chromosomes 21 and 22. <i>Science</i> , 2002, 296, 916-919.	6.0	793
103	Microarrays and genetic epidemiology: A multipurpose tool for a multifaceted field. <i>Genetic Epidemiology</i> , 2002, 23, 4-20.	0.6	19
104	Flexible Use of High-Density Oligonucleotide Arrays for Single-Nucleotide Polymorphism Discovery and Validation. <i>Genome Research</i> , 2001, 11, 1418-1424.	2.4	66
105	Reprogramming of the Macrophage Transcriptome in Response to Interferon- β and <i>Mycobacterium tuberculosis</i> . <i>Journal of Experimental Medicine</i> , 2001, 194, 1123-1140.	4.2	437
106	Temporal Gene Regulation During HIV-1 Infection of Human CD4+ T Cells. <i>Genome Research</i> , 2001, 11, 1198-1204.	2.4	89
107	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</i> (1999), 2000, 23, 26-34.	0.9	7
108	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</i> (1999), 2000, 23, 26-34.	0.9	36

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109	Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse. <i>Nature Genetics</i> , 2000, 24, 381-386.	9.4	395
110	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, 13847-13852.	3.3	145
111	Detection of Deleted Genomic DNA Using a Semiautomated Computational Analysis of GeneChip Data. <i>Genome Research</i> , 2000, 10, 2044-2054.	2.4	10
112	HIV-1 infectability of CD4+ lymphocytes with relation to β -chemokines and the CCR5 coreceptor. <i>Immunology Letters</i> , 1999, 66, 71-75.	1.1	27
113	High density synthetic oligonucleotide arrays. <i>Nature Genetics</i> , 1999, 21, 20-24.	9.4	2,085
114	Reduced HIV-1 Infectability of CD4+Lymphocytes from Exposed-Uninfected Individuals: Association with Low Expression of CCR5 and High Production of β -Chemokines. <i>Virology</i> , 1998, 244, 66-73.	1.1	153
115	Simultaneous Genotyping and Species Identification Using Hybridization Pattern Recognition Analysis of GenericMycobacteriumDNA%Arrays. <i>Genome Research</i> , 1998, 8, 435-448.	2.4	243
116	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, 14470-14475.	3.3	413
117	Deciphering Molecular Circuitry Using High-Density DNA Arrays. , 1998, , 85-108.		2
118	Extensive polymorphisms observed in HIV-1 clade B protease gene using high-density oligonucleotide arrays. <i>Nature Medicine</i> , 1996, 2, 753-759.	15.2	558
119	The Use of Transcription-based Amplification Systems in the Diagnosis of HIV-1 Infections. , 1994, , 33-58.		0
120	Blunt-end and single-strand ligations by <i>Escherichia coli</i> ligase: influence on an in vitro amplification scheme. <i>Gene</i> , 1990, 89, 117-122.	1.0	41
121	Hybridization properties of immobilized nucleic acids. <i>Nucleic Acids Research</i> , 1987, 15, 5373-5390.	6.5	63
122	Expression of the <i>lacZ</i> gene from two methanol-regulated promoters in <i>Pichia pastoris</i> . <i>Nucleic Acids Research</i> , 1987, 15, 3859-3876.	6.5	327
123	Introduction and expression of the bacterial <i>PaeR7</i> methylase gene in mammalian cells.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 7713-7717.	3.3	16
124	Nucleotide sequence of the <i>PaeR7</i> restriction/modification system and partial characterization of its protein products. <i>Nucleic Acids Research</i> , 1985, 13, 8441-8461.	6.5	91
125	The Isolation and Characterization of the <i>Escherichia Coli</i> DNA adenine methylase (<i>dam</i>) gene. <i>Nucleic Acids Research</i> , 1983, 11, 837-851.	6.5	187
126	A semi-automated method for the reading of nucleic acid sequencing gels. <i>Nucleic Acids Research</i> , 1982, 10, 103-114.	6.5	20

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127	ScrFI: a new sequence-specific endonuclease from <i>Streptococcus cremoris</i> . <i>Nucleic Acids Research</i> , 1982, 10, 8171-8179.	6.5	89
128	A computer assisted method for the determination of restriction enzyme recognition sites. <i>Nucleic Acids Research</i> , 1978, 5, 4105-4128.	6.5	80