

Jason Gertz

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

9,047
citations

136950

32
h-index

128289

60
g-index

75
all docs

75
docs citations

75
times ranked

18933
citing authors

#	ARTICLE	IF	CITATIONS
1	Hotspot <i>ESR1</i> Mutations Are Multimodal and Contextual Modulators of Breast Cancer Metastasis. <i>Cancer Research</i> , 2022, 82, 1321-1339.	0.9	30
2	A human breast cancer-derived xenograft and organoid platform for drug discovery and precision oncology. <i>Nature Cancer</i> , 2022, 3, 232-250.	13.2	133
3	<i>ESR1</i> mutant breast cancers show elevated basal cytokeratins and immune activation. <i>Nature Communications</i> , 2022, 13, 2011.	12.8	29
4	Comprehensive evaluation and efficient classification of BRCA1 RING domain missense substitutions. <i>American Journal of Human Genetics</i> , 2022, 109, 1153-1174.	6.2	6
5	Estrogen Receptor Alpha Mutations in Breast Cancer Cells Cause Gene Expression Changes through Constant Activity and Secondary Effects. <i>Cancer Research</i> , 2021, 81, 539-551.	0.9	35
6	Steroid Hormone Receptor and Infiltrating Immune Cell Status Reveals Therapeutic Vulnerabilities of <i>ESR1</i> -Mutant Breast Cancer. <i>Cancer Research</i> , 2021, 81, 732-746.	0.9	34
7	A Positive Feedback Loop Between <i>TGFβ2</i> and Androgen Receptor Supports Triple-negative Breast Cancer Anoikis Resistance. <i>Endocrinology</i> , 2021, 162, .	2.8	13
8	Reciprocal regulation of pancreatic ductal adenocarcinoma growth and molecular subtype by <i>HNF4α</i> and <i>SIX1/4</i> . <i>Gut</i> , 2021, 70, 900-914.	12.1	19
9	<i>Brd4</i> -bound enhancers drive cell-intrinsic sex differences in glioblastoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	28
10	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design. <i>GigaScience</i> , 2021, 10, .	6.4	17
11	A predominant enhancer co-amplified with the <i>SOX2</i> oncogene is necessary and sufficient for its expression in squamous cancer. <i>Nature Communications</i> , 2021, 12, 7139.	12.8	12
12	Regulatory sharing between estrogen receptor α bound enhancers. <i>Nucleic Acids Research</i> , 2020, 48, 6597-6610.	14.5	7
13	<i>MYC</i> Drives Temporal Evolution of Small Cell Lung Cancer Subtypes by Reprogramming Neuroendocrine Fate. <i>Cancer Cell</i> , 2020, 38, 60-78.e12.	16.8	262
14	Synergistic CRISPRa-Regulated Chondrogenic Extracellular Matrix Deposition Without Exogenous Growth Factors. <i>Tissue Engineering - Part A</i> , 2020, 26, 1169-1179.	3.1	11
15	<i>ETV4</i> Is Necessary for Estrogen Signaling and Growth in Endometrial Cancer Cells. <i>Cancer Research</i> , 2020, 80, 1234-1245.	0.9	39
16	XPRESSyourself: Enhancing, standardizing, and automating ribosome profiling computational analyses yields improved insight into data. <i>PLoS Computational Biology</i> , 2020, 16, e1007625.	3.2	15
17	Estrogen-independent molecular actions of mutant estrogen receptor 1 in endometrial cancer. <i>Genome Research</i> , 2019, 29, 1429-1441.	5.5	27
18	FFPEcap-seq: a method for sequencing capped RNAs in formalin-fixed paraffin-embedded samples. <i>Genome Research</i> , 2019, 29, 1826-1835.	5.5	9

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19	Lentiviral CRISPR Epigenome Editing of Inflammatory Receptors as a Gene Therapy Strategy for Disc Degeneration. <i>Human Gene Therapy</i> , 2019, 30, 1161-1175.	2.7	44
20	MYC-Driven Small-Cell Lung Cancer is Metabolically Distinct and Vulnerable to Arginine Depletion. <i>Clinical Cancer Research</i> , 2019, 25, 5107-5121.	7.0	117
21	Estrogen Signaling in Endometrial Cancer: a Key Oncogenic Pathway with Several Open Questions. <i>Hormones and Cancer</i> , 2019, 10, 51-63.	4.9	164
22	Sufficiency analysis of estrogen responsive enhancers using synthetic activators. <i>Life Science Alliance</i> , 2019, 2, e201900497.	2.8	10
23	GIGGLE: a search engine for large-scale integrated genome analysis. <i>Nature Methods</i> , 2018, 15, 123-126.	19.0	154
24	Clinical and Genomic Crosstalk between Glucocorticoid Receptor and Estrogen Receptor β In Endometrial Cancer. <i>Cell Reports</i> , 2018, 22, 2995-3005.	6.4	52
25	Dissection of Enhancer Function Using Multiplex CRISPR-based Enhancer Interference in Cell Lines. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	7
26	MYC Drives Progression of Small Cell Lung Cancer to a Variant Neuroendocrine Subtype with Vulnerability to Aurora Kinase Inhibition. <i>Cancer Cell</i> , 2017, 31, 270-285.	16.8	406
27	Multiplex Enhancer Interference Reveals Collaborative Control of Gene Regulation by Estrogen Receptor β -Bound Enhancers. <i>Cell Systems</i> , 2017, 5, 333-344.e5.	6.2	85
28	CRISPR Epigenome Editing of AKAP150 in DRG Neurons Abolishes Degenerative IVD-Induced Neuronal Activation. <i>Molecular Therapy</i> , 2017, 25, 2014-2027.	8.2	35
29	Post-mortem molecular profiling of three psychiatric disorders. <i>Genome Medicine</i> , 2017, 9, 72.	8.2	147
30	Genomic regulation of invasion by STAT3 in triple negative breast cancer. <i>Oncotarget</i> , 2017, 8, 8226-8238.	1.8	69
31	GENT-18. DIFFERENTIAL BRD4-BOUND STRETCH/SUPER ENHANCERS DRIVE CRITICAL SEX DIFFERENCES IN GBM PHENOTYPE. <i>Neuro-Oncology</i> , 2016, 18, vi77-vi77.	1.2	0
32	Discordant Haplotype Sequencing Identifies Functional Variants at the 2q33 Breast Cancer Risk Locus. <i>Cancer Research</i> , 2016, 76, 1916-1925.	0.9	7
33	Cooperative Dynamics of AR and ER Activity in Breast Cancer. <i>Molecular Cancer Research</i> , 2016, 14, 1054-1067.	3.4	114
34	Distinct gene regulatory programs define the inhibitory effects of liver X receptors and PPAR γ on cancer cell proliferation. <i>Genome Medicine</i> , 2016, 8, 74.	8.2	43
35	RNA sequencing of pancreatic adenocarcinoma tumors yields novel expression patterns associated with long-term survival and reveals a role for <i>ANGPTL4</i> . <i>Molecular Oncology</i> , 2016, 10, 1169-1182.	4.6	70
36	Improved survival among colon cancer patients with increased differentially expressed pathways. <i>BMC Medicine</i> , 2015, 13, 75.	5.5	18

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37	Promoter-distal RNA polymerase II binding discriminates active from inactive CCAAT/ enhancer-binding protein beta binding sites. <i>Genome Research</i> , 2015, 25, 1791-1800.	5.5	30
38	From single-cell to cell-pool transcriptomes: Stochasticity in gene expression and RNA splicing. <i>Genome Research</i> , 2014, 24, 496-510.	5.5	470
39	Recurrent read-through fusion transcripts in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2014, 146, 287-297.	2.5	141
40	Distinct Properties of Cell-Type-Specific and Shared Transcription Factor Binding Sites. <i>Molecular Cell</i> , 2013, 52, 25-36.	9.7	283
41	Mapping genome-wide transcription factor binding sites in frozen tissues. <i>Epigenetics and Chromatin</i> , 2013, 6, 30.	3.9	29
42	Dynamic DNA methylation across diverse human cell lines and tissues. <i>Genome Research</i> , 2013, 23, 555-567.	5.5	614
43	Early de novo DNA methylation and prolonged demethylation in the muscle lineage. <i>Epigenetics</i> , 2013, 8, 317-332.	2.7	85
44	Research Resource: Enhanced Genome-Wide Occupancy of Estrogen Receptor β by the Cochaperone p23 in Breast Cancer Cells. <i>Molecular Endocrinology</i> , 2012, 26, 194-202.	3.7	19
45	Widespread plasticity in CTCF occupancy linked to DNA methylation. <i>Genome Research</i> , 2012, 22, 1680-1688.	5.5	494
46	Transposase mediated construction of RNA-seq libraries. <i>Genome Research</i> , 2012, 22, 134-141.	5.5	85
47	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	5.5	1,708
48	The Hypersensitive Glucocorticoid Response Specifically Regulates Period 1 and Expression of Circadian Genes. <i>Molecular and Cellular Biology</i> , 2012, 32, 3756-3767.	2.3	122
49	Genistein and bisphenol A exposure cause estrogen receptor 1 to bind thousands of sites in a cell type-specific manner. <i>Genome Research</i> , 2012, 22, 2153-2162.	5.5	121
50	CTCF/cohesin-mediated DNA looping is required for protocadherin β promoter choice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21081-21086.	7.1	218
51	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	27.8	1,384
52	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. <i>Genome Research</i> , 2012, 22, 860-869.	5.5	150
53	Allele-specific distribution of RNA polymerase II on female X chromosomes. <i>Human Molecular Genetics</i> , 2011, 20, 3964-3973.	2.9	34
54	$\text{I}\kappa\text{B}$ kinase β (IKK β) regulates the balance between type I and type II interferon responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 21170-21175.	7.1	105

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55	Analysis of DNA Methylation in a Three-Generation Family Reveals Widespread Genetic Influence on Epigenetic Regulation. <i>PLoS Genetics</i> , 2011, 7, e1002228.	3.5	256
56	Epistasis in a quantitative trait captured by a molecular model of transcription factor interactions. <i>Theoretical Population Biology</i> , 2010, 77, 1-5.	1.1	29
57	Environment-specific combinatorial <i>cis</i> -regulation in synthetic promoters. <i>Molecular Systems Biology</i> , 2009, 5, 244.	7.2	45
58	Analysis of combinatorial <i>cis</i> -regulation in synthetic and genomic promoters. <i>Nature</i> , 2009, 457, 215-218.	27.8	287
59	A <i>cis</i> -regulatory logic simulator. <i>BMC Bioinformatics</i> , 2007, 8, 272.	2.6	1
60	Phylogeny based discovery of regulatory elements. <i>BMC Bioinformatics</i> , 2006, 7, 266.	2.6	9
61	Discovery, validation, and genetic dissection of transcription factor binding sites by comparative and functional genomics. <i>Genome Research</i> , 2005, 15, 1145-1152.	5.5	31