Houtan Noushmehr

List of Publications by Year
in descending order

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92 papers	40,190 citations	61945 43 h-index	76872 74 g-index
112 all docs	112 docs citations	112 times ranked	52559 citing authors

#	Article	IF	Citations
1	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	13.7	6,541
2	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
3	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
4	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
5	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. Nucleic Acids Research, 2016, 44, e71-e71.	6.5	2,519
6	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
7	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	7.7	2,078
8	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
9	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
10	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	13.5	1,695
11	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
12	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
13	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
14	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. Genome Research, 2010, 20, 440-446.	2.4	740
15	Glucagon-Like Peptide 1 Inhibits Cell Apoptosis and Improves Glucose Responsiveness of Freshly Isolated Human Islets. Endocrinology, 2003, 144, 5149-5158.	1.4	593
16	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear laminaâ€“associated domains. Nature Genetics, 2012, 44, 40-46.	9.4	588
17	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. Genome Research, 2012, 22, 271-282.	2.4	527
18	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326

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19	Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120.	13.7	320
20	New functionalities in the TCGAbiolinks package for the study and integration of cancer data from GDC and GTEx. PLoS Computational Biology, 2019, 15, e1006701.	1.5	319
21	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
22	Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. Neuro-Oncology, 2018, 20, 608-620.	0.6	194
23	DNA methylation profiling to predict recurrence risk in meningioma: development and validation of a nomogram to optimize clinical management. Neuro-Oncology, 2019, 21, 901-910.	0.6	184
24	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. PLoS Genetics, 2014, 10, e1004102.	1.5	167
25	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	13.5	164
26	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 0, 5, 1542.	0.8	155
27	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 2016, 5, 1542.	0.8	140
28	A Distinct DNA Methylation Shift in a Subset of Glioma CpG Island Methylator Phenotypes during Tumor Recurrence. Cell Reports, 2018, 23, 637-651.	2.9	137
29	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. Neuro-Oncology, 2018, 20, 873-884.	0.6	119
30	Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant IDH1. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10743-10748.	3.3	109
31	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	5.8	98
32	FunciSNP: an R/bioconductor tool integrating functional non-coding data sets with genetic association studies to identify candidate regulatory SNPs. Nucleic Acids Research, 2012, 40, e139-e139.	6.5	97
33	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nature Genetics, 2019, 51, 815-823.	9.4	89
34	ELMER v.2: an R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles. Bioinformatics, 2019, 35, 1974-1977.	1.8	87
35	Fatty Acid Translocase (FAT/CD36) Is Localized on Insulin-Containing Granules in Human Pancreatic Â-Cells and Mediates Fatty Acid Effects on Insulin Secretion. Diabetes, 2005, 54, 472-481.	0.3	84
36	Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. Acta Neuropathologica, 2020, 140, 919-949.	3.9	72

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37	Interpreting pathways to discover cancer driver genes with Moonlight. Nature Communications, 2020, 11, 69.	5.8	66
38	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. IScience, 2019, 17, 242-255.	1.9	60
39	A serum-based DNA methylation assay provides accurate detection of glioma. Neuro-Oncology, 2021, 23, 1494-1508.	0.6	53
40	Gene Reactivation by 5-Aza-2â€²-Deoxycytidineâ€“Induced Demethylation Requires SRCAPâ€“Mediated H2A.Z Insertion to Establish Nucleosome Depleted Regions. PLoS Genetics, 2012, 8, e1002604.	1.5	52
41	The Somatic Genomic Landscape of Glioblastoma. Cell, 2014, 157, 753.	13.5	51
42	An early requirement for maternal FoxH1 during zebrafish gastrulation. Developmental Biology, 2007, 310, 10-22.	0.9	50
43	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. International Journal of Molecular Sciences, 2017, 18, 274.	1.8	50
44	Post-Sepsis State Induces Tumor-Associated Macrophage Accumulation through CXCR4/CXCL12 and Favors Tumor Progression in Mice. Cancer Immunology Research, 2016, 4, 312-322.	1.6	45
45	Optimizing exosomal RNA isolation for RNA-Seq analyses of archival sera specimens. PLoS ONE, 2018, 13, e0196913.	1.1	42
46	Comprehensive Functional Annotation of Seventy-One Breast Cancer Risk Loci. PLoS ONE, 2013, 8, e63925.	1.1	41
47	Nucleosome positioning and histone modifications define relationships between regulatory elements and nearby gene expression in breast epithelial cells. BMC Genomics, 2014, 15, 331.	1.2	40
48	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
49	Transcriptional profiling of endogenous germ layer precursor cells identifies dusp4 as an essential gene in zebrafish endoderm specification. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12337-12342.	3.3	39
50	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. Cell Reports, 2019, 29, 3726-3735.e4.	2.9	39
51	Genome-wide Runx2 occupancy in prostate cancer cells suggests a role in regulating secretion. Nucleic Acids Research, 2012, 40, 3538-3547.	6.5	38
52	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. Human Molecular Genetics, 2014, 23, 2198-2209.	1.4	36
53	Prognostic significance of genome-wide DNA methylation profiles within the randomized, phase 3, EORTC CATNON trial on non-1p/19q deleted anaplastic glioma. Neuro-Oncology, 2021, 23, 1547-1559.	0.6	34
54	RGBM: regularized gradient boosting machines for identification of the transcriptional regulators of discrete glioma subtypes. Nucleic Acids Research, 2018, 46, e39-e39.	6.5	32

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55	Metabolic reprogramming associated with aggressiveness occurs in the G-CIMP-high molecular subtypes of IDH1mut lower grade gliomas. Neuro-Oncology, 2020, 22, 480-492.	0.6	31
56	Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123.	4.7	30
57	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. Gynecologic Oncology, 2019, 153, 343-355.	0.6	28
58	Identification of subsets of IDH-mutant glioblastomas with distinct epigenetic and copy number alterations and stratified clinical risks. Neuro-Oncology Advances, 2019, 1, vdz015.	0.4	22
59	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.4	22
60	Molecular landscape of IDH-mutant primary astrocytoma Grade IV/glioblastomas. Modern Pathology, 2021, 34, 1245-1260.	2.9	21
61	Machine Learning Applications in the Neuro ICU: A Solution to Big Data Mayhem?. Frontiers in Neurology, 2020, 11, 554633.	1.1	17
62	Targeting the E3 Ubiquitin Ligase PJA1 Enhances Tumor-Suppressing TGFÎ² Signaling. Cancer Research, 2020, 80, 1819-1832.	0.4	17
63	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. F1000Research, 0, 7, 439.	0.8	14
64	SIRT1 regulates Mxd1 during malignant melanoma progression. Oncotarget, 2017, 8, 114540-114553.	0.8	12
65	Gene expression profiling of bone marrow mesenchymal stem cells from Osteogenesis Imperfecta patients during osteoblast differentiation. European Journal of Medical Genetics, 2017, 60, 326-334.	0.7	10
66	Detection of tumor-specific DNA methylation markers in the blood of patients with pituitary neuroendocrine tumors. Neuro-Oncology, 2022, 24, 1126-1139.	0.6	9
67	Molecular landscape of <scp>IDH</scp>â€wild type, <scp>pTERT</scp>â€wild type adult glioblastomas. Brain Pathology, 2022, 32, .	2.1	9
68	Src as a novel therapeutic target for endometriosis. Gynecologic Oncology, 2014, 135, 100-107.	0.6	8
69	DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. Neuro-Oncology, 2021, 23, 1292-1303.	0.6	6
70	A non-functional galanin receptor-2 in a multiple sclerosis patient. Pharmacogenomics Journal, 2019, 19, 72-82.	0.9	5
71	Expression and regulatory roles of lncRNAs in G-CIMP-low vs G-CIMP-high Glioma: an in-silico analysis. Journal of Translational Medicine, 2021, 19, 182.	1.8	5
72	Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer. , 2011, , .		5

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73	Clinical and research applications of a brain tumor tissue bank in the age of precision medicine. Personalized Medicine, 2019, 16, 145-156.	0.8	4
74	Identification and functional annotation of GWAS risk SNPs. Cell Cycle, 2011, 10, 3999-3998.	1.3	1
75	The Functionality of Prostate Cancer Predisposition Risk Regions Is Revealed by AR Enhancers. , 2013, , 59-84.		1
76	EPIG-14EPIGENOMIC (DNA METHYLATION AND EXPRESSION) SIGNATURES DEFINE SUBSETS OF BOTH IDHmut AND IDHwt GLIOMA WITH DISTINCT CLINICAL OUTCOMES. Neuro-Oncology, 2015, 17, v89.2-v89.	0.6	0
77	GENT-33. EPIGENETIC ALTERATIONS AT INTERGENIC REGIONS ASSOCIATED WITH PROGRESSION IN AÂSUBSET OF IDH MUTANT GLIOMAS. Neuro-Oncology, 2016, 18, vi81-vi81.	0.6	0
78	GENT-34. EPIGENOMIC STEMNESS SIGNATURE ASSOCIATED WITH GLIOMA MOLECULAR SUBTYPES. Neuro-Oncology, 2016, 18, vi81-vi81.	0.6	0
79	GENE-26. PREDICTIVE SIGNATURE OF MALIGNANT RECURRENCE IN G-CIMP TUMORS. Neuro-Oncology, 2017, 19, vi98-vi98.	0.6	0
80	GENE-52. EPIGENOMIC GLIOMA SUBTYPE EVALUATION ACROSS 31 TUMOR TYPES. Neuro-Oncology, 2017, 19, vi103-vi104.	0.6	0
81	Abstract 1646: Integrative analysis identifies functional prostate cancer risk SNPs in genomic regulatory regions defined as enhancers. , 2012, , .		0
82	Abstract 1380: Genome-wide fingerprinting of regulatory chromatin to evaluate the tissue specific origins of high-grade serous ovarian cancer. , 2014, , .		0
83	Effect of tumor-associated macrophages on neoplastic progression in sepsis-surviving mice through CXCL12/CXCR4.. Journal of Clinical Oncology, 2015, 33, e22107-e22107.	0.8	0
84	Abstract 4767: DNA sequences differentially associated with Sirt1 and Dnmt3b during melanoma progression. , 2015, , .		0
85	Abstract 780: Multi-omic profiling of gliomas reveals distinct DNA methylation changes at tumor recurrence. , 2016, , .		0
86	Abstract LB-004: Molecular hallmarks of cancer: Stemness. , 2017, , .		0
87	Abstract 2417: Large scale integrated transcriptomic and epigenetic profiling defines the molecular hallmarks of HGSOC and disease origins. , 2017, , .		0
88	Abstract 2413: SIRT1 regulatesMxd1throughout melanoma progression. , 2017, , .		0
89	LncRNA Interpreter: A Protein-Centric Pipeline for Mechanistic Analysis of Long Noncoding RNAs. SSRN Electronic Journal, 0, , .	0.4	0
90	Global expression of microRNAs in neurospheres in primary cultures of glioblastoma treated with temozolomide and ionizing radiation.. FASEB Journal, 2018, 32, lb542.	0.2	0

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91	IDO1 expression in glioma molecular subtypes.. Journal of Clinical Oncology, 2018, 36, e14029-e14029.	0.8	0
92	Neurosurgery's Impact on Neuro-Oncologyâ€”â€œCan We Do Better?â€â€”Lessons Learned Over 50 Years. Neurosurgery, 2022, 68, 17-26.	0.6	0