

Houtan Noushmehr

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

40,190
citations

61984

43
h-index

76900

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. <i>Nature</i> , 2011, 474, 609-615.	27.8	6,541
2	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	28.9	3,979
3	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
4	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	27.0	2,582
5	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. <i>Nucleic Acids Research</i> , 2016, 44, e71-e71.	14.5	2,519
6	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	28.9	2,435
7	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. <i>Cancer Cell</i> , 2010, 17, 510-522.	16.8	2,078
8	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	28.9	1,794
9	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	28.9	1,718
10	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	28.9	1,695
11	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428
12	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
13	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	28.9	1,242
14	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. <i>Genome Research</i> , 2010, 20, 440-446.	5.5	740
15	Glucagon-Like Peptide 1 Inhibits Cell Apoptosis and Improves Glucose Responsiveness of Freshly Isolated Human Islets. <i>Endocrinology</i> , 2003, 144, 5149-5158.	2.8	593
16	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. <i>Nature Genetics</i> , 2012, 44, 40-46.	21.4	588
17	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012, 22, 271-282.	5.5	527
18	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	21.4	326

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19	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019, 576, 112-120.	27.8	320
20	New functionalities in the TCGAblinks package for the study and integration of cancer data from GDC and GTEx. <i>PLoS Computational Biology</i> , 2019, 15, e1006701.	3.2	319
21	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	21.4	221
22	Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. <i>Neuro-Oncology</i> , 2018, 20, 608-620.	1.2	194
23	DNA methylation profiling to predict recurrence risk in meningioma: development and validation of a nomogram to optimize clinical management. <i>Neuro-Oncology</i> , 2019, 21, 901-910.	1.2	184
24	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. <i>PLoS Genetics</i> , 2014, 10, e1004102.	3.5	167
25	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
26	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , 0, 5, 1542.	1.6	155
27	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , 2016, 5, 1542.	1.6	140
28	A Distinct DNA Methylation Shift in a Subset of Glioma CpG Island Methylator Phenotypes during Tumor Recurrence. <i>Cell Reports</i> , 2018, 23, 637-651.	6.4	137
29	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018, 20, 873-884.	1.2	119
30	Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant <i>IDH1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10743-10748.	7.1	109
31	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	12.8	98
32	FunciSNP: an R/bioconductor tool integrating functional non-coding data sets with genetic association studies to identify candidate regulatory SNPs. <i>Nucleic Acids Research</i> , 2012, 40, e139-e139.	14.5	97
33	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. <i>Nature Genetics</i> , 2019, 51, 815-823.	21.4	89
34	ELMER v.2: an R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles. <i>Bioinformatics</i> , 2019, 35, 1974-1977.	4.1	87
35	Fatty Acid Translocase (FAT/CD36) Is Localized on Insulin-Containing Granules in Human Pancreatic β -Cells and Mediates Fatty Acid Effects on Insulin Secretion. <i>Diabetes</i> , 2005, 54, 472-481.	0.6	84
36	Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. <i>Acta Neuropathologica</i> , 2020, 140, 919-949.	7.7	72

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37	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020, 11, 69.	12.8	66
38	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. <i>IScience</i> , 2019, 17, 242-255.	4.1	60
39	A serum-based DNA methylation assay provides accurate detection of glioma. <i>Neuro-Oncology</i> , 2021, 23, 1494-1508.	1.2	53
40	Gene Reactivation by 5-Aza-2-Deoxycytidine-Induced Demethylation Requires SRCAP-Mediated H2A.Z Insertion to Establish Nucleosome Depleted Regions. <i>PLoS Genetics</i> , 2012, 8, e1002604.	3.5	52
41	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2014, 157, 753.	28.9	51
42	An early requirement for maternal FoxH1 during zebrafish gastrulation. <i>Developmental Biology</i> , 2007, 310, 10-22.	2.0	50
43	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 274.	4.1	50
44	Post-Sepsis State Induces Tumor-Associated Macrophage Accumulation through CXCR4/CXCL12 and Favors Tumor Progression in Mice. <i>Cancer Immunology Research</i> , 2016, 4, 312-322.	3.4	45
45	Optimizing exosomal RNA isolation for RNA-Seq analyses of archival sera specimens. <i>PLoS ONE</i> , 2018, 13, e0196913.	2.5	42
46	Comprehensive Functional Annotation of Seventy-One Breast Cancer Risk Loci. <i>PLoS ONE</i> , 2013, 8, e63925.	2.5	41
47	Nucleosome positioning and histone modifications define relationships between regulatory elements and nearby gene expression in breast epithelial cells. <i>BMC Genomics</i> , 2014, 15, 331.	2.8	40
48	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2015, 24, 3595-3607.	2.9	40
49	Transcriptional profiling of endogenous germ layer precursor cells identifies <i>dusp4</i> as an essential gene in zebrafish endoderm specification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12337-12342.	7.1	39
50	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. <i>Cell Reports</i> , 2019, 29, 3726-3735.e4.	6.4	39
51	Genome-wide Runx2 occupancy in prostate cancer cells suggests a role in regulating secretion. <i>Nucleic Acids Research</i> , 2012, 40, 3538-3547.	14.5	38
52	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. <i>Human Molecular Genetics</i> , 2014, 23, 2198-2209.	2.9	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. <i>Neuro-Oncology</i> , 2021, 23, 1547-1559.	1.2	34
54	RGBM: regularized gradient boosting machines for identification of the transcriptional regulators of discrete glioma subtypes. <i>Nucleic Acids Research</i> , 2018, 46, e39-e39.	14.5	32

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55	Metabolic reprogramming associated with aggressiveness occurs in the G-CIMP-high molecular subtypes of IDH1mut lower grade gliomas. <i>Neuro-Oncology</i> , 2020, 22, 480-492.	1.2	31
56	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	10.3	30
57	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	1.4	28
58	Identification of subsets of IDH-mutant glioblastomas with distinct epigenetic and copy number alterations and stratified clinical risks. <i>Neuro-Oncology Advances</i> , 2019, 1, vdz015.	0.7	22
59	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. <i>Cancer Research</i> , 2019, 79, 467-481.	0.9	22
60	Molecular landscape of IDH-mutant primary astrocytoma Grade IV/glioblastomas. <i>Modern Pathology</i> , 2021, 34, 1245-1260.	5.5	21
61	Machine Learning Applications in the Neuro ICU: A Solution to Big Data Mayhem?. <i>Frontiers in Neurology</i> , 2020, 11, 554633.	2.4	17
62	Targeting the E3 Ubiquitin Ligase PJA1 Enhances Tumor-Suppressing TGF β 2 Signaling. <i>Cancer Research</i> , 2020, 80, 1819-1832.	0.9	17
63	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. <i>F1000Research</i> , 0, 7, 439.	1.6	14
64	SIRT1 regulates Mxd1 during malignant melanoma progression. <i>Oncotarget</i> , 2017, 8, 114540-114553.	1.8	12
65	Gene expression profiling of bone marrow mesenchymal stem cells from Osteogenesis Imperfecta patients during osteoblast differentiation. <i>European Journal of Medical Genetics</i> , 2017, 60, 326-334.	1.3	10
66	Detection of tumor-specific DNA methylation markers in the blood of patients with pituitary neuroendocrine tumors. <i>Neuro-Oncology</i> , 2022, 24, 1126-1139.	1.2	9
67	Molecular landscape of IDH-wild type, pTERT-wild type adult glioblastomas. <i>Brain Pathology</i> , 2022, 32, .	4.1	9
68	Src as a novel therapeutic target for endometriosis. <i>Gynecologic Oncology</i> , 2014, 135, 100-107.	1.4	8
69	DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. <i>Neuro-Oncology</i> , 2021, 23, 1292-1303.	1.2	6
70	A non-functional galanin receptor-2 in a multiple sclerosis patient. <i>Pharmacogenomics Journal</i> , 2019, 19, 72-82.	2.0	5
71	Expression and regulatory roles of lncRNAs in G-CIMP-low vs G-CIMP-high Glioma: an in-silico analysis. <i>Journal of Translational Medicine</i> , 2021, 19, 182.	4.4	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. <i>Personalized Medicine</i> , 2019, 16, 145-156.	1.5	4
74	Identification and functional annotation of GWAS risk SNPs. <i>Cell Cycle</i> , 2011, 10, 3999-3998.	2.6	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. <i>Neuro-Oncology</i> , 2015, 17, v89.2-v89.	1.2	0
77	GENT-33. EPIGENETIC ALTERATIONS AT INTERGENIC REGIONS ASSOCIATED WITH PROGRESSION IN A SUBSET OF IDH MUTANT GLIOMAS. <i>Neuro-Oncology</i> , 2016, 18, vi81-vi81.	1.2	0
78	GENT-34. EPIGENOMIC STEMNESS SIGNATURE ASSOCIATED WITH GLIOMA MOLECULAR SUBTYPES. <i>Neuro-Oncology</i> , 2016, 18, vi81-vi81.	1.2	0
79	GENE-26. PREDICTIVE SIGNATURE OF MALIGNANT RECURRENCE IN G-CIMP TUMORS. <i>Neuro-Oncology</i> , 2017, 19, vi98-vi98.	1.2	0
80	GENE-52. EPIGENOMIC GLIOMA SUBTYPE EVALUATION ACROSS 31 TUMOR TYPES. <i>Neuro-Oncology</i> , 2017, 19, vi103-vi104.	1.2	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.. <i>Journal of Clinical Oncology</i> , 2015, 33, e22107-e22107.	1.6	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 HGSOE and disease origins. , 2017, , .		0
88	Abstract 2413: SIRT1 regulates Mxd1 throughout melanoma progression. , 2017, , .		0
89	LncRNA Interpreter: A Protein-Centric Pipeline for Mechanistic Analysis of Long Noncoding RNAs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
90	Global expression of microRNAs in neurospheres in primary cultures of glioblastoma treated with temozolomide and ionizing radiation.. <i>FASEB Journal</i> , 2018, 32, lb542.	0.5	0

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91	IDO1 expression in glioma molecular subtypes.. Journal of Clinical Oncology, 2018, 36, e14029-e14029.	1.6	0
92	Neurosurgery's Impact on Neuro-Oncologyâ€™â€œCan We Do Better?â€™â€œ”Lessons Learned Over 50 Years. Neurosurgery, 2022, 68, 17-26.	1.1	0