

# Houtan Noushmehr

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Detection of tumor-specific DNA methylation markers in the blood of patients with pituitary neuroendocrine tumors. <i>Neuro-Oncology</i> , 2022, 24, 1126-1139.	0.6	9
2	Neurosurgery's Impact on Neuro-Oncologyâ€”â€œCan We Do Better?â€”Lessons Learned Over 50 Years. <i>Neurosurgery</i> , 2022, 68, 17-26.	0.6	0
3	Molecular landscape of <scp><i>IDH</i></scp>â€wild type, <scp>p<i>TERT</i></scp>â€wild type adult glioblastomas. <i>Brain Pathology</i> , 2022, 32, .	2.1	9
4	DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. <i>Neuro-Oncology</i> , 2021, 23, 1292-1303.	0.6	6
5	A serum-based DNA methylation assay provides accurate detection of glioma. <i>Neuro-Oncology</i> , 2021, 23, 1494-1508.	0.6	53
6	Molecular landscape of IDH-mutant primary astrocytoma Grade IV/glioblastomas. <i>Modern Pathology</i> , 2021, 34, 1245-1260.	2.9	21
7	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.	1.8	5
8	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.	0.6	34
9	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	13.5	164
10	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	4.7	30
11	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.	0.6	31
12	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020, 11, 69.	5.8	66
13	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.	3.9	72
14	Machine Learning Applications in the Neuro ICU: A Solution to Big Data Mayhem?. <i>Frontiers in Neurology</i> , 2020, 11, 554633.	1.1	17
15	Targeting the E3 Ubiquitin Ligase PJA1 Enhances Tumor-Suppressing TGF $\beta$ <sup>2</sup> Signaling. <i>Cancer Research</i> , 2020, 80, 1819-1832.	0.4	17
16	A non-functional galanin receptor-2 in a multiple sclerosis patient. <i>Pharmacogenomics Journal</i> , 2019, 19, 72-82.	0.9	5
17	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.	1.9	60
18	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.	0.4	22

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19	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.	0.6	184
20	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.	9.4	89
21	New functionalities in the TCGAbiolinks package for the study and integration of cancer data from GDC and GTEx. <i>PLoS Computational Biology</i> , 2019, 15, e1006701.	1.5	319
22	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	0.6	28
23	Clinical and research applications of a brain tumor tissue bank in the age of precision medicine. <i>Personalized Medicine</i> , 2019, 16, 145-156.	0.8	4
24	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019, 576, 112-120.	13.7	320
25	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.	2.9	39
26	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.	1.8	87
27	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. <i>Cancer Research</i> , 2019, 79, 467-481.	0.4	22
28	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.	13.5	1,718
29	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
30	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
31	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.	2.9	137
32	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018, 20, 873-884.	0.6	119
33	RGBM: regularized gradient boosting machines for identification of the transcriptional regulators of discrete glioma subtypes. <i>Nucleic Acids Research</i> , 2018, 46, e39-e39.	6.5	32
34	Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. <i>Neuro-Oncology</i> , 2018, 20, 608-620.	0.6	194
35	Optimizing exosomal RNA isolation for RNA-Seq analyses of archival sera specimens. <i>PLoS ONE</i> , 2018, 13, e0196913.	1.1	42
36	Global expression of microRNAs in neurospheres in primary cultures of glioblastoma treated with temozolomide and ionizing radiation.. <i>FASEB Journal</i> , 2018, 32, lb542.	0.2	0

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37	IDO1 expression in glioma molecular subtypes.. Journal of Clinical Oncology, 2018, 36, e14029-e14029.	0.8	0
38	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
39	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
40	Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant <i>IDH1</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10743-10748.	3.3	109
41	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
42	GENE-26. PREDICTIVE SIGNATURE OF MALIGNANT RECURRENCE IN G-CIMP TUMORS. Neuro-Oncology, 2017, 19, vi98-vi98.	0.6	0
43	SIRT1 regulates Mxd1 during malignant melanoma progression. Oncotarget, 2017, 8, 114540-114553.	0.8	12
44	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. International Journal of Molecular Sciences, 2017, 18, 274.	1.8	50
45	GENE-52. EPIGENOMIC GLIOMA SUBTYPE EVALUATION ACROSS 31 TUMOR TYPES. Neuro-Oncology, 2017, 19, vi103-vi104.	0.6	0
46	Abstract LB-004: Molecular hallmarks of cancer: Stemness. , 2017, , .		0
47	Abstract 2417: Large scale integrated transcriptomic and epigenetic profiling defines the molecular hallmarks of HGSOc and disease origins. , 2017, , .		0
48	Abstract 2413: SIRT1 regulatesMxd1throughout melanoma progression. , 2017, , .		0
49	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
50	GENT-34. EPIGENOMIC STEMNESS SIGNATURE ASSOCIATED WITH GLIOMA MOLECULAR SUBTYPES. Neuro-Oncology, 2016, 18, vi81-vi81.	0.6	0
51	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
52	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	13.5	1,695
53	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. Nucleic Acids Research, 2016, 44, e71-e71.	6.5	2,519
54	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 2016, 5, 1542.	0.8	140

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55	Abstract 780: Multi-omic profiling of gliomas reveals distinct DNA methylation changes at tumor recurrence. , 2016, , .		0
56	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
57	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
58	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
59	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
60	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
61	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
62	Abstract 4767: DNA sequences differentially associated with Sirt1 and Dnmt3b during melanoma progression. , 2015, , .		0
63	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. PLoS Genetics, 2014, 10, e1004102.	1.5	167
64	Src as a novel therapeutic target for endometriosis. Gynecologic Oncology, 2014, 135, 100-107.	0.6	8
65	The Somatic Genomic Landscape of Glioblastoma. Cell, 2014, 157, 753.	13.5	51
66	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
67	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
68	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
69	Abstract 1380: Genome-wide fingerprinting of regulatory chromatin to evaluate the tissue specific origins of high-grade serous ovarian cancer. , 2014, , .		0
70	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
71	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
72	The Functionality of Prostate Cancer Predisposition Risk Regions Is Revealed by AR Enhancers. , 2013, , 59-84.		1

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73	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	5.8	98
74	Comprehensive Functional Annotation of Seventy-One Breast Cancer Risk Loci. <i>PLoS ONE</i> , 2013, 8, e63925.	1.1	41
75	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.	1.5	52
76	Genome-wide Runx2 occupancy in prostate cancer cells suggests a role in regulating secretion. <i>Nucleic Acids Research</i> , 2012, 40, 3538-3547.	6.5	38
77	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012, 22, 271-282.	2.4	527
78	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.	6.5	97
79	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.	9.4	588
80	Abstract 1646: Integrative analysis identifies functional prostate cancer risk SNPs in genomic regulatory regions defined as enhancers. , 2012, , .		0
81	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011, 474, 609-615.	13.7	6,541
82	Identification and functional annotation of GWAS risk SNPs. <i>Cell Cycle</i> , 2011, 10, 3999-3998.	1.3	1
83	Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer. , 2011, , .		5
84	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. <i>Cancer Cell</i> , 2010, 17, 510-522.	7.7	2,078
85	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.	2.4	740
86	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.	3.3	39
87	An early requirement for maternal FoxH1 during zebrafish gastrulation. <i>Developmental Biology</i> , 2007, 310, 10-22.	0.9	50
88	Fatty Acid Translocase (FAT/CD36) Is Localized on Insulin-Containing Granules in Human Pancreatic $\beta$ -Cells and Mediates Fatty Acid Effects on Insulin Secretion. <i>Diabetes</i> , 2005, 54, 472-481.	0.3	84
89	Glucagon-Like Peptide 1 Inhibits Cell Apoptosis and Improves Glucose Responsiveness of Freshly Isolated Human Islets. <i>Endocrinology</i> , 2003, 144, 5149-5158.	1.4	593
90	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. <i>F1000Research</i> , 0, 7, 439.	0.8	14

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91	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 0, 5, 1542.	0.8	155
92	LncRNA Interpreter: A Protein-Centric Pipeline for Mechanistic Analysis of Long Noncoding RNAs. SSRN Electronic Journal, 0, , .	0.4	0