

Mehdi Manoochehri

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,650
citations

471509

17
h-index

345221

36
g-index

36
all docs

36
docs citations

36
times ranked

2765
citing authors

#	ARTICLE	IF	CITATIONS
1	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
2	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	7.1	51
3	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	8.2	19
4	Breast Cancer Risk Genes Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	27.0	532
5	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. <i>Cancers</i> , 2021, 13, 2370.	3.7	4
6	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	6.2	6
7	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. <i>Breast Cancer Research</i> , 2021, 23, 86.	5.0	7
8	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	6.4	9
9	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 623-642.	2.5	19
10	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , 2021, 11, 19787.	3.3	2
11	Epigenetic quantification of circulating immune cells in peripheral blood of triple-negative breast cancer patients. <i>Clinical Epigenetics</i> , 2021, 13, 207.	4.1	2
12	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
13	DNA methylation of the long intergenic noncoding RNA 299 gene in triple-negative breast cancer: results from a prospective study. <i>Scientific Reports</i> , 2020, 10, 11762.	3.3	10
14	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	6.2	39
15	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	21.4	265
16	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	3.3	2
17	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32
18	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	12.8	30

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19	<i>SST</i> gene hypermethylation acts as a pan-cancer marker for pancreatic ductal adenocarcinoma and multiple other tumors: toward its use for blood-based diagnosis. <i>Molecular Oncology</i> , 2020, 14, 1252-1267.	4.6	24
20	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. <i>Breast Cancer Research and Treatment</i> , 2020, 181, 423-434.	2.5	14
21	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	5.2	28
22	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	3.3	5
23	<i>GHR</i> DNA hypermethylation is a new epigenetic biomarker for gastric adenocarcinoma and beyond. <i>Journal of Cellular Physiology</i> , 2019, 234, 15320-15329.	4.1	15
24	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	12.8	90
25	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	6.4	52
26	Prediction and clinical utility of a contralateral breast cancer risk model. <i>Breast Cancer Research</i> , 2019, 21, 144.	5.0	24
27	Long intergenic noncoding RNA 299 methylation in peripheral blood is a biomarker for triple-negative breast cancer. <i>Epigenomics</i> , 2019, 11, 81-93.	2.1	32
28	Tissue-Specific Down-Regulation of the Long Non-Coding RNAs PCAT18 and LINC01133 in Gastric Cancer Development. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3881.	4.1	37
29	Neuroprotective effects of astaxanthin in a rat model of spinal cord injury. <i>Behavioural Brain Research</i> , 2017, 329, 104-110.	2.2	46
30	Promoter hypermethylation and downregulation of the FAS gene may be involved in colorectal carcinogenesis. <i>Oncology Letters</i> , 2016, 12, 285-290.	1.8	14
31	Downregulation of external death receptor genes FAS and DR5 in colorectal cancer samples positive for human papillomavirus infection. <i>Pathology Research and Practice</i> , 2015, 211, 444-448.	2.3	18
32	<i>GHR</i> DNA hypermethylation is a common epigenetic alteration of high diagnostic value in a broad spectrum of cancers. <i>Oncotarget</i> , 2015, 6, 4418-4427.	1.8	25
33	Down-Regulation of BAX Gene During Carcinogenesis and Acquisition of Resistance to 5-FU in Colorectal Cancer. <i>Pathology and Oncology Research</i> , 2014, 20, 301-307.	1.9	35
34	Ccr2-64i and Ccr5 \uparrow 32 Polymorphisms in Patients with Late-Onset Alzheimer's disease; A Study from Iran (Ccr2-64i And Ccr5 \uparrow 32 Polymorphisms in Alzheimer's disease). <i>Iranian Journal of Basic Medical Sciences</i> , 2012, 15, 937-44.	1.0	15
35	Association of CALHM1 Gene Polymorphism with Late Onset Alzheimer's Disease in Iranian Population. <i>Avicenna Journal of Medical Biotechnology</i> , 2010, 2, 153-7.	0.3	6
36	Lack of Association between Tumor Necrosis Factor-alpha -308 G/A Polymorphism and Risk of Developing Late-Onset Alzheimer's Disease in an Iranian Population. <i>Avicenna Journal of Medical Biotechnology</i> , 2009, 1, 193-7.	0.3	6