Enes Makalic

List of Publications by Year
in descending order

72 papers	6,849 citations	147801 31 h-index	88630 70 g-index
80 all docs	80 docs citations	80 times ranked	10473 citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
3	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
4	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
5	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
6	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
7	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
8	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
9	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	2.9	168
10	DNA methylationâ€based biological aging and cancer risk and survival: Pooled analysis of seven prospective studies. International Journal of Cancer, 2018, 142, 1611-1619.	5.1	153
11	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
12	A Simple Sampler for the Horseshoe Estimator. IEEE Signal Processing Letters, 2016, 23, 179-182.	3.6	124
13	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
14	Association of DNA Methylation-Based Biological Age With Health Risk Factors and Overall and Cause-Specific Mortality. American Journal of Epidemiology, 2018, 187, 529-538.	3.4	106
15	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.9	100
16	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
17	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
18	A Genome-wide Association Study of Early-Onset Breast Cancer Identifies PFKM as a Novel Breast Cancer Gene and Supports a Common Genetic Spectrum for Breast Cancer at Any Age. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 658-669.	2.5	77

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19	Characterization of brainâ€derived extracellular vesicle lipids in Alzheimer's disease. Journal of Extracellular Vesicles, 2021, 10, e12089.	12.2	64
20	Smoking and blood DNA methylation: an epigenome-wide association study and assessment of reversibility. Epigenetics, 2020, 15, 358-368.	2.7	56
21	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
22	Novel associations between blood DNA methylation and body mass index in middle-aged and older adults. International Journal of Obesity, 2018, 42, 887-896.	3.4	52
23	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
24	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
25	Alcohol consumption is associated with widespread changes in blood DNA methylation: Analysis of crossâ€sectional and longitudinal data. Addiction Biology, 2021, 26, e12855.	2.6	49
26	Quantifying the utility of single nucleotide polymorphisms to guide colorectal cancer screening. Future Oncology, 2016, 12, 503-513.	2.4	42
27	Melanoma risk for CDKN2A mutation carriers who are relatives of population-based case carriers in Australia and the UK. Journal of Medical Genetics, 2011, 48, 266-272.	3.2	41
28	Biological Aging Measures Based on Blood DNA Methylation and Risk of Cancer: A Prospective Study. JNCI Cancer Spectrum, 2021, 5, pkaa109.	2.9	40
29	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38
30	Genome-wide measures of DNA methylation in peripheral blood and the risk of urothelial cell carcinoma: a prospective nested caseâ€“control study. British Journal of Cancer, 2016, 115, 664-673.	6.4	38
31	Explaining Variance in the Cumulus Mammographic Measures That Predict Breast Cancer Risk: A Twins and Sisters Study. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 2395-2403.	2.5	36
32	Global measures of peripheral blood-derived DNA methylation as a risk factor in the development of mature B-cell neoplasms. Epigenomics, 2016, 8, 55-66.	2.1	35
33	Dietary intake of one-carbon metabolism nutrients and DNA methylation in peripheral blood. American Journal of Clinical Nutrition, 2018, 108, 611-621.	4.7	35
34	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
35	Genomeâ€Wide Measures of Peripheral Blood Dna Methylation and Prostate Cancer Risk in a Prospective Nested Caseâ€Control Study. Prostate, 2017, 77, 471-478.	2.3	31
36	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28

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37	The Consistency of MDL for Linear Regression Models With Increasing Signal-to-Noise Ratio. IEEE Transactions on Signal Processing, 2012, 60, 1508-1510.	5.3	26
38	High performance computing enabling exhaustive analysis of higher order single nucleotide polymorphism interaction in Genome Wide Association Studies. Health Information Science and Systems, 2015, 3, S3.	5.2	24
39	Cirrus: An Automated Mammography-Based Measure of Breast Cancer Risk Based on Textural Features. JNCI Cancer Spectrum, 2018, 2, pky057.	2.9	24
40	Strategies for Integrated Analysis of Genetic, Epigenetic, and Gene Expression Variation in Cancer: Addressing the Challenges. Frontiers in Genetics, 2016, 7, 2.	2.3	23
41	Ability of known susceptibility SNPs to predict colorectal cancer risk for persons with and without a family history. Familial Cancer, 2019, 18, 389-397.	1.9	23
42	Going Beyond Conventional Mammographic Density to Discover Novel Mammogram-Based Predictors of Breast Cancer Risk. Journal of Clinical Medicine, 2020, 9, 627.	2.4	23
43	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	6.4	21
44	Universal Models for the Exponential Distribution. IEEE Transactions on Information Theory, 2009, 55, 3087-3090.	2.4	20
45	Childhood body mass index and adult mammographic density measures that predict breast cancer risk. Breast Cancer Research and Treatment, 2016, 156, 163-170.	2.5	19
46	Stochastic Epigenetic Mutations Are Associated with Risk of Breast Cancer, Lung Cancer, and Mature B-cell Neoplasms. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2026-2037.	2.5	18
47	Novel mammogramâ€based measures improve breast cancer risk prediction beyond an established mammographic density measure. International Journal of Cancer, 2021, 148, 2193-2202.	5.1	18
48	FAN1 variants identified in multiple-case early-onset breast cancer families via exome sequencing: no evidence for association with risk for breast cancer. Breast Cancer Research and Treatment, 2011, 130, 1043-1049.	2.5	16
49	Physical Activity, Television Viewing Time, and DNA Methylation in Peripheral Blood. Medicine and Science in Sports and Exercise, 2019, 51, 490-498.	0.4	16
50	Heritable methylation marks associated with breast and prostate cancer risk. Prostate, 2018, 78, 962-969.	2.3	15
51	Assessment of a Polygenic Risk Score for Colorectal Cancer to Predict Risk of Lynch Syndrome Colorectal Cancer. JNCI Cancer Spectrum, 2021, 5, pkab022.	2.9	15
52	Estimating the Order of an Autoregressive Model Using Normalized Maximum Likelihood. IEEE Transactions on Signal Processing, 2011, 59, 479-487.	5.3	13
53	Minimum Message Length shrinkage estimation. Statistics and Probability Letters, 2009, 79, 1155-1161.	0.7	9
54	Fast Computation of the Kullbackâ€“Leibler Divergence and Exact Fisher Information for the First-Order Moving Average Model. IEEE Signal Processing Letters, 2010, 17, 391-393.	3.6	9

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55	Genetic susceptibility markers for a breast-colorectal cancer phenotype: Exploratory results from genome-wide association studies. PLoS ONE, 2018, 13, e0196245.	2.5	9
56	Epigenetic Drift Association with Cancer Risk and Survival, and Modification by Sex. Cancers, 2021, 13, 1881.	3.7	9
57	Demographic and lifestyle risk factors for gastroesophageal reflux disease and Barrettâ€™s esophagus in Australia. Ecological Management and Restoration, 2022, 35, .	0.4	9
58	Estimation of stationary autoregressive models with the Bayesian LASSO. Journal of Time Series Analysis, 2013, 34, 517-531.	1.2	8
59	Diet and risk of gastro-oesophageal reflux disease in the Melbourne Collaborative Cohort Study. Public Health Nutrition, 2021, 24, 5034-5046.	2.2	8
60	Use of a Novel Nonparametric Version of DEPTH to Identify Genomic Regions Associated with Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1619-1624.	2.5	7
61	Overall lack of replication of associations between dietary intake of folate and vitamin B-12 and DNA methylation in peripheral blood. American Journal of Clinical Nutrition, 2020, 111, 228-230.	4.7	6
62	Association of FOXO3 Blood DNA Methylation with Cancer Risk, Cancer Survival, and Mortality. Cells, 2021, 10, 3384.	4.1	6
63	Supercomputing enabling exhaustive statistical analysis of genome wide association study data: Preliminary results. , 2012, 2012, 1258-61.		5
64	An open-source, integrated pedigree data management and visualization tool for genetic epidemiology. International Journal of Epidemiology, 2018, 47, 1034-1039.	1.9	5
65	Smoking Methylation Marks for Prediction of Urothelial Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2197-2206.	2.5	4
66	Minimum message length analysis of multiple short time series. Statistics and Probability Letters, 2016, 110, 318-328.	0.7	3
67	Minimum message length inference of the Poisson and geometric models using heavy-tailed prior distributions. Journal of Mathematical Psychology, 2018, 83, 1-11.	1.8	3
68	An efficient algorithm for sampling from sinkâ€‰(x) for generating random correlation matrices. Communications in Statistics Part B: Simulation and Computation, 2020, , 1-5.	1.2	3
69	Does genetic predisposition modify the effect of lifestyle-related factors on DNA methylation?. Epigenetics, 2022, 17, 1838-1847.	2.7	2
70	Quantifying the cumulative effect of lowâ€penetrance genetic variants on breast cancer risk. Molecular Genetics & Genomic Medicine, 2015, 3, 182-188.	1.2	1
71	Minimum Message Length Inference of the Exponential Distribution with Type I Censoring. Entropy, 2021, 23, 1439.	2.2	1
72	Aberrant DNA Methylation Patterns in Peripheral Blood Are Detectable Years before the Diagnosis of Mature B Cell Neoplasms. Blood, 2016, 128, 1521-1521.	1.4	0