

Michael T Parsons

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

3,818
citations

201674

27
h-index

138484

58
g-index

69
all docs

69
docs citations

69
times ranked

5996
citing authors

#	ARTICLE	IF	CITATIONS
1	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	6.3	19
2	The splicing effect of variants at branchpoint elements in cancer genes. <i>Genetics in Medicine</i> , 2022, 24, 398-409.	2.4	9
3	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in <i>BRCA1</i> and <i>BRCA2</i> compared with those harboring protein truncating variants. <i>Genetics in Medicine</i> , 2022, 24, 119-129.	2.4	10
4	Cancer Risks Associated With <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>Journal of Clinical Oncology</i> , 2022, 40, 1529-1541.	1.6	90
5	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	2.8	23
6	Value of the loss of heterozygosity to <i>BRCA1</i> variant classification. <i>Npj Breast Cancer</i> , 2022, 8, 9.	5.2	2
7	TRACEBACK: Testing of Historical Tubo-Ovarian Cancer Patients for Hereditary Risk Genes as a Cancer Prevention Strategy in Family Members. <i>Journal of Clinical Oncology</i> , 2022, , JCO2102108.	1.6	3
8	Federated analysis of <i>BRCA1</i> and <i>BRCA2</i> variation in a Japanese cohort. <i>Cell Genomics</i> , 2022, 2, 100109.	6.5	1
9	Expansion of Cancer Risk Profile for <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2022, 8, 871.	7.1	70
10	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	8.2	19
11	Under-ascertainment of breast cancer susceptibility gene carriers in a cohort of New Zealand female breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2021, 185, 583-590.	2.5	0
12	Classification of genetic variants in hereditary cancer genes. , 2021, , 349-387.		0
13	A case-only study to identify genetic modifiers of breast cancer risk for <i>BRCA1/BRCA2</i> mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	12.8	19
14	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
15	Considerations for using population frequency data in germline variant interpretation: Cancer syndrome genes as a model. <i>Human Mutation</i> , 2021, 42, 530-536.	2.5	8
16	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous <i>BRCA1</i> or <i>BRCA2</i> pathogenic variant. <i>Genetics in Medicine</i> , 2021, 23, 1726-1737.	2.4	16
17	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.9	39
18	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120

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19	Classification of variants of uncertain significance in BRCA1 and BRCA2 using personal and family history of cancer from individuals in a large hereditary cancer multigene panel testing cohort. <i>Genetics in Medicine</i> , 2020, 22, 701-708.	2.4	28
20	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	2.4	82
21	Considerations in assessing germline variant pathogenicity using cosegregation analysis. <i>Genetics in Medicine</i> , 2020, 22, 2052-2059.	2.4	15
22	Contribution of mRNA Splicing to Mismatch Repair Gene Sequence Variant Interpretation. <i>Frontiers in Genetics</i> , 2020, 11, 798.	2.3	19
23	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 44.	5.2	5
24	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
25	Characterization of the Cancer Spectrum in Men With Germline <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2020, 6, 1218.	7.1	48
26	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32
27	Assessment of blind predictions of the clinical significance of <i>BRCA1</i> and <i>BRCA2</i> variants. <i>Human Mutation</i> , 2019, 40, 1546-1556.	2.5	19
28	The <i>FANCM</i> :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	5.2	28
29	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
30	GFP-Fragment Reassembly Screens for the Functional Characterization of Variants of Uncertain Significance in Protein Interaction Domains of the <i>BRCA1</i> and <i>BRCA2</i> Genes. <i>Cancers</i> , 2019, 11, 151.	3.7	4
31	Large scale multifactorial likelihood quantitative analysis of <i>BRCA1</i> and <i>BRCA2</i> variants: An ENIGMA resource to support clinical variant classification. <i>Human Mutation</i> , 2019, 40, 1557-1578.	2.5	102
32	The spectrum of <i>BRCA1</i> and <i>BRCA2</i> pathogenic sequence variants in Middle Eastern, North African, and South European countries. <i>Human Mutation</i> , 2019, 40, e1-e23.	2.5	34
33	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. <i>British Journal of Cancer</i> , 2019, 121, 180-192.	6.4	19
34	<i>BRCA1</i> and <i>BRCA2</i> pathogenic sequence variants in women of African origin or ancestry. <i>Human Mutation</i> , 2019, 40, 1781-1796.	2.5	26
35	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. <i>Journal of Medical Genetics</i> , 2019, 56, 347-357.	3.2	32
36	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

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37	Comprehensive Assessment of BARD1 Messenger Ribonucleic Acid Splicing With Implications for Variant Classification. <i>Frontiers in Genetics</i> , 2019, 10, 1139.	2.3	10
38	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. <i>Bioinformatics</i> , 2019, 35, 2315-2317.	4.1	52
39	The <i>BRCA2</i> c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018, 39, 729-741.	2.5	19
40	Mutational spectrum in a worldwide study of 29,700 families with <i>BRCA1</i> or <i>BRCA2</i> mutations. <i>Human Mutation</i> , 2018, 39, 593-620.	2.5	224
41	BRCA Challenge: BRCA Exchange as a global resource for variants in <i>BRCA1</i> and <i>BRCA2</i> . <i>PLoS Genetics</i> , 2018, 14, e1007752.	3.5	148
42	Germline pathogenic variants of 11 breast cancer genes in 7,051 Japanese patients and 11,241 controls. <i>Nature Communications</i> , 2018, 9, 4083.	12.8	179
43	<i>BRCA1</i> and <i>BRCA2</i> 5' noncoding region variants identified in breast cancer patients alter promoter activity and protein binding. <i>Human Mutation</i> , 2018, 39, 2025-2039.	2.5	15
44	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.9	54
45	Novel diagnostic tool for prediction of variant spliceogenicity derived from a set of 395 combined in silico/in vitro studies: an international collaborative effort. <i>Nucleic Acids Research</i> , 2018, 46, 7913-7923.	14.5	71
46	Substantial evidence for the clinical significance of missense variant <i>BRCA1</i> c.5309G>Tp.(Gly1770Val). <i>Breast Cancer Research and Treatment</i> , 2018, 172, 497-503.	2.5	7
47	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for <i>BRCA1</i> pathogenic variant carriers. <i>European Journal of Human Genetics</i> , 2017, 25, 432-438.	2.8	26
48	Adding In Silico Assessment of Potential Splice Aberration to the Integrated Evaluation of <i>BRCA</i> Gene Unclassified Variants. <i>Human Mutation</i> , 2016, 37, 627-639.	2.5	52
49	Naturally occurring <i>BRCA2</i> alternative mRNA splicing events in clinically relevant samples. <i>Journal of Medical Genetics</i> , 2016, 53, 548-558.	3.2	69
50	Combined genetic and splicing analysis of <i>BRCA1</i> c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. <i>Human Molecular Genetics</i> , 2016, 25, 2256-2268.	2.9	106
51	DNA methylation profiling to assess pathogenicity of <i>BRCA1</i> unclassified variants in breast cancer. <i>Epigenetics</i> , 2015, 10, 1121-1132.	2.7	12
52	<i>BRCA1</i> and <i>BRCA2</i> genetic testing "pitfalls" and recommendations for managing variants of uncertain clinical significance. <i>Annals of Oncology</i> , 2015, 26, 2057-2065.	1.2	163
53	Consequences of germline variation disrupting the constitutional translational initiation codon start sites of <i>MLH1</i> and <i>BRCA2</i> : Use of potential alternative start sites and implications for predicting variant pathogenicity. <i>Molecular Carcinogenesis</i> , 2015, 54, 513-522.	2.7	14
54	Reply to J. Moline et al. <i>Journal of Clinical Oncology</i> , 2014, 32, 2278-2279.	1.6	5

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55	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419.	5.0	97
56	Tumor Mismatch Repair Immunohistochemistry and DNA <i>MLH1</i> Methylation Testing of Patients With Endometrial Cancer Diagnosed at Age Younger Than 60 Years Optimizes Triage for Population-Level Germline Mismatch Repair Gene Mutation Testing. <i>Journal of Clinical Oncology</i> , 2014, 32, 90-100.	1.6	195
57	Multifactorial Likelihood Assessment of BRCA1 and BRCA2 Missense Variants Confirms That BRCA1:c.122A>G(p.His41Arg) Is a Pathogenic Mutation. <i>PLoS ONE</i> , 2014, 9, e86836.	2.5	17
58	A Multifactorial Likelihood Model for MMR Gene Variant Classification Incorporating Probabilities Based on Sequence Bioinformatics and Tumor Characteristics: A Report from the Colon Cancer Family Registry. <i>Human Mutation</i> , 2013, 34, 200-209.	2.5	81
59	Correlation of tumour BRAF mutations and <i>MLH1</i> methylation with germline mismatch repair (MMR) gene mutation status: a literature review assessing utility of tumour features for MMR variant classification. <i>Journal of Medical Genetics</i> , 2012, 49, 151-157.	3.2	253