Rodney J Scott

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1304451/publications.pdf

Version: 2024-02-01

579	59,937	2975	1536
papers	citations	93 h-index	218 g-index

608	608	608	62744
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	27.8	6,934
2	Genetic Heterogeneity and Penetrance Analysis of the BRCA1 and BRCA2 Genes in Breast Cancer Families. American Journal of Human Genetics, 1998, 62, 676-689.	6.2	2,662
3	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
4	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
5	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	21.4	1,758
6	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
7	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
8	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
9	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
10	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
11	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
12	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
13	Long-term effect of aspirin on cancer risk in carriers of hereditary colorectal cancer: an analysis from the CAPP2 randomised controlled trial. Lancet, The, 2011, 378, 2081-2087.	13.7	849
14	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
15	Inflammatory subtypes in asthma: Assessment and identification using induced sputum. Respirology, 2006, 11, 54-61.	2.3	787
16	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750
17	Frequency and Spectrum of Cancers in the Peutz-Jeghers Syndrome. Clinical Cancer Research, 2006, 12, 3209-3215.	7.0	746
18	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711

#	Article	IF	Citations
19	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
20	Multifactorial Analysis of Differences Between Sporadic Breast Cancers and Cancers Involving BRCA1 and BRCA2 Mutations. Journal of the National Cancer Institute, 1998, 90, 1138-1145.	6.3	652
21	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	21.4	629
22	Cortical Brain Abnormalities in 4474 Individuals With Schizophrenia and 5098 Control Subjects via the Enhancing Neuro Imaging Genetics Through Meta Analysis (ENIGMA) Consortium. Biological Psychiatry, 2018, 84, 644-654.	1.3	627
23	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
24	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	21.4	536
25	Widespread white matter microstructural differences in schizophrenia across 4322 individuals: results from the ENIGMA Schizophrenia DTI Working Group. Molecular Psychiatry, 2018, 23, 1261-1269.	7.9	522
26	Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. Nature Genetics, 2009, 41, 824-828.	21.4	501
27	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
28	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
29	Clarithromycin Targets Neutrophilic Airway Inflammation in Refractory Asthma. American Journal of Respiratory and Critical Care Medicine, 2008, 177, 148-155.	5.6	450
30	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	12.6	450
31	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
32	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
33	Application of a 5-tiered scheme for standardized classification of 2,360 unique mismatch repair gene variants in the InSiGHT locus-specific database. Nature Genetics, 2014, 46, 107-115.	21.4	410
34	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
35	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53â€‰949). Molecular Psychiatry, 2015, 20, 183-192.	7.9	344
36	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326

#	Article	IF	Citations
37	Genomeâ€wide metaâ€analysis identifies novel multiple sclerosis susceptibility loci. Annals of Neurology, 2011, 70, 897-912.	5.3	314
38	Dysregulation of miRNA 181b in the temporal cortex in schizophrenia. Human Molecular Genetics, 2008, 17, 1156-1168.	2.9	312
39	Genome-wide association study identifies FCGR2A as a susceptibility locus for Kawasaki disease. Nature Genetics, 2011, 43, 1241-1246.	21.4	297
40	Innate immune activation in neutrophilic asthma and bronchiectasis. Thorax, 2007, 62, 211-218.	5.6	290
41	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
42	Effect of Aspirin or Resistant Starch on Colorectal Neoplasia in the Lynch Syndrome. New England Journal of Medicine, 2008, 359, 2567-2578.	27.0	273
43	Transcriptional phenotypes of asthma defined by gene expression profiling of induced sputum samples. Journal of Allergy and Clinical Immunology, 2011, 127, 153-160.e9.	2.9	258
44	Genome-wide association meta-analysis identifies new endometriosis risk loci. Nature Genetics, 2012, 44, 1355-1359.	21.4	257
45	BRCA1 sequence analysis in women at high risk for susceptibility mutations. Risk factor analysis and implications for genetic testing. JAMA - Journal of the American Medical Association, 1997, 278, 1242-1250.	7.4	255
46	Relative frequency and morphology of cancers in STK11 mutation carriers1 â˜†. Gastroenterology, 2004, 126, 1788-1794.	1.3	228
47	MicroRNAs miR-17 and miR-20a Inhibit T Cell Activation Genes and Are Under-Expressed in MS Whole Blood. PLoS ONE, 2010, 5, e12132.	2.5	225
48	Cancer prevention with aspirin in hereditary colorectal cancer (Lynch syndrome), 10-year follow-up and registry-based 20-year data in the CAPP2 study: a double-blind, randomised, placebo-controlled trial. Lancet, The, 2020, 395, 1855-1863.	13.7	220
49	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217
50	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
51	Imprinted DLK1-DIO3 region of 14q32 defines a schizophrenia-associated miRNA signature in peripheral blood mononuclear cells. Molecular Psychiatry, 2012, 17, 827-840.	7.9	210
52	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	14.8	204
53	Meta-Analysis of 13 Genome Scans Reveals Multiple Cleft Lip/Palate Genes with Novel Loci on 9q21 and 2q32-35. American Journal of Human Genetics, 2004, 75, 161-173.	6.2	200
54	Submicroscopic Duplications of the Hydroxysteroid Dehydrogenase HSD17B10 and the E3 Ubiquitin Ligase HUWE1 Are Associated with Mental Retardation. American Journal of Human Genetics, 2008, 82, 432-443.	6.2	187

#	Article	IF	Citations
55	Hereditary Nonpolyposis Colorectal Cancer in 95 Families: Differences and Similarities between Mutation-Positive and Mutation-Negative Kindreds. American Journal of Human Genetics, 2001, 68, 118-127.	6.2	186
56	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
57	MLH1 Germline Epimutations as a Factor in Hereditary Nonpolyposis Colorectal Cancer. Gastroenterology, 2005, 129, 1392-1399.	1.3	179
58	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
59	Sputum gene expression signature of 6 biomarkers discriminates asthma inflammatory phenotypes. Journal of Allergy and Clinical Immunology, 2014, 133, 997-1007.	2.9	175
60	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
61	Germline mutations in the 3â€² part of APC exon 15 do not result in truncated proteins and are associated with attenuated adenomatous polyposis coli. Human Genetics, 1996, 98, 727-734.	3.8	167
62	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. Nature Communications, 2015, 6, 5899.	12.8	162
63	Panel Testing for Familial Breast Cancer: Calibrating the Tension Between Research and Clinical Care. Journal of Clinical Oncology, 2016, 34, 1455-1459.	1.6	154
64	Common variants at 6p21.1 are associated with large artery atherosclerotic stroke. Nature Genetics, 2012, 44, 1147-1151.	21.4	152
65	Haplotype and Phenotype Analysis of Nine Recurrent BRCA2 Mutations in 111 Families: Results of an International Study. American Journal of Human Genetics, 1998, 62, 1381-1388.	6.2	150
66	Cancer Risks for PMS2-Associated Lynch Syndrome. Journal of Clinical Oncology, 2018, 36, 2961-2968.	1.6	147
67	Ischemic stroke is associated with the ABO locus: The EuroCLOT study. Annals of Neurology, 2013, 73, 16-31.	5.3	144
68	Differential Proteolytic Enzyme Activity in Eosinophilic and Neutrophilic Asthma. American Journal of Respiratory and Critical Care Medicine, 2005, 172, 559-565.	5.6	142
69	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	21.4	141
70	Epigenetically reprogrammed methylation landscape drives the DNA self-assembly and serves as a universal cancer biomarker. Nature Communications, 2018, 9, 4915.	12.8	135
71	Increased power by harmonizing structural MRI site differences with the ComBat batch adjustment method in ENIGMA. NeuroImage, 2020, 218, 116956.	4.2	135
72	Familial infiltrative fibromatosis (desmoid tumours) (MIM135290) caused by a recurrent 3' APC gene mutation. Human Molecular Genetics, 1996, 5, 1921-1924.	2.9	134

#	Article	IF	Citations
73	Four Novel Loci (19q13, 6q24, 12q24, and 5q14) Influence the Microcirculation In Vivo. PLoS Genetics, 2010, 6, e1001184.	3.5	134
74	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	7.9	134
75	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
76	Genome-wide supported variant MIR137 and severe negative symptoms predict membership of an impaired cognitive subtype of schizophrenia. Molecular Psychiatry, 2013, 18, 774-780.	7.9	129
77	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2015, 107, .	6.3	129
78	The multiple sclerosis whole blood mRNA transcriptome and genetic associations indicate dysregulation of specific T cell pathways in pathogenesis. Human Molecular Genetics, 2010, 19, 2134-2143.	2.9	128
79	Bloodâ€based detection of <scp>RAS</scp> mutations to guide antiâ€<scp>EGFR</scp> therapy in colorectal cancer patients: concordance of results from circulating tumor <scp>DNA</scp> and tissueâ€based <scp>RAS</scp> testing. Molecular Oncology, 2017, 11, 208-219.	4.6	125
80	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
81	Methylation differences at the HLA-DRB1 locus in CD4+ T-Cells are associated with multiple sclerosis. Multiple Sclerosis Journal, 2014, 20, 1033-1041.	3.0	120
82	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
83	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	6.2	119
84	How to Use an Article About Genetic Association. JAMA - Journal of the American Medical Association, 2009, 301, 191.	7.4	115
85	Small Molecular Weight Variants of p53 Are Expressed in Human Melanoma Cells and Are Induced by the DNA-Damaging Agent Cisplatin. Clinical Cancer Research, 2008, 14, 1659-1668.	7.0	112
86	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
87	Insights into the Genetic Architecture of Early Stage Age-Related Macular Degeneration: A Genome-Wide Association Study Meta-Analysis. PLoS ONE, 2013, 8, e53830.	2.5	108
88	A Multicenter Blinded Study to Evaluate KRAS Mutation Testing Methodologies in the Clinical Setting. Journal of Molecular Diagnostics, 2009, 11, 543-552.	2.8	107
89	Preliminary investigation of gene expression profiles in peripheral blood lymphocytes in schizophrenia. Schizophrenia Research, 2006, 82, 175-183.	2.0	106
90	Cohort Profile: The Hunter Community Study. International Journal of Epidemiology, 2010, 39, 1452-1463.	1.9	106

#	Article	IF	Citations
91	The NOD2 3020insC Mutation and the Risk of Colorectal Cancer: Table 1. Cancer Research, 2004, 64, 1604-1606.	0.9	105
92	Nerve fibers infiltrate the tumor microenvironment and are associated with nerve growth factor production and lymph node invasion in breast cancer. Molecular Oncology, 2015, 9, 1626-1635.	4.6	105
93	Prevalence of BRCA1 and BRCA2 germline mutations in patients with triple-negative breast cancer. Breast Cancer Research and Treatment, 2015, 150, 71-80.	2.5	103
94	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	103
95	Genome-wide association meta-analysis of functional outcome after ischemic stroke. Neurology, 2019, 92, e1271-e1283.	1.1	99
96	Parental Prenatal Smoking and Risk of Childhood Acute Lymphoblastic Leukemia. American Journal of Epidemiology, 2012, 175, 43-53.	3.4	98
97	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
98	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
99	BRIP1, PALB2, and RAD51C mutation analysis reveals their relative importance as genetic susceptibility factors for breast cancer. Breast Cancer Research and Treatment, 2011, 127, 853-859.	2.5	95
100	Long-term effect of resistant starch on cancer risk in carriers of hereditary colorectal cancer: an analysis from the CAPP2 randomised controlled trial. Lancet Oncology, The, 2012, 13, 1242-1249.	10.7	95
101	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
102	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
103	Obesity, Aspirin, and Risk of Colorectal Cancer in Carriers of Hereditary Colorectal Cancer: A Prospective Investigation in the CAPP2 Study. Journal of Clinical Oncology, 2015, 33, 3591-3597.	1.6	91
104	Direct integrin Î±vÎ²6-ERK binding: implications for tumour growth. Oncogene, 2002, 21, 1370-1380.	5.9	90
105	Phenotype-Genotype Correlations in a Series of Wolfram Syndrome Families. Diabetes Care, 2004, 27, 2003-2009.	8.6	90
106	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. Human Molecular Genetics, 2014, 23, 3054-3068.	2.9	90
107	Australian Schizophrenia Research Bank: a database of comprehensive clinical, endophenotypic and genetic data for aetiological studies of schizophrenia. Australian and New Zealand Journal of Psychiatry, 2010, 44, 1029-35.	2.3	90
108	Demethylation by 5-aza-2'-deoxycytidine in colorectal cancer cells targets genomic DNA whilst promoter CpG island methylation persists. BMC Cancer, 2010, 10, 366.	2.6	89

#	Article	IF	Citations
109	Transcriptome Sequencing Revealed Significant Alteration of Cortical Promoter Usage and Splicing in Schizophrenia. PLoS ONE, 2012, 7, e36351.	2.5	89
110	P53 in human melanoma fails to regulate target genes associated with apoptosis and the cell cycle and may contribute to proliferation. BMC Cancer, 2011, 11, 203.	2.6	88
111	An X-Linked Haplotype of Neandertal Origin Is Present Among All Non-African Populations. Molecular Biology and Evolution, 2011, 28, 1957-1962.	8.9	87
112	Genome-wide DNA methylation profiling of CD8+ T cells shows a distinct epigenetic signature to CD4+ T cells in multiple sclerosis patients. Clinical Epigenetics, 2015, 7, 118.	4.1	85
113	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
114	Differential gene expression and cytokine production from neutrophils in asthma phenotypes. European Respiratory Journal, 2010, 35, 522-531.	6.7	84
115	How to Use an Article About Genetic Association. JAMA - Journal of the American Medical Association, 2009, 301, 74.	7.4	83
116	Gene expression analysis reveals schizophrenia-associated dysregulation ofÂimmune pathways in peripheral blood mononuclear cells. Journal of Psychiatric Research, 2013, 47, 425-437.	3.1	83
117	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
118	Correlation between the development of extracolonic manifestations in FAP patients and mutations beyond codon 1403 in the APC gene.. Journal of Medical Genetics, 1996, 33, 274-280.	3.2	80
119	Germline 657del5 mutation in the NBS1 gene in breast cancer patients. International Journal of Cancer, 2003, 106, 379-381.	5.1	80
120	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
121	Novel germline APC gene mutation in a large familial adenomatous polyposis kindred displaying variable phenotypes.. Gut, 1995, 36, 731-736.	12.1	76
122	Cytokine responses and sudden infant death syndrome: genetic, developmental, and environmental risk factors. Journal of Leukocyte Biology, 2005, 78, 1242-1254.	3.3	76
123	BRCA2 gene mutations in families with aggregations of breast and stomach cancers. British Journal of Cancer, 2002, 87, 888-891.	6.4	75
124	Is hemochromatosis a risk factor for Alzheimer's disease?. Journal of Alzheimer's Disease, 2001, 3, 471-477.	2.6	74
125	Transcriptome-wide mega-analyses reveal joint dysregulation of immunologic genes and transcription regulators in brain and blood in schizophrenia. Schizophrenia Research, 2016, 176, 114-124.	2.0	74
126	Somatic deletion mapping on chromosome 10 and sequence analysis of PTEN/MMAC1 point to the 10q25-26 region as the primary target in low-grade and high-grade gliomas. Oncogene, 1998, 16, 3331-3335.	5.9	73

#	Article	IF	Citations
127	Temozolomide induces senescence but not apoptosis in human melanoma cells. British Journal of Cancer, 2007, 97, 1225-1233.	6.4	73
128	Decreased expression of key tumour suppressor microRNAs is associated with lymph node metastases in triple negative breast cancer. BMC Cancer, 2014, 14, 51.	2.6	73
129	Catechol-O-methyltransferase (COMT) genotype moderates the effects of childhood trauma on cognition and symptoms in schizophrenia. Journal of Psychiatric Research, 2014, 49, 43-50.	3.1	73
130	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
131	Leiden open variation database of the MUTYH gene. Human Mutation, 2010, 31, 1205-1215.	2.5	72
132	Systemic upregulation of neutrophil Â-defensins and serine proteases in neutrophilic asthma. Thorax, 2011, 66, 942-947.	5.6	71
133	Review and meta-analysis of genetic polymorphisms associated with exceptional human longevity. Mechanisms of Ageing and Development, 2018, 175, 24-34.	4.6	71
134	BRCA1-associated breast and ovarian cancer risks in Poland: no association with commonly studied polymorphisms. Breast Cancer Research and Treatment, 2010, 119, 201-211.	2.5	70
135	IL12A, MPHOSPH9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. Genes and Immunity, 2010, 11, 397-405.	4.1	70
136	c-Myc inactivation of p53 through the pan-cancer lncRNA MILIP drives cancer pathogenesis. Nature Communications, 2020, 11, 4980.	12.8	70
137	Serum Concentrations of Selenium and Copper in Patients Diagnosed with Pancreatic Cancer. Cancer Research and Treatment, 2016, 48, 1056-1064.	3.0	69
138	Phenotypic differences in familial adenomatous polyposis based on APC gene mutation status. Gut, 1998, 43, 675-679.	12.1	68
139	Genetic polymorphisms and childhood acute lymphoblastic leukemia: GWAS of the ESCALE study (SFCE). Leukemia, 2012, 26, 2561-2564.	7.2	68
140	The relative mRNA expression of p53 isoforms in breast cancer is associated with clinical features and outcome. Carcinogenesis, 2014, 35, 586-596.	2.8	67
141	Detection of new mutations in six out of 10 Swiss HNPCC families by genomic sequencing of the hMSH2 and hMLH1 genes.. Journal of Medical Genetics, 1995, 32, 909-912.	3.2	65
142	Altered gene expression in the superior temporal gyrus in schizophrenia. BMC Genomics, 2008, 9, 199.	2.8	65
143	Xeroderma pigmentosum-Cockayne syndrome complex in two patients: Absence of slun tumors despite severe deficiency of DNA excision repair. Journal of the American Academy of Dermatology, 1993, 29, 883-889.	1.2	64
144	Cis-Expression Quantitative Trait Loci Mapping Reveals Replicable Associations with Heroin Addiction in OPRM1. Biological Psychiatry, 2015, 78, 474-484.	1.3	64

#	Article	IF	Citations
145	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1503-1510.	2.5	64
146	Differential methylation at MHC in CD4+ T cells is associated with multiple sclerosis independently of HLA-DRB1. Clinical Epigenetics, 2017, 9, 71.	4.1	63
147	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
148	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
149	Epigenome-wide association studies: current knowledge, strategies and recommendations. Clinical Epigenetics, 2021, 13, 214.	4.1	62
150	Characterisation of autoantibodies to peripheral myelin protein 22 in patients with hereditary and acquired neuropathies. Journal of Neuroimmunology, 2000, 104, 155-163.	2.3	61
151	Maternal folate and other vitamin supplementation during pregnancy and risk of acute lymphoblastic leukemia in the offspring. International Journal of Cancer, 2010, 126, 2690-2699.	5.1	61
152	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. Human Molecular Genetics, 2013, 22, 2754-2764.	2.9	60
153	Colorectal carcinoma in the course of inflammatory bowel diseases. Hereditary Cancer in Clinical Practice, 2019, 17, 18.	1.5	60
154	Mutation analysis of the STK11/LKB1 gene and clinical characteristics of an Australian series of Peutz-Jeghers syndrome patients. Clinical Genetics, 2002, 62, 282-287.	2.0	59
155	The RAD51 135 G>C Polymorphism Modifies Breast Cancer and Ovarian Cancer Risk in Polish BRCA1 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 270-275.	2.5	59
156	Maternal Use of Folic Acid and Other Supplements and Risk of Childhood Brain Tumors. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1933-1941.	2.5	59
157	Gene expression profiling in treatment-naive schizophrenia patients identifies abnormalities in biological pathways involving AKT1 that are corrected by antipsychotic medication. International Journal of Neuropsychopharmacology, 2013, 16, 1483-1503.	2.1	59
158	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	7.9	59
159	Proteotranscriptomic Profiling of 231-BR Breast Cancer Cells: Identification of Potential Biomarkers and Therapeutic Targets for Brain Metastasis. Molecular and Cellular Proteomics, 2015, 14, 2316-2330.	3.8	59
160	Association between endometriosis and the interleukin 1A (IL1A) locus. Human Reproduction, 2015, 30, 239-248.	0.9	58
161	Variation in the risk of colorectal cancer in families with Lynch syndrome: a retrospective cohort study. Lancet Oncology, The, 2021, 22, 1014-1022.	10.7	58
162	Cell-Free DNA as a Diagnostic Blood-Based Biomarker for Colorectal Cancer: A Systematic Review. Journal of Surgical Research, 2019, 236, 184-197.	1.6	57

#	Article	IF	Citations
163	Polymorphisms in genes of the steroid hormone biosynthesis and metabolism pathways and endometrial cancer risk. Cancer Epidemiology, 2010, 34, 328-337.	1.9	56
164	miRNAs and Other Epigenetic Changes as Biomarkers in Triple Negative Breast Cancer. International Journal of Molecular Sciences, 2015, 16, 28347-28376.	4.1	56
165	DNA methylation profile of triple negative breast cancer-specific genes comparing lymph node positive patients to lymph node negative patients. Scientific Reports, 2016, 6, 33435.	3.3	56
166	Factor V Leiden is associated with pre-eclampsia but not with fetal growth restriction: a genetic association study and meta-analysis. Journal of Thrombosis and Haemostasis, 2008, 6, 1868-1875.	3.8	55
167	A Polymorphism in the HLA-DPB1 Gene Is Associated with Susceptibility to Multiple Sclerosis. PLoS ONE, 2010, 5, e13454.	2.5	55
168	Potential association of vitamin D receptor polymorphismTaq1with multiple sclerosis. Multiple Sclerosis Journal, 2012, 18, 16-22.	3.0	55
169	The â€œunnaturalâ€•history of colorectal cancer in Lynch syndrome: Lessons from colonoscopy surveillance. International Journal of Cancer, 2021, 148, 800-811.	5.1	55
170	Altered gene expression in the amygdala in schizophrenia: Up-regulation of genes located in the cytomatrix active zone. Molecular and Cellular Neurosciences, 2006, 31, 243-250.	2.2	54
171	Buccal DNA Collection: Comparison of Buccal Swabs with FTA Cards. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 816-819.	2.5	54
172	Toll-Like Receptor (TLR) and Nucleosome-binding Oligomerization Domain (NOD) gene polymorphisms and endometrial cancer risk. BMC Cancer, 2010, 10, 382.	2.6	53
173	A rare P2X7 variant Arg307Gln with absent pore formation function protects against neuroinflammation in multiple sclerosis. Human Molecular Genetics, 2015, 24, 5644-5654.	2.9	53
174	ONCOSTATIN M (OSM) IS INCREASED IN ASTHMA WITH INCOMPLETELY REVERSIBLE AIRFLOW OBSTRUCTION. Experimental Lung Research, 2009, 35, 781-794.	1.2	52
175	How to Use an Article About Genetic Association. JAMA - Journal of the American Medical Association, 2009, 301, 304.	7.4	52
176	INPP4B is an oncogenic regulator in human colon cancer. Oncogene, 2016, 35, 3049-3061.	5.9	52
177	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
178	A Transcription Factor Map as Revealed by a Genome-Wide Gene Expression Analysis of Whole-Blood mRNA Transcriptome in Multiple Sclerosis. PLoS ONE, 2010, 5, e14176.	2.5	51
179	Impact of COX-2 rs5275 and rs20417 and GPIIIa rs5918 Polymorphisms on 90-Day Ischemic Stroke Functional Outcome: A Novel Finding. Journal of Stroke and Cerebrovascular Diseases, 2011, 20, 134-144.	1.6	51
180	Identification of TPIT and other novel autoantigens in lymphocytic hypophysitis; immunoscreening of a pituitary cDNA library and development of immunoprecipitation assays. European Journal of Endocrinology, 2012, 166, 391-398.	3.7	51

#	Article	IF	Citations
181	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	11.0	51
182	New deletion in low-grade oligodendroglioma at the glioblastoma suppressor locus on chromosome 10q25-26. Oncogene, 1997, 15, 997-1000.	5.9	50
183	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
184	Mutational analysis of the first 14 exons of the adenomatous polyposis coli (APC) gene. European Journal of Cancer, 1994, 30, 1709-1713.	2.8	49
185	Identification of a modifier gene locus on chromosome 1p35-36 in familial adenomatous polyposis. Human Genetics, 1997, 99, 653-657.	3.8	49
186	Hereditary non-polyposis colorectal cancer and the role of hPMS2 and hEXO1 mutations. Clinical Genetics, 2004, 65, 215-225.	2.0	49
187	Exposure to pesticides and the risk of childhood brain tumors. Cancer Causes and Control, 2013, 24, 1269-1278.	1.8	49
188	CX3CR1 is dysregulated in blood and brain from schizophrenia patients. Schizophrenia Research, 2015, 168, 434-443.	2.0	49
189	Novel genes associated with lymph node metastasis in triple negative breast cancer. Scientific Reports, 2015, 5, 15832.	3.3	48
190	XPD Common Variants and their Association with Melanoma and Breast Cancer Risk. Breast Cancer Research and Treatment, 2006, 98, 209-215.	2.5	47
191	Altered expression of regulator of G-protein signalling 4 (RGS4) mRNA in the superior temporal gyrus in schizophrenia. Schizophrenia Research, 2007, 89, 165-168.	2.0	47
192	Methylenetetrahydrofolate reductase polymorphisms modify BRCA1-associated breast and ovarian cancer risks. Breast Cancer Research and Treatment, 2007, 104, 299-308.	2.5	47
193	Xeroderma pigmentosum genes and melanoma risk. International Journal of Cancer, 2013, 133, 1094-1100.	5.1	47
194	The VEGF_936_C>T 3â€²UTR polymorphism reduces BRCA1-associated breast cancer risk in Polish women. Cancer Letters, 2008, 262, 71-76.	7.2	46
195	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	6.3	45
196	Mutation analysis of MLH1 and MSH2 genes performed by denaturing high-performance liquid chromatography. Journal of Proteomics, 2002, 51, 89-100.	2.4	44
197	Integrin Î±vÎ²6-associated ERK2 mediates MMP-9 secretion in colon cancer cells. British Journal of Cancer, 2002, 87, 348-351.	6.4	44
198	Ethnicity, infection and sudden infant death syndrome. FEMS Immunology and Medical Microbiology, 2004, 42, 53-65.	2.7	44

#	Article	IF	Citations
199	STK11 status and intussusception risk in Peutz-Jeghers syndrome. Journal of Medical Genetics, 2006, 43, e41-e41.	3.2	44
200	Estrogen receptor polymorphisms and the risk of endometrial cancer. BJOG: an International Journal of Obstetrics and Gynaecology, 2009, 116, 1053-1061.	2.3	44
201	Colorectal cancer susceptibility loci on chromosome 8q23.3 and 11q23.1 as modifiers for disease expression in lynch syndrome. Journal of Medical Genetics, 2011, 48, 279-284.	3.2	44
202	A variant at 9p21.3 functionally implicates CDKN2B in paediatric B-cell precursor acute lymphoblastic leukaemia aetiology. Nature Communications, 2016, 7, 10635.	12.8	44
203	Interleukin-10 and sudden infant death syndrome. FEMS Immunology and Medical Microbiology, 2004, 42, 130-138.	2.7	43
204	Mutation analysis of theMYH gene in an Australian series of colorectal polyposis patients with or without germlineAPC mutations. International Journal of Cancer, 2005, 116, 73-77.	5.1	43
205	COGENT (COlorectal cancer GENeTics): an international consortium to study the role of polymorphic variation on the risk of colorectal cancer. British Journal of Cancer, 2010, 102, 447-454.	6.4	43
206	Next-generation sequencing reveals broad down-regulation of microRNAs in secondary progressive multiple sclerosis CD4+ T cells. Clinical Epigenetics, 2016, 8, 87.	4.1	43
207	EBV and MS: Major cause, minor contribution or red-herring?. Multiple Sclerosis and Related Disorders, 2017, 16, 24-30.	2.0	43
208	Paternal impacts on development: identification of genomic regions vulnerable to oxidative DNA damage in human spermatozoa. Human Reproduction, 2019, 34, 1876-1890.	0.9	43
209	LncRNA REG1CP promotes tumorigenesis through an enhancer complex to recruit FANCJ helicase for REG3A transcription. Nature Communications, 2019, 10, 5334.	12.8	43
210	CDKN2A common variants and their association with melanoma risk: a population-based study. Cancer Research, 2005, 65, 835-9.	0.9	43
211	Integrin expression in colon cancer cells is regulated by the cytoplasmic domain of the ?6 integrin subunit. International Journal of Cancer, 2002, 99, 529-537.	5.1	42
212	IL6 G-174C Associated With Sudden Infant Death Syndrome in a Caucasian Australian Cohort. Human Immunology, 2006, 67, 819-825.	2.4	42
213	Capturing all disease-causing mutations for clinical and research use: Toward an effortless system for the Human Variome Project. Genetics in Medicine, 2009, 11, 843-849.	2.4	42
214	Genome-wide association study of endometrial cancer in E2C2. Human Genetics, 2014, 133, 211-224.	3.8	42
215	Expression of reninâ€“angiotensin system (RAS) components in endometrial cancer. Endocrine Connections, 2017, 6, 9-19.	1.9	42
216	Genome-wide DNA methylation changes in CD19+ B cells from relapsing-remitting multiple sclerosis patients. Scientific Reports, 2018, 8, 17418.	3.3	42

#	Article	IF	Citations
217	Lack of association between screening interval and cancer stage in Lynch syndrome may be accounted for by over-diagnosis; a prospective Lynch syndrome database report. Hereditary Cancer in Clinical Practice, 2019, 17, 8.	1.5	42
218	Polymorphisms in the Receptor Tyrosine Kinase MERTK Gene Are Associated with Multiple Sclerosis Susceptibility. PLoS ONE, 2011, 6, e16964.	2.5	42
219	MDM2 SNP309 T>G alone or in combination with theTP53 R72P polymorphism does not appear to influence disease expression and age of diagnosis of colorectal cancer in HNPCC patients. International Journal of Cancer, 2007, 120, 563-565.	5.1	41
220	Inflammatory response gene polymorphisms and their relationship with colorectal cancer risk. BMC Cancer, 2008, 8, 112.	2.6	41
221	Polymorphisms in TP53 and MDM2 combined are associated with high grade endometrial cancer. Gynecologic Oncology, 2009, 113, 109-114.	1.4	41
222	Use of multigeneâ€panel identifies pathogenic variants in several <scp>CRC</scp>â€predisposing genes in patients previously tested for Lynch Syndrome. Clinical Genetics, 2017, 92, 405-414.	2.0	41
223	Iron levels, genes involved in iron metabolism and antioxidative processes and lung cancer incidence. PLoS ONE, 2019, 14, e0208610.	2.5	41
224	Fetal Growth and Risk of Childhood Acute Lymphoblastic Leukemia: Results From an Australian Case-Control Study. American Journal of Epidemiology, 2009, 170, 221-228.	3.4	40
225	HLAâ€DRB1 associations with disease susceptibility and clinical course in Australians with multiple sclerosis. Tissue Antigens, 2009, 74, 17-21.	1.0	40
226	Schizophrenia genetic variants are not associated with intelligence. Psychological Medicine, 2013, 43, 2563-2570.	4.5	40
227	Association of paediatric mastocytosis with a polymorphism resulting in an amino acid substitution (M541L) in the transmembrane domain of c-KIT. British Journal of Dermatology, 2008, 159, 1160-9.	1.5	39
228	Haemochromatosis HFE gene polymorphisms as potential modifiers of hereditary nonpolyposis colorectal cancer risk and onset age. International Journal of Cancer, 2009, 125, 78-83.	5.1	39
229	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
230	Influence of selection criteria on mutation detection in patients with hereditary nonpolyposis colorectal cancer. , 1999, 85, 2512-2518.		38
231	MC1R common variants, CDKN2A and their association with melanoma and breast cancer risk. International Journal of Cancer, 2006, 119, 2597-2602.	5.1	38
232	GENETIC ANALYSIS OF ANTHERIDIOGEN SENSITIVITY IN CERATOPTERIS RICHARDII. American Journal of Botany, 1987, 74, 1872-1877.	1.7	37
233	Smoking Related Cancers and Loci at Chromosomes 15q25, 5p15, 6p22.1 and 6p21.33 in the Polish Population. PLoS ONE, 2011, 6, e25057.	2.5	37
234	Combined analysis of exon splicing and genome wide polymorphism data predict schizophrenia risk loci. Journal of Psychiatric Research, 2014, 52, 44-49.	3.1	37

#	Article	IF	Citations
235	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	6.2	37
236	Increased DNA methylation of SLFN12 in CD4+ and CD8+ T cells from multiple sclerosis patients. PLoS ONE, 2018, 13, e0206511.	2.5	37
237	Common variants of DNA repair genes and malignant melanoma. European Journal of Cancer, 2008, 44, 110-114.	2.8	36
238	Maternal Dietary Intake of Folate and Vitamins B6 and B12 During Pregnancy and the Risk of Childhood Acute Lymphoblastic Leukemia. Nutrition and Cancer, 2012, 64, 1122-1130.	2.0	36
239	The Architecture of Risk for Type 2 Diabetes: Understanding Asia in the Context of Global Findings. International Journal of Endocrinology, 2014, 2014, 1-21.	1.5	36
240	Prevalence of PALB2 mutations in Australian familial breast cancer cases and controls. Breast Cancer Research, 2015, 17, 111.	5.0	36
241	A Clinical Review of Generalized Overgrowth Syndromes in the Era of Massively Parallel Sequencing. Molecular Syndromology, 2018, 9, 70-82.	0.8	36
242	Comprehensive mismatch repair gene panel identifies variants in patients with Lynchâ€like syndrome. Molecular Genetics & Genomic Medicine, 2019, 7, e850.	1.2	36
243	Familial adenomatous polyposis: more evidence for disease diversity and genetic heterogeneity. Gut, 2001, 48, 508-514.	12.1	35
244	Interleukin 1-? responses to bacterial toxins and sudden infant death syndrome. FEMS Immunology and Medical Microbiology, 2004, 42, 139-145.	2.7	35
245	The PAI-1 4G/5G Gene Polymorphism and Ischemic Stroke: An Association Study and Meta-Analysis. Journal of Stroke and Cerebrovascular Diseases, 2007, 16, 173-179.	1.6	35
246	Exposure to professional pest control treatments and the risk of childhood acute lymphoblastic leukemia. International Journal of Cancer, 2011, 129, 1678-1688.	5.1	35
247	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	3.3	35
248	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	5.1	35
249	BRCA2 mutations in a population-based series of patients with ocular melanoma. International Journal of Cancer, 2002, 102, 188-191.	5.1	34
250	A high frequency of BRCA2 gene mutations in Polish families with ovarian and stomach cancer. European Journal of Human Genetics, 2003, 11, 955-958.	2.8	34
251	Germline MSH2 and MLH1 mutational spectrum including large rearrangements in HNPCC families from Poland (update study). Clinical Genetics, 2005, 69, 40-47.	2.0	34
252	Age of diagnosis of colorectal cancer in HNPCC patients is more complex than that predicted by R72P polymorphism inTP53. International Journal of Cancer, 2006, 118, 2479-2484.	5.1	34

#	Article	IF	Citations
253	Genetic Overlap Between Diagnostic Subtypes of Ischemic Stroke. Stroke, 2015, 46, 615-619.	2.0	34
254	Candidate locus analysis of the TERTâ€“CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	3.8	34
255	Lessons learnt from implementation of a Lynch syndrome screening program for patients with gynaecological malignancy. Pathology, 2017, 49, 457-464.	0.6	34
256	Vitamin D receptor variants and the malignant melanoma risk: A population-based study. Cancer Epidemiology, 2009, 33, 103-107.	1.9	33
257	Can selenium levels act as a marker of colorectal cancer risk?. BMC Cancer, 2013, 13, 214.	2.6	33
258	STaRRRT: a table of short tandem repeats in regulatory regions of the human genome. BMC Genomics, 2013, 14, 795.	2.8	33
259	Analysis of the global methylation status of human spermatozoa and its association with the tendency of these cells to enter apoptosis. Andrologia, 2013, 45, 424-429.	2.1	33
260	Parental alcohol consumption and risk of childhood acute lymphoblastic leukemia and brain tumors. Cancer Causes and Control, 2013, 24, 391-402.	1.8	33
261	Combined analysis of three lynch syndrome cohorts confirms the modifying effects of 8q23.3 and 11q23.1 in MLH1 mutation carriers. International Journal of Cancer, 2013, 132, 1556-1564.	5.1	33
262	Preliminary evidence of an interaction between the FOXP2 gene and childhood emotional abuse predicting likelihood of auditory verbal hallucinations in schizophrenia. Journal of Psychiatric Research, 2014, 50, 66-72.	3.1	33
263	Comparison of genomic abnormalities between BRCAX and sporadic breast cancers studied by comparative genomic hybridization. International Journal of Cancer, 2005, 114, 230-236.	5.1	32
264	IMMUNE RESPONSES OF AIRWAY NEUTROPHILS ARE IMPAIRED IN ASTHMA. Experimental Lung Research, 2009, 35, 554-569.	1.2	32
265	Gastrointestinal polyps in McCune Albright syndrome. Journal of Medical Genetics, 2011, 48, 458-461.	3.2	32
266	Genome-Wide Association Study Identifies a Possible Susceptibility Locus for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 980-987.	2.5	32
267	Polymorphisms in nucleotide excision repair genes and susceptibility to colorectal cancer in the Polish population. Molecular Biology Reports, 2015, 42, 755-764.	2.3	32
268	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. American Journal of Human Genetics, 2016, 98, 1159-1169.	6.2	32
269	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
270	Prevalence of the NOD2 3020insC mutation in aggregations of breast and lung cancer. Breast Cancer Research and Treatment, 2006, 95, 141-145.	2.5	31

#	Article	IF	Citations
271	MSH6 and PMS2 mutation positive Australian Lynch syndrome families: novel mutations, cancer risk and age of diagnosis of colorectal cancer. Hereditary Cancer in Clinical Practice, 2010, 8, 5.	1.5	31
272	Parental smoking and risk of childhood brain tumors. International Journal of Cancer, 2013, 133, 253-259.	5.1	31
273	The expression of Dicer and Drosha in matched normal tissues, tumours and lymph node metastases in triple negative breast cancer. BMC Cancer, 2014, 14, 253.	2.6	30
274	Genetic burden associated with varying degrees of disease severity in endometriosis. Molecular Human Reproduction, 2015, 21, 594-602.	2.8	30
275	Altered neural signaling and immune pathways in peripheral blood mononuclear cells of schizophrenia patients with cognitive impairment: A transcriptome analysis. Brain, Behavior, and Immunity, 2016, 53, 194-206.	4.1	30
276	Association of zinc level and polymorphism in MMP-7 gene with prostate cancer in Polish population. PLoS ONE, 2018, 13, e0201065.	2.5	30
277	Germline mutations in the CHEK2 kinase gene are associated with an increased risk of bladder cancer. International Journal of Cancer, 2008, 122, 583-586.	5.1	29
278	Long Term Transcriptional Reactivation of Epigenetically Silenced Genes in Colorectal Cancer Cells Requires DNA Hypomethylation and Histone Acetylation. PLoS ONE, 2011, 6, e23127.	2.5	29
279	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29
280	Relationship between APC genotype, polyp distribution, and oral sulindac treatment in the colon and rectum of patients with familial adenomatous polyposis. Diseases of the Colon and Rectum, 2001, 44, 1090-1097.	1.3	28
281	Auroraâ€A and Cyclin D1 polymorphisms and the age of onset of colorectal cancer in hereditary nonpolyposis colorectal cancer. International Journal of Cancer, 2008, 122, 1273-1277.	5.1	28
282	Variant alleles of the CYP1B1 gene are associated with colorectal cancer susceptibility. BMC Cancer, 2010, 10, 420.	2.6	28
283	Blood cadmium levels as a marker for early lung cancer detection. Journal of Trace Elements in Medicine and Biology, 2021, 64, 126682.	3.0	28
284	Confirmation of Childhood Acute Lymphoblastic Leukemia Variants, ARID5B and IKZF1, and Interaction with Parental Environmental Exposures. PLoS ONE, 2014, 9, e110255.	2.5	28
285	Impact of microsatellite testing and mismatch repair protein expression on the clinical interpretation of genetic testing in hereditary non-polyposis colorectal cancer. Journal of Cancer Research and Clinical Oncology, 2002, 128, 403-411.	2.5	27
286	An updated mutation spectrum in an Australian series of PJS patients provides further evidence for only one gene locus. Clinical Genetics, 2006, 70, 409-414.	2.0	27
287	Vitamin D receptor variants and breast cancer risk in the Polish population. Breast Cancer Research and Treatment, 2009, 115, 629-633.	2.5	27
288	A high-throughput protocol for mutation scanning of the BRCA1 and BRCA2genes. BMC Cancer, 2011, 11, 265.	2.6	27

#	Article	IF	Citations
289	Association of PHB 1630 C>T and MTHFR 677 C>T polymorphisms with breast and ovarian cancer risk in BRCA1/2 mutation carriers: results from a multicenter study. British Journal of Cancer, 2012, 106, 2016-2024.	6.4	27
290	Genetic Loci for Retinal Arteriolar Microcirculation. PLoS ONE, 2013, 8, e65804.	2.5	27
291	Survival by colon cancer stage and screening interval in Lynch syndrome: a prospective Lynch syndrome database report. Hereditary Cancer in Clinical Practice, 2019, 17, 28.	1.5	27
292	Characterization and genetic analysis of antheridiogen-insensitive mutants in the fern Ceratopteris. Botanical Journal of the Linnean Society, 1988, 96, 371-379.	1.6	26
293	Secretory phospholipase A 2 does not appear to be associated with phenotypic variation in familial adenomatous polyposis. Human Genetics, 1996, 98, 386-390.	3.8	26
294	Complex genetic predisposition to cancer in an extended HNPCC family with an ancestral hMLH1 mutation.. Journal of Medical Genetics, 1996, 33, 636-640.	3.2	26
295	Elevated frequency of p53-independent apoptosis after irradiation increases levels of DNA breaks in ataxia telangiectasia lymphoblasts. International Journal of Radiation Biology, 1997, 72, 257-269.	1.8	26
296	CDKN2A common variant and multi-organ cancer riskâ€"a population-based study. International Journal of Cancer, 2006, 118, 3180-3182.	5.1	26
297	Maternal consumption of coffee and tea during pregnancy and risk of childhood ALL: results from an Australian caseâ€"control study. Cancer Causes and Control, 2011, 22, 207-218.	1.8	26
298	Genetic Association of Refractive Error and Axial Length with 15q14 but Not 15q25 in the Blue Mountains Eye Study Cohort. Ophthalmology, 2013, 120, 292-297.	5.2	26
299	Maternal Dietary Intake of Folate and Vitamins B6 and B12 During Pregnancy and Risk of Childhood Brain Tumors. Nutrition and Cancer, 2014, 66, 800-809.	2.0	26
300	Reevaluation of the BRCA2 truncating allele c.9976Aâ€‰>â€‰T (p.Lys3326Ter) in a familial breast cancer context. Scientific Reports, 2015, 5, 14800.	3.3	26
301	Exploring the Risk Factors for Sudden Infant Deaths and Their Role in Inflammatory Responses to Infection. Frontiers in Immunology, 2015, 6, 44.	4.8	26
302	Do common genotypes of FK506 binding protein 5 (FKBP5) moderate the effects of childhood maltreatment on cognition in schizophrenia and healthy controls?. Journal of Psychiatric Research, 2015, 70, 9-17.	3.1	26
303	Extracellular Matrix (ECM) Activates Î²-catenin Signaling in Uterine Fibroids. Reproduction, 2018, 155, 61-71.	2.6	26
304	IGF1 is a modifier of disease risk in hereditary nonâ€polyposis colorectal cancer. International Journal of Cancer, 2008, 123, 1339-1343.	5.1	25
305	DNA repair gene polymorphisms and risk of early onset colorectal cancer in Lynch syndrome. Cancer Epidemiology, 2012, 36, 183-189.	1.9	25
306	Are Myocardial Infarctionâ€"Associated Single-Nucleotide Polymorphisms Associated With Ischemic Stroke?. Stroke, 2012, 43, 980-986.	2.0	25

#	Article	IF	Citations
307	Progesterone Activates Multiple Innate Immune Pathways in <scp>C</scp>hlamydia trachomatisâ€infected Endocervical Cells. American Journal of Reproductive Immunology, 2014, 71, 165-177.	1.2	25
308	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	3.1	25
309	Targeted nextâ€generation sequencing of 22 mismatch repair genes identifies Lynch syndrome families. Cancer Medicine, 2016, 5, 929-941.	2.8	25
310	Influence of the selenium level on overall survival in lung cancer. Journal of Trace Elements in Medicine and Biology, 2019, 56, 46-51.	3.0	25
311	Clinical use of SNP-microarrays for the detection of genome-wide changes in haematological malignancies. Critical Reviews in Oncology/Hematology, 2019, 142, 58-67.	4.4	25
312	Germline mutation and large deletion analysis of theCDKN2A andARF genes in families with multiple melanoma or an aggregation of malignant melanoma and breast cancer. International Journal of Cancer, 2004, 110, 558-562.	5.1	24
313	VariantSpark: population scale clustering of genotype information. BMC Genomics, 2015, 16, 1052.	2.8	24
314	Genetic Polymorphisms in Xenobiotic Clearance Genes and Their Influence on Disease Expression in Hereditary Nonpolyposis Colorectal Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2307-2310.	2.5	23
315	Lack of support for association between the KIF1B rs10492972[C] variant and multiple sclerosis. Nature Genetics, 2010, 42, 469-470.	21.4	23
316	Nucleotide Excision Repair Gene Expression after Cisplatin Treatment in Melanoma. Cancer Research, 2010, 70, 7918-7926.	0.9	23
317	Genome-Wide Association Study Identifies Two Novel Genomic Regions in Irritable Bowel Syndrome. American Journal of Gastroenterology, 2014, 109, 770-772.	0.4	23
318	Prevalence of the E318K and V320I MITF germline mutations in Polish cancer patients and multiorgan cancer risk-a population-based study. Cancer Genetics, 2014, 207, 128-132.	0.4	23
319	Common variants of xeroderma pigmentosum genes and prostate cancer risk. Gene, 2014, 546, 156-161.	2.2	23
320	Breastfeeding and Nutrition to 2 Years of Age and Risk of Childhood Acute Lymphoblastic Leukemia and Brain Tumors. Nutrition and Cancer, 2015, 67, 431-441.	2.0	23
321	Influence of the Levels of Arsenic, Cadmium, Mercury and Lead on Overall Survival in Lung Cancer. Biomolecules, 2021, 11, 1160.	4.0	23
322	Association of Extracolonic Manifestations of Familial Adenomatous Polyposis with Acetylation Phenotype in a Large FAP Kindred. European Journal of Human Genetics, 1997, 5, 43-49.	2.8	23
323	Genome-Wide Association Study of Retinopathy in Individuals without Diabetes. PLoS ONE, 2013, 8, e54232.	2.5	22
324	The male excess in sudden infant deaths. Innate Immunity, 2014, 20, 24-29.	2.4	22

#	Article	IF	Citations
325	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
326	Timeâ€resolved proteomic profiling of cigarette smokeâ€induced experimental chronic obstructive pulmonary disease. Respirology, 2021, 26, 960-973.	2.3	22
327	Detection of germline mutations in the BRCA1 gene by RNA-based sequencing. Human Mutation, 2001, 18, 149-156.	2.5	21
328	Investigation of the expression of genes affecting cytomatrix active zone function in the amygdala in schizophrenia: Effects of antipsychotic drugs. Journal of Psychiatric Research, 2009, 43, 282-290.	3.1	21
329	Continuing difficulties in interpreting CNV data: lessons from a genome-wide CNV association study of Australian HNPCC/lynch syndrome patients. BMC Medical Genomics, 2013, 6, 10.	1.5	21
330	Polygenic Overlap Between Kidney Function and Large Artery Atherosclerotic Stroke. Stroke, 2014, 45, 3508-3513.	2.0	21
331	Reninâ€“angiotensin system gene polymorphisms and endometrial cancer. Endocrine Connections, 2016, 5, 128-135.	1.9	21
332	GISCOME â€“ Genetics of Ischaemic Stroke Functional Outcome network: A protocol for an international multicentre genetic association study. European Stroke Journal, 2017, 2, 229-237.	5.5	21
333	Copy number variation in tripleÂnegative breast cancer samples associated with lymph node metastasis. Neoplasia, 2021, 23, 743-753.	5.3	21
334	Disease expression in Swiss hereditary non-polyposis colorectal cancer (HNPCC) kindreds. , 1997, 74, 281-285.		20
335	Resequencing and fine-mapping of the chromosome 12q13-14 locus associated with multiple sclerosis refines the number of implicated genes. Human Molecular Genetics, 2013, 22, 2283-2292.	2.9	20
336	Genome-wide significant results identified for plasma apolipoprotein H levels in middle-aged and older adults. Scientific Reports, 2016, 6, 23675.	3.3	20
337	The potential role of miRNAs in therapy of breast and ovarian cancers associated with BRCA1 mutation. Hereditary Cancer in Clinical Practice, 2017, 15, 15.	1.5	20
338	German family study on hereditary breast and/or ovarian cancer: Germline mutation analysis of theBRCA1 gene. Genes Chromosomes and Cancer, 1997, 18, 126-132.	2.8	19
339	Optimization of experimental conditions for RNA-based sequencing of MLH1 and MSH2 genes. Human Mutation, 2001, 17, 52-60.	2.5	19
340	Lack of association between genetic polymorphisms in cytokine genes and disease expression in patients with hereditary non-polyposis colorectal cancer. Scandinavian Journal of Gastroenterology, 2007, 42, 628-632.	1.5	19
341	Base excision repair and the role of MUTYH. Hereditary Cancer in Clinical Practice, 2007, 5, 199.	1.5	19
342	Whole genome amplification and its impact on CGH array profiles. BMC Research Notes, 2008, 1, 56.	1.4	19

#	Article	IF	Citations
343	Genetic modifiers of cancer risk in Lynch syndrome: a review. Familial Cancer, 2013, 12, 207-216.	1.9	19
344	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	2.9	19
345	Mutations in RECQL are not associated with breast cancer risk in an Australian population. Nature Genetics, 2018, 50, 1346-1348.	21.4	19
346	TAPES: A tool for assessment and prioritisation in exome studies. PLoS Computational Biology, 2019, 15, e1007453.	3.2	19
347	Meta-Analysis of Mismatch Repair Polymorphisms within the Cogent Consortium for Colorectal Cancer Susceptibility. PLoS ONE, 2013, 8, e72091.	2.5	19
348	Cancer Familial Aggregation (CFA) and G446A polymorphism in ARLTS1 gene. Breast Cancer Research and Treatment, 2006, 99, 59-62.	2.5	18
349	CYP1B1 and predisposition to breast cancer in Poland. Breast Cancer Research and Treatment, 2007, 106, 383-388.	2.5	18
350	Microarraysâ€"Identifying Molecular Portraits for Prostate Tumors with Different Gleason Patterns. Methods in Molecular Medicine, 2008, 141, 131-151.	0.8	18
351	Detecting Genotyping Error Using Measures of Degree of Hardy-Weinberg Disequilibrium. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 5.	0.6	18
352	Array comparative genomic hybridization for the detection of submicroscopic copy number variations of the X chromosome in women with premature ovarian failure. Human Reproduction, 2010, 25, 3159-3160.	0.9	18
353	MicroRNA-16 Is Down-Regulated in Mutated FLT3 Expressing Murine Myeloid FDC-P1 Cells and Interacts with Pim-1. PLoS ONE, 2012, 7, e44546.	2.5	18
354	Identity-by-Descent Mapping to Detect Rare Variants Conferring Susceptibility to Multiple Sclerosis. PLoS ONE, 2013, 8, e56379.	2.5	18
355	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131.	2.5	18
356	Genetically Determined Risk of Depression and Functional Outcome After Ischemic Stroke. Stroke, 2019, 50, 2219-2222.	2.0	18
357	Transcriptomic abnormalities in peripheral blood in bipolar disorder, and discrimination of the major psychoses. Schizophrenia Research, 2020, 217, 124-135.	2.0	18
358	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	3.8	18
359	Apoptosis is not involved in the hypersensitivity of fanconi anemia cells to mitomycin C. Cancer Genetics and Cytogenetics, 1994, 75, 67-71.	1.0	17
360	MTHFR 677 C>T and 1298 A>C polymorphisms and the age of onset of colorectal cancer in hereditary nonpolyposis colorectal cancer. European Journal of Human Genetics, 2009, 17, 629-635.	2.8	17

#	Article	IF	Citations
361	Genome-Wide Analysis of Blood Pressure Variability and Ischemic Stroke. Stroke, 2013, 44, 2703-2709.	2.0	17
362	Genetic and Environmental Factors Affecting TNF-Î± Responses in Relation to Sudden Infant Death Syndrome. Frontiers in Immunology, 2015, 6, 374.	4.8	17
363	Virus Infections and Sudden Death in Infancy: The Role of Interferon-ÃŽÂ³. Frontiers in Immunology, 2015, 6, 107.	4.8	17
364	Proteomic Profiling of Human Uterine Fibroids Reveals Upregulation of the Extracellular Matrix Protein Periostin. Endocrinology, 2018, 159, 1106-1118.	2.8	17
365	DNA methylation changes in CD4⁺ T cells isolated from multiple sclerosis patients on dimethyl fumarate. Multiple Sclerosis Journal - Experimental, Translational and Clinical, 2018, 4, 205521731878782.	1.0	17
366	Survival of Patients with Turcot's Syndrome and Glioblastoma. New England Journal of Medicine, 1996, 334, 736-737.	27.0	16
367	DNA Double Strand Break Repair and its Association with Inherited Predispositions to Breast Cancer. Hereditary Cancer in Clinical Practice, 2004, 2, 37.	1.5	16
368	Genetic variants in MUTYH are not associated with endometrial cancer risk. Hereditary Cancer in Clinical Practice, 2009, 7, 3.	1.5	16
369	Familial recurrence risks for multiple sclerosis in Australia. Journal of Neurology, Neurosurgery and Psychiatry, 2011, 82, 1351-1354.	1.9	16
370	Understanding Xeroderma Pigmentosum Complementation Groups Using Gene Expression Profiling after UV-Light Exposure. International Journal of Molecular Sciences, 2015, 16, 15985-15996.	4.1	16
371	Folate Pathway Gene Polymorphisms, Maternal Folic Acid Use, and Risk of Childhood Acute Lymphoblastic Leukemia. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 48-56.	2.5	16
372	Do founder mutations characteristic of some cancer sites also predispose to pancreatic cancer?. International Journal of Cancer, 2016, 139, 601-606.	5.1	16
373	Lynch syndrome mutation spectrum in New South Wales, Australia, including 55 novel mutations. Molecular Genetics & Genomic Medicine, 2016, 4, 223-231.	1.2	16
374	Reevaluation of RINT1 as a breast cancer predisposition gene. Breast Cancer Research and Treatment, 2016, 159, 385-392.	2.5	16
375	The presence of the intron 3 16 bp duplication polymorphism ofp53(rs17878362) in breast cancer is associated with a low Î”40p53:p53 ratio and better outcome. Carcinogenesis, 2016, 37, 81-86.	2.8	16
376	Serum 25(OH)D concentration, common variants of the VDR gene and lung cancer occurrence. International Journal of Cancer, 2017, 141, 336-341.	5.1	16
377	Molecular patterns of cancer colonisation in lymph nodes of breast cancer patients. Breast Cancer Research, 2018, 20, 143.	5.0	16
378	Low frequency of BRCA1 germline mutations in 45 German breast/ovarian cancer families.. Journal of Medical Genetics, 1997, 34, 884-888.	3.2	15

#	Article	IF	Citations
379	Gene Expression Profiling in Familial Adenomatous Polyposis Adenomas and Desmoid Disease. Hereditary Cancer in Clinical Practice, 2007, 5, 79.	1.5	15
380	The 3â€² untranslated region CÂ›ÂT polymorphism of prohibitin is a breast cancer risk modifier in Polish women carrying a BRCA1 mutation. Breast Cancer Research and Treatment, 2007, 104, 67-74.	2.5	15
381	Expanding the genetic basis of copy number variation in familial breast cancer. Hereditary Cancer in Clinical Practice, 2014, 12, 15.	1.5	15
382	Genetics of hand grip strength in mid to late life. Age, 2015, 37, 9745.	3.0	15
383	Alteration of miRNA-mRNA interactions in lymphocytes of individuals with schizophrenia. Journal of Psychiatric Research, 2019, 112, 89-98.	3.1	15
384	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
385	Brain transcriptome perturbations in the Hfeâˆ’/âˆ’ mouse model of genetic iron loading. Brain Research, 2012, 1448, 144-152.	2.2	14
386	Cytokine gene polymorphism among Indigenous Australians. Innate Immunity, 2014, 20, 431-439.	2.4	14
387	Biobank Classification in an Australian Setting. Biopreservation and Biobanking, 2015, 13, 212-218.	1.0	14
388	Letter to the editor: blood processing and sample storage have negligible effects on methylation. Clinical Epigenetics, 2018, 10, 22.	4.1	14
389	Genetic association and causal inference converge on hyperglycaemia as a modifiable factor to improve lung function. ELife, 2021, 10, .	6.0	14
390	Genetic testing for homologous recombination repair (HRR) in metastatic castration-resistant prostate cancer (mCRPC): challenges and solutions. Oncotarget, 2021, 12, 1600-1614.	1.8	14
391	Low prevalence of CDKN2A/ARF mutations among early-onset cancers of breast, pancreas and malignant melanoma in Poland. European Journal of Cancer Prevention, 2008, 17, 389-391.	1.3	13
392	Genetic contribution to all cancers: the first demonstration using the model of breast cancers from Poland stratified by age at diagnosis and tumour pathology. Breast Cancer Research and Treatment, 2009, 114, 121-126.	2.5	13
393	Comparison of cytokine gene polymorphisms among Greek patients with invasive meningococcal disease or viral meningitis. Journal of Medical Microbiology, 2013, 62, 694-700.	1.8	13
394	Low prevalence of germline PALB2 mutations in Australian tripleâ€negative breast cancer. International Journal of Cancer, 2014, 134, 301-305.	5.1	13
395	Concordance between Direct and Imputed APOE Genotypes using 1000 Genomes Data. Journal of Alzheimer's Disease, 2014, 42, 391-393.	2.6	13
396	Rare germline copy number deletions of likely functional importance are implicated in endometrial cancer predisposition. Human Genetics, 2015, 134, 269-278.	3.8	13

#	Article	IF	Citations
397	The effect of a muscarinic receptor 1 gene variant on grey matter volume in schizophrenia. Psychiatry Research - Neuroimaging, 2015, 234, 182-187.	1.8	13
398	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	5.1	13
399	Lung Cancer Occurrenceâ€"Correlation with Serum Chromium Levels and Genotypes. Biological Trace Element Research, 2021, 199, 1228-1236.	3.5	13
400	Survival of Laryngeal Cancer Patients Depending on Zinc Serum Level and Oxidative Stress Genotypes. Biomolecules, 2021, 11, 865.	4.0	13
401	BRCA1 and BRCA2 mutation analysis in 86 early onset breast/ovarian cancer patients.. Journal of Medical Genetics, 1997, 34, 990-995.	3.2	12
402	Frequency of the Common MYH Mutations (G382D and Y165C) in MMR Mutation Positive and Negative HNPCC Patients. Hereditary Cancer in Clinical Practice, 2005, 3, 65.	1.5	12
403	Brain transcriptome perturbations in the transferrin receptor 2 mutant mouse support the case for brain changes in iron loading disorders, including effects relating to long-term depression and long-term potentiation. Neuroscience, 2013, 235, 119-128.	2.3	12
404	Evaluation of Different Normalization and Analysis Procedures for Illumina Gene Expression Microarray Data Involving Small Changes. Microarrays (Basel, Switzerland), 2013, 2, 131-152.	1.4	12
405	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
406	Effects of gender, cytokine gene polymorphisms and environmental factors on inflammatory responses. Innate Immunity, 2015, 21, 523-530.	2.4	12
407	Erythrocyte microRNA sequencing reveals differential expression in relapsing-remitting multiple sclerosis. BMC Medical Genomics, 2018, 11, 48.	1.5	12
408	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	2.5	12
409	Investigation of monogenic causes of familial breast cancer: data from the BEACCON case-control study. Npj Breast Cancer, 2021, 7, 76.	5.2	12
410	Contribution of BRCA2 germline mutations to hereditary breast/ovarian cancer in Germany. Journal of Medical Genetics, 2002, 39, 12e-12.	3.2	11
411	Integrin Â3 Leu33Pro polymorphism increases BRCA1-associated ovarian cancer risk. Journal of Medical Genetics, 2007, 44, 408-411.	3.2	11
412	Changes in Brain Transcripts Related to Alzheimer's Disease in a Model of HFE Hemochromatosis are not Consistent with Increased Alzheimer's Disease Risk. Journal of Alzheimer's Disease, 2012, 30, 791-803.	2.6	11
413	Management of ovarian and endometrial cancers in women belonging to HNPCC carrier families: review of the literature and results of cancer risk assessment in Polish HNPCC families. Hereditary Cancer in Clinical Practice, 2015, 13, 3.	1.5	11
414	Associations Between Methylenetetrahydrofolate Reductase Polymorphisms, Serum Homocysteine Levels, and Incident Cortical Cataract. JAMA Ophthalmology, 2016, 134, 522.	2.5	11

#	Article	IF	Citations
415	Predicting type 2 diabetes using genetic and environmental risk factors in a multi-ethnic Malaysian cohort. Public Health, 2017, 149, 31-38.	2.9	11
416	Characterization of the early molecular changes in the glomeruli of Cd151 â^'/â^' mice highlights induction of mindin and MMP-10. Scientific Reports, 2017, 7, 15987.	3.3	11
417	Low-level parental mosaicism in an apparent de novo case of Peutzâ€"Jeghers syndrome. Familial Cancer, 2019, 18, 109-112.	1.9	11
418	Multi-tissue transcriptome-wide association study identifies eight candidate genes and tissue-specific gene expression underlying endometrial cancer susceptibility. Communications Biology, 2021, 4, 1211.	4.4	11
419	Genetic variation and its role in malignancy. International Journal of Biomedical Science, 2011, 7, 158-71.	0.1	11
420	Virtual Ontogeny of Cortical Growth Preceding Mental Illness. Biological Psychiatry, 2022, 92, 299-313.	1.3	11
421	Familial and genetic aspects of colorectal carcinogenesis. European Journal of Cancer, 1993, 29, 2163-2167.	2.8	10
422	The Association of the COMT V158M Polymorphism with Endometrial/Ovarian Cancer in HNPCC Families Adhering to the Amsterdam Criteria. Hereditary Cancer in Clinical Practice, 2006, 4, 94.	1.5	10
423	Association between early-onset breast and laryngeal cancers. Breast Cancer Research and Treatment, 2006, 97, 215-219.	2.5	10
424	Germline epimutations of APC are not associated with inherited colorectal polyposis. Gut, 2006, 55, 586-587.	12.1	10
425	The influence of the Cyclin D1 870 G>A polymorphism as an endometrial cancer risk factor. BMC Cancer, 2008, 8, 272.	2.6	10
426	The â^'149C>T SNP within the Î"DNMT3B gene, is not associated with early disease onset in hereditary non-polyposis colorectal cancer. Cancer Letters, 2008, 265, 39-44.	7.2	10
427	Evidence-Based Medicine in the Era of Biomarkers: Teaching a New Dog Old Tricks?. Clinical Pharmacology and Therapeutics, 2010, 88, 740-742.	4.7	10
428	Can a familial gastrointestinal tumour syndrome be allelic with Waardenburg syndrome?. Clinical Genetics, 2011, 79, 554-560.	2.0	10
429	Cell cycleâ€"related genes as modifiers of age of onset of colorectal cancer in Lynch syndrome: a large-scale study in non-Hispanic white patients. Carcinogenesis, 2013, 34, 299-306.	2.8	10
430	The importance of a large sample cohort for studies on modifier genes influencing disease severity in FAP patients. Hereditary Cancer in Clinical Practice, 2013, 11, 20.	1.5	10
431	Altered expression of the plasminogen activation pathway in peripheral blood mononuclear cells in multiple sclerosis: possible pathomechanism of matrix metalloproteinase activation. Multiple Sclerosis Journal, 2013, 19, 1268-1274.	3.0	10
432	Erythrocytes in multiple sclerosis â€" forgotten contributors to the pathophysiology?. Multiple Sclerosis Journal - Experimental, Translational and Clinical, 2016, 2, 205521731664998.	1.0	10

#	Article	IF	Citations
433	Differing Contributions of Classical Risk Factors to Type 2 Diabetes in Multi-Ethnic Malaysian Populations. International Journal of Environmental Research and Public Health, 2018, 15, 2813.	2.6	10
434	Prevalence of germline TP53 variants among early-onset breast cancer patients from Polish population. Breast Cancer, 2021, 28, 226-235.	2.9	10
435	Germline Missense Changes in the APC Gene and Their Relationship to Disease. Hereditary Cancer in Clinical Practice, 2004, 2, 81.	1.5	9
436	Exposure to household painting and floor treatments, and parental occupational paint exposure and risk of childhood brain tumors: results from an Australian caseâ€“control study. Cancer Causes and Control, 2014, 25, 283-291.	1.8	9
437	Dupuytrenâ€™s disease and the risk of malignant neoplasms. Hereditary Cancer in Clinical Practice, 2014, 12, 6.	1.5	9
438	Narrowing the critical region for overgrowth within 13q14.2-q14.3 microdeletions. European Journal of Medical Genetics, 2015, 58, 629-633.	1.3	9
439	Comparison of Three Different Methods for Determining Cell Proliferation in Breast Cancer Cell Lines. Journal of Visualized Experiments, 2016, , .	0.3	9
440	Genome-wide miRNA, gene and methylation analysis of triple negative breast cancer to identify changes associated with lymph node metastases. Genomics Data, 2017, 14, 1-4.	1.3	9
441	Differential effect of disease-associated ST8SIA2 haplotype on cerebral white matter diffusion properties in schizophrenia and healthy controls. Translational Psychiatry, 2018, 8, 21.	4.8	9
442	Genomic integrity in the male germ line: evidence in support of the disposable soma hypothesis. Reproduction, 2018, 156, 269-282.	2.6	9
443	Exceptional Longevity and Polygenic Risk for Cardiovascular Health. Genes, 2019, 10, 227.	2.4	9
444	Wnt receptor gene FZD1 was associated with schizophrenia in genome-wide SNP analysis of the Australian Schizophrenia Research Bank cohort. Australian and New Zealand Journal of Psychiatry, 2020, 54, 902-908.	2.3	9
445	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
446	Epigenetic differences at the HTR2A locus in progressive multiple sclerosis patients. Scientific Reports, 2020, 10, 22217.	3.3	9
447	Appearance of the liver form of pyruvate kinase in differentiating cultured foetal hepatocytes. Differentiation, 1984, 25, 64-69.	1.9	8
448	A 1q44 deletion, paternal UPD of chromosome 2 and a deletion due to a complex translocation detected in children with abnormal phenotypes using new SNP array technology. Cytogenetic and Genome Research, 2009, 124, 94-101.	1.1	8
449	Combined iPLEX and TaqMan Assays to Screen for 45 Common Mutations in Lynch Syndrome and FAP Patients. Journal of Molecular Diagnostics, 2010, 12, 82-90.	2.8	8
450	Regulators of Global Genome Repair Do Not Respond to DNA Damaging Therapy but Correlate with Survival in Melanoma. PLoS ONE, 2013, 8, e70424.	2.5	8

#	Article	IF	Citations
451	Copy Number Variation in Hereditary Non-Polyposis Colorectal Cancer. Genes, 2013, 4, 536-555.	2.4	8
452	Childhood and parental diagnostic radiological procedures and risk of childhood brain tumors. Cancer Causes and Control, 2014, 25, 375-383.	1.8	8
453	Methylation of the Corticotropin Releasing Hormone Gene Promoter in BeWo Cells: Relationship to Gene Activity. International Journal of Endocrinology, 2015, 2015, 1-8.	1.5	8
454	Thyroid cancer in a patient with Lynch syndrome – case report and literature review. Therapeutics and Clinical Risk Management, 2017, Volume 13, 915-918.	2.0	8
455	Concentrations of plasma-borne extracellular particles differ between multiple sclerosis disease courses and compared to healthy controls. Multiple Sclerosis and Related Disorders, 2020, 45, 102446.	2.0	8
456	Founder Mutations for Early Onset Melanoma as Revealed by Whole Exome Sequencing Suggests That This is Not Associated with the Increasing Incidence of Melanoma in Poland. Cancer Research and Treatment, 2019, 51, 337-344.	3.0	8
457	Sertraline hydrochloride for reducing impulsive behaviour in male, repeat-violent offenders (ReINVEST): protocol for a phase IV, double-blind, placebo-controlled, randomised clinical trial. BMJ Open, 2021, 11, e044656.	1.9	8
458	Re: IGF-1 Gene Polymorphism and Risk for Hereditary Nonpolyposis Colorectal Cancer. Journal of the National Cancer Institute, 2006, 98, 1664-1665.	6.3	7
459	Sifting the wheat from the chaff: prioritizing GWAS results by identifying consistency across analytical methods. Genetic Epidemiology, 2011, 35, 745-754.	1.3	7
460	Bilateral dysgerminoma associated with gonadoblastoma and sex-cord stromal tumour with annular tubules in a 28-year-old fertile woman with normal karyotype. Pathology, 2012, 44, 257-260.	0.6	7
461	Nodular prurigo of the vulva. Pathology, 2012, 44, 565-567.	0.6	7
462	Development of an experimental model for assessing the effects of cigarette smoke and virus infections on inflammatory responses to bacterial antigens. Innate Immunity, 2014, 20, 647-658.	2.4	7
463	Characterizing the genetic risk for Type 2 diabetes in a Malaysian multiâ€ethnic cohort. Diabetic Medicine, 2015, 32, 1377-1384.	2.3	7
464	Vehicle refuelling, use of domestic wood heaters and the risk of childhood brain tumours: Results from an Australian caseâ€“control study. Pediatric Blood and Cancer, 2015, 62, 229-234.	1.5	7
465	Copy number variants associated with 18p11.32, DCC and the promoter 1B region of APC in colorectal polyposis patients. Meta Gene, 2016, 7, 95-104.	0.6	7
466	Detection of complex genomic signatures associated with risk in plasma cell disorders. Cancer Genetics, 2017, 218-219, 1-9.	0.4	7
467	Erythrocyte microRNAs show biomarker potential and implicate multiple sclerosis susceptibility genes. Clinical and Translational Medicine, 2020, 10, 74-90.	4.0	7
468	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. Npj Breast Cancer, 2021, 7, 52.	5.2	7

#	Article	IF	Citations
469	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. Breast Cancer Research, 2021, 23, 86.	5.0	7
470	Pyruvate kinase isoenzyme transitions in cultures of fetal rat hepatocytes. Cell Differentiation and Development, 1988, 25, 109-118.	0.4	6
471	BRCA1 mutations in a selected series of breast/ovarian cancer patients.. Journal of Medical Genetics, 1996, 33, 721-725.	3.2	6
472	Cell cycle dependent DNA break increase in ataxia telangiectasia lymphoblasts after radiation exposure. Journal of Clinical Pathology, 2001, 54, 347-350.	1.9	6
473	Profuse familial adenomatous polyposis with an adenomatous polyposis coli exon 3 mutation. Familial Cancer, 2001, 1, 3-7.	1.9	6
474	Epimutations, Inheritance and Causes of Aberrant DNA Methylation in Cancer. Hereditary Cancer in Clinical Practice, 2006, 4, 75.	1.5	6
475	Frequency and nature of hMSH6 germline mutations in Polish patients with colorectal, endometrial and ovarian cancers. Clinical Genetics, 2006, 70, 68-70.	2.0	6
476	DNA and RNA analyses in detection of genetic predisposition to cancer. Hereditary Cancer in Clinical Practice, 2012, 10, 17.	1.5	6
477	<scp>KRAS</scp> mutation testing of metastatic colorectal cancer in <scp>A</scp>ustralia: Where are we at?. Asia-Pacific Journal of Clinical Oncology, 2014, 10, 261-265.	1.1	6
478	When is a mutation not a mutation: the case of the c.594-2A>C splice variant in a woman harbouring another BRCA1 mutation in trans. Hereditary Cancer in Clinical Practice, 2016, 14, 6.	1.5	6
479	New <scp>EPCAM</scp> founder deletion in Polish population. Clinical Genetics, 2017, 92, 649-653.	2.0	6
480	Critical evaluation of linear regression models for cell-subtype specific methylation signal from mixed blood cell DNA. PLoS ONE, 2018, 13, e0208915.	2.5	6
481	BRCA1/2 mutations are not a common cause of malignant melanoma in the Polish population. PLoS ONE, 2018, 13, e0204768.	2.5	6
482	Evaluating the associations between obesity and age-related cataract: a Mendelian randomization study. American Journal of Clinical Nutrition, 2019, 110, 969-976.	4.7	6
483	Enrichment of atypical hyperdiploidy and IKZF1 deletions detected by SNP-microarray in high-risk Australian AIEOP-BFM B-cell acute lymphoblastic leukaemia cohort. Cancer Genetics, 2020, 242, 8-14.	0.4	6
484	A genetic variant in telomerase reverse transcriptase (TERT) modifies cancer risk in Lynch syndrome patients harbouring pathogenic MSH2 variants. Scientific Reports, 2021, 11, 11401.	3.3	6
485	Comparison of the QuantiGene 2.0 Assay and Real-Time RT-PCR in the Detection of p53 Isoform mRNA Expression in Formalin-Fixed Paraffin-Embedded Tissues- A Preliminary Study. PLoS ONE, 2016, 11, e0165930.	2.5	6
486	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6

#	Article	IF	Citations
487	Ethnic Diversity of DPD Activity and the DPYD Gene: Review of the Literature. Pharmacogenomics and Personalized Medicine, 2021, Volume 14, 1603-1617.	0.7	6
488	Gene Expression Profiling of Xeroderma Pigmentosum. Hereditary Cancer in Clinical Practice, 2006, 4, 103.	1.5	5
489	Modifier Genes and HNPCC: Variable phenotypic expression in HNPCC and the search for modifier genes. European Journal of Human Genetics, 2008, 16, 531-532.	2.8	5
490	Ovarian cancer risk in Polish BRCA1 mutation carriers is not associated with the prohibitin 3' untranslated region polymorphism. BMC Cancer, 2008, 8, 90.	2.6	5
491	Colorectal cancer: lessons for genetic counselling and care for families. Clinical Genetics, 1994, 46, 106-114.	2.0	5
492	8q23.3 and 11q23.1 as modifying loci influencing the risk for CRC in Lynch syndrome. European Journal of Human Genetics, 2012, 20, 487-488.	2.8	5
493	Lynch syndrome mutations shared by the Baltic States and Poland. Clinical Genetics, 2014, 86, 190-193.	2.0	5
494	Cumulative Small Effect Genetic Markers and the Risk of Colorectal Cancer in Poland, Estonia, Lithuania, and Latvia. Gastroenterology Research and Practice, 2015, 2015, 1-10.	1.5	5
495	Folate Pathway Gene Polymorphisms and Risk of Childhood Brain Tumors: Results from an Australian Caseâ€“Control Study. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 931-937.	2.5	5
496	Paternal Dietary Folate, B6 and B12 Intake, and the Risk of Childhood Brain Tumors. Nutrition and Cancer, 2015, 67, 224-230.	2.0	5
497	Cumulative effects of genetic markers and the detection of advanced colorectal neoplasias by population screening. Clinical Genetics, 2015, 88, 234-240.	2.0	5
498	Identification of endothelin-converting enzyme-2 as an autoantigen in autoimmune polyendocrine syndrome type 1. Autoimmunity, 2017, 50, 223-231.	2.6	5
499	The intron 3 16Âbp duplication polymorphism of p53 (rs17878362) is not associated with increased risk of developing triple-negative breast cancer. Breast Cancer Research and Treatment, 2019, 173, 727-733.	2.5	5
500	Reply to: New Meta- and Mega-analyses of Magnetic Resonance Imaging Findings in Schizophrenia: Do They Really Increase Our Knowledge About the Nature of the Disease Process?. Biological Psychiatry, 2019, 85, e35-e39.	1.3	5
501	Promoter Methylation Pattern Controls Corticotropin Releasing Hormone Gene Activity in Human Trophoblasts. PLoS ONE, 2017, 12, e0170671.	2.5	5
502	Familial Breast and Bowel Cancer: Does It Exist?. Hereditary Cancer in Clinical Practice, 2004, 2, 25.	1.5	4
503	Missense Mutations in Cancer Predisposing Genes: Can We Make Sense of Them?. Hereditary Cancer in Clinical Practice, 2005, 3, 123-7.	1.5	4
504	Have the roles of two functional polymorphisms in breast cancer, R72P in P53 and MDM2-309 in MDM2, become clearer?. Breast Cancer Research, 2010, 12, 102.	5.0	4

#	Article	IF	Citations
505	Review Selenium as aÂmarker of cancer risk and of selection for control examinations in surveillance. Wspolczesna Onkologia, 2015, 1A, 60-61.	1.4	4
506	Early changes of endometrial neoplasia revealed by loss of mismatch repair gene protein expression in a patient diagnosed with Lynch syndrome. Pathology, 2016, 48, 78-80.	0.6	4
507	Genetic and Environmental Modifiers of Cancer Risk in Lynch Syndrome. , 2018, , 67-89.		4
508	Mind Over Matter: Confronting Challenges in Post-Mortem Brain Biobanking for Glioblastoma Multiforme. Biomarker Insights, 2021, 16, 117727192110133.	2.5	4
509	A requirement for DNA synthesis in foetal hepatocyte differentiation. Differentiation, 1984, 28, 49-52.	1.9	3
510	BRCA1 mutations found in archived early onset breast tumours. European Journal of Cancer, 1997, 33, 683-686.	2.8	3
511	Case Report: Familial Gastric Cancer and Chordoma in the Same Family. Hereditary Cancer in Clinical Practice, 2005, 3, 81-4.	1.5	3
512	Common genetic variants in the plasminogen activation pathway are not associated with multiple sclerosis. Multiple Sclerosis Journal, 2014, 20, 489-491.	3.0	3
513	Intermediate lobe immunoreactivity in a patient with suspected lymphocytic hypophysitis. Pituitary, 2014, 17, 22-29.	2.9	3
514	Identification of Genome-Wide SNPâ€“SNP and SNPâ€“Clinical Boolean Interactions in Age-Related Macular Degeneration. Methods in Molecular Biology, 2015, 1253, 217-255.	0.9	3
515	Somaticâ€gonadal mosaicism causing Sotos syndrome. American Journal of Medical Genetics, Part A, 2016, 170, 3360-3362.	1.2	3
516	The prevalence of unique <scp>SNP</scp>s in the reninâ€angiotensin system highlights the need for pharmacogenetics in Indigenous Australians. Clinical and Experimental Pharmacology and Physiology, 2016, 43, 157-160.	1.9	3
517	Gene expression profiles in whole blood and associations with metabolic dysregulation in obesity. Obesity Research and Clinical Practice, 2018, 12, 204-213.	1.8	3
518	CD36 â€“ a plausible modifier of disease phenotype in familial adenomatous polyposis. Hereditary Cancer in Clinical Practice, 2018, 16, 14.	1.5	3
519	Constitutional variants in POT1, TERF2IP, and ACD genes in patients with melanoma in the Polish population. European Journal of Cancer Prevention, 2020, 29, 511-519.	1.3	3
520	CD36 polymorphisms and the age of disease onset in patients with pathogenic variants within the mutation cluster region of APC. Hereditary Cancer in Clinical Practice, 2021, 19, 25.	1.5	3
521	Genetic Epidemiology Studies in Hereditary Non-Polyposis Colorectal Cancer. Methods in Molecular Biology, 2009, 472, 89-102.	0.9	3
522	Prognostic Implications of Cancer Susceptibility Genes: Any News?. Recent Results in Cancer Research, 1999, 151, 71-84.	1.8	3

#	Article	IF	Citations
523	Electro-Oculographic and Electroretinographic Studies in HNPCC Gene Mutation Carriers. Ophthalmic Research, 2003, 35, 281-294.	1.9	2
524	Intronic TP53 Germline Sequence Variants Modify the Risk in German Breast/Ovarian Cancer Families. Hereditary Cancer in Clinical Practice, 2004, 2, 139.	1.5	2
525	Deletion Mutations in an Australian Series of HNPCC Patients. Hereditary Cancer in Clinical Practice, 2005, 3, 43.	1.5	2
526	Clinical and epidemiological features of familial laryngeal cancer in Poland. Cancer Detection and Prevention, 2007, 31, 270-275.	2.1	2
527	Clinical characteristics of tumors derived from colorectal cancer patients who harbor the Tumor Necrosis Factor Î±-1031T/T and NOD2 3020insC polymorphism. Cancer Epidemiology, 2009, 33, 161-163.	1.9	2
528	Epithelioid trophoblastic tumour simulating a high grade carcinoma. Pathology, 2014, 46, 248-250.	0.6	2
529	Genetics, Mucosal Inflammation and the Environment in Post-Infectious Chronic Gut Syndromes. American Journal of Gastroenterology Supplements (Print), 2016, 3, 46-51.	0.7	2
530	Prevalence of clinically actionable genotypes and medication exposure of older adults in the community. Pharmacogenomics and Personalized Medicine, 2017, Volume10, 17-27.	0.7	2
531	Exome sequencing of familial adenomatous polyposisâ€like individuals identifies both known and novel causative genes. Clinical Genetics, 2021, 100, 478-483.	2.0	2
532	Changes in the expression of class I major histocompatibility complex antigen RNA induced by interferon in rat hepatoma cells. Cancer Letters, 1990, 50, 209-213.	7.2	1
533	Informed consent and BRCA1 mutation detection in archived breast tumour specimens. Lancet, The, 1996, 347, 1189.	13.7	1
534	DNA Mismatch Repair and Hereditary Nonpolyposis Colorectal Cancer. Oncology Research and Treatment, 1997, 20, 42-47.	1.2	1
535	Tumour site, sex, and survival in colorectal cancer. Lancet, The, 2000, 356, 857.	13.7	1
536	Reply to Vasen et al.. American Journal of Human Genetics, 2001, 68, 1534-1535.	6.2	1
537	A Comparison Between Denaturing Gradient Gel Electrophoresis and Denaturing High Performance Liquid Chromatography in Detecting Mutations in Genes Associated with Hereditary Non-Polyposis Colorectal Cancer (HNPCC) and the Identification of 9 New Mutations Previously Unidentified by DGGE. Hereditary Cancer in Clinical Practice, 2003, 1, 39.	1.5	1
538	Low-risk Genes and Multi-organ Cancer Risk in the Polish Population. Hereditary Cancer in Clinical Practice, 2006, 4, 52.	1.5	1
539	Hereditary Cancer in Clinical Practice transfers to BioMed Central. Hereditary Cancer in Clinical Practice, 2009, 7, .	1.5	1
540	<scp>cDNA</scp> analysis of the <scp>BRCA1</scp> unclassified variant c.5194â€<scp>12G</scp>><scp>A</scp>. Clinical Genetics, 2013, 84, 505-506.	2.0	1

#	Article	IF	Citations
541	First recurrent large genomic rearrangement in the BRCA1 gene found in Poland. Cancer Epidemiology, 2014, 38, 382-385.	1.9	1
542	A novel polymorphic repeat in the upstream regulatory region of the estrogen-induced gene EIG121 is not associated with the risk of developing breast or endometrial cancer. BMC Research Notes, 2016, 9, 287.	1.4	1
543	A polymorphic repeat in the IGF1 promoter influences the risk of endometrial cancer. Endocrine Connections, 2016, 5, 115-122.	1.9	1
544	A Simple Migration/Invasion Workflow Using an Automated Live-cell Imager. Journal of Visualized Experiments, 2019, , .	0.3	1
545	Finding Needles in Haystacks: The Use of Quantitative Proteomics for the Early Detection of Colorectal Cancer. , 0, , .		1
546	The MinION as a cost-effective technology for diagnostic screening of the SCN1A gene in epilepsy patients. Epilepsy Research, 2021, 172, 106593.	1.6	1
547	Survival of bladder or renal cancer in patients with CHEK2 mutations. PLoS ONE, 2021, 16, e0257132.	2.5	1
548	Genetic feedback to reduce alcohol consumption in hospital outpatients with risky drinking: feasibility and acceptability. Public Health Research and Practice, 2016, 26, .	1.5	1
549	CHAPTER 22. Selenium and Cancer. Food and Nutritional Components in Focus, 2015, , 377-390.	0.1	1
550	Gene symbol: STK11. Disease: Peutz-Jeghers Syndrome. Human Genetics, 2008, 124, 300.	3.8	1
551	Verification and Validation of a Four-Gene Panel as a Prognostic Indicator in Triple Negative Breast Cancer. Frontiers in Oncology, 2022, 12, 821334.	2.8	1
552	Contribution of large genomic rearrangements inPALB2to familial breast cancer: implications for genetic testing. Journal of Medical Genetics, 2023, 60, 112-118.	3.2	1
553	Capturing SNP Association across the NK Receptor and HLA Gene Regions in Multiple Sclerosis by Targeted Penalised Regression Models. Genes, 2022, 13, 87.	2.4	1
554	How Common is Hereditary Cancer?. Annals of Medicine, 1994, 26, 173-175.	3.8	0
555	Epidemiology of Colorectal Cancer: Questions Answered and Questions Remaining. , 1996, , 84-92.		0
556	Genetic Testing Redefines Hereditary Nonpolyposis Colon Cancer. , 1996, , 74-83.		0
557	Mutations in the APC Gene and the Related Phenotypes of Swiss Patients with Familial Adenomatous Polyposis. , 1996, , 52-58.		0
558	Response to De Vos et al.. Clinical Genetics, 2004, 66, 568-568.	2.0	0

#	Article	IF	Citations
559	Genetic testing: a round table conversation. Internal Medicine Journal, 2004, 34, 587-588.	0.8	0
560	DNA mismatch repair genes and hereditary non-polyposis colorectal cancer. Journal of Gastroenterology and Hepatology (Australia), 2004, 19, 465-466.	2.8	0
561	Response to â€œVariability in the clinical phenotype among families with HNPCCâ€• The potential importance of the location of the mutation in the gene by Dr. Prathap Bandipalliam. International Journal of Cancer, 2007, 120, 2278-2278.	5.1	0
562	Familial association of laryngeal, lung, stomach and early-onset breast cancer. Breast Cancer Research and Treatment, 2008, 112, 359-361.	2.5	0
563	BRAF and NRAS mutational status are prognostically important in thick and locally advanced cutaneous melanoma. Pathology, 2012, 44, S99.	0.6	0
564	Poster #114 GENOME-WIDE SUPPORTED VARIANTS (MIR137) PREDICTS MEMBERSHIP OF A COGNITIVE SUBTYPE OF SCHIZOPHRENIA. Schizophrenia Research, 2012, 136, S226.	2.0	0
565	Reply to Win and Jenkins. International Journal of Cancer, 2013, 133, 1764-1764.	5.1	0
566	KRAS mutation testing in colorectal cancer: the model for molecular pathology testing in the future. Colorectal Cancer, 2016, 5, 73-80.	0.8	0
567	Genetic Contributors to Hereditary Cancer Predispositions: Do We Have Enough Information?. , 0, , .		0
568	Low Blood-As Levels and Selected Genotypes Appears to Be Promising Biomarkers for Occurrence of Colorectal Cancer in Women. Biomedicines, 2021, 9, 1105.	3.2	0
569	Sertraline hydrochloride for reducing impulsive behaviour in male, repeat-violent offenders (ReINVEST): protocol for a phase IV, double-blind, placebo-controlled, randomised clinical trial. BMJ Open, 2021, 11, e044656.	1.9	0
570	Integration of tumour sequencing and caseâ€“control data to assess pathogenicity of RAD51C missense variants in familial breast cancer. Npj Breast Cancer, 2022, 8, 10.	5.2	0
571	Optical genome mapping using Bionano: A comparative study of genomic changes in haematological malignancies performed at the John Hunter hospital. Pathology, 2022, 54, S16-S17.	0.6	0
572	A Protein Truncation Test for BRCA1. , 0, , 6-10.		0
573	TAPES: A tool for assessment and prioritisation in exome studies. , 2019, 15, e1007453.		0
574	TAPES: A tool for assessment and prioritisation in exome studies. , 2019, 15, e1007453.		0
575	TAPES: A tool for assessment and prioritisation in exome studies. , 2019, 15, e1007453.		0
576	TAPES: A tool for assessment and prioritisation in exome studies. , 2019, 15, e1007453.		0

#	Article	IF	Citations
577	TAPES: A tool for assessment and prioritisation in exome studies. , 2019, 15, e1007453.		0
578	TAPES: A tool for assessment and prioritisation in exome studies. , 2019, 15, e1007453.		0
579	Bladder cancer survival in patients with NOD2 or CDKN2A variants. Oncotarget, 2022, 13, 628-640.	1.8	0