

Vijai Joseph

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6191803/publications.pdf>

Version: 2024-02-01

148
papers

12,739
citations

34016

52
h-index

28224

105
g-index

155
all docs

155
docs citations

155
times ranked

19933
citing authors

#	ARTICLE	IF	CITATIONS
1	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	3.0	19
2	Multiple Primary Cancers in Patients Undergoing Tumor-Normal Sequencing Define Novel Associations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 362-371.	1.1	7
3	Inherited TP53 Variants and Risk of Prostate Cancer. <i>European Urology</i> , 2022, 81, 243-250.	0.9	40
4	SNPs at SMG7 associated with time from biochemical recurrence to prostate cancer death. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, , .	1.1	1
5	A breast cancer (BC) risk model incorporating Tyrer-Cuzick version 8 (TCv8) and a polygenic risk score (PRS) for diverse ancestries.. <i>Journal of Clinical Oncology</i> , 2022, 40, 557-557.	0.8	1
6	Inherited Germline Cancer Susceptibility Gene Variants in Individuals with Non-Muscle-Invasive Bladder Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 4267-4277.	3.2	4
7	Targeting Germline- and Tumor-Associated Nucleotide Excision Repair Defects in Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 1997-2010.	3.2	15
8	Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217.		0
9	A case-only study to identify genetic modifiers of breast cancer risk for <i>BRCA1/BRCA2</i> mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	5.8	19
10	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. <i>Nature Cancer</i> , 2021, 2, 357-365.	5.7	74
11	Sequencing at lymphoid neoplasm susceptibility loci maps six myeloma risk genes. <i>Human Molecular Genetics</i> , 2021, 30, 1142-1153.	1.4	2
12	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. <i>Neuron</i> , 2021, 109, 1465-1478.e4.	3.8	21
13	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous <i>BRCA1</i> or <i>BRCA2</i> pathogenic variant. <i>Genetics in Medicine</i> , 2021, 23, 1726-1737.	1.1	16
14	Prevalence of Germline Alterations on Targeted Tumor-Normal Sequencing of Esophagogastric Cancer. <i>JAMA Network Open</i> , 2021, 4, e2114753.	2.8	15
15	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	2.6	6
16	A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1683-1692.	3.0	66
17	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	2.9	9
18	Germline Variants Identified in Patients with Early-onset Renal Cell Carcinoma Referred for Germline Genetic Testing. <i>European Urology Oncology</i> , 2021, 4, 993-1000.	2.6	16

#	ARTICLE	IF	CITATIONS
19	Clonal hematopoiesis is associated with risk of severe Covid-19. <i>Nature Communications</i> , 2021, 12, 5975.	5.8	81
20	The context-specific role of germline pathogenicity in tumorigenesis. <i>Nature Genetics</i> , 2021, 53, 1577-1585.	9.4	44
21	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.4	39
22	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. <i>Human Molecular Genetics</i> , 2020, 29, 70-79.	1.4	17
23	Fumarate hydratase <i>FH</i> c.1431_1433dupAAA (p.Lys477dup) variant is not associated with cancer including renal cell carcinoma. <i>Human Mutation</i> , 2020, 41, 103-109.	1.1	25
24	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
25	Cancer Susceptibility Mutations in Patients With Urothelial Malignancies. <i>Journal of Clinical Oncology</i> , 2020, 38, 406-414.	0.8	60
26	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of <i>BRCA1</i> and <i>BRCA2</i> pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	1.1	82
27	A Rare <i>TP53</i> Mutation Predominant in Ashkenazi Jews Confers Risk of Multiple Cancers. <i>Cancer Research</i> , 2020, 80, 3732-3744.	0.4	32
28	Mutation Rates in Cancer Susceptibility Genes in Patients With Breast Cancer With Multiple Primary Cancers. <i>JCO Precision Oncology</i> , 2020, 4, 916-925.	1.5	9
29	Characterization of the Cancer Spectrum in Men With Germline <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2020, 6, 1218.	3.4	48
30	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
31	Cascading After Peridiagnostic Cancer Genetic Testing: An Alternative to Population-Based Screening. <i>Journal of Clinical Oncology</i> , 2020, 38, 1398-1408.	0.8	60
32	11p15.5 epimutations in children with Wilms tumor and hepatoblastoma detected in peripheral blood. <i>Cancer</i> , 2020, 126, 3114-3121.	2.0	23
33	Lipid Trait Variants and the Risk of Non-Hodgkin Lymphoma Subtypes: A Mendelian Randomization Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1074-1078.	1.1	13
34	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 146-157.	3.0	129
35	Genetic overlap between autoimmune diseases and non-Hodgkin lymphoma subtypes. <i>Genetic Epidemiology</i> , 2019, 43, 844-863.	0.6	28
36	Two truncating variants in <i>FANCC</i> and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	1.6	5

#	ARTICLE	IF	CITATIONS
37	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90
38	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. <i>Journal of Clinical Oncology</i> , 2019, 37, 286-295.	0.8	397
39	Case-control analysis identifies shared properties of rare germline variation in cancer predisposing genes. <i>European Journal of Human Genetics</i> , 2019, 27, 824-828.	1.4	4
40	Toward automation of germline variant curation in clinical cancer genetics. <i>Genetics in Medicine</i> , 2019, 21, 2116-2125.	1.1	27
41	Understanding Inherited Risk in Unselected Newly Diagnosed Patients With Endometrial Cancer. <i>JCO Precision Oncology</i> , 2019, 3, 1-15.	1.5	7
42	Germline deletion of ETV6 in familial acute lymphoblastic leukemia. <i>Blood Advances</i> , 2019, 3, 1039-1046.	2.5	21
43	Understanding Inherited Risk in Unselected Newly Diagnosed Patients With Endometrial Cancer. <i>Obstetrical and Gynecological Survey</i> , 2019, 74, 473-474.	0.2	0
44	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
45	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019, 51, 76-87.	9.4	377
46	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. <i>Frontiers in Oncology</i> , 2019, 9, 1539.	1.3	6
47	Prospective Evaluation of Germline Alterations in Patients With Exocrine Pancreatic Neoplasms. <i>Journal of the National Cancer Institute</i> , 2018, 110, 1067-1074.	3.0	170
48	Mutational spectrum in a worldwide study of 29,700 families with <i>BRCA1</i> or <i>BRCA2</i> mutations. <i>Human Mutation</i> , 2018, 39, 593-620.	1.1	224
49	High-depth whole genome sequencing of an Ashkenazi Jewish reference panel: enhancing sensitivity, accuracy, and imputation. <i>Human Genetics</i> , 2018, 137, 343-355.	1.8	24
50	Germline Lysine-Specific Demethylase 1 (<i>LSD1/KDM1A</i>) Mutations Confer Susceptibility to Multiple Myeloma. <i>Cancer Research</i> , 2018, 78, 2747-2759.	0.4	56
51	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. <i>Nature Communications</i> , 2018, 9, 4182.	5.8	15
52	Prevalence of Germline Mutations in Cancer Susceptibility Genes in Patients With Advanced Renal Cell Carcinoma. <i>JAMA Oncology</i> , 2018, 4, 1228.	3.4	132
53	HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. <i>Cancer Research</i> , 2018, 78, 4086-4096.	0.4	34
54	Germline <i>SDHA</i> mutations in children and adults with cancer. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002584.	0.5	33

#	ARTICLE	IF	CITATIONS
55	Frequency of actionable cancer predisposing germline mutations in patients with lung cancers.. Journal of Clinical Oncology, 2018, 36, 1504-1504.	0.8	2
56	DNA damage repair (DDR) germline mutations in patients (Pts) with urothelial carcinoma (UC).. Journal of Clinical Oncology, 2018, 36, 1516-1516.	0.8	2
57	Novel pedigree analysis implicates DNA repair and chromatin remodeling in multiple myeloma risk. PLoS Genetics, 2018, 14, e1007111.	1.5	30
58	Inherited mutations in breast cancer patients with and without multiple primary cancers.. Journal of Clinical Oncology, 2018, 36, 1503-1503.	0.8	0
59	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
60	The contribution of pathogenic variants in breast cancer susceptibility genes to familial breast cancer risk. Npj Breast Cancer, 2017, 3, 22.	2.3	108
61	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
62	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
63	Mutation Detection in Patients With Advanced Cancer by Universal Sequencing of Cancer-Related Genes in Tumor and Normal DNA vs Guideline-Based Germline Testing. JAMA - Journal of the American Medical Association, 2017, 318, 825.	3.8	366
64	Integrative clinical genomics of metastatic cancer. Nature, 2017, 548, 297-303.	13.7	685
65	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	1.1	15
66	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	1.1	18
67	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. JCO Precision Oncology, 2017, 2017, 1-16.	1.5	286
68	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
69	Prospective assessment for pathogenic germline alterations (PGA) in pancreas cancer (PAC).. Journal of Clinical Oncology, 2017, 35, 4102-4102.	0.8	4
70	Evaluating the association of multiple single nucleotide polymorphisms with response to gemcitabine and platinum combination chemotherapy in urothelial carcinoma of the bladder. International Journal of Clinical Pharmacology and Therapeutics, 2017, 55, 203-209.	0.3	2
71	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	1.1	10
72	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.	13.9	1,205

#	ARTICLE	IF	CITATIONS
73	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	2.2	31
74	Evaluation of ACMG-Guideline-Based Variant Classification of Cancer Susceptibility and Non-Cancer-Associated Genes in Families Affected by Breast Cancer. <i>American Journal of Human Genetics</i> , 2016, 98, 801-817.	2.6	113
75	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. <i>Breast Cancer Research</i> , 2016, 18, 15.	2.2	88
76	Conflicting Interpretation of Genetic Variants and Cancer Risk by Commercial Laboratories as Assessed by the Prospective Registry of Multiplex Testing. <i>Journal of Clinical Oncology</i> , 2016, 34, 4071-4078.	0.8	147
77	A Recurrent ERCC3 Truncating Mutation Confers Moderate Risk for Breast Cancer. <i>Cancer Discovery</i> , 2016, 6, 1267-1275.	7.7	41
78	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
79	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , 2016, 7, 10933.	5.8	94
80	Clinical Evaluation of Cisplatin Sensitivity of Germline Polymorphisms in Neoadjuvant Chemotherapy for Urothelial Cancer. <i>Clinical Genitourinary Cancer</i> , 2016, 14, 511-517.	0.9	5
81	Germline Variants in Targeted Tumor Sequencing Using Matched Normal DNA. <i>JAMA Oncology</i> , 2016, 2, 104.	3.4	270
82	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. <i>Human Molecular Genetics</i> , 2016, 25, 1663-1676.	1.4	52
83	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. <i>Human Molecular Genetics</i> , 2016, 25, 1203-1214.	1.4	38
84	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	9.4	125
85	Collaborative science in the next-generation sequencing era: a viewpoint on how to combine exome sequencing data across sites to identify novel disease susceptibility genes. <i>Briefings in Bioinformatics</i> , 2016, 17, 672-677.	3.2	6
86	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	0.6	18
87	Genome Sequencing of Multiple Primary Tumors Reveals a Novel PALB2 Variant. <i>Journal of Clinical Oncology</i> , 2016, 34, e61-e67.	0.8	6
88	A Germline Variant on Chromosome 4q31.1 Associates with Susceptibility to Developing Colon Cancer Metastasis. <i>PLoS ONE</i> , 2016, 11, e0146435.	1.1	2
89	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2015, 17, 61.	2.2	26
90	Genetic susceptibility to diffuse large B-cell lymphoma in a pooled study of three Eastern Asian populations. <i>European Journal of Haematology</i> , 2015, 95, 442-448.	1.1	30

#	ARTICLE	IF	CITATIONS
91	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
92	Germline ETV6 Mutations Confer Susceptibility to Acute Lymphoblastic Leukemia and Thrombocytopenia. PLoS Genetics, 2015, 11, e1005262.	1.5	128
93	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	5.8	58
94	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
95	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
96	<i>FANCM</i>c.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. Human Molecular Genetics, 2015, 24, 5345-5355.	1.4	91
97	An analysis of the association between prostate cancer risk loci, PSA levels, disease aggressiveness and disease-specific mortality. British Journal of Cancer, 2015, 113, 166-172.	2.9	16
98	Association of Type and Location of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
99	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	1.1	22
100	Tissue-Specific Enrichment of Lymphoma Risk Loci in Regulatory Elements. PLoS ONE, 2015, 10, e0139360.	1.1	5
101	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	1.5	47
102	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	2.2	97
103	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	2.2	57
104	Variants at IRX4 as prostate cancer expression quantitative trait loci. European Journal of Human Genetics, 2014, 22, 558-563.	1.4	36
105	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
106	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	2.6	96
107	Cancer Genomics and Inherited Risk. Journal of Clinical Oncology, 2014, 32, 687-698.	0.8	121
108	Sequencing an Ashkenazi reference panel supports population-targeted personal genomics and illuminates Jewish and European origins. Nature Communications, 2014, 5, 4835.	5.8	156

#	ARTICLE	IF	CITATIONS
109	Genetic Association Analysis of ATP Binding Cassette Protein Family Reveals a Novel Association of ABCB1 Genetic Variants with Epilepsy Risk, but Not with Drug-Resistance. PLoS ONE, 2014, 9, e89253.	1.1	26
110	Genetic Variation in DNA Repair Pathways and Risk of Non-Hodgkin's Lymphoma. PLoS ONE, 2014, 9, e101685.	1.1	19
111	COMPLEXO: identifying the missing heritability of breast cancer via next generation collaboration. Breast Cancer Research, 2013, 15, 402.	2.2	36
112	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1226-1231.	9.4	270
113	Major vault protein (MVP) gene polymorphisms and drug resistance in mesial temporal lobe epilepsy with hippocampal sclerosis. Gene, 2013, 526, 449-453.	1.0	15
114	Prevalence of HOXB13 mutation in a population of Ashkenazi Jewish men treated for prostate cancer. Familial Cancer, 2013, 12, 597-600.	0.9	10
115	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	9.4	179
116	Germline single nucleotide polymorphisms associated with response of urothelial carcinoma to platinum-based therapy: the role of the host. Annals of Oncology, 2013, 24, 2414-2421.	0.6	10
117	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
118	A Recessive Founder Mutation in Regulator of Telomere Elongation Helicase 1, RTEL1, Underlies Severe Immunodeficiency and Features of Hoyeraal Hreidarsson Syndrome. PLoS Genetics, 2013, 9, e1003695.	1.5	106
119	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244
120	Susceptibility Loci Associated with Specific and Shared Subtypes of Lymphoid Malignancies. PLoS Genetics, 2013, 9, e1003220.	1.5	44
121	GABRG2, rs211037 is associated with epilepsy susceptibility, but not with antiepileptic drug resistance and febrile seizures. Pharmacogenetics and Genomics, 2013, 23, 605-610.	0.7	40
122	Assessment of SLX4 Mutations in Hereditary Breast Cancers. PLoS ONE, 2013, 8, e66961.	1.1	37
123	Saliva samples for genomic testing for preventive oncology: Improving the yield.. Journal of Clinical Oncology, 2013, 31, e12555-e12555.	0.8	0
124	Transcriptional regulation and prostate cancer risk loci.. Journal of Clinical Oncology, 2013, 31, 1554-1554.	0.8	6
125	A Nonsynonymous Polymorphism in <i>IRS1</i> Modifies Risk of Developing Breast and Ovarian Cancers in <i>BRCA1</i> and Ovarian Cancer in <i>BRCA2</i> Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1362-1370.	1.1	23
126	Common Variants at the 19p13.1 and <i>ZNF365</i> Loci Are Associated with ER Subtypes of Breast Cancer and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 645-657.	1.1	47

#	ARTICLE	IF	CITATIONS
127	566 IDENTIFICATION OF GENETIC MARKERS ASSOCIATED WITH RESPONSE TO BACILLUS CALMETTE-GUÉRIN INTRAVESICAL THERAPY IN NON-MUSCLE-INVASIVE BLADDER CANCER. <i>Journal of Urology</i> , 2012, 187, .	0.2	0
128	Rare De Novo Germline Copy-Number Variation in Testicular Cancer. <i>American Journal of Human Genetics</i> , 2012, 91, 379-383.	2.6	21
129	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2012, 14, R33.	2.2	78
130	Prevalence of BRCA1 and BRCA2 mutations in Ashkenazi Jewish families with breast and pancreatic cancer. <i>Cancer</i> , 2012, 118, 493-499.	2.0	83
131	Ovarian cancer susceptibility alleles and risk of ovarian cancer in BRCA1 and BRCA2 mutation carriers. <i>Human Mutation</i> , 2012, 33, 690-702.	1.1	34
132	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). <i>PLoS ONE</i> , 2012, 7, e42380.	1.1	51
133	Genetic architecture of prostate cancer in the Ashkenazi Jewish population. <i>British Journal of Cancer</i> , 2011, 105, 864-869.	2.9	10
134	995 ANALYSIS OF STATIN MEDICATION, GENETIC VARIATION AND PROSTATE CANCER OUTCOMES. <i>Journal of Urology</i> , 2011, 185, .	0.2	2
135	Discriminatory accuracy and potential clinical utility of genomic profiling for breast cancer risk in BRCA-negative women. <i>Breast Cancer Research and Treatment</i> , 2011, 127, 479-487.	1.1	15
136	Haplotype structure in Ashkenazi Jewish BRCA1 and BRCA2 mutation carriers. <i>Human Genetics</i> , 2011, 130, 685-699.	1.8	18
137	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 4693-4706.	1.4	71
138	Genetic Variation at 9p22.2 and Ovarian Cancer Risk for BRCA1 and BRCA2 Mutation Carriers. <i>Journal of the National Cancer Institute</i> , 2011, 103, 105-116.	3.0	40
139	A locus for juvenile myoclonic epilepsy maps to 2q33-q36. <i>Human Genetics</i> , 2010, 128, 123-130.	1.8	14
140	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. <i>Nature Genetics</i> , 2010, 42, 885-892.	9.4	309
141	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. <i>PLoS Genetics</i> , 2010, 6, e1001183.	1.5	85
142	Susceptibility Loci Associated with Prostate Cancer Progression and Mortality. <i>Clinical Cancer Research</i> , 2010, 16, 2819-2832.	3.2	74
143	Genome-wide Association Studies of Cancer Predisposition. <i>Hematology/Oncology Clinics of North America</i> , 2010, 24, 973-996.	0.9	34
144	The role of PAK-1 in activation of MAP kinase cascade and oncogenic transformation by Akt. <i>Oncogene</i> , 2009, 28, 2365-2369.	2.6	53

#	ARTICLE	IF	CITATIONS
145	Protective and susceptibility effects of hSKCa3 allelic variants on juvenile myoclonic epilepsy. Journal of Medical Genetics, 2005, 42, 439-442.	1.5	9
146	Absence of GABRA1 Ala322Asp mutation in juvenile myoclonic epilepsy families from India. Journal of Genetics, 2003, 82, 17-21.	0.4	15
147	Genetic association analysis of KCNQ3 and juvenile myoclonic epilepsy in a South Indian population. Human Genetics, 2003, 113, 461-463.	1.8	15
148	Clinical characteristics of a South Indian cohort of juvenile myoclonic epilepsy probands. Seizure: the Journal of the British Epilepsy Association, 2003, 12, 490-496.	0.9	42