Vijai Joseph

List of Publications by Year
in descending order

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	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.	13.9	1,205
2	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
3	Integrative clinical genomics of metastatic cancer. Nature, 2017, 548, 297-303.	13.7	685
4	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
5	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. Journal of Clinical Oncology, 2019, 37, 286-295.	0.8	397
6	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
7	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
8	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
9	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
10	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	9.4	309
11	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
12	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
13	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1226-1231.	9.4	270
14	Germline Variants in Targeted Tumor Sequencing Using Matched Normal DNA. JAMA Oncology, 2016, 2, 104.	3.4	270
15	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
16	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
17	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
18	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	9.4	179

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19	Prospective Evaluation of Germline Alterations in Patients With Exocrine Pancreatic Neoplasms. Journal of the National Cancer Institute, 2018, 110, 1067-1074.	3.0	170
20	Sequencing an Ashkenazi reference panel supports population-targeted personal genomics and illuminates Jewish and European origins. Nature Communications, 2014, 5, 4835.	5.8	156
21	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
22	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
23	Conflicting Interpretation of Genetic Variants and Cancer Risk by Commercial Laboratories as Assessed by the Prospective Registry of Multiplex Testing. Journal of Clinical Oncology, 2016, 34, 4071-4078.	0.8	147
24	Prevalence of Germline Mutations in Cancer Susceptibility Genes in Patients With Advanced Renal Cell Carcinoma. JAMA Oncology, 2018, 4, 1228.	3.4	132
25	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129
26	Germline ETV6 Mutations Confer Susceptibility to Acute Lymphoblastic Leukemia and Thrombocytopenia. PLoS Genetics, 2015, 11, e1005262.	1.5	128
27	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
28	Cancer Genomics and Inherited Risk. Journal of Clinical Oncology, 2014, 32, 687-698.	0.8	121
29	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
30	Evaluation of ACMG-Guideline-Based Variant Classification of Cancer Susceptibility and Non-Cancer-Associated Genes in Families Affected by Breast Cancer. American Journal of Human Genetics, 2016, 98, 801-817.	2.6	113
31	The contribution of pathogenic variants in breast cancer susceptibility genes to familial breast cancer risk. Npj Breast Cancer, 2017, 3, 22.	2.3	108
32	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
33	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
34	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.	2.2	97
35	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
36	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94

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37	FANCMc.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
38	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
39	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	2.2	88
40	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	1.5	85
41	Prevalence of BRCA1 and BRCA2 mutations in Ashkenazi Jewish families with breast and pancreatic cancer. Cancer, 2012, 118, 493-499.	2.0	83
42	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	1.1	82
43	Clonal hematopoiesis is associated with risk of severe Covid-19. Nature Communications, 2021, 12, 5975.	5.8	81
44	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	2.2	78
45	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
46	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
47	Susceptibility Loci Associated with Prostate Cancer Progression and Mortality. Clinical Cancer Research, 2010, 16, 2819-2832.	3.2	74
48	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. Nature Cancer, 2021, 2, 357-365.	5.7	74
49	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 Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	1.4	71
50	A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. Journal of the National Cancer Institute, 2021, 113, 1683-1692.	3.0	66
51	Cancer Susceptibility Mutations in Patients With Urothelial Malignancies. Journal of Clinical Oncology, 2020, 38, 406-414.	0.8	60
52	Cascading After Peridiagnostic Cancer Genetic Testing: An Alternative to Population-Based Screening. Journal of Clinical Oncology, 2020, 38, 1398-1408.	0.8	60
53	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	5.8	58
54	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

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55	Germline Lysine-Specific Demethylase 1 (LSD1/KDM1A) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759.	0.4	56
56	The role of PAK-1 in activation of MAP kinase cascade and oncogenic transformation by Akt. Oncogene, 2009, 28, 2365-2369.	2.6	53
57	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	1.4	52
58	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	1.1	51
59	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
60	Common Variants at the 19p13.1 and ZNF365 Loci Are Associated with ER Subtypes of Breast Cancer and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 645-657.	1.1	47
61	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
62	Susceptibility Loci Associated with Specific and Shared Subtypes of Lymphoid Malignancies. PLoS Genetics, 2013, 9, e1003220.	1.5	44
63	The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.	9.4	44
64	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
65	A Recurrent ERCC3 Truncating Mutation Confers Moderate Risk for Breast Cancer. Cancer Discovery, 2016, 6, 1267-1275.	7.7	41
66	Genetic Variation at 9p22.2 and Ovarian Cancer Risk for BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2011, 103, 105-116.	3.0	40
67	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
68	Inherited TP53 Variants and Risk of Prostate Cancer. European Urology, 2022, 81, 243-250.	0.9	40
69	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
70	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. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
71	Assessment of SLX4 Mutations in Hereditary Breast Cancers. PLoS ONE, 2013, 8, e66961.	1.1	37
72	COMPLEXO: identifying the missing heritability of breast cancer via next generation collaboration. Breast Cancer Research, 2013, 15, 402.	2.2	36

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73	Variants at IRX4 as prostate cancer expression quantitative trait loci. European Journal of Human Genetics, 2014, 22, 558-563.	1.4	36
74	Genome-wide Association Studies of Cancer Predisposition. Hematology/Oncology Clinics of North America, 2010, 24, 973-996.	0.9	34
75	Ovarian cancer susceptibility alleles and risk of ovarian cancer inBRCA1andBRCA2mutation carriers. Human Mutation, 2012, 33, 690-702.	1.1	34
76	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
77	HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. Cancer Research, 2018, 78, 4086-4096.	0.4	34
78	Germline SDHA mutations in children and adults with cancer. Journal of Physical Education and Sports Management, 2018, 4, a002584.	0.5	33
79	A Rare TP53 Mutation Predominant in Ashkenazi Jews Confers Risk of Multiple Cancers. Cancer Research, 2020, 80, 3732-3744.	0.4	32
80	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
81	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	2.2	31
82	Genetic susceptibility to diffuse large Bâ€cell lymphoma in a pooled study of three Eastern Asian populations. European Journal of Haematology, 2015, 95, 442-448.	1.1	30
83	Novel pedigree analysis implicates DNA repair and chromatin remodeling in multiple myeloma risk. PLoS Genetics, 2018, 14, e1007111.	1.5	30
84	Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863.	0.6	28
85	Toward automation of germline variant curation in clinical cancer genetics. Genetics in Medicine, 2019, 21, 2116-2125.	1.1	27
86	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	2.2	26
87	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
88	Fumarate hydrataseFHc.1431_1433dupAAA (p.Lys477dup) variant is not associated with cancer including renal cell carcinoma. Human Mutation, 2020, 41, 103-109.	1.1	25
89	High-depth whole genome sequencing of an Ashkenazi Jewish reference panel: enhancing sensitivity, accuracy, and imputation. Human Genetics, 2018, 137, 343-355.	1.8	24
90	A Nonsynonymous Polymorphism in IRS1 Modifies Risk of Developing Breast and Ovarian Cancers in BRCA1 and Ovarian Cancer in BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1362-1370.	1.1	23

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91	11p15.5 epimutations in children with Wilms tumor and hepatoblastoma detected in peripheral blood. Cancer, 2020, 126, 3114-3121.	2.0	23
92	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	1.1	22
93	Rare De Novo Germline Copy-Number Variation in Testicular Cancer. American Journal of Human Genetics, 2012, 91, 379-383.	2.6	21
94	Germline deletion of ETV6 in familial acute lymphoblastic leukemia. Blood Advances, 2019, 3, 1039-1046.	2.5	21
95	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. Neuron, 2021, 109, 1465-1478.e4.	3.8	21
96	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
97	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
98	Genetic Variation in DNA Repair Pathways and Risk of Non-Hodgkin's Lymphoma. PLoS ONE, 2014, 9, e101685.	1.1	19
99	Haplotype structure in Ashkenazi Jewish BRCA1 and BRCA2 mutation carriers. Human Genetics, 2011, 130, 685-699.	1.8	18
100	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
101	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
102	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. Human Molecular Genetics, 2020, 29, 70-79.	1.4	17
103	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
104	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	1.1	16
105	Germline Variants Identified in Patients with Early-onset Renal Cell Carcinoma Referred for Germline Genetic Testing. European Urology Oncology, 2021, 4, 993-1000.	2.6	16
106	Absence ofGABRA1 Ala322Asp mutation in juvenile myoclonic epilepsy families from India. Journal of Genetics, 2003, 82, 17-21.	0.4	15
107	Genetic association analysis of KCNQ3 and juvenile myoclonic epilepsy in a South Indian population. Human Genetics, 2003, 113, 461-463.	1.8	15
108	Discriminatory accuracy and potential clinical utility of genomic profiling for breast cancer risk in BRCA-negative women. Breast Cancer Research and Treatment, 2011, 127, 479-487.	1.1	15

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109	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
110	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	1.1	15
111	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for WaldenstrÃ¶m macroglobulinemia. Nature Communications, 2018, 9, 4182.	5.8	15
112	Targeting Germline- and Tumor-Associated Nucleotide Excision Repair Defects in Cancer. Clinical Cancer Research, 2021, 27, 1997-2010.	3.2	15
113	Prevalence of Germline Alterations on Targeted Tumor-Normal Sequencing of Esophagogastric Cancer. JAMA Network Open, 2021, 4, e2114753.	2.8	15
114	A locus for juvenile myoclonic epilepsy maps to 2q33â€“q36. Human Genetics, 2010, 128, 123-130.	1.8	14
115	Lipid Trait Variants and the Risk of Non-Hodgkin Lymphoma Subtypes: A Mendelian Randomization Study. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1074-1078.	1.1	13
116	Genetic architecture of prostate cancer in the Ashkenazi Jewish population. British Journal of Cancer, 2011, 105, 864-869.	2.9	10
117	Prevalence of HOXB13 mutation in a population of Ashkenazi Jewish men treated for prostate cancer. Familial Cancer, 2013, 12, 597-600.	0.9	10
118	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
119	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
120	Protective and susceptibility effects of hSKCa3 allelic variants on juvenile myoclonic epilepsy. Journal of Medical Genetics, 2005, 42, 439-442.	1.5	9
121	Mutation Rates in Cancer Susceptibility Genes in Patients With Breast Cancer With Multiple Primary Cancers. JCO Precision Oncology, 2020, 4, 916-925.	1.5	9
122	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
123	Understanding Inherited Risk in Unselected Newly Diagnosed Patients With Endometrial Cancer. JCO Precision Oncology, 2019, 3, 1-15.	1.5	7
124	Multiple Primary Cancers in Patients Undergoing Tumor-Normal Sequencing Define Novel Associations. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 362-371.	1.1	7
125	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. Briefings in Bioinformatics, 2016, 17, 672-677.	3.2	6
126	Genome Sequencing of Multiple Primary Tumors Reveals a Novel PALB2 Variant. Journal of Clinical Oncology, 2016, 34, e61-e67.	0.8	6

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127	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539.	1.3	6
128	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6
129	Transcriptional regulation and prostate cancer risk loci.. Journal of Clinical Oncology, 2013, 31, 1554-1554.	0.8	6
130	Clinical Evaluation of Cisplatin Sensitivity of Germline Polymorphisms in Neoadjuvant Chemotherapy for Urothelial Cancer. Clinical Genitourinary Cancer, 2016, 14, 511-517.	0.9	5
131	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
132	Tissue-Specific Enrichment of Lymphoma Risk Loci in Regulatory Elements. PLoS ONE, 2015, 10, e0139360.	1.1	5
133	Caseâ€“control analysis identifies shared properties of rare germline variation in cancer predisposing genes. European Journal of Human Genetics, 2019, 27, 824-828.	1.4	4
134	Prospective assessment for pathogenic germline alterations (PGA) in pancreas cancer (PAC).. Journal of Clinical Oncology, 2017, 35, 4102-4102.	0.8	4
135	Inherited Germline Cancer Susceptibility Gene Variants in Individuals with Nonâ€“Muscle-Invasive Bladder Cancer. Clinical Cancer Research, 2022, 28, 4267-4277.	3.2	4
136	995 ANALYSIS OF STATIN MEDICATION, GENETIC VARIATION AND PROSTATE CANCER OUTCOMES. Journal of Urology, 2011, 185, .	0.2	2
137	Sequencing at lymphoid neoplasm susceptibility loci maps six myeloma risk genes. Human Molecular Genetics, 2021, 30, 1142-1153.	1.4	2
138	Frequency of actionable cancer predisposing germline mutations in patients with lung cancers.. Journal of Clinical Oncology, 2018, 36, 1504-1504.	0.8	2
139	DNA damage repair (DDR) germline mutations in patients (Pts) with urothelial carcinoma (UC).. Journal of Clinical Oncology, 2018, 36, 1516-1516.	0.8	2
140	A Germline Variant on Chromosome 4q31.1 Associates with Susceptibility to Developing Colon Cancer Metastasis. PLoS ONE, 2016, 11, e0146435.	1.1	2
141	Evaluating the association of multiple single nucleotide polymorphisms with response to gemcitabine and platinum combination chemotherapy in urothelial carcinoma of theÂbladder. International Journal of Clinical Pharmacology and Therapeutics, 2017, 55, 203-209.	0.3	2
142	SNPs at SMG7 associated with time from biochemical recurrence to prostate cancer death. Cancer Epidemiology Biomarkers and Prevention, 2022, , .	1.1	1
143	A breast cancer (BC) risk model incorporating Tyrer-Cuzick version 8 (TCv8) and a polygenic risk score (PRS) for diverse ancestries.. Journal of Clinical Oncology, 2022, 40, 557-557.	0.8	1
144	566 IDENTIFICATION OF GENETIC MARKERS ASSOCIATED WITH RESPONSE TO BACILLUS CALMETTE-GUÃ‰RIN INTRAVESICAL THERAPY IN NON-MUSCLE-INVASIVE BLADDER CANCER. Journal of Urology, 2012, 187, .	0.2	0

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145	Understanding Inherited Risk in Unselected Newly Diagnosed Patients With Endometrial Cancer. Obstetrical and Gynecological Survey, 2019, 74, 473-474.	0.2	0
146	Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217.		0
147	Saliva samples for genomic testing for preventive oncology: Improving the yield.. Journal of Clinical Oncology, 2013, 31, e12555-e12555.	0.8	0
148	Inherited mutations in breast cancer patients with and without multiple primary cancers.. Journal of Clinical Oncology, 2018, 36, 1503-1503.	0.8	0