Robert J Klein

List of Publications by Year
in descending order

106 papers	14,102 citations	66343 42 h-index	36028 97 g-index
119 all docs	119 docs citations	119 times ranked	23856 citing authors

#	Article	IF	Citations
1	Complement Factor H Polymorphism in Age-Related Macular Degeneration. Science, 2005, 308, 385-389.	12.6	4,018
2	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
3	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
4	Computational identification of noncoding RNAs in E. coli by comparative genomics. Current Biology, 2001, 11, 1369-1373.	3.9	363
5	Strong Association of the Y402H Variant in Complement Factor H at 1q32 with Susceptibility to Age-Related Macular Degeneration. American Journal of Human Genetics, 2005, 77, 149-153.	6.2	327
6	A germline JAK2 SNP is associated with predisposition to the development of JAK2V617F-positive myeloproliferative neoplasms. Nature Genetics, 2009, 41, 455-459.	21.4	322
7	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. Nature Genetics, 2012, 44, 1330-1335.	21.4	286
8	Genome-wide association study provides evidence for a breast cancer risk locus at 6q22.33. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4340-4345.	7.1	274
9	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1226-1231.	21.4	270
10	Germline BRCA Mutations Denote a Clinicopathologic Subset of Prostate Cancer. Clinical Cancer Research, 2010, 16, 2115-2121.	7.0	263
11	RSEARCH: finding homologs of single structured RNA sequences. BMC Bioinformatics, 2003, 4, 44.	2.6	224
12	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	21.4	179
13	Toward a resolution of the introns early/late debate: Only phase zero introns are correlated with the structure of ancient proteins. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 5094-5099.	7.1	178
14	Genome-Wide Association Studies of Cancer. Journal of Clinical Oncology, 2010, 28, 4255-4267.	1.6	159
15	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
16	Noncoding RNA genes identified in AT-rich hyperthermophiles. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7542-7547.	7.1	154
17	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
18	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	6.3	152

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19	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	21.4	147
20	Comprehensive Genetic Landscape of Uveal Melanoma by Whole-Genome Sequencing. American Journal of Human Genetics, 2016, 99, 1190-1198.	6.2	135
21	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
22	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. American Journal of Human Genetics, 2015, 97, 139-152.	6.2	122
23	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
24	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
25	WGSA: an annotation pipeline for human genome sequencing studies. Journal of Medical Genetics, 2016, 53, 111-112.	3.2	96
26	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	12.8	95
27	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	2.9	90
28	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
29	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	3.5	85
30	Analysis of Genetic Variants in Never-Smokers with Lung Cancer Facilitated by an Internet-Based Blood Collection Protocol: A Preliminary Report. Clinical Cancer Research, 2010, 16, 755-763.	7.0	82
31	Estimating rates of alternative splicing in mammals and invertebrates. Nature Genetics, 2004, 36, 915-916.	21.4	81
32	Power analysis for genome-wide association studies. BMC Genetics, 2007, 8, 58.	2.7	80
33	Susceptibility Loci Associated with Prostate Cancer Progression and Mortality. Clinical Cancer Research, 2010, 16, 2819-2832.	7.0	74
34	<scp>G</scp>enetic variants associated with longer telomere length are associated with increased lung cancer risk among neverâ€smoking women in Asia: a report from the female lung cancer consortium in Asia. International Journal of Cancer, 2015, 137, 311-319.	5.1	72
35	Blood Biomarker Levels to Aid Discovery of Cancer-Related Single-Nucleotide Polymorphisms: Kallikreins and Prostate Cancer. Cancer Prevention Research, 2010, 3, 611-619.	1.5	60
36	Genome-wide association study of prostate-specific antigen levels identifies novel loci independent of prostate cancer. Nature Communications, 2017, 8, 14248.	12.8	58

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37	Germline Lysine-Specific Demethylase 1 (LSD1/KDM1A) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759.	0.9	56
38	A Heroin Addiction Severity-Associated Intronic Single Nucleotide Polymorphism Modulates Alternative Pre-mRNA Splicing of the Â Opioid Receptor Gene OPRM1 via hnRNPH Interactions. Journal of Neuroscience, 2014, 34, 11048-11066.	3.6	52
39	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	2.9	52
40	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	2.9	50
41	A Novel Genetic Variant in Long Non-coding RNA Gene NEXN-AS1 is Associated with Risk of Lung Cancer. Scientific Reports, 2016, 6, 34234.	3.3	48
42	Genome-wide Scan Identifies Role for AOX1 in Prostate Cancer Survival. European Urology, 2018, 74, 710-719.	1.9	47
43	Evaluation of Multiple Riskâ€“Associated Single Nucleotide Polymorphisms Versus Prostate-Specific Antigen at Baseline to Predict Prostate Cancer in Unscreened Men. European Urology, 2012, 61, 471-477.	1.9	46
44	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. American Journal of Human Genetics, 2017, 100, 51-63.	6.2	45
45	Susceptibility Loci Associated with Specific and Shared Subtypes of Lymphoid Malignancies. PLoS Genetics, 2013, 9, e1003220.	3.5	44
46	A Replication Study and Genome-Wide Scan of Single-Nucleotide Polymorphisms Associated with Pancreatic Cancer Risk and Overall Survival. Clinical Cancer Research, 2012, 18, 3942-3951.	7.0	40
47	Variants at IRX4 as prostate cancer expression quantitative trait loci. European Journal of Human Genetics, 2014, 22, 558-563.	2.8	36
48	Exome sequencing identifies germline variants in DIS3 in familial multiple myeloma. Leukemia, 2019, 33, 2324-2330.	7.2	33
49	Analysis of genetic variation in Ashkenazi Jews by high density SNP genotyping. BMC Genetics, 2008, 9, 14.	2.7	31
50	Successes of Genome-wide Association Studies. Cell, 2010, 142, 350-351.	28.9	31
51	Rare, Pathogenic Germline Variants in Fanconi Anemia Genes Increase Risk for Squamous Lung Cancer. Clinical Cancer Research, 2019, 25, 1517-1525.	7.0	31
52	Novel pedigree analysis implicates DNA repair and chromatin remodeling in multiple myeloma risk. PLoS Genetics, 2018, 14, e1007111.	3.5	30
53	Identification of 31 loci for mammographic density phenotypes and their associations with breast cancer risk. Nature Communications, 2020, 11, 5116.	12.8	29
54	Genetic markers of pigmentation are novel risk loci for uveal melanoma. Scientific Reports, 2016, 6, 31191.	3.3	28

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55	Polymorphisms at the Microseminoprotein-Î² Locus Associated with Physiologic Variation in Î²-Microseminoprotein and Prostate-Specific Antigen Levels. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2035-2042.	2.5	27
56	High-depth whole genome sequencing of an Ashkenazi Jewish reference panel: enhancing sensitivity, accuracy, and imputation. Human Genetics, 2018, 137, 343-355.	3.8	24
57	Inherited Rare, Deleterious Variants in ATM Increase Lung Adenocarcinoma Risk. Journal of Thoracic Oncology, 2020, 15, 1871-1879.	1.1	24
58	The 6q22.33 Locus and Breast Cancer Susceptibility. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2468-2475.	2.5	22
59	Rare De Novo Germline Copy-Number Variation in Testicular Cancer. American Journal of Human Genetics, 2012, 91, 379-383.	6.2	21
60	Genetic Variation in KLK2 and KLK3 Is Associated with Concentrations of hK2 and PSA in Serum and Seminal Plasma in Young Men. Clinical Chemistry, 2014, 60, 490-499.	3.2	21
61	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. Neuron, 2021, 109, 1465-1478.e4.	8.1	21
62	Outcome of genetic evaluation of patients with kidney cancer referred for suspected hereditary cancer syndromes. Urologic Oncology: Seminars and Original Investigations, 2016, 34, 238.e1-238.e7.	1.6	20
63	Prostate cancer polygenic risk score and prediction of lethal prostate cancer. Npj Precision Oncology, 2022, 6, 25.	5.4	20
64	Genetic Variation in DNA Repair Pathways and Risk of Non-Hodgkin's Lymphoma. PLoS ONE, 2014, 9, e101685.	2.5	19
65	Haplotype structure in Ashkenazi Jewish BRCA1 and BRCA2 mutation carriers. Human Genetics, 2011, 130, 685-699.	3.8	18
66	Validation and genomic interrogation of the <scp>MET</scp> variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma. Cancer, 2016, 122, 402-410.	4.1	18
67	A Common Prostate Cancer Risk Variant 5â€² of Microseminoprotein-Î² (MSMB) Is a Strong Predictor of Circulating Î²-Microseminoprotein (MSP) Levels in Multiple Populations. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2639-2646.	2.5	17
68	Including Additional Controls from Public Databases Improves the Power of a Genome-Wide Association Study. Human Heredity, 2011, 72, 21-34.	0.8	17
69	Prostate Cancer Risk-Associated Single-Nucleotide Polymorphism Affects Prostate-Specific Antigen Glycosylation and Its Function. Clinical Chemistry, 2019, 65, e1-e9.	3.2	17
70	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.	6.4	16
71	Genetic signature of prostate cancer mouse models resistant to optimized hK2 targeted Î±-particle therapy. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15172-15181.	7.1	16
72	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	2.7	15

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73	Genome-wide analysis of the role of copy-number variation in pancreatic cancer risk. Frontiers in Genetics, 2014, 5, 29.	2.3	13
74	Predicting functionally important SNP classes based on negative selection. BMC Bioinformatics, 2011, 12, 26.	2.6	12
75	Variation in Genes Related to Obesity, Weight, and Weight Change and Risk of Contralateral Breast Cancer in the WECARE Study Population. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 2261-2267.	2.5	11
76	Genetic architecture of prostate cancer in the Ashkenazi Jewish population. British Journal of Cancer, 2011, 105, 864-869.	6.4	10
77	Validation of prostate cancer risk variants rs10993994 and rs7098889 by CRISPR/Cas9 mediated genome editing. Gene, 2021, 768, 145265.	2.2	10
78	Germline Pathogenic Variants Impact Clinicopathology of Advanced Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1450-1459.	2.5	10
79	Prostate cancer risk SNP rs10993994 is a trans-eQTL for SNHG11 mediated through MSMB. Human Molecular Genetics, 2020, 29, 1581-1591.	2.9	8
80	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.	6.5	6
81	Genome Sequencing of Multiple Primary Tumors Reveals a Novel PALB2 Variant. Journal of Clinical Oncology, 2016, 34, e61-e67.	1.6	6
82	Transcriptional regulation and prostate cancer risk loci.. Journal of Clinical Oncology, 2013, 31, 1554-1554.	1.6	6
83	Genome-wide association study identifies a role for the progesterone receptor in benign prostatic hyperplasia risk. Prostate Cancer and Prostatic Diseases, 2021, 24, 492-498.	3.9	5
84	Linkage Disequilibrium Mapping for Complex Disease Genes. Methods in Molecular Biology, 2007, 376, 85-107.	0.9	5
85	Tissue-Specific Enrichment of Lymphoma Risk Loci in Regulatory Elements. PLoS ONE, 2015, 10, e0139360.	2.5	5
86	ImmuneRegulation: a web-based tool for identifying human immune regulatory elements. Nucleic Acids Research, 2019, 47, W142-W150.	14.5	4
87	Caseâ€“control analysis identifies shared properties of rare germline variation in cancer predisposing genes. European Journal of Human Genetics, 2019, 27, 824-828.	2.8	4
88	Genetic and Functional Investigation of Germline JAK2 Alleles That Predispose to Myeloproliferative Neoplasms. Blood, 2011, 118, 124-124.	1.4	4
89	Genomeâ€wide association study identifies novel single nucleotide polymorphisms having ageâ€specific effect on prostateâ€specific antigen levels. Prostate, 2020, 80, 1405-1412.	2.3	3
90	995 ANALYSIS OF STATIN MEDICATION, GENETIC VARIATION AND PROSTATE CANCER OUTCOMES. Journal of Urology, 2011, 185, .	0.4	2

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91	Sequencing at lymphoid neoplasm susceptibility loci maps six myeloma risk genes. Human Molecular Genetics, 2021, 30, 1142-1153.	2.9	2
92	Expansion of symmetric exon-bordering domains does not explain evolution of lineage specific genes in mammals. Genetica, 2007, 131, 59-68.	1.1	1
93	MP30-12 RENAL CELL CARCINOMA AND NON-HODGKINâ€™S LYMPHOMA: GENOMIC APPROACHES TO IDENTIFICATION OF SHARED SUSCEPTIBILITY. Journal of Urology, 2014, 191, .	0.4	1
94	Validation and genomic interrogation of the MET variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma.. Journal of Clinical Oncology, 2014, 32, 395-395.	1.6	1
95	SNPs at SMG7 associated with time from biochemical recurrence to prostate cancer death. Cancer Epidemiology Biomarkers and Prevention, 2022, , .	2.5	1
96	Susceptibility loci in a molecular subtype of prostate cancer. Nature Reviews Urology, 2009, 6, 357-358.	3.8	0
97	MP36-02 VALIDATION AND GENOMIC INTERROGATION OF THE MET VARIANT RS11762213 AS A PREDICTOR OF ADVERSE OUTCOMES IN CLEAR CELL RENAL CELL CARCINOMA. Journal of Urology, 2014, 191, .	0.4	0
98	PD10-05 OUTCOME OF GENETIC EVALUATION OF KIDNEY CANCER PATIENTS REFERRED FOR SUSPECTED HEREDITARY CANCER SYNDROMES. Journal of Urology, 2014, 191, .	0.4	0
99	MP6-16 GERMLINE VARIANTS WITHIN THE PTEN/PI3K AXIS AND ASSOCIATION WITH CASTRATE RESISTANT PROSTATE CANCER AND PROSTATE CANCER SPECIFIC MORTALITY. Journal of Urology, 2015, 193, .	0.4	0
100	Prostate Cancer Risk: Single Nucleotide Polymorphisms (SNPs). Molecular Pathology Library, 2018, , 117-128.	0.1	0
101	Functional Common and Rare ERBB2 Germline Variants Cooperate in Familial and Sporadic Cancer Susceptibility. Cancer Prevention Research, 2021, 14, 441-454.	1.5	0
102	Clinical and preclinical evaluation of taxane sensitivity in gastric cancer (GC): Relevance of GC histology.. Journal of Clinical Oncology, 2013, 31, 37-37.	1.6	0
103	Abstract 2566: Comprehensive analysis to identify functional basis of prostate cancer risk SNPs. , 2016, , .		0
104	Abstract 1444: Validation of prostate cancer risk variants by CRISPR/Cas9 mediated genome editing at the MSMB locus. , 2017, , .		0
105	Abstract 1297: Genetic reclassification of prostate-specific antigen levels for personalized prostate cancer screening. , 2017, , .		0
106	Polygenic risk scores and prostate cancer screening: a recipe for more overdiagnosis?. BJU International, 2022, 129, 271-271.	2.5	0