Belynda D Hicks

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1443985/publications.pdf

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78	4,534	186265	123424
papers	citations	28 h-index	61 g-index

81	81	81	9546
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
2	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
3	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	2.5	278
4	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
5	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. Nature Biotechnology, 2014, 32, 915-925.	17.5	217
6	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
7	Somatic Genomics and Clinical Features of Lung Adenocarcinoma: A Retrospective Study. PLoS Medicine, 2016, 13, e1002162.	8.4	148
8	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	7.1	139
9	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
10	Hoyeraal-Hreidarsson syndrome caused by a germline mutation in the TEL patch of the telomere protein TPP1. Genes and Development, 2014, 28, 2090-2102.	5.9	106
11	Genomic Classification and Clinical Outcome in Rhabdomyosarcoma: A Report From an International Consortium. Journal of Clinical Oncology, 2021, 39, 2859-2871.	1.6	101
12	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	9.4	88
13	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
14	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85
15	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
16	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. Nature Communications, 2020, 11, 2459.	12.8	77
17	Novel and known ribosomal causes of Diamond-Blackfan anaemia identified through comprehensive genomic characterisation. Journal of Medical Genetics, 2017, 54, 417-425.	3.2	71
18	Genome-Wide Association Study to Identify Susceptibility Loci That Modify Radiation-Related Risk for Breast Cancer After Childhood Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	66

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19	Whole genome sequencing of skull-base chordoma reveals genomic alterations associated with recurrence and chordoma-specific survival. Nature Communications, 2021, 12, 757.	12.8	55
20	Effect of pre-analytic variables on the reproducibility of qPCR relative telomere length measurement. PLoS ONE, 2017, 12, e0184098.	2.5	55
21	Association between GWAS-identified lung adenocarcinoma susceptibility loci andEGFRmutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	2.9	50
22	Germline mutations in Protection of Telomeres 1 in two families with Hodgkin lymphoma. British Journal of Haematology, 2018, 181, 372-377.	2.5	48
23	Immune gene expression profiling reveals heterogeneity in luminal breast tumors. Breast Cancer Research, 2019, 21, 147.	5.0	43
24	Correlation of Leukocyte Telomere Length Measurement Methods in Patients with Dyskeratosis Congenita and in Their Unaffected Relatives. International Journal of Molecular Sciences, 2017, 18, 1765.	4.1	42
25	Oral microbial community composition is associated with pancreatic cancer: A caseâ€control study in Iran. Cancer Medicine, 2020, 9, 797-806.	2.8	42
26	Whole exome sequencing in families at high risk for Hodgkin lymphoma: identification of a predisposing mutation in the KDR gene. Haematologica, 2016, 101, 853-860.	3.5	40
27	Comparing the performance of selected variant callers using synthetic data and genome segmentation. BMC Bioinformatics, 2018, 19, 429.	2.6	40
28	Rare germline variants in known melanoma susceptibility genes in familial melanoma. Human Molecular Genetics, 2017, 26, 4886-4895.	2.9	37
29	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. Breast Cancer Research, 2019, 21, 62.	5.0	34
30	Prevalence and spectrum of germline rare variants in BRCA1/2 and PALB2 among breast cancer cases in Sarawak, Malaysia. Breast Cancer Research and Treatment, 2017, 165, 687-697.	2.5	26
31	Genome-wide Association Study Identifies HLA-DPB1 as a Significant Risk Factor for Severe Aplastic Anemia. American Journal of Human Genetics, 2020, 106, 264-271.	6.2	25
32	Multiple rare variants in high-risk pancreatic cancer-related genes may increase risk for pancreatic cancer in a subset of patients with and without germline CDKN2A mutations. Human Genetics, 2016, 135, 1241-1249.	3.8	24
33	Temporal Variability of Oral Microbiota over 10 Months and the Implications for Future Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 594-600.	2.5	24
34	Telomere Length Calibration from qPCR Measurement: Limitations of Current Method. Cells, 2018, 7, 183.	4.1	23
35	Effect of Recipient Age and Stem Cell Source on the Association between Donor Telomere Length and Survival after Allogeneic Unrelated Hematopoietic Cell Transplantation for Severe Aplastic Anemia. Biology of Blood and Marrow Transplantation, 2016, 22, 2276-2282.	2.0	22
36	Survey on Scientific Shared Resource Rigor and Reproducibility. Journal of Biomolecular Techniques, 2019, 30, 36-44.	1.5	20

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37	SomaticCombiner: improving the performance of somatic variant calling based on evaluation tests and a consensus approach. Scientific Reports, 2020, 10, 12898.	3.3	19
38	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19
39	Genome-Wide Association Study in Irradiated Childhood Cancer Survivors Identifies HTR2A forÂSubsequent Basal Cell Carcinoma. Journal of Investigative Dermatology, 2019, 139, 2042-2045.e8.	0.7	18
40	Telomere length and epigenetic clocks as markers of cellular aging: a comparative study. GeroScience, 2022, 44, 1861-1869.	4.6	18
41	Genetic testing in severe aplastic anemia is required forÂoptimal hematopoietic cell transplant outcomes. Blood, 2022, 140, 909-921.	1.4	18
42	Comparison of Oral Microbiota Collected Using Multiple Methods and Recommendations for New Epidemiologic Studies. MSystems, 2020, 5, .	3.8	17
43	Successful use of whole genome amplified DNA from multiple source types for high-density Illumina SNP microarrays. BMC Genomics, 2018, 19, 182.	2.8	16
44	Wholeâ€exome sequencing of nevoid basal cell carcinoma syndrome families and review of Human Gene Mutation Database PTCH1 mutation data. Molecular Genetics & Genomic Medicine, 2018, 6, 1168-1180.	1.2	16
45	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	3.4	16
46	Whole exome sequencing in families with CLL detects a variant in Integrin Î² 2 associated with disease susceptibility. Blood, 2016, 128, 2261-2263.	1.4	15
47	Prevalence of pathogenic/likely pathogenic variants in the 24 cancer genes of the ACMG Secondary Findings v2.0 list in a large cancer cohort and ethnicity-matched controls. Genome Medicine, 2018, 10, 99.	8.2	15
48	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	2.9	15
49	Rare Germline Copy Number Variations and Disease Susceptibility in Familial Melanoma. Journal of Investigative Dermatology, 2016, 136, 2436-2443.	0.7	13
50	No association between donor telomere length and outcomes after allogeneic unrelated hematopoietic cell transplant in patients with acute leukemia. Bone Marrow Transplantation, 2018, 53, 383-391.	2.4	13
51	Whole exome sequencing in 75 high-risk families with validation and replication in independent case-control studies identifies TANGO2, OR5H14, and CHAD as new prostate cancer susceptibility genes. Oncotarget, 2017, 8, 1495-1507.	1.8	11
52	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in the Childhood Cancer Survivor Study. JNCI Cancer Spectrum, 2021, 5, pkab007.	2.9	11
53	DNA-methylation-based telomere length estimator: comparisons with measurements from flow FISH and qPCR. Aging, 2021, 13, 14675-14686.	3.1	11
54	Telomere Length and Survival of Patients with Hepatocellular Carcinoma in the United States. PLoS ONE, 2016, 11, e0166828.	2.5	10

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55	RPS29 is Mutated in a Multi-Case Diamond Blackfan Anemia Family. Blood, 2012, 120, 511-511.	1.4	10
56	Relative Telomere Length before Hematopoietic Cell Transplantation and Outcome after Unrelated Donor Hematopoietic Cell Transplantation for Acute Leukemia. Biology of Blood and Marrow Transplantation, 2017, 23, 1054-1058.	2.0	9
57	Preâ€transplant short telomeres are associated with high mortality risk after unrelated donor haematopoietic cell transplant for severe aplastic anaemia. British Journal of Haematology, 2020, 188, 309-316.	2.5	9
58	Subsequent Neoplasm Risk Associated With Rare Variants in DNA Damage Response and Clinical Radiation Sensitivity Syndrome Genes in the Childhood Cancer Survivor Study. JCO Precision Oncology, 2020, 4, 926-936.	3.0	9
59	Age-related DNA methylation in paired normal and tumour breast tissue in Chinese breast cancer patients. Epigenetics, 2021, 16, 677-691.	2.7	9
60	Using whole-exome sequencing and protein interaction networks to prioritize candidate genes for germline cutaneous melanoma susceptibility. Scientific Reports, 2020, 10, 17198.	3.3	8
61	Epigenetic Aging and Hematopoietic Cell Transplantation in Patients With Severe Aplastic Anemia. Transplantation and Cellular Therapy, 2021, 27, 313.e1-313.e8.	1.2	8
62	Population Frequency of Fanconi Pathway Gene Variants and Their Association with Survival After Hematopoietic Cell Transplantation for Severe Aplastic Anemia. Biology of Blood and Marrow Transplantation, 2020, 26, 817-822.	2.0	6
63	Endemic Burkitt Lymphoma in second-degree relatives in Northern Uganda: in-depth genome-wide analysis suggests clues about genetic susceptibility. Leukemia, 2021, 35, 1209-1213.	7.2	5
64	Rare Germline Variants in Chordoma-Related Genes and Chordoma Susceptibility. Cancers, 2021, 13, 2704.	3.7	5
65	Leukocyte telomere length in patients with myotonic dystrophy type I: a pilot study. Annals of Clinical and Translational Neurology, 2020, 7, 126-131.	3.7	4
66	Integrated Analysis of Coexpression and Exome Sequencing to Prioritize Susceptibility Genes for Familial Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 2464-2475.e5.	0.7	4
67	Comparison of somatic mutation landscapes in Chinese versus European breast cancer patients. Human Genetics and Genomics Advances, 2021, 3, 100076.	1.7	3
68	Breast Cancer Risk in Women from Ghana Carrying Rare Germline Pathogenic Mutations. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1593-1601.	2.5	3
69	Rare germline variants in PALB2 and BRCA2 in familial and sporadic chordoma. Human Mutation, 2022, 43, 1396-1407.	2.5	3
70	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355.	1.9	1
71	Novel and Known Ribosomal Causes of Diamond-Blackfan Anemia Identified through Comprehensive Genomic Characterization. Blood, 2016, 128, 1495-1495.	1.4	1
72	Donor Telomere Length and Outcomes after Allogeneic Unrelated Hematopoietic Cell Transplant in Patients with Acute Leukemia. Blood, 2016, 128, 520-520.	1.4	1

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73	Subsequent neoplasm risk associated with rare variants in DNA repair and clinical radiation sensitivity syndrome genes: A report from the Childhood Cancer Survivor Study.. Journal of Clinical Oncology, 2019, 37, 10028-10028.	1.6	1
74	Pre-HCT Telomere Abnormalities and Mortality after Unrelated Donor Hematopoietic Cell Transplant for Severe Aplastic Anemia. Biology of Blood and Marrow Transplantation, 2019, 25, S417.	2.0	0
75	Germline Mutations in RTEL1 cause Dyskeratosis Congenita. Blood, 2012, 120, 515-515.	1.4	0
76	Functional Consequences Of RPS29 Germline Mutations In Diamond-Blackfan Anemia. Blood, 2013, 122, 2465-2465.	1.4	0
77	Germline Mutations in Patients Receiving Unrelated Donor Hematopoietic Cell Transplant for Severe Aplastic Anemia. Blood, 2016, 128, 68-68.	1.4	0
78	Whole Exome Sequencing in Severe Aplastic Anemia Identifies Unrecognized Inherited Subset with Inferior Survival after Hematopoietic Cell Transplant. Blood, 2021, 138, 605-605.	1.4	0