Belynda D Hicks

List of Publications by Year
in descending order

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

Version: 2024-02-01

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	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355.	1.9	1
2	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
3	Telomere length and epigenetic clocks as markers of cellular aging: a comparative study. GeroScience, 2022, 44, 1861-1869.	4.6	18
4	Breast Cancer Risk in Women from Ghana Carrying Rare Germline Pathogenic Mutations. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1593-1601.	2.5	3
5	Genetic testing in severe aplastic anemia is required forÂoptimal hematopoietic cell transplant outcomes. Blood, 2022, 140, 909-921.	1.4	18
6	Rare germline variants in PALB2 and BRCA2 in familial and sporadic chordoma. Human Mutation, 2022, 43, 1396-1407.	2.5	3
7	Age-related DNA methylation in paired normal and tumour breast tissue in Chinese breast cancer patients. Epigenetics, 2021, 16, 677-691.	2.7	9
8	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	3.4	16
9	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
10	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in the Childhood Cancer Survivor Study. JNCI Cancer Spectrum, 2021, 5, pkab007.	2.9	11
11	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
12	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
13	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85
14	Rare Germline Variants in Chordoma-Related Genes and Chordoma Susceptibility. Cancers, 2021, 13, 2704.	3.7	5
15	DNA-methylation-based telomere length estimator: comparisons with measurements from flow FISH and qPCR. Aging, 2021, 13, 14675-14686.	3.1	11
16	Genomic Classification and Clinical Outcome in Rhabdomyosarcoma: A Report From an International Consortium. Journal of Clinical Oncology, 2021, 39, 2859-2871.	1.6	101
17	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
18	Comparison of somatic mutation landscapes in Chinese versus European breast cancer patients. Human Genetics and Genomics Advances, 2021, 3, 100076.	1.7	3

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19	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
20	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
21	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
22	Oral microbial community composition is associated with pancreatic cancer: A caseâ€control study in Iran. Cancer Medicine, 2020, 9, 797-806.	2.8	42
23	SomaticCombiner: improving the performance of somatic variant calling based on evaluation tests and a consensus approach. Scientific Reports, 2020, 10, 12898.	3.3	19
24	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
25	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
26	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. Nature Communications, 2020, 11, 2459.	12.8	77
27	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19
28	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	7.1	139
29	Comparison of Oral Microbiota Collected Using Multiple Methods and Recommendations for New Epidemiologic Studies. MSystems, 2020, 5, .	3.8	17
30	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
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	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
33	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
34	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. Breast Cancer Research, 2019, 21, 62.	5.0	34
35	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
36	Immune gene expression profiling reveals heterogeneity in luminal breast tumors. Breast Cancer Research, 2019, 21, 147.	5.0	43

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37	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
38	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
39	Survey on Scientific Shared Resource Rigor and Reproducibility. Journal of Biomolecular Techniques, 2019, 30, 36-44.	1.5	20
40	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
41	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
42	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
43	Germline mutations in Protection of Telomeres 1 in two families with Hodgkin lymphoma. British Journal of Haematology, 2018, 181, 372-377.	2.5	48
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	Comparing the performance of selected variant callers using synthetic data and genome segmentation. BMC Bioinformatics, 2018, 19, 429.	2.6	40
46	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
47	Telomere Length Calibration from qPCR Measurement: Limitations of Current Method. Cells, 2018, 7, 183.	4.1	23
48	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
49	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
50	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
51	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
52	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
53	Rare germline variants in known melanoma susceptibility genes in familial melanoma. Human Molecular Genetics, 2017, 26, 4886-4895.	2.9	37
54	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099

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55	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
56	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
57	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
58	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
59	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
60	Effect of pre-analytic variables on the reproducibility of qPCR relative telomere length measurement. PLoS ONE, 2017, 12, e0184098.	2.5	55
61	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
62	Rare Germline Copy Number Variations and Disease Susceptibility in Familial Melanoma. Journal of Investigative Dermatology, 2016, 136, 2436-2443.	0.7	13
63	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
64	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
65	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
66	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
67	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
68	Novel and Known Ribosomal Causes of Diamond-Blackfan Anemia Identified through Comprehensive Genomic Characterization. Blood, 2016, 128, 1495-1495.	1.4	1
69	Donor Telomere Length and Outcomes after Allogeneic Unrelated Hematopoietic Cell Transplant in Patients with Acute Leukemia. Blood, 2016, 128, 520-520.	1.4	1
70	Somatic Genomics and Clinical Features of Lung Adenocarcinoma: A Retrospective Study. PLoS Medicine, 2016, 13, e1002162.	8.4	148
71	Telomere Length and Survival of Patients with Hepatocellular Carcinoma in the United States. PLoS ONE, 2016, 11, e0166828.	2.5	10
72	Germline Mutations in Patients Receiving Unrelated Donor Hematopoietic Cell Transplant for Severe Aplastic Anemia. Blood, 2016, 128, 68-68.	1.4	0

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73	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	9.4	88
74	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
75	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
76	Functional Consequences Of RPS29 Germline Mutations In Diamond-Blackfan Anemia. Blood, 2013, 122, 2465-2465.	1.4	0
77	Germline Mutations in RTEL1 cause Dyskeratosis Congenita. Blood, 2012, 120, 515-515.	1.4	0
78	RPS29 is Mutated in a Multi-Case Diamond Blackfan Anemia Family. Blood, 2012, 120, 511-511.	1.4	10