

Lara E Sucheston-Campbell

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,186
citations

430874

18
h-index

414414

32
g-index

52
all docs

52
docs citations

52
times ranked

2875
citing authors

#	ARTICLE	IF	CITATIONS
1	Polygenic risk scores for prediction of breast cancer risk in women of African ancestry: a cross-ancestry approach. <i>Human Molecular Genetics</i> , 2022, 31, 3133-3143.	2.9	11
2	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1168-1176.	6.3	41
3	Genome-Wide Association Analyses Identify Variants in IRF4 Associated With Acute Myeloid Leukemia and Myelodysplastic Syndrome Susceptibility. <i>Frontiers in Genetics</i> , 2021, 12, 554948.	2.3	8
4	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021, 12, 4198.	12.8	24
5	Prognostic impact of pre-transplant chromosomal aberrations in peripheral blood of patients undergoing unrelated donor hematopoietic cell transplant for acute myeloid leukemia. <i>Scientific Reports</i> , 2021, 11, 15004.	3.3	4
6	Novel genetic variants associated with mortality after unrelated donor allogeneic hematopoietic cell transplantation. <i>EClinicalMedicine</i> , 2021, 40, 101093.	7.1	8
7	Pre-HCT mosaicism increases relapse risk and lowers survival in acute lymphoblastic leukemia patients post-unrelated HCT. <i>Blood Advances</i> , 2021, 5, 66-70.	5.2	6
8	Dietary Supplement Use During Chemotherapy and Survival Outcomes of Patients With Breast Cancer Enrolled in a Cooperative Group Clinical Trial (SWOG S0221). <i>Journal of Clinical Oncology</i> , 2020, 38, 804-814.	1.6	142
9	High dimensional model representation of log likelihood ratio: binary classification with SNP data. <i>BMC Medical Genomics</i> , 2020, 13, 133.	1.5	1
10	Meta-Analysis of Genome-Wide Association Studies of Acute Myeloid Leukemia (AML) Patients Identifies Variants Associated with Risk of 11q23/KMT2A-Translocated and Core-Binding Factor (CBF) AML and Suggests a Role for Transcription Elongation in Leukemogenesis. <i>Blood</i> , 2020, 136, 29-30.	1.4	0
11	Population Distribution of GvL and GvH Minor Histocompatibility Antigens. <i>Blood</i> , 2020, 136, 23-25.	1.4	0
12	Associations of Clinical Outcomes after Allogeneic Hematopoietic Cell Transplantation with Number of Predicted Class II Restricted mHA. <i>Blood</i> , 2020, 136, 2-2.	1.4	0
13	Pre-Transplant Clonal Mosaicism Is Associated with Increased Relapse and Lower Survival in Acute Lymphoblastic Leukemia Patients Undergoing Allogeneic Hematopoietic Cell Transplant. <i>Blood</i> , 2020, 136, 9-10.	1.4	0
14	The miR-96 and RAR β signaling axis governs androgen signaling and prostate cancer progression. <i>Oncogene</i> , 2019, 38, 421-444.	5.9	45
15	Validation of genetic associations with acute GVHD and nonrelapse mortality in DISCOVeRY-BMT. <i>Blood Advances</i> , 2019, 3, 2337-2341.	5.2	8
16	Multiple functional variants in the IL1RL1 region are pretransplant markers for risk of GVHD and infection deaths. <i>Blood Advances</i> , 2019, 3, 2512-2524.	5.2	7
17	gwasurvivr: an R package for genome-wide survival analysis. <i>Bioinformatics</i> , 2019, 35, 1968-1970.	4.1	72
18	De Novo and Therapy-Related Acute Myeloid Leukemia and Myelodysplastic Syndrome: Similarities and Differences in SNP-Array Detected Chromosomal Aberrations in Pre-Transplant Blood Samples. <i>Blood</i> , 2019, 134, 1430-1430.	1.4	2

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19	Exome chip analyses identify genes affecting mortality after HLA-matched unrelated-donor blood and marrow transplantation. <i>Blood</i> , 2018, 131, 2490-2499.	1.4	21
20	Genetic Variants in Immune-Related Pathways and Breast Cancer Risk in African American Women in the AMBER Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 321-330.	2.5	16
21	Physical activity modifies genetic susceptibility to obesity in postmenopausal women. <i>Menopause</i> , 2018, 25, 1131-1137.	2.0	7
22	A survey of microRNA single nucleotide polymorphisms identifies novel breast cancer susceptibility loci in a case-control, population-based study of African-American women. <i>Breast Cancer Research</i> , 2018, 20, 45.	5.0	15
23	Genetic ancestry and population differences in levels of inflammatory cytokines in women: Role for evolutionary selection and environmental factors. <i>PLoS Genetics</i> , 2018, 14, e1007368.	3.5	47
24	OATP1B2 deficiency protects against paclitaxel-induced neurotoxicity. <i>Journal of Clinical Investigation</i> , 2018, 128, 816-825.	8.2	57
25	Multiple Functional Donor Polymorphisms in IL1RL1 region Associate with Death Due to GvHD or Infection after Unrelated Donor Allogeneic Hematopoietic Stem Cell Transplantation (HCT) for AML and MDS. <i>Blood</i> , 2018, 132, 312-312.	1.4	0
26	The influence of genetic susceptibility and calcium plus vitamin D supplementation on fracture risk. <i>American Journal of Clinical Nutrition</i> , 2017, 105, 970-979.	4.7	15
27	Gene-Hormone Therapy Interaction and Fracture Risk in Postmenopausal Women. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 1908-1916.	3.6	5
28	Characterizing Genetic Susceptibility to Breast Cancer in Women of African Ancestry. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1016-1026.	2.5	24
29	Replication and validation of genetic polymorphisms associated with survival after allogeneic blood or marrow transplant. <i>Blood</i> , 2017, 130, 1585-1596.	1.4	45
30	Integration of VDR genome wide binding and GWAS genetic variation data reveals co-occurrence of VDR and NF- κ B binding that is linked to immune phenotypes. <i>BMC Genomics</i> , 2017, 18, 132.	2.8	35
31	No Evidence That Genetic Variation in the Myeloid-Derived Suppressor Cell Pathway Influences Ovarian Cancer Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 420-424.	2.5	3
32	Single nucleotide variants in metastasis-related genes are associated with breast cancer risk, by lymph node involvement and estrogen receptor status, in women with European and African ancestry. <i>Molecular Carcinogenesis</i> , 2017, 56, 1000-1009.	2.7	12
33	Supplement Use and Chemotherapy-Induced Peripheral Neuropathy in a Cooperative Group Trial (S0221): The DELCaP Study. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	30
34	A methodological study of genome-wide DNA methylation analyses using matched archival formalin-fixed paraffin embedded and fresh frozen breast tumors. <i>Oncotarget</i> , 2017, 8, 14821-14829.	1.8	8
35	Genetic association with B-cell acute lymphoblastic leukemia in allogeneic transplant patients differs by age and sex. <i>Blood Advances</i> , 2017, 1, 1717-1728.	5.2	15
36	<i>PALB2</i>,<i>CHEK2</i>and<i>ATM</i>rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	3.2	174

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37	Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. <i>Human Molecular Genetics</i> , 2016, 25, ddw305.	2.9	50
38	An exome-wide analysis of low frequency and rare variants in relation to risk of breast cancer in African American Women: the AMBER Consortium. <i>Carcinogenesis</i> , 2016, 37, 870-877.	2.8	22
39	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. <i>Oncotarget</i> , 2016, 7, 69097-69110.	1.8	5
40	Replication of Candidate SNP Survival Analyses and Gene-Based Tests of Association with Survival Outcomes after an Unrelated Donor Blood or Marrow Transplant: Results from the Discovery-BMT Study. <i>Blood</i> , 2016, 128, 71-71.	1.4	0
41	Exome Array Analyses Identify Low-Frequency Germline Variants Associated with Increased Risk of AML in a HLA-Matched Unrelated Donor Blood and Marrow Transplant Population. <i>Blood</i> , 2016, 128, 42-42.	1.4	0
42	VDR regulation of microRNA differs across prostate cell models suggesting extremely flexible control of transcription. <i>Epigenetics</i> , 2015, 10, 40-49.	2.7	15
43	Identification and Utilization of Donor and Recipient Genetic Variants to Predict Survival After HCT: Are We Ready for Primetime?. <i>Current Hematologic Malignancy Reports</i> , 2015, 10, 45-58.	2.3	11
44	Vitamin D Receptor and RXR in the Post-Genomic Era. <i>Journal of Cellular Physiology</i> , 2015, 230, 758-766.	4.1	35
45	Hormone-related pathways and risk of breast cancer subtypes in African American women. <i>Breast Cancer Research and Treatment</i> , 2015, 154, 145-154.	2.5	30
46	Establishment of Definitions and Review Process for Consistent Adjudication of Cause-specific Mortality after Allogeneic Unrelated-donor Hematopoietic Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2015, 21, 1679-1686.	2.0	37
47	Serum microRNA expression patterns that predict early treatment failure in prostate cancer patients. <i>Oncotarget</i> , 2014, 5, 824-840.	1.8	52
48	Cooperative behavior of the nuclear receptor superfamily and its deregulation in prostate cancer. <i>Carcinogenesis</i> , 2014, 35, 262-271.	2.8	19