

Zachary C Fogarty

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/281403/publications.pdf>

Version: 2024-02-01

24
papers

1,293
citations

623734

14
h-index

610901

24
g-index

27
all docs

27
docs citations

27
times ranked

3958
citing authors

#	ARTICLE	IF	CITATIONS
1	PSMA as a Theranostic Target in Hepatocellular Carcinoma: Immunohistochemistry and ^{68}Ga -PSMA PET Using Cyclotron-Produced ^{68}Ga . <i>Hepatology Communications</i> , 2022, 6, 1172-1185.	4.3	15
2	<i>CELSR1</i> Risk Alleles in Familial Bicuspid Aortic Valve and Hypoplastic Left Heart Syndrome. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003523.	3.6	11
3	A microRNA Transcriptome-wide Association Study of Prostate Cancer Risk. <i>Frontiers in Genetics</i> , 2022, 13, 836841.	2.3	3
4	Two-stage Study of Familial Prostate Cancer by Whole-exome Sequencing and Custom Capture Identifies 10 Novel Genes Associated with the Risk of Prostate Cancer. <i>European Urology</i> , 2021, 79, 353-361.	1.9	28
5	Frequent POLE-driven hypermutation in ovarian endometrioid cancer revealed by mutational signatures in RNA sequencing. <i>BMC Medical Genomics</i> , 2021, 14, 165.	1.5	10
6	Patient-specific genomics and cross-species functional analysis implicate LRP2 in hypoplastic left heart syndrome. <i>ELife</i> , 2020, 9, .	6.0	29
7	An expanded variant list and assembly annotation identifies multiple novel coding and noncoding genes for prostate cancer risk using a normal prostate tissue eQTL data set. <i>PLoS ONE</i> , 2019, 14, e0214588.	2.5	5
8	Genome-wide analyses as part of the international FTLT-TDP whole-genome sequencing consortium reveals novel disease risk factors and increases support for immune dysfunction in FTLT. <i>Acta Neuropathologica</i> , 2019, 137, 879-899.	7.7	90
9	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. <i>Human Molecular Genetics</i> , 2019, 28, 1331-1342.	2.9	19
10	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	21.4	356
11	Mapping Complex Traits in a Diversity Outbred F1 Mouse Population Identifies Germline Modifiers of Metastasis in Human Prostate Cancer. <i>Cell Systems</i> , 2017, 4, 31-45.e6.	6.2	44
12	Dose-Response Association of CD8^{+} Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. <i>JAMA Oncology</i> , 2017, 3, e173290.	7.1	260
13	Targeted sequencing of 36 known or putative colorectal cancer susceptibility genes. <i>Molecular Genetics & Genomic Medicine</i> , 2017, 5, 553-569.	1.2	32
14	An integrative approach to assess X-chromosome inactivation using allele-specific expression with applications to epithelial ovarian cancer. <i>Genetic Epidemiology</i> , 2017, 41, 898-914.	1.3	16
15	Germline miRNA DNA variants and the risk of colorectal cancer by subtype. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 177-184.	2.8	7
16	<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
17	The inflammatory microenvironment in epithelial ovarian cancer: a role for TLR4 and MyD88 and related proteins. <i>Tumor Biology</i> , 2016, 37, 13279-13286.	1.8	41
18	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 446-454.	2.5	9

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19	A targeted genetic association study of epithelial ovarian cancer susceptibility. <i>Oncotarget</i> , 2016, 7, 7381-7389.	1.8	7
20	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. <i>Clinical Cancer Research</i> , 2015, 21, 5264-5276.	7.0	33
21	Variation in NF- κ B Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1421-1427.	2.5	13
22	Risk of Ovarian Cancer and the NF- κ B Pathway: Genetic Association with <i>IL1A</i> and <i>TNFSF10</i> . <i>Cancer Research</i> , 2014, 74, 852-861.	0.9	48
23	Large-Scale Evaluation of Common Variation in Regulatory T Cell-Related Genes and Ovarian Cancer Outcome. <i>Cancer Immunology Research</i> , 2014, 2, 332-340.	3.4	21
24	Analysis of Over 10,000 Cases Finds No Association between Previously Reported Candidate Polymorphisms and Ovarian Cancer Outcome. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 987-992.	2.5	20