

Shuwei Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1041464/publications.pdf>

Version: 2024-02-01

19
papers

1,135
citations

840776

11
h-index

940533

16
g-index

19
all docs

19
docs citations

19
times ranked

3047
citing authors

#	ARTICLE	IF	CITATIONS
1	Diagnostic exome sequencing provides a molecular diagnosis for a significant proportion of patients with epilepsy. <i>Genetics in Medicine</i> , 2016, 18, 898-905.	2.4	299
2	Association of Breast and Ovarian Cancers With Predisposition Genes Identified by Large-Scale Sequencing. <i>JAMA Oncology</i> , 2019, 5, 51.	7.1	145
3	Sanger Confirmation Is Required to Achieve Optimal Sensitivity and Specificity in Next-Generation Sequencing Panel Testing. <i>Journal of Molecular Diagnostics</i> , 2016, 18, 923-932.	2.8	143
4	Multigene Panel Testing Provides a New Perspective on Lynch Syndrome. <i>Journal of Clinical Oncology</i> , 2017, 35, 2568-2575.	1.6	122
5	Male breast cancer in a multi-gene panel testing cohort: insights and unexpected results. <i>Breast Cancer Research and Treatment</i> , 2017, 161, 575-586.	2.5	116
6	Clinical features and cancer risk in families with pathogenic <i>CDH1</i> variants irrespective of clinical criteria. <i>Journal of Medical Genetics</i> , 2019, 56, 838-843.	3.2	84
7	Candidate-gene criteria for clinical reporting: diagnostic exome sequencing identifies altered candidate genes among 8% of patients with undiagnosed diseases. <i>Genetics in Medicine</i> , 2017, 19, 224-235.	2.4	47
8	Breast cancer risk is similar for CHEK2 founder and non-founder mutation carriers. <i>Cancer Genetics</i> , 2016, 209, 403-407.	0.4	41
9	Rare Germline Pathogenic Mutations of DNA Repair Genes Are Most Strongly Associated with Grade Group 5 Prostate Cancer. <i>European Urology Oncology</i> , 2020, 3, 224-230.	5.4	41
10	A hyperactive quantitative trait locus allele of <i>Arabidopsis BRX</i> contributes to natural variation in root growth vigor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8475-8480.	7.1	33
11	Validation of a prostate cancer polygenic risk score. <i>Prostate</i> , 2020, 80, 1314-1321.	2.3	23
12	A Bayesian framework for efficient and accurate variant prediction. <i>PLoS ONE</i> , 2018, 13, e0203553.	2.5	12
13	Tumour characteristics provide evidence for germline mismatch repair missense variant pathogenicity. <i>Journal of Medical Genetics</i> , 2020, 57, 62-69.	3.2	11
14	Prevalence of Germline Pathogenic and Likely Pathogenic Variants in Patients With Second Breast Cancers. <i>JNCI Cancer Spectrum</i> , 2020, 4, pkaa094.	2.9	10
15	Clinical germline diagnostic exome sequencing for hereditary cancer: Findings within novel candidate genes are prevalent. <i>Cancer Genetics</i> , 2018, 224-225, 12-20.	0.4	7
16	Functional and evolutionary correlates of gene constellations in the <i>Drosophila melanogaster</i> genome that deviate from the stereotypical gene architecture. <i>BMC Genomics</i> , 2010, 11, 322.	2.8	1
17	Abstract P4-12-16: Teasing out the PALB2 phenotype. , 2015, , .		0
18	Women with breast and uterine cancer in relation to genetic mutation risk: A case-control analysis.. <i>Journal of Clinical Oncology</i> , 2015, 33, 1549-1549.	1.6	0

#	ARTICLE	IF	CITATIONS
19	Diagnosing Hereditary Cancer Susceptibility Through Multigene Panel Testing. , 2017, , 123-153.		0