Liying Zhang

List of Publications by Year
in descending order

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70 papers	5,832 citations	186265 28 h-index	102487 66 g-index
75 all docs	75 docs citations	75 times ranked	9859 citing authors

#	Article	IF	Citations
1	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.	27.0	1,205
2	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. Journal of Clinical Oncology, 2019, 37, 286-295.	1.6	397
3	Mutation Detection in Patients With Advanced Cancer by Universal Sequencing of Cancer-Related Genes in Tumor and Normal DNA vs Guideline-Based Germline Testing. JAMA - Journal of the American Medical Association, 2017, 318, 825.	7.4	366
4	Tumour lineage shapes BRCA-mediated phenotypes. Nature, 2019, 571, 576-579.	27.8	295
5	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. JCO Precision Oncology, 2017, 2017, 1-16.	3.0	286
6	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. Cancer Discovery, 2018, 8, 49-58.	9.4	275
7	Germline Variants in Targeted Tumor Sequencing Using Matched Normal DNA. JAMA Oncology, 2016, 2, 104.	7.1	270
8	Hereditary diffuse gastric cancer: updated clinical practice guidelines. Lancet Oncology, The, 2020, 21, e386-e397.	10.7	237
9	Reliable Pan-Cancer Microsatellite Instability Assessment by Using Targeted Next-Generation Sequencing Data. JCO Precision Oncology, 2017, 2017, 1-17.	3.0	209
10	Immunohistochemistry versus Microsatellite Instability Testing for Screening Colorectal Cancer Patients at Risk for Hereditary Nonpolyposis Colorectal Cancer Syndrome. Journal of Molecular Diagnostics, 2008, 10, 301-307.	2.8	177
11	Identification of germline genetic mutations in patients with pancreatic cancer. Cancer, 2015, 121, 4382-4388.	4.1	167
12	NF-Î¹B Regulates Androgen Receptor Expression and Prostate Cancer Growth. American Journal of Pathology, 2009, 175, 489-499.	3.8	163
13	Prevalence of Clonal Hematopoiesis Mutations in Tumor-Only Clinical Genomic Profiling of Solid Tumors. JAMA Oncology, 2018, 4, 1589.	7.1	139
14	Specifications of the ACMG/AMP variant curation guidelines for the analysis of germline CDH1 sequence variants. Human Mutation, 2018, 39, 1553-1568.	2.5	138
15	Prevalence of Germline Mutations in Cancer Susceptibility Genes in Patients With Advanced Renal Cell Carcinoma. JAMA Oncology, 2018, 4, 1228.	7.1	132
16	Geneâ€specific criteria for PTEN variant curation: Recommendations from the ClinGen PTEN Expert Panel. Human Mutation, 2018, 39, 1581-1592.	2.5	123
17	Colorectal Carcinomas Containing Hypermethylated MLH1 Promoter and Wild-Type BRAF/KRAS Are Enriched for Targetable Kinase Fusions. Cancer Research, 2019, 79, 1047-1053.	0.9	112
18	Comprehensive detection of germline variants by MSK-IMPACT, a clinical diagnostic platform for solid tumor molecular oncology and concurrent cancer predisposition testing. BMC Medical Genomics, 2017, 10, 33.	1.5	111

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19	ClinGen Myeloid Malignancy Variant Curation Expert Panel recommendations for germline RUNX1 variants. Blood Advances, 2019, 3, 2962-2979.	5.2	110
20	Specifications of the ACMG/AMP variant interpretation guidelines for germline TP53 variants. Human Mutation, 2021, 42, 223-236.	2.5	81
21	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. Nature Cancer, 2021, 2, 357-365.	13.2	74
22	A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. Journal of the National Cancer Institute, 2021, 113, 1683-1692.	6.3	66
23	The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.	21.4	44
24	Immunohistochemical detection of ARID1A in colorectal carcinoma: loss of staining is associated with sporadic microsatellite unstable tumors with medullary histology and high TNM stage. Human Pathology, 2014, 45, 2430-2436.	2.0	41
25	A Recurrent ERCC3 Truncating Mutation Confers Moderate Risk for Breast Cancer. Cancer Discovery, 2016, 6, 1267-1275.	9.4	41
26	Integrating somatic variant data and biomarkers for germline variant classification in cancer predisposition genes. Human Mutation, 2018, 39, 1542-1552.	2.5	40
27	The emerging significance of secondary germline testing in cancer genomics. Journal of Pathology, 2018, 244, 610-615.	4.5	37
28	Germline SDHA mutations in children and adults with cancer. Journal of Physical Education and Sports Management, 2018, 4, a002584.	1.2	33
29	Prevalence and Prognostic Role of BRCA1/2 Variants in Unselected Chinese Breast Cancer Patients. PLoS ONE, 2016, 11, e0156789.	2.5	30
30	Cellular localization of PD-L1 expression in mismatch-repair-deficient and proficient colorectal carcinomas. Modern Pathology, 2019, 32, 110-121.	5.5	28
31	Toward automation of germline variant curation in clinical cancer genetics. Genetics in Medicine, 2019, 21, 2116-2125.	2.4	27
32	Germline alterations in patients with biliary tract cancers: A spectrum of significant and previously underappreciated findings. Cancer, 2020, 126, 1995-2002.	4.1	26
33	Fumarate hydrataseFHc.1431_1433dupAAA (p.Lys477dup) variant is not associated with cancer including renal cell carcinoma. Human Mutation, 2020, 41, 103-109.	2.5	25
34	Reliable Clinical MLH1 Promoter Hypermethylation Assessment Using a High-Throughput Genome-Wide Methylation Array Platform. Journal of Molecular Diagnostics, 2020, 22, 368-375.	2.8	25
35	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	2.5	22
36	Expression of androgen receptor and its phosphorylated forms in breast cancer progression. Cancer, 2013, 119, 2532-2540.	4.1	20

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37	A Rapid and Reliable Test for BRCA1 and BRCA2 Founder Mutation Analysis in Paraffin Tissue Using Pyrosequencing. Journal of Molecular Diagnostics, 2009, 11, 176-181.	2.8	18
38	Immunohistochemical null-phenotype for mismatch repair proteins in colonic carcinoma associated with concurrent MLH1 hypermethylation and MSH2 somatic mutations. Familial Cancer, 2018, 17, 225-228.	1.9	17
39	CDH1 Missense Variant c.1679C>G (p.T560R) Completely Disrupts Normal Splicing through Creation of a Novel 5â€™ Splice Site. PLoS ONE, 2016, 11, e0165654.	2.5	16
40	Characterization of a novel germline PALB2 duplication in a hereditary breast and ovarian cancer family. Breast Cancer Research and Treatment, 2016, 160, 447-456.	2.5	16
41	Accurate germline RUNX1 variant interpretation and its clinical significance. Blood Advances, 2020, 4, 6199-6203.	5.2	13
42	Morphologic and Genomic Characteristics of Breast Cancers Occurring in Individuals with Lynch Syndrome. Clinical Cancer Research, 2022, 28, 404-413.	7.0	13
43	Detecting mismatch repair deficiency in solid neoplasms: immunohistochemistry, microsatellite instability, or both?. Modern Pathology, 2022, 35, 1515-1528.	5.5	13
44	BRCA1 R71K missense mutation contributes to cancer predisposition by increasing alternative transcript levels. Breast Cancer Research and Treatment, 2011, 130, 1051-1056.	2.5	12
45	Colorectal carcinoma with double somatic mismatch repair gene inactivation: clinical and pathological characteristics and response to immune checkpoint blockade. Modern Pathology, 2019, 32, 1551-1562.	5.5	12
46	The germline CDH1 c.48 G > C substitution contributes to cancer predisposition through generation of a pro-invasive mutation. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2014, 770, 106-111.	1.0	11
47	Assessment of individuals with BRCA1 and BRCA2 large rearrangements in high-risk breast and ovarian cancer families. Breast Cancer Research and Treatment, 2014, 145, 625-634.	2.5	11
48	Fumarate hydratase variant prevalence and manifestations among individuals receiving germline testing. Cancer, 2022, 128, 675-684.	4.1	11
49	Contiguous gene deletion of chromosome 2p16.3-p21 as a cause of Lynch syndrome. Familial Cancer, 2018, 17, 71-77.	1.9	10
50	Prevalence and Preliminary Validation of Screening Criteria to Identify Carriers of Germline BAP1 Mutations. Journal of Thoracic Oncology, 2019, 14, 1989-1994.	1.1	10
51	cDNA analysis demonstrates that the BRCA2 intronic variant IVS4-12del5 is a deleterious mutation. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2009, 663, 84-89.	1.0	9
52	BAP1 Missense Mutation c.2054 A>T (p.E685V) Completely Disrupts Normal Splicing through Creation of a Novel 5â€™ Splice Site in a Human Mesothelioma Cell Line. PLoS ONE, 2015, 10, e0119224.	2.5	9
53	Germline RAD51B variants confer susceptibility to breast and ovarian cancers deficient in homologous recombination. Npj Breast Cancer, 2021, 7, 135.	5.2	9
54	Discordant DNA mismatch repair protein status between synchronous or metachronous gastrointestinal carcinomas: frequency, patterns, and molecular etiologies. Familial Cancer, 2020, 20, 201-213.	1.9	8

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55	Understanding Inherited Risk in Unselected Newly Diagnosed Patients With Endometrial Cancer. JCO Precision Oncology, 2019, 3, 1-15.	3.0	7
56	Insertion of an <scp>SVA</scp> element in <scp>MSH2</scp> as a novel cause of Lynch syndrome. Genes Chromosomes and Cancer, 2021, 60, 571-576.	2.8	6
57	Characterization of a novel germline BRCA1 splice variant, c.5332+4delA. Breast Cancer Research and Treatment, 2018, 168, 543-550.	2.5	5
58	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions. Cancer Genetics, 2022, 264-265, 50-59.	0.4	5
59	A synonymous germline variant PALB2 c.18G>T (p.Gly6=) disrupts normal splicing in a family with pancreatic and breast cancers. Breast Cancer Research and Treatment, 2019, 173, 79-86.	2.5	4
60	Insertion of an Aluâ€like element in MLH1 intron 7 as a novel cause of Lynch syndrome. Molecular Genetics & Genomic Medicine, 2020, 8, e1523.	1.2	4
61	Inherited Germline Cancer Susceptibility Gene Variants in Individuals with Nonâ€“Muscle-Invasive Bladder Cancer. Clinical Cancer Research, 2022, 28, 4267-4277.	7.0	4
62	The RAD51D c.82G>A (p.Val28Met) variant disrupts normal splicing and is associated with hereditary ovarian cancer. Breast Cancer Research and Treatment, 2021, 185, 869-877.	2.5	2
63	Fumarate hydratase c.914TÂ>ÂC (p.Phe305Ser) is a pathogenic variant associated with hereditary leiomyomatosis and renal cell cancer syndrome. Molecular Genetics & Genomic Medicine, 2020, 8, e1293.	1.2	1
64	Characterization of a germline splice site variant MLH1 c.678-3T>A in a Lynch syndrome family. Familial Cancer, 2020, 19, 315-322.	1.9	1
65	Resolving pathogenicity classification for the CDH1 c.[715G>A] (p.Gly239Arg) Variant. European Journal of Human Genetics, 2021, 29, 1103-1109.	2.8	1
66	The p.Ser64Leu and p.Pro104Leu missense variants of PALB2 identified in familial pancreatic cancer patients compromise the DNA damage response. Human Mutation, 2021, 42, 150-163.	2.5	0
67	Abstract 449: A standard operating procedure for the curation of gene fusions. , 2021, , .		0
68	Expert Curation of Somatic FLT3 Variants By the Clingen Somatic Hematologic Cancer Taskforce (ClinGen HCT). Blood, 2021, 138, 4387-4387.	1.4	0
69	Expert Curation of Somatic Variants in Hematological Malignancies By the Clingen Somatic Hematological Cancer Taskforce (ClinGen HCT). Blood, 2020, 136, 23-23.	1.4	0
70	Integrated, Integral, and Exploratory Biomarkers in the Development of Poly(ADP-Ribose) Polymerase Inhibitors. Cancer Journal (Sudbury, Mass), 2021, 27, 482-490.	2.0	0