Jie He

List of Publications by Year in descending order

65 papers	3,875 citations	331670 21 h-index	233421 45 g-index
65 all docs	65 docs citations	65 times ranked	8204 citing authors

#	Article	IF	Citations
1	Intensity modulated radiation therapy may improve survival for tracheal-bronchial adenoid cystic carcinoma: A retrospective study of 133 cases. Lung Cancer, 2021, 157, 116-123.	2.0	4
2	Co-occurring gain-of-function mutations in HER2 and HER3 modulate HER2/HER3 activation, oncogenesis, and HER2 inhibitor sensitivity. Cancer Cell, 2021, 39, 1099-1114.e8.	16.8	45
3	Prognostic impact of somatic mutations in diffuse large B-cell lymphoma and relationship to cell-of-origin: data from the phase III GOYA study. Haematologica, 2020, 105, 2298-2307.	3.5	34
4	Clonal diversity predicts adverse outcome in chronic lymphocytic leukemia. Leukemia, 2019, 33, 390-402.	7.2	44
5	Genomic profiling of cell-free circulating tumor DNA in patients with colorectal cancer and its fidelity to the genomics of the tumor biopsy. Journal of Gastrointestinal Oncology, 2019, 10, 831-840.	1.4	31
6	Combined Blockade of Activating ERBB2 Mutations and ER Results in Synthetic Lethality of ER+/HER2 Mutant Breast Cancer. Clinical Cancer Research, 2019, 25, 277-289.	7.0	74
7	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. Journal of Clinical Investigation, 2019, 129, 4276-4289.	8.2	134
8	Acid-Based Decalcification Methods Compromise Genomic Profiling from DNA and RNA. Blood, 2019, 134, 4659-4659.	1.4	3
9	PIK3CA C2 Domain Deletions Hyperactivate Phosphoinositide 3-kinase (PI3K), Generate Oncogene Dependence, and Are Exquisitely Sensitive to PI3KÎ± Inhibitors. Clinical Cancer Research, 2018, 24, 1426-1435.	7.0	27
10	Analytical Validation of a Hybrid Captureâ€"Based Next-Generation Sequencing Clinical Assay for Genomic Profiling of Cell-Free Circulating Tumor DNA. Journal of Molecular Diagnostics, 2018, 20, 686-702.	2.8	149
11	A Next-Generation Sequencing-Based Karyotyping Algorithm Reveals the Genomic Structure of Acute Myeloid Leukemia. Blood, 2018, 132, 2773-2773.	1.4	1
12	Genomic alterations (GA) predicted to confer lack of benefit from trastuzumab in advanced esophagogastric cancers (EGC): Analysis of 527 HER2-amplified (HER2amp) cases.. Journal of Clinical Oncology, 2018, 36, 44-44.	1.6	4
13	Comprehensive genomic profiling of ctDNA in patients with colon cancer and its fidelity to the genomics of the tumor biopsy.. Journal of Clinical Oncology, 2018, 36, 569-569.	1.6	4
14	Distinct age-associated molecular profiles in acute myeloid leukemia defined by comprehensive clinical genomic profiling. Oncotarget, 2018, 9, 26417-26430.	1.8	25
15	Co-existing alterations in cell-cycle pathway genes and impact on benefit from trastuzumab in advanced esophagogastric cancers (EGC): Analysis of 527 Her2-amplified cases.. Journal of Clinical Oncology, 2018, 36, 4063-4063.	1.6	0
16	Genomic Profiling of a Large Set of Diverse Pediatric Cancers Identifies Known and Novel Mutations across Tumor Spectra. Cancer Research, 2017, 77, 509-519.	0.9	75
17	An Acquired HER2â€ˆT798I Gatekeeper Mutation Induces Resistance to Neratinib in a Patient with HER2 Mutantâ€"Driven Breast Cancer. Cancer Discovery, 2017, 7, 575-585.	9.4	85
18	High-Throughput Genomic Profiling of Adult Solid Tumors Reveals Novel Insights into Cancer Pathogenesis. Cancer Research, 2017, 77, 2464-2475.	0.9	93

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19	Genomics of primary chemoresistance and remission induction failure in paediatric and adult acute myeloid leukaemia. British Journal of Haematology, 2017, 176, 86-91.	2.5	29
20	Development and validation of a real-world clinicogenomic database.. Journal of Clinical Oncology, 2017, 35, 2514-2514.	1.6	9
21	Comprehensive genomic profiling (CGP) of esophageal and tubular GI tumors to identify frequencies of ErbB family member amplification with therapeutic implications.. Journal of Clinical Oncology, 2017, 35, 8-8.	1.6	0
22	Genomic profiling of circulating tumor DNA (ctDNA) from patients (pts) with pancreatic ductal adenocarcinoma (PDA).. Journal of Clinical Oncology, 2017, 35, 4128-4128.	1.6	0
23	Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. Blood, 2016, 127, 3004-3014.	1.4	244
24	Comprehensive Genomic Profiling of Advanced Penile Carcinoma Suggests a High Frequency of Clinically Relevant Genomic Alterations. Oncologist, 2016, 21, 33-39.	3.7	69
25	Clinical Relevant Alterations Identified By Comprehensive Genomic Profiling Can Potentially Improve Therapeutic Option and Change Prognosis in Hematologic Malignancies. Blood, 2016, 128, 5109-5109.	1.4	2
26	Total mutation burden (TMB) in lung cancer (LC) and relationship with response to PD-1/PD-L1 targeted therapies.. Journal of Clinical Oncology, 2016, 34, 9017-9017.	1.6	129
27	MDM2 amplification (Amp) to mediate cabozantinib resistance in patients (Pts) with advanced RET-rearranged lung cancers.. Journal of Clinical Oncology, 2016, 34, 9068-9068.	1.6	15
28	Analytic validation of a clinical circulating tumor DNA assay for patients with solid tumors.. Journal of Clinical Oncology, 2016, 34, e23049-e23049.	1.6	2
29	Comprehensive genomic profiling in colorectal cancer (CRC) to identify differing frequencies of clinically relevant genomic alterations (CRGA) in tumors of patients (pts) less than age 50 as compared to those of pts over age 65.. Journal of Clinical Oncology, 2016, 34, 570-570.	1.6	0
30	Distinct age-associated genomic profiles in acute myeloid leukemia (AML) using FoundationOne heme.. Journal of Clinical Oncology, 2016, 34, 7041-7041.	1.6	1
31	A Survey of Fusion Genes in Myeloma Identifies Kinase Domain Activation Which Could be Targeted with Available Treatments. Blood, 2016, 128, 117-117.	1.4	1
32	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. Blood, 2016, 128, 4416-4416.	1.4	1
33	Aberrant Phosphorylation of MEF2C Is Dispensable for Hematopoiesis, and Induces Chemotherapy Resistance and Susceptibility to MARK Kinase Inhibition Therapy in Acute Myeloid Leukemia. Blood, 2016, 128, 436-436.	1.4	0
34	Comprehensive Clinical Genomic Profiling Defines Age-Associated Molecular Targets in Pediatric and Adult Acute Myeloid Leukemia. Blood, 2016, 128, 596-596.	1.4	0
35	Comprehensive Genomic Profiling for Improved Diagnosis and Therapy of Pediatric Acute Leukemias. Blood, 2016, 128, 1605-1605.	1.4	0
36	Multiple Myeloma with a Deletion of Chromosome 17p: TP53 Mutations Are Highly Prevalent and Negatively Affect Prognosis. Blood, 2016, 128, 3271-3271.	1.4	2

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37	Tumor-specific HSP90 inhibition as a therapeutic approach in JAK-mutant acute lymphoblastic leukemias. Blood, 2015, 126, 2479-2483.	1.4	36
38	Detection of Crizotinib-Sensitive Lung Adenocarcinomas With MET, ALK, and ROS1 Genomic Alterations via Comprehensive Genomic Profiling. Clinical Lung Cancer, 2015, 16, e105-e109.	2.6	10
39	Comprehensive Genomic Profiling (CGP) of Angioimmunoblastic T-Cell Lymphoma (AITL) to Prospectively Inform Diagnosis and Clinical Management. Blood, 2015, 126, 3898-3898.	1.4	1
40	Frequency of clinically relevant genomic alterations using comprehensive genomic profiling (CGP) for the management of advanced gynecologic malignancies in a community setting.. Journal of Clinical Oncology, 2015, 33, e22068-e22068.	1.6	0
41	Comprehensive genomic profiling identifies clinically relevant genomic alterations in relapsed and metastatic penile squamous cell carcinoma.. Journal of Clinical Oncology, 2015, 33, e15628-e15628.	1.6	0
42	Integrated DNA/RNA Profiling for Somatic Alterations in Adult B-Cell ALL. Blood, 2015, 126, 1422-1422.	1.4	0
43	Genomic and Proteomic Analysis of Primary Chemoresistance and Induction Failure in Acute Myeloid Leukemia. Blood, 2015, 126, 88-88.	1.4	0
44	Defining the Incidence and Clinical Impact of Genomic Alterations Across Different Histologic Types of Lymphoma Using a Clinically Validated Comprehensive Targeted Sequencing Assay. Blood, 2015, 126, 2668-2668.	1.4	0
45	Predictive and Prognostic Significance of Comprehensive Genomic Profiling in Patients with Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 2651-2651.	1.4	0
46	Unique metastases of ALK mutated lung cancer activated to the adnexa of the uterus. Case Reports in Clinical Pathology, 2014, 1, 151-154.	0.0	10
47	Kinase fusions are frequent in Spitz tumours and spitzoid melanomas. Nature Communications, 2014, 5, 3116.	12.8	521
48	Advanced urothelial carcinoma: next-generation sequencing reveals diverse genomic alterations and targets of therapy. Modern Pathology, 2014, 27, 271-280.	5.5	122
49	Sclerosing epithelioid fibrosarcoma presenting as intraabdominal sarcomatosis with a novel EWSR1-CREB3L1 gene fusion. Human Pathology, 2014, 45, 2173-2178.	2.0	30
50	Novel Chromatin Modifying Gene Alterations and Significant Survival Association of ATM and P53 in Mantle Cell Lymphoma. Blood, 2014, 124, 3033-3033.	1.4	2
51	Identifying ALK rearrangements that are not detected by FISH with targeted next-generation sequencing of lung carcinoma.. Journal of Clinical Oncology, 2014, 32, 8049-8049.	1.6	11
52	Genomic Analysis of Serial Samples from CLL Patients Identifies Clonal Events Associated with Disease Progression. Blood, 2014, 124, 1954-1954.	1.4	0
53	A Comprehensive Clinical Next Generation Sequencing-Based Assay Can Impact Hematopathologic Diagnosis in a Significant Subset of Patients with Hematologic Malignancies. Blood, 2014, 124, 2984-2984.	1.4	0
54	Clinical Utility of Comprehensive Profiling of Genomic Alterations in Hematologic Malignancies. Blood, 2014, 124, 1072-1072.	1.4	0

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55	Identification of Actionable Genomic Alterations Across Different Lymphoma Histologies Using a Comprehensive Next Generation Genomic Sequencing Clinical Assay. Blood, 2014, 124, 3000-3000.	1.4	0
56	Utility of Combined DNA and RNA Next Generation Sequencing in Leukemias for Identification of Prognostic and Therapeutically Relevant Genomic Alterations in Clinical Practice. Blood, 2014, 124, 1039-1039.	1.4	0
57	Genomic Profiling Combining DNA and RNA Analysis of 112 Formalin-Fixed Paraffin-Embedded Diffuse Large B Cell Lymphoma Specimens Identifies a High Frequency of Clinically Relevant Genomic Alterations. Blood, 2014, 124, 704-704.	1.4	0
58	Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. Nature Biotechnology, 2013, 31, 1023-1031.	17.5	1,785
59	Integrated Genetic Profiling Of JAK2 Wildtype Chronic-Phase Myeloproliferative Neoplasms. Blood, 2013, 122, 1588-1588.	1.4	1
60	Profiling Genomic Alterations Of Diffuse Large B-Cell Lymphoma (DLBCL) At Diagnosis, Relapse, and Transformation, Using a Novel Clinical Diagnostic Targeted Sequencing Platform. Blood, 2013, 122, 1761-1761.	1.4	3
61	Identification Of Actionable Genomic Alterations In Hematologic Malignancies By a Clinical Next Generation Sequencing-Based Assay. Blood, 2013, 122, 230-230.	1.4	2
62	Extensive High-Depth Sequencing Of Longitudinal CLL Samples Identifies Frequent Mutations In MAP Kinase Signaling and Novel Mutations Activating Notch and Beta-Catenin. Blood, 2013, 122, 2858-2858.	1.4	2
63	Next-generation sequencing of genomic and cDNA to identify a high frequency of kinase fusions involving ROS1, ALK, RET, NTRK1, and BRAF in Spitz tumors.. Journal of Clinical Oncology, 2013, 31, 9002-9002.	1.6	2
64	Clinical next generation sequencing (NGS) of fine needle aspiration (FNA) biopsies in non-small cell lung (NSCLC) and pancreatic cancers.. Journal of Clinical Oncology, 2013, 31, 11100-11100.	1.6	1
65	Overview Of The Genomic Landscape Of High Risk Diffuse Large B-Cell Lymphoma Using Targeted DNA and RNA Sequencing. Blood, 2013, 122, 501-501.	1.4	0