

# Xinjie Xu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1616004/publications.pdf>

Version: 2024-02-01

19  
papers

104  
citations

1684188

5  
h-index

1372567

10  
g-index

19  
all docs

19  
docs citations

19  
times ranked

203  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Novel <i>USP25::PDGFRA</i> Gene Fusion in a 78 Year Old Patient with a Myeloid Neoplasm. <i>Laboratory Medicine</i> , 2022, 53, e134-e138.	1.2	1
2	Identification of <i>EWSR1</i> rearrangements in patients with immature hematopoietic neoplasms: A case series and review of literature. <i>Annals of Diagnostic Pathology</i> , 2022, 58, 151942.	1.3	1
3	Guiding the global evolution of cytogenetic testing for hematologic malignancies. <i>Blood</i> , 2022, 139, 2273-2284.	1.4	29
4	Apparent coexistence of <i>ETV6::RUNX1</i> and <i>KMT2A::MLLT3</i> fusions due to a nonproductive <i>KMT2A</i> rearrangement in B-ALL. <i>Leukemia and Lymphoma</i> , 2022, , 1-4.	1.3	1
5	A community approach to the cancer-variant-interpretation bottleneck. <i>Nature Cancer</i> , 2022, 3, 522-525.	13.2	3
6	Identification of a novel <i>KMT2A</i> / <i>GIMAP8</i> gene fusion in a pediatric patient with acute undifferentiated leukemia. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 108-111.	2.8	5
7	Myeloid malignancies with 5q and 7q deletions are associated with extreme genomic complexity, biallelic TP53 variants, and very poor prognosis. <i>Blood Cancer Journal</i> , 2021, 11, 18.	6.2	8
8	Clinical utility of next generation sequencing to detect <i>IGH/IL3</i> rearrangements [t(5;14)(q31.1;q32.1)] in B-lymphoblastic leukemia/lymphoma. <i>Annals of Diagnostic Pathology</i> , 2021, 53, 151761.	1.3	8
9	OUP accepted manuscript. <i>Laboratory Medicine</i> , 2021, , .	1.2	1
10	Utilizing next-generation sequencing to characterize a case of acute myeloid leukemia with t(4;12)(q12;p13) in the absence of <i>ETV6/CHIC2</i> and <i>ETV6/PDGFR</i> gene fusions. <i>Cancer Genetics</i> , 2021, 260-261, 1-5.	0.4	0
11	<i>MYC</i> break-apart FISH probe set reveals frequent unbalanced patterns of uncertain significance when evaluating aggressive B-cell lymphoma. <i>Blood Cancer Journal</i> , 2021, 11, 184.	6.2	6
12	Expert Curation of Somatic <i>FLT3</i> Variants By the Clingen Somatic Hematologic Cancer Taskforce (ClinGen HCT). <i>Blood</i> , 2021, 138, 4387-4387.	1.4	0
13	Siblings with <i>ETV6/RUNX1</i> -positive B-lymphoblastic leukemia: A single site experience and review of the literature. <i>Annals of Diagnostic Pathology</i> , 2020, 48, 151588.	1.3	1
14	Detection of cryptic <i>CCND1</i> rearrangements in mantle cell lymphoma by next generation sequencing. <i>Annals of Diagnostic Pathology</i> , 2020, 46, 151533.	1.3	8
15	Cryptic and atypical <i>KMT2A</i> / <i>USP2</i> and <i>KMT2A</i> / <i>USP8</i> rearrangements identified by mate pair sequencing in infant and childhood leukemia. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 422-427.	2.8	7
16	Expert Variant Curation Combined with in-Silico analysis for Clinical Interpretation of <i>BCL2</i> variants in Resistance to <i>BCL2</i> Inhibitors in Chronic Lymphocytic Leukemia/ Small Lymphocytic Lymphoma. <i>Blood</i> , 2020, 136, 42-43.	1.4	0
17	Clinical Value of Next Generation Sequencing in the Detection of Recurring Structural Rearrangements and Copy Number Abnormalities in Acute Myeloid Leukemia. <i>Blood</i> , 2020, 136, 21-22.	1.4	0
18	Expert Curation of Somatic Variants in Hematological Malignancies By the Clingen Somatic Hematological Cancer Taskforce (ClinGen HCT). <i>Blood</i> , 2020, 136, 23-23.	1.4	0

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19	Assessing copy number aberrations and copy neutral loss of heterozygosity across the genome as best practice: An evidence based review of clinical utility from the cancer genomics consortium (CGC) working group for myelodysplastic syndrome, myelodysplastic/myeloproliferative and myeloproliferative neoplasms. <i>Cancer Genetics</i> , 2018, 228-229, 197-217.	0.4	25