Linda B Baughn

List of Publications by Year
in descending order

117 papers	1,767 citations	331670 21 h-index	330143 37 g-index
119 all docs	119 docs citations	119 times ranked	3152 citing authors

#	Article	IF	Citations
1	A Novel Orally Active Small Molecule Potently Induces G1 Arrest in Primary Myeloma Cells and Prevents Tumor Growth by Specific Inhibition of Cyclin-Dependent Kinase 4/6. Cancer Research, 2006, 66, 7661-7667.	0.9	209
2	Functional convergence of histone methyltransferases EHMT1 and KMT2C involved in intellectual disability and autism spectrum disorder. PLoS Genetics, 2017, 13, e1006864.	3.5	116
3	Mutually Exclusive Cyclin-Dependent Kinase 4/Cyclin D1 and Cyclin-Dependent Kinase 6/Cyclin D2 Pairing Inactivates Retinoblastoma Protein and Promotes Cell Cycle Dysregulation in Multiple Myeloma. Cancer Research, 2005, 65, 11345-11353.	0.9	101
4	Targeting TMPRSS2 in SARS-CoV-2 Infection. Mayo Clinic Proceedings, 2020, 95, 1989-1999.	3.0	100
5	Molecular signatures of multiple myeloma progression through single cell RNA-Seq. Blood Cancer Journal, 2019, 9, 2.	6.2	74
6	Profiling Bortezomib Resistance Identifies Secondary Therapies in a Mouse Myeloma Model. Molecular Cancer Therapeutics, 2013, 12, 1140-1150.	4.1	68
7	Cytogenetic abnormalities in multiple myeloma: association with disease characteristics and treatment response. Blood Cancer Journal, 2020, 10, 82.	6.2	59
8	Clinical characteristics and treatment outcomes of newly diagnosed multiple myeloma with chromosome 1q abnormalities. Blood Advances, 2020, 4, 3509-3519.	5.2	58
9	Differences in genomic abnormalities among African individuals with monoclonal gammopathies using calculated ancestry. Blood Cancer Journal, 2018, 8, 96.	6.2	47
10	The future of myeloma precision medicine: integrating the compendium of known drug resistance mechanisms with emerging tumor profiling technologies. Leukemia, 2019, 33, 863-883.	7.2	45
11	False-negative rates for MYC fluorescence in situ hybridization probes in B-cell neoplasms. Haematologica, 2019, 104, e248-e251.	3.5	43
12	Expression of Germinal Center B Cell Markers in Bortezomib-Resistant Multiple Myeloma Cells. Blood, 2011, 118, 129-129.	1.4	39
13	Mate pair sequencing improves detection of genomic abnormalities in acute myeloid leukemia. European Journal of Haematology, 2019, 102, 87-96.	2.2	35
14	CDK2 Phosphorylation of Smad2 Disrupts TGF-Î² Transcriptional Regulation in Resistant Primary Bone Marrow Myeloma Cells. Journal of Immunology, 2009, 182, 1810-1817.	0.8	34
15	Implications of MYC Rearrangements in Newly Diagnosed Multiple Myeloma. Clinical Cancer Research, 2020, 26, 6581-6588.	7.0	32
16	Integration of cytogenomic data for furthering the characterization of pediatric B-cell acute lymphoblastic leukemia: a multi-institution, multi-platform microarray study. Cancer Genetics, 2015, 208, 1-18.	0.4	30
17	A simple additive staging system for newly diagnosed multiple myeloma. Blood Cancer Journal, 2022, 12, 21.	6.2	30
18	Guiding the global evolution of cytogenetic testing for hematologic malignancies. Blood, 2022, 139, 2273-2284.	1.4	29

#	Article	IF	Citations
19	CNV-RF Is a Random Forestâ€“Based Copy Number Variation Detection Method Using Next-Generation Sequencing. Journal of Molecular Diagnostics, 2016, 18, 872-881.	2.8	28
20	Mate pair sequencing outperforms fluorescence in situ hybridization in the genomic characterization of multiple myeloma. Blood Cancer Journal, 2019, 9, 103.	6.2	27
21	Secondary cytogenetic abnormalities in core-binding factor AML harboring inv(16) vs t(8;21). Blood Advances, 2021, 5, 2481-2489.	5.2	25
22	KMT2A (MLL) rearrangements observed in pediatric/young adult Tâ€lymphoblastic leukemia/lymphoma: A 10â€year review from a single cytogenetic laboratory. Genes Chromosomes and Cancer, 2018, 57, 541-546.	2.8	21
23	Utilization of Translational Bioinformatics to Identify Novel Biomarkers of Bortezomib Resistance in Multiple Myeloma. Journal of Cancer, 2014, 5, 720-727.	2.5	20
24	Metaphase cytogenetics and plasma cell proliferation index for risk stratification in newly diagnosed multiple myeloma. Blood Advances, 2020, 4, 2236-2244.	5.2	20
25	Acute leukemias harboring KMT2A/MLLT10 fusion: a 10â€year experience from a single genomics laboratory. Genes Chromosomes and Cancer, 2019, 58, 567-577.	2.8	19
26	Phenotypic and functional characterization of a bortezomib-resistant multiple myeloma cell line by flow and mass cytometry. Leukemia and Lymphoma, 2017, 58, 1931-1940.	1.3	17
27	Coreâ€binding factor acute myeloid leukemia with t(8;21): Risk factors and a novel scoring system (Iâ€•CBF) Tj ETQq1 1 0.784314 rg	2.8	17
28	Bortezomib Resistance Can Be Reversed by Induced Expression of Plasma Cell Maturation Markers in a Mouse In Vitro Model of Multiple Myeloma. PLoS ONE, 2013, 8, e77608.	2.5	17
29	Characterization of a cryptic IGH/CCND1 rearrangement in a case of mantle cell lymphoma with negative CCND1 FISH studies. Blood Advances, 2019, 3, 1298-1302.	5.2	16
30	Characterization of TCF3 rearrangements in pediatric B-lymphoblastic leukemia/lymphoma by mate-pair sequencing (MPseq) identifies complex genomic rearrangements and a novel TCF3/TEF gene fusion. Blood Cancer Journal, 2019, 9, 81.	6.2	14
31	Elucidating a false-negative MYC break-apart fluorescence in situ hybridization probe study by next-generation sequencing in a patient with high-grade B-cell lymphoma with IGH/MYC and IGH/BCL2 rearrangements. Journal of Physical Education and Sports Management, 2019, 5, a004077.	1.2	14
32	Evidence-based review of genomic aberrations in B-lymphoblastic leukemia/lymphoma: Report from the cancer genomics consortium working group for lymphoblastic leukemia. Cancer Genetics, 2020, 243, 52-72.	0.4	14
33	The Prognostic Role of MYC Structural Variants Identified by NGS and FISH in Multiple Myeloma. Clinical Cancer Research, 2021, 27, 5430-5439.	7.0	14
34	Lymphoid blast transformation in an MPN with BCR-JAK2 treated with ruxolitinib: putative mechanisms of resistance. Blood Advances, 2021, 5, 3492-3496.	5.2	14
35	Characterization of unusual <scp>iAMP21</scp> Bâ€lymphoblastic leukemia (<scp>iAMP21â€ALL</scp>) from the Mayo Clinic and Children's Oncology Group. Genes Chromosomes and Cancer, 2022, 61, 710-719.	2.8	14
36	The Utilization of Chromosomal Microarray Technologies for Hematologic Neoplasms. American Journal of Clinical Pathology, 2018, 150, 375-384.	0.7	13

#	Article	IF	Citations
37	Tetraploidy is associated with poor prognosis at diagnosis in multiple myeloma. American Journal of Hematology, 2019, 94, E117-E120.	4.1	13
38	Rapid assessment of hyperdiploidy in plasma cell disorders using a novel multiâ€parametric flow cytometry method. American Journal of Hematology, 2019, 94, 424-430.	4.1	11
39	Bosutinib, a <scp>L</scp>yn/<scp>B</scp>tk inhibiting tyrosine kinase inhibitor, is ineffective in advanced systemic mastocytosis. American Journal of Hematology, 2015, 90, E74.	4.1	10
40	Hyperhaploid plasma cell myeloma characterized by poor outcome and monosomy 17 with frequently co-occurring TP53 mutations. Blood Cancer Journal, 2019, 9, 20.	6.2	10
41	In vitro and ex vivo gene expression profiling reveals differential kinetic response of HSPs and UPR genes is associated with PI resistance in multiple myeloma. Blood Cancer Journal, 2020, 10, 78.	6.2	9
42	Disruption of the Shc/Grb2 Complex during Abelson Virus Transformation Affects Proliferation, but Not Apoptosis. Journal of Virology, 2005, 79, 2325-2334.	3.4	8
43	Detection of a cryptic NUP214/ABL1 gene fusion by mate-pair sequencing (MPseq) in a newly diagnosed case of pediatric T-lymphoblastic leukemia. Journal of Physical Education and Sports Management, 2019, 5, a003533.	1.2	8
44	Constitutional chromosome rearrangements that mimic the 2017 world health organization â€œacute myeloid leukemia with recurrent genetic abnormalitiesâ€: A study of three cases and review of the literature. Cancer Genetics, 2019, 230, 37-46.	0.4	8
45	Fluorescence inâ€situ hybridisation for TP63 rearrangements in T cell lymphomas: singleâ€site experience of 470 patients and implications for clinical testing. Histopathology, 2020, 76, 481-485.	2.9	8
46	Detection of cryptic CCND1 rearrangements in mantle cell lymphoma by next generation sequencing. Annals of Diagnostic Pathology, 2020, 46, 151533.	1.3	8
47	Myeloid malignancies with 5q and 7q deletions are associated with extreme genomic complexity, biallelic TP53 variants, and very poor prognosis. Blood Cancer Journal, 2021, 11, 18.	6.2	8
48	Clinical utility of next generation sequencing to detect IGH/IL3 rearrangements [t(5;14)(q31.1;q32.1)] in B-lymphoblastic leukemia/lymphoma. Annals of Diagnostic Pathology, 2021, 53, 151761.	1.3	8
49	In Silico Prediction of Novel Drug Combinations to Combat Bortezomib-Resistant Multiple Myeloma. Blood, 2012, 120, 1344-1344.	1.4	8
50	Assessing the prognostic utility of smoldering multiple myeloma risk stratification scores applied serially post diagnosis. Blood Cancer Journal, 2021, 11, 186.	6.2	8
51	Identification of a Novel ZBTB20-JAK2 Fusion by Mate-Pair Sequencing in a Young Adult With B-Lymphoblastic Leukemia/Lymphoma. Mayo Clinic Proceedings, 2019, 94, 1381-1384.	3.0	7
52	Use of mate-pair sequencing to characterize a complex cryptic BCR/ABL1 rearrangement observed in a newly diagnosed case of chronic myeloid leukemia. Human Pathology, 2019, 89, 109-114.	2.0	7
53	Characterization of a cryptic PML-RARA fusion by mate-pair sequencing in a case of acute promyelocytic leukemia with a normal karyotype and negative RARA FISH studies. Leukemia and Lymphoma, 2020, 61, 975-978.	1.3	7
54	Integrated genomic analysis using chromosomal microarray, fluorescence in situ hybridization and mate pair analyses: Characterization of a cryptic t(9;22)(p24.1;q11.2)/BCR-JAK2 in myeloid/lymphoid neoplasm with eosinophilia. Cancer Genetics, 2020, 246-247, 44-47.	0.4	7

#	Article	IF	Citations
55	Cryptic and atypical <scp>KMT2Aâ€USP2</scp> and <scp>KMT2Aâ€USP8</scp> rearrangements identified by mate pair sequencing in infant and childhood leukemia. Genes Chromosomes and Cancer, 2020, 59, 422-427.	2.8	7
56	Typical, atypical and cryptic t(15;17)(q24;q21) (PML::RARA) observed in acute promyelocytic leukemia: A retrospective review of 831 patients with concurrent chromosome and PML::RARA dualâ€color dualâ€fusion FISH studies. Genes Chromosomes and Cancer, 2022, 61, 629-634.	2.8	7
57	Characterizing false-positive fluorescence in situ hybridization results by mate-pair sequencing in a patient with chronic myeloid leukemia and progression to myeloid blast crisis. Cancer Genetics, 2020, 243, 48-51.	0.4	6
58	Coreâ€binding factor acute myeloid leukemia with inv(16): Older age and high white blood cell count are risk factors for treatment failure. International Journal of Laboratory Hematology, 2021, 43, e19-e25.	1.3	6
59	Comparative study of therapyâ€related and de novo adult bâ€cell acute lymphoblastic leukaemia. British Journal of Haematology, 2022, 196, 963-968.	2.5	6
60	Prognostic significance of acquired 1q22 gain in multiple myeloma. American Journal of Hematology, 2021, , .	4.1	6
61	MYC break-apart FISH probe set reveals frequent unbalanced patterns of uncertain significance when evaluating aggressive B-cell lymphoma. Blood Cancer Journal, 2021, 11, 184.	6.2	6
62	Necrotizing Enterocolitis in Two Siblings and an Unrelated Infant with Overlapping Chromosome 6q25 Deletions. Molecular Syndromology, 2018, 9, 141-148.	0.8	5
63	Characterization of a rarely reported STAT5B/RARA gene fusion in a young adult with newly diagnosed acute promyelocytic leukemia with resistance to ATRA therapy. Cancer Genetics, 2019, 237, 51-54.	0.4	5
64	An intragenic duplication of TRPS1 leading to abnormal transcripts and causing trichorhinophalangeal syndrome type I. Journal of Physical Education and Sports Management, 2019, 5, a004655.	1.2	5
65	Identification of a novel <scp>KMT2A</scp>/<scp>GIMAP8</scp> gene fusion in a pediatric patient with acute undifferentiated leukemia. Genes Chromosomes and Cancer, 2021, 60, 108-111.	2.8	5
66	The Genetics of Sudden Infant Death Syndromeâ€"Towards a Gene Reference Resource. Genes, 2021, 12, 216.	2.4	5
67	Modeling Proteasome Inhibition in Lymphoma. Blood, 2011, 118, 4946-4946.	1.4	5
68	secDrug: a pipeline to discover novel drug combinations to kill drug-resistant multiple myeloma cells using a greedy set cover algorithm and single-cell multi-omics. Blood Cancer Journal, 2022, 12, 39.	6.2	5
69	Clinical utility of fluorescence in situ hybridizationâ€based diagnosis of BCRâ€ABL1 like (<scp>P</scp>hiladelphia chromosome like) <scp>B</scp>â€cute lymphoblastic leukemia. American Journal of Hematology, 2020, 95, E68-E72.	4.1	4
70	The CCND1 c.870G risk allele is enriched in individuals of African ancestry with plasma cell dyscrasias. Blood Cancer Journal, 2020, 10, 39.	6.2	4
71	IGH rearrangement in myeloid neoplasms. Haematologica, 2020, 105, e315-e317.	3.5	4
72	Identification of adult Philadelphia-like acute lymphoblastic leukemia using a FISHâ€based algorithm distinguishes prognostic groups and outcomes. Blood Cancer Journal, 2021, 11, 156.	6.2	4

#	Article	IF	Citations
73	A nearâ€haploid clone harboring a BCR/ABL1 gene fusion in an adult patient with newly diagnosed Bâ€lymphoblastic leukemia. Genes Chromosomes and Cancer, 2019, 58, 665-668.	2.8	3
74	Secondary acquisition of BCR-ABL1 fusion in de novo GATA2-MECOM positive acute myeloid leukemia with subsequent emergence of a rare KMT2A-ASXL2 fusion. Cancer Genetics, 2020, 241, 67-71.	0.4	3
75	Establishing a Novel Pipeline That Combines in-Silico Prediction with in-Vitro and Ex-Vivo Validation to Discover Secondary Drug Combinations Against Relapsed and/or Refractory Multiple Myeloma. Blood, 2021, 138, 1615-1615.	1.4	3
76	Family history of plasma cell disorders is associated with improved survival in MGUS, multiple myeloma, and systemic AL amyloidosis. Leukemia, 2022, 36, 1058-1065.	7.2	3
77	Buccal epithelial cells display somatic, bone marrowâ€“derived CALR mutation. Blood Advances, 2017, 1, 2302-2306.	5.2	2
78	Whole Genome Mate-pair Sequencing of Plasma Cell Neoplasm as a Novel Diagnostic Strategy: AÂCase of Unrecognized t(2;11) Structural Variation. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, 598-602.	0.4	2
79	Limited diagnostic impact of duplications <1 Mb of uncertain clinical significance: a 10-year retrospective analysis of reporting practices at the Mayo Clinic. Genetics in Medicine, 2020, 22, 2120-2124.	2.4	2
80	Increased complexity of t(11;14) rearrangements in plasma cell neoplasms compared with mantle cell lymphoma. Genes Chromosomes and Cancer, 2021, 60, 678-686.	2.8	2
81	SH2-Containing Inositol 5'-Phosphatase Inhibits Transformation of Abelson Murine Leukemia Virus. Journal of Virology, 2011, 85, 9239-9242.	3.4	1
82	Standardization of Minimal Residual Disease Testing in Multiple Myeloma. journal of applied laboratory medicine, The, 2017, 2, 118-122.	1.3	1
83	Characterization of a cryptic KMT2A/AFF1 gene fusion by mate-pair sequencing (MPseq) in a young adult with newly diagnosed B-lymphoblastic leukemia. Journal of Hematopathology, 2019, 12, 99-104.	0.4	1
84	Siblings with ETV6/RUNX1-positive B-lymphoblastic leukemia: A single site experience and review of the literature. Annals of Diagnostic Pathology, 2020, 48, 151588.	1.3	1
85	OUP accepted manuscript. Laboratory Medicine, 2021, , .	1.2	1
86	Strategies To Identify Effective Treatments For Proteasome Inhibitor Resistant Multiple Myeloma. Blood, 2013, 122, 278-278.	1.4	1
87	Germline Calr Mutation and Thrombocytosis Presenting with Concomitant BCR-ABL1+ CML. Blood, 2016, 128, 5494-5494.	1.4	1
88	A Novel Approach to Risk Stratification in Multiple Myeloma Using ISS Stage and FISH. Blood, 2019, 134, 1800-1800.	1.4	1
89	Detection of a Cryptic KMT2A/AFDN Gene Fusion [ins(6;11)(q27;q23q23)] in a Pediatric Patient with Newly Diagnosed Acute Myeloid Leukemia. Laboratory Medicine, 2022, 53, e95-e99.	1.2	1
90	Characterization of Atypical t(11;14) CCND1/IGH Translocations in Multiple Myeloma. Blood, 2021, 138, 3771-3771.	1.4	1

#	Article	IF	Citations
91	A Novel USP25::PDGFRA Gene Fusion in a 78 Year Old Patient with a Myeloid Neoplasm. Laboratory Medicine, 2022, 53, e134-e138.	1.2	1
92	Identification of EWSR1 rearrangements in patients with immature hematopoietic neoplasms: A case series and review of literature. Annals of Diagnostic Pathology, 2022, 58, 151942.	1.3	1
93	Apparent coexistence of ETV6::RUNX1 and KMT2A::MLLT3 fusions due to a nonproductive KMT2A rearrangement in B-ALL. Leukemia and Lymphoma, 2022, , 1-4.	1.3	1
94	Stabilization of activation induced cytidine deaminase by bortezomib does not confer increased drug target mutation frequency. Leukemia and Lymphoma, 2014, 55, 220-222.	1.3	0
95	Utility of Genome-Wide Characterization of B-Cell Acute Lymphoblastic Leukemia Using SNP-Based Microarray. Cancer Genetics, 2016, 209, 292.	0.4	0
96	Characterization of a Novel Inverted Tandem Duplication by Mate Pair Sequencing (MPseq). Cancer Genetics, 2016, 209, 296-297.	0.4	0
97	Characterization of a t(1;2)(p36;p21) involving the PRDM16 gene region by mate-pair sequencing (MPseq) in a patient with newly diagnosed acute myeloid leukemia with myelodysplasia-related changes. Journal of Hematopathology, 2019, 12, 85-90.	0.4	0
98	67. NUP98 rearrangements in hematologic malignancies: A 4-year review from the genomics laboratory. Cancer Genetics, 2020, 244, 25-26.	0.4	0
99	Detection of a Cryptic EP300/ZNF384 Gene Fusion by Chromosomal Microarray and Next-Generation Sequencing Studies in a Pediatric Patient with B-Lymphoblastic Leukemia. Laboratory Medicine, 2021, 52, 297-302.	1.2	0
100	Lymphoma-like double-hit genetic abnormalities (MYC/IGH and IGH/BCL2) in a case of non-secretory multiple myeloma. Leukemia and Lymphoma, 2021, 62, 243-246.	1.3	0
101	Prenatal characterization of a novel inverted SMAD2 duplication by mate pair sequencing in a fetus with dextrocardia. Clinical Case Reports (discontinued), 2021, 9, 769-774.	0.5	0
102	Detection of t(5;14)(q31.1;q32.1) [IGH/IL3] in B-lymphoblastic leukemia by next generation sequencing. Molecular Genetics and Metabolism, 2021, 132, S46-S47.	1.1	0
103	Dual Primary IGH Translocations in Multiple Myeloma: A Novel Finding. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, e710-e713.	0.4	0
104	Good and Poor Response Gene Expression Signatures to Proteasome Inhibitors Using a Mouse Model of Multiple Myeloma. Blood, 2011, 118, 1843-1843.	1.4	0
105	Low Expression of CXCR4 in Bortezomib-Resistant Multiple Myeloma Correlates with Extramedullary Disease in a Murine Mouse Model. Blood, 2012, 120, 442-442.	1.4	0
106	Genomic Abnormalities Among African Individuals with Monoclonal Gammopathies Using Calculated Ancestry. Blood, 2018, 132, 4458-4458.	1.4	0
107	Metaphase Cytogenetics for Risk Stratification in Newly Diagnosed Multiple Myeloma. Blood, 2019, 134, 4396-4396.	1.4	0
108	The CCND1 870G Risk Allele Is Enriched in African Individuals with Plasma Cell Dyscrasias. Blood, 2019, 134, 4362-4362.	1.4	0

#	Article	IF	Citations
109	Differentiating between Hyperdiploidy and Pseudo-Hyperdiploidy in B-Lymphoblastic Leukemia Utilizing Low-Coverage Mate-Pair Sequencing. Blood, 2019, 134, 5212-5212.	1.4	0
110	Utilizing next-generation sequencing to characterize a case of acute myeloid leukemia with t(4;12)(q12;p13) in the absence of ETV6/CHIC2 and ETV6/PDGFRA gene fusions. Cancer Genetics, 2021, 260-261, 1-5.	0.4	0
111	False-Negative Centromere 15 Probe Results in Association with African Ancestry in Plasma Cell Dyscrasias. Blood, 2021, 138, 4101-4101.	1.4	0
112	Assessing the Prognostic Utility of the Mayo 2018 and IMWG 2020 Smoldering Multiple Myeloma Risk Stratification Scores When Applied Post Diagnosis. Blood, 2021, 138, 543-543.	1.4	0
113	The Prognostic Significance of Acquired 1q22 Gain in Multiple Myeloma. Blood, 2020, 136, 9-10.	1.4	0
114	Phenotypic and Functional Characterization of Multiple Myeloma By Single Cell Mass Cytometry (CyTOF). Blood, 2020, 136, 40-41.	1.4	0
115	Heterogeneity of MYC Abnormalities in Multiple Myeloma. Blood, 2020, 136, 2-3.	1.4	0
116	Clinical Value of Next Generation Sequencing in the Detection of Recurring Structural Rearrangements and Copy Number Abnormalities in Acute Myeloid Leukemia. Blood, 2020, 136, 21-22.	1.4	0
117	eP406: Germline 16p13.1 microdeletion identified during routine hematologic testing. Genetics in Medicine, 2022, 24, S255-S256.	2.4	0