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	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
2	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
3	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
4	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
5	A simple additive staging system for newly diagnosed multiple myeloma. Blood Cancer Journal, 2022, 12, 21.	6.2	30
6	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
7	eP406: Germline 16p13.1 microdeletion identified during routine hematologic testing. Genetics in Medicine, 2022, 24, S255-S256.	2.4	0
8	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
9	Guiding the global evolution of cytogenetic testing for hematologic malignancies. Blood, 2022, 139, 2273-2284.	1.4	29
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	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
18	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

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19	The Genetics of Sudden Infant Death Syndromeâ€"Towards a Gene Reference Resource. Genes, 2021, 12, 216.	2.4	5
20	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
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	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
23	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
24	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
25	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
26	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
27	Dual Primary IGH Translocations in Multiple Myeloma: A Novel Finding. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, e710-e713.	0.4	0
28	OUP accepted manuscript. Laboratory Medicine, 2021, , .	1.2	1
29	Prognostic significance of acquired 1q22 gain in multiple myeloma. American Journal of Hematology, 2021, , .	4.1	6
30	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
31	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
32	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
33	Assessing the prognostic utility of smoldering multiple myeloma risk stratification scores applied serially post diagnosis. Blood Cancer Journal, 2021, 11, 186.	6.2	8
34	Characterization of Atypical t(11;14) CCND1/IGH Translocations in Multiple Myeloma. Blood, 2021, 138, 3771-3771.	1.4	1
35	False-Negative Centromere 15 Probe Results in Association with African Ancestry in Plasma Cell Dyscrasias. Blood, 2021, 138, 4101-4101.	1.4	0
36	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

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37	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
38	Clinical utility of fluorescence in situ hybridizationâ€based diagnosis of BCRâ€ABL1 like (<scp>P</scp>hiladelphia chromosome like) <scp>B</scp>â€acute lymphoblastic leukemia. American Journal of Hematology, 2020, 95, E68-E72.	4.1	4
39	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
40	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
41	Implications of MYC Rearrangements in Newly Diagnosed Multiple Myeloma. Clinical Cancer Research, 2020, 26, 6581-6588.	7.0	32
42	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
43	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
44	Targeting TMPRSS2 in SARS-CoV-2 Infection. Mayo Clinic Proceedings, 2020, 95, 1989-1999.	3.0	100
45	Clinical characteristics and treatment outcomes of newly diagnosed multiple myeloma with chromosome 1q abnormalities. Blood Advances, 2020, 4, 3509-3519.	5.2	58
46	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
47	Cytogenetic abnormalities in multiple myeloma: association with disease characteristics and treatment response. Blood Cancer Journal, 2020, 10, 82.	6.2	59
48	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
49	Detection of cryptic CCND1 rearrangements in mantle cell lymphoma by next generation sequencing. Annals of Diagnostic Pathology, 2020, 46, 151533.	1.3	8
50	67. NUP98 rearrangements in hematologic malignancies: A 4-year review from the genomics laboratory. Cancer Genetics, 2020, 244, 25-26.	0.4	0
51	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
52	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
53	IGH rearrangement in myeloid neoplasms. Haematologica, 2020, 105, e315-e317.	3.5	4
54	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

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55	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
56	Metaphase cytogenetics and plasma cell proliferation index for risk stratification in newly diagnosed multiple myeloma. Blood Advances, 2020, 4, 2236-2244.	5.2	20
57	The Prognostic Significance of Acquired 1q22 Gain in Multiple Myeloma. Blood, 2020, 136, 9-10.	1.4	0
58	Phenotypic and Functional Characterization of Multiple Myeloma By Single Cell Mass Cytometry (CyTOF). Blood, 2020, 136, 40-41.	1.4	0
59	Heterogeneity of MYC Abnormalities in Multiple Myeloma. Blood, 2020, 136, 2-3.	1.4	0
60	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
61	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
62	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
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	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
65	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
66	Tetraploidy is associated with poor prognosis at diagnosis in multiple myeloma. American Journal of Hematology, 2019, 94, E117-E120.	4.1	13
67	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
68	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
69	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
70	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
71	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
72	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

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73	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
74	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
75	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
76	Mate pair sequencing outperforms fluorescence in situ hybridization in the genomic characterization of multiple myeloma. Blood Cancer Journal, 2019, 9, 103.	6.2	27
77	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
78	Molecular signatures of multiple myeloma progression through single cell RNA-Seq. Blood Cancer Journal, 2019, 9, 2.	6.2	74
79	False-negative rates for MYC fluorescence in situ hybridization probes in B-cell neoplasms. Haematologica, 2019, 104, e248-e251.	3.5	43
80	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
81	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
82	Mate pair sequencing improves detection of genomic abnormalities in acute myeloid leukemia. European Journal of Haematology, 2019, 102, 87-96.	2.2	35
83	Metaphase Cytogenetics for Risk Stratification in Newly Diagnosed Multiple Myeloma. Blood, 2019, 134, 4396-4396.	1.4	0
84	The CCND1 870G Risk Allele Is Enriched in African Individuals with Plasma Cell Dyscrasias. Blood, 2019, 134, 4362-4362.	1.4	0
85	A Novel Approach to Risk Stratification in Multiple Myeloma Using ISS Stage and FISH. Blood, 2019, 134, 1800-1800.	1.4	1
86	Differentiating between Hyperdiploidy and Pseudo-Hyperdiploidy in B-Lymphoblastic Leukemia Utilizing Low-Coverage Mate-Pair Sequencing. Blood, 2019, 134, 5212-5212.	1.4	0
87	Differences in genomic abnormalities among African individuals with monoclonal gammopathies using calculated ancestry. Blood Cancer Journal, 2018, 8, 96.	6.2	47
88	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
89	Necrotizing Enterocolitis in Two Siblings and an Unrelated Infant with Overlapping Chromosome 6q25 Deletions. Molecular Syndromology, 2018, 9, 141-148.	0.8	5
90	The Utilization of Chromosomal Microarray Technologies for Hematologic Neoplasms. American Journal of Clinical Pathology, 2018, 150, 375-384.	0.7	13

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91	Coreâ€binding factor acute myeloid leukemia with t(8;21): Risk factors and a novel scoring system (Iâ€•CBF) Tj ETQq1 1 0.784314 rgBT	2.8	17
92	Genomic Abnormalities Among African Individuals with Monoclonal Gammopathies Using Calculated Ancestry. Blood, 2018, 132, 4458-4458.	1.4	0
93	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
94	Buccal epithelial cells display somatic, bone marrowâ€“derived CALR mutation. Blood Advances, 2017, 1, 2302-2306.	5.2	2
95	Functional convergence of histone methyltransferases EHMT1 and KMT2C involved in intellectual disability and autism spectrum disorder. PLoS Genetics, 2017, 13, e1006864.	3.5	116
96	Standardization of Minimal Residual Disease Testing in Multiple Myeloma. journal of applied laboratory medicine, The, 2017, 2, 118-122.	1.3	1
97	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
98	Utility of Genome-Wide Characterization of B-Cell Acute Lymphoblastic Leukemia Using SNP-Based Microarray. Cancer Genetics, 2016, 209, 292.	0.4	0
99	Characterization of a Novel Inverted Tandem Duplication by Mate Pair Sequencing (MPseq). Cancer Genetics, 2016, 209, 296-297.	0.4	0
100	Germline Calr Mutation and Thrombocytosis Presenting with Concomitant BCR-ABL1+ CML. Blood, 2016, 128, 5494-5494.	1.4	1
101	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
102	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
103	Utilization of Translational Bioinformatics to Identify Novel Biomarkers of Bortezomib Resistance in Multiple Myeloma. Journal of Cancer, 2014, 5, 720-727.	2.5	20
104	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
105	Profiling Bortezomib Resistance Identifies Secondary Therapies in a Mouse Myeloma Model. Molecular Cancer Therapeutics, 2013, 12, 1140-1150.	4.1	68
106	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
107	Strategies To Identify Effective Treatments For Proteasome Inhibitor Resistant Multiple Myeloma. Blood, 2013, 122, 278-278.	1.4	1
108	In Silico Prediction of Novel Drug Combinations to Combat Bortezomib-Resistant Multiple Myeloma. Blood, 2012, 120, 1344-1344.	1.4	8

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109	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
110	SH2-Containing Inositol 5'-Phosphatase Inhibits Transformation of Abelson Murine Leukemia Virus. Journal of Virology, 2011, 85, 9239-9242.	3.4	1
111	Expression of Germinal Center B Cell Markers in Bortezomib-Resistant Multiple Myeloma Cells. Blood, 2011, 118, 129-129.	1.4	39
112	Modeling Proteasome Inhibition in Lymphoma. Blood, 2011, 118, 4946-4946.	1.4	5
113	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
114	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
115	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
116	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
117	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