Beth A Pitel

List of Publications by Year
in descending order

45	385	840776 11	839539 18
papers	citations	h-index	g-index

46	46	46	726
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Re: Stanley Weng, Renzo G. DiNatale, Andrew Silagy, et al. The Clinicopathologic and Molecular Landscape of Clear Cell Papillary Renal Cell Carcinoma: Implications in Diagnosis and Management. Eur Urol 2021;79:468â€“77. European Urology, 2021, 80, e62-e63.	1.9	2
3	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
4	Assessment of Risk of Hereditary Predisposition in Patients With Melanoma and/or Mesothelioma and Renal Neoplasia. JAMA Network Open, 2021, 4, e2132615.	5.9	4
5	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
6	Identification of a Novel Homozygous Multi-Exon Duplication in RYR2 Among Children With Exertion-Related Unexplained Sudden Deaths in the Amish Community. JAMA Cardiology, 2020, 5, 340.	6.1	17
7	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
8	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
9	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
10	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. JCO Clinical Cancer Informatics, 2020, 4, 602-613.	2.1	26
11	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
12	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
13	IGH rearrangement in myeloid neoplasms. Haematologica, 2020, 105, e315-e317.	3.5	4
14	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
15	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
16	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
17	Cryptic ETV6â€“PDGFRB fusion in a highly complex rearrangement of chromosomes 1, 5, and 12 due to a chromothripsis-like event in a myelodysplastic syndrome/myeloproliferative neoplasm. Leukemia and Lymphoma, 2019, 60, 1304-1307.	1.3	8
18	8. Mate pair sequencing characterization of 5q/7q co-deleted acute myeloid leukemia: a prospective study to discover novel co-abnormalities in complex karyotypes. Cancer Genetics, 2019, 233-234, S4.	0.4	0

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19	13. NGS-based detection of translocations in plasma cell myeloma. Cancer Genetics, 2019, 233-234, S5-S6.	0.4	0
20	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
21	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
22	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
23	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
24	RNA sequencing identifies a novel USP9Xâ€ USP6 promoter swap gene fusion in a primary aneurysmal bone cyst. Genes Chromosomes and Cancer, 2019, 58, 589-594.	2.8	27
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	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
27	Mate pair sequencing outperforms fluorescence in situ hybridization in the genomic characterization of multiple myeloma. Blood Cancer Journal, 2019, 9, 103.	6.2	27
28	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
29	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
30	Mate pair sequencing improves detection of genomic abnormalities in acute myeloid leukemia. European Journal of Haematology, 2019, 102, 87-96.	2.2	35
31	Differentiating between Hyperdiploidy and Pseudo-Hyperdiploidy in B-Lymphoblastic Leukemia Utilizing Low-Coverage Mate-Pair Sequencing. Blood, 2019, 134, 5212-5212.	1.4	0
32	SVAtools for junction detection of genome-wide chromosomal rearrangements by mate-pair sequencing (MPseq). Cancer Genetics, 2018, 221, 1-18.	0.4	65
33	Use of Mate-Pair Sequencing (MPseq) to Elucidate a Complex BCR-ABL1 Rearrangement Observed in a Newly Diagnosed Case of Chronic Myeloid Leukemia. American Journal of Clinical Pathology, 2018, 150, S131-S132.	0.7	0
34	12. Mate pair sequencing: Unveiling underappreciated complexity and providing clarity to the previously unanswered questions of cytogenetics. Cancer Genetics, 2018, 224-225, 54-55.	0.4	0
35	1. Clinical utility of mate pair sequencing to detect diagnostic and prognostic chromosomal rearrangements and copy number changes in patients with acute myeloid leukemia. Cancer Genetics, 2018, 226-227, 36.	0.4	0
36	19. Evidence-based review of genomic aberrations in T-ALL: Strategy and progress of CGC T-ALL Working Group. Cancer Genetics, 2018, 226-227, 43.	0.4	1

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37	28. Creation, maintenance, and utility of a comprehensive and informative pan-cancer gene list to aid in interpretation of whole genomes in cancer. Cancer Genetics, 2018, 226-227, 46-47.	0.4	0
38	43. Evidence-based review of genomic aberrations in pediatric B-Cell Acute Lymphoblastic Leukemia (B-ALL): Progress from Cancer Genomics Consortium (CGC) B-ALL Workgroup. Cancer Genetics, 2018, 226-227, 52.	0.4	0
39	Introduction to Publicly Available Knowledgebases to Aid Interpretations of Genomic Findings in Oncology. Cancer Genetics, 2017, 214-215, 40-41.	0.4	0
40	Development of a Custom, Sensitive and Specific PCR Strategy for the Detection of ERG Deletions in Pediatric B- Lymphoblastic Leukemia/Lymphoma (B-ALL). Cancer Genetics, 2017, 214-215, 49.	0.4	0
41	A novel deletion of SNURF/SNRPN exon 1 in a patient with Prader-Willi-like phenotype. European Journal of Medical Genetics, 2017, 60, 416-420.	1.3	11
42	Development of a Clinical Grade Interpretive Tool for Neoplastic Genomic Microarray Testing. Cancer Genetics, 2016, 209, 285.	0.4	0
43	Molecular Characterization of Recurrent Partial Gene Duplications by Whole Genome Mate-Pair Sequencing (MPseq) to Improve the Accuracy of Chromosomal Microarray Reporting. Cancer Genetics, 2016, 209, 299-300.	0.4	0
44	Clinical Impact of Genomic Duplications: A Discussion of Reporting Practices. Cancer Genetics, 2016, 209, 230-231.	0.4	0
45	Postnatal Chromosomal Microarray Reveals a False Positive Trisomy 21 NIPS Result. Cancer Genetics, 2015, 208, 357.	0.4	0