Beth A Pitel

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4855887/publications.pdf

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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	SVAtools for junction detection of genome-wide chromosomal rearrangements by mate-pair sequencing (MPseq). Cancer Genetics, 2018, 221, 1-18.	0.4	65
2	Mate pair sequencing improves detection of genomic abnormalities in acute myeloid leukemia. European Journal of Haematology, 2019, 102, 87-96.	2.2	35
3	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
4	Mate pair sequencing outperforms fluorescence in situ hybridization in the genomic characterization of multiple myeloma. Blood Cancer Journal, 2019, 9, 103.	6.2	27
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	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
18	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

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19	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
20	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
21	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
22	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
23	IGH rearrangement in myeloid neoplasms. Haematologica, 2020, 105, e315-e317.	3.5	4
24	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
25	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
26	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
27	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
28	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
29	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
30	Postnatal Chromosomal Microarray Reveals a False Positive Trisomy 21 NIPS Result. Cancer Genetics, 2015, 208, 357.	0.4	0
31	Development of a Clinical Grade Interpretive Tool for Neoplastic Genomic Microarray Testing. Cancer Genetics, 2016, 209, 285.	0.4	0
32	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
33	Clinical Impact of Genomic Duplications: A Discussion of Reporting Practices. Cancer Genetics, 2016, 209, 230-231.	0.4	0
34	Introduction to Publicly Available Knowledgebases to Aid Interpretations of Genomic Findings in Oncology. Cancer Genetics, 2017, 214-215, 40-41.	0.4	0
35	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
36	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

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37	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
38	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
39	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
40	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
41	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
42	13. NGS-based detection of translocations in plasma cell myeloma. Cancer Genetics, 2019, 233-234, S5-S6.	0.4	0
43	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
44	Differentiating between Hyperdiploidy and Pseudo-Hyperdiploidy in B-Lymphoblastic Leukemia Utilizing Low-Coverage Mate-Pair Sequencing. Blood, 2019, 134, 5212-5212.	1.4	0
45	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