

Hutton M Kearney

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,684
citations

687363

13
h-index

642732

23
g-index

25
all docs

25
docs citations

25
times ranked

2569
citing authors

#	ARTICLE	IF	CITATIONS
1	Stankiewicz-Isidor syndrome: expanding the clinical and molecular phenotype. <i>Genetics in Medicine</i> , 2022, 24, 179-191.	2.4	9
2	Best practices for the interpretation and reporting of clinical whole genome sequencing. <i>Npj Genomic Medicine</i> , 2022, 7, 27.	3.8	48
3	Prenatal characterization of a novel inverted <i>SMAD2</i> duplication by mate pair sequencing in a fetus with dextrocardia. <i>Clinical Case Reports (discontinued)</i> , 2021, 9, 769-774.	0.5	0
4	Exome and genome sequencing for pediatric patients with congenital anomalies or intellectual disability: an evidence-based clinical guideline of the American College of Medical Genetics and Genomics (ACMG). <i>Genetics in Medicine</i> , 2021, 23, 2029-2037.	2.4	229
5	Lymphoid blast transformation in an MPN with <i>BCR-JAK2</i> treated with ruxolitinib: putative mechanisms of resistance. <i>Blood Advances</i> , 2021, 5, 3492-3496.	5.2	14
6	Conventional Cytogenetic Analysis of Hematologic Neoplasms: A 20-Year Review of Proficiency Test Results From the College of American Pathologists/American College of Medical Genetics and Genomics Cytogenetics Committee. <i>Archives of Pathology and Laboratory Medicine</i> , 2021, 145, 176-190.	2.5	3
7	Molecular characterization of Novel <i>ATM</i> fusions in chronic lymphocytic leukemia and T-cell prolymphocytic leukemia. <i>Leukemia and Lymphoma</i> , 2021, , 1-11.	1.3	0
8	Best practices for the analytical validation of clinical whole-genome sequencing intended for the diagnosis of germline disease. <i>Npj Genomic Medicine</i> , 2020, 5, 47.	3.8	67
9	Limited diagnostic impact of duplications <1 Mb of uncertain clinical significance: a 10-year retrospective analysis of reporting practices at the Mayo Clinic. <i>Genetics in Medicine</i> , 2020, 22, 2120-2124.	2.4	2
10	The Medical Genome Initiative: moving whole-genome sequencing for rare disease diagnosis to the clinic. <i>Genome Medicine</i> , 2020, 12, 48.	8.2	40
11	Response to Maya et al.. <i>Genetics in Medicine</i> , 2020, 22, 1278-1279.	2.4	4
12	Most noninvasive prenatal screens failing due to inadequate fetal cell free <i>scp>DNA</scp></i> are negative for trisomy when repeated. <i>Prenatal Diagnosis</i> , 2020, 40, 831-837.	2.3	12
13	Biallelic variants in <i>CTU2</i> cause DREAMâ€PL syndrome and impair thiolation of tRNA wobble U34. <i>Human Mutation</i> , 2019, 40, 2108-2120.	2.5	25
14	Points to consider in the reevaluation and reanalysis of genomic test results: a statement of the American College of Medical Genetics and Genomics (ACMG). <i>Genetics in Medicine</i> , 2019, 21, 1267-1270.	2.4	147
15	Interstitial 4q Deletion Syndrome Including <i>NR3C2</i> ; Causing Pseudohypoaldosteronism. <i>Molecular Syndromology</i> , 2019, 10, 327-331.	0.8	6
16	Mate pair sequencing outperforms fluorescence in situ hybridization in the genomic characterization of multiple myeloma. <i>Blood Cancer Journal</i> , 2019, 9, 103.	6.2	27
17	Constitutional chromosome rearrangements that mimic the 2017 world health organization â€acute myeloid leukemia with recurrent genetic abnormalitiesâ€. A study of three cases and review of the literature. <i>Cancer Genetics</i> , 2019, 230, 37-46.	0.4	8
18	Use of mate-pair sequencing to characterize a complex cryptic <i>BCR/ABL1</i> rearrangement observed in a newly diagnosed case of chronic myeloid leukemia. <i>Human Pathology</i> , 2019, 89, 109-114.	2.0	7

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19	Mate pair sequencing improves detection of genomic abnormalities in acute myeloid leukemia. <i>European Journal of Haematology</i> , 2019, 102, 87-96.	2.2	35
20	SVAtools for junction detection of genome-wide chromosomal rearrangements by mate-pair sequencing (MPseq). <i>Cancer Genetics</i> , 2018, 221, 1-18.	0.4	65
21	The Utilization of Chromosomal Microarray Technologies for Hematologic Neoplasms. <i>American Journal of Clinical Pathology</i> , 2018, 150, 375-384.	0.7	13
22	<sc>C</sc>opy number variant analysis using genome-wide mate-pair sequencing. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 459-470.	2.8	44
23	Diagnostic cytogenetic testing following positive noninvasive prenatal screening results: a clinical laboratory practice resource of the American College of Medical Genetics and Genomics (ACMG). <i>Genetics in Medicine</i> , 2017, 19, 845-850.	2.4	31