

Marcus Häy Hansen

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

143
citations

1478280

6
h-index

1281743

11
g-index

27
all docs

27
docs citations

27
times ranked

231
citing authors

#	ARTICLE	IF	CITATIONS
1	Sensitive ligand-based protein quantification using immuno-PCR: A critical review of single-probe and proximity ligation assays. <i>BioTechniques</i> , 2014, 56, 217-228.	0.8	24
2	A decade with whole exome sequencing in haematology. <i>British Journal of Haematology</i> , 2020, 188, 367-382.	1.2	24
3	Myeloproliferative and lymphoproliferative malignancies occurring in the same patient: a nationwide discovery cohort. <i>Haematologica</i> , 2020, 105, 2432-2439.	1.7	16
4	Systematic evaluation of signal-to-noise ratio in variant detection from single cell genome multiple displacement amplification and exome sequencing. <i>BMC Genomics</i> , 2018, 19, 681.	1.2	12
5	Diagnosing and following adult patients with acute myeloid leukaemia in the genomic age. <i>British Journal of Haematology</i> , 2014, 167, 162-176.	1.2	11
6	Perspective: sensitive detection of residual lymphoproliferative disease by NGS and clonal rearrangements—how low can you go?. <i>Experimental Hematology</i> , 2021, 98, 14-24.	0.2	8
7	The concept of leukaemic stem cells in acute myeloid leukaemia 25 years on: hitting a moving target. <i>British Journal of Haematology</i> , 2019, 187, 144-156.	1.2	7
8	Molecular characterization of sorted malignant B cells from patients clinically identified with mantle cell lymphoma. <i>Experimental Hematology</i> , 2020, 84, 7-18.e12.	0.2	7
9	Novel scripts for improved annotation and selection of variants from whole exome sequencing in cancer research. <i>MethodsX</i> , 2015, 2, 145-153.	0.7	5
10	Case report: Exome sequencing identifies T-ALL with myeloid features as a IKZF1-struck early precursor T-cell malignancy. <i>Leukemia Research Reports</i> , 2018, 9, 1-4.	0.2	5
11	Nature and nurture: a case of transcending haematological pre-malignancies in a pair of monozygotic twins adding possible clues on the pathogenesis of B-cell proliferations. <i>British Journal of Haematology</i> , 2015, 169, 391-400.	1.2	4
12	Combination of RNA- and exome sequencing: Increasing specificity for identification of somatic point mutations and indels in acute leukaemia. <i>Leukemia Research</i> , 2016, 51, 27-31.	0.4	4
13	Clonal evolution in patients developing therapy-related myeloid neoplasms following autologous stem cell transplantation. <i>Bone Marrow Transplantation</i> , 2022, 57, 460-465.	1.3	4
14	Detailed characterization of the transcriptome of single B cells in mantle cell lymphoma suggesting a potential use for SOX4. <i>Scientific Reports</i> , 2021, 11, 19092.	1.6	3
15	Unraveling clonal heterogeneity at the stem cell level in myelodysplastic syndrome: In pursuit of cell subsets driving disease progression. <i>Leukemia Research</i> , 2020, 92, 106350.	0.4	2
16	Distal chromosome 1q aberrations and initial response to ibrutinib in central nervous system relapsed mantle cell lymphoma. <i>Leukemia Research Reports</i> , 2021, 15, 100255.	0.2	2
17	Investigation of circulating DNA integrity after blood collection. <i>BioTechniques</i> , 2021, 71, 550-555.	0.8	2
18	Kinetics of del(7q) driven leukemogenesis in a patient with JAK2 V617F and TET2 mutated chronic myeloproliferative neoplasm. <i>Leukemia Research Reports</i> , 2013, 2, 51-53.	0.2	1

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19	Shared Genomic Alterations in Patients with Co-Existing Myeloproliferative Neoplasms and Angioimmunoblastic T-Cell Lymphoma. <i>Blood</i> , 2019, 134, 2776-2776.	0.6	1
20	Mantle cell lymphoma and the evidence of an immature lymphoid component. <i>Leukemia Research</i> , 2022, 115, 106824.	0.4	1
21	Can exome scans be expected to be part of real-time decision-making in patients with haematological cancers?. <i>British Journal of Haematology</i> , 2016, 174, 486-492.	1.2	0
22	Acute myeloid/T-cell lymphoblastic leukaemia (<scp>ATML</scp>) â€” a disease entity to look out for. <i>British Journal of Haematology</i> , 2019, 185, 178-178.	1.2	0
23	Replicate whole-genome next-generation sequencing data derived from Caucasian donor saliva samples. <i>Data in Brief</i> , 2021, 38, 107349.	0.5	0
24	Therapy-Related Myeloid Neoplasms Following Autologous Stem Cell Transplantation: The Prevalence of Chip Mutations at Time of Transplantation â€” a Single Center Experience. <i>Blood</i> , 2018, 132, 1529-1529.	0.6	0