Sylvain Mareschal

List of Publications by Year
in descending order

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47 papers	1,751 citations	304368 22 h-index	301761 39 g-index
48 all docs	48 docs citations	48 times ranked	2911 citing authors

#	Article	IF	Citations
1	Challenging conventional karyotyping by next-generation karyotyping in 281 intensively treated patients with AML. Blood Advances, 2021, 5, 1003-1016.	2.5	12
2	Chronic T cell receptor stimulation unmasks NK receptor signaling in peripheral T cell lymphomas via epigenetic reprogramming. Journal of Clinical Investigation, 2021, 131, .	3.9	4
3	Chromatin Accessibility Profiling to Increase Diagnostic Accuracy and Refine Cell-of-Origin Classification of Mature T-Cell Lymphomas. Blood, 2021, 138, 809-809.	0.6	1
4	Integrated transcriptomic and genomic analysis improves prediction of complete remission and survival in elderly patients with acute myeloid leukemia. Blood Cancer Journal, 2020, 10, 67.	2.8	6
5	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. Clinical Cancer Research, 2020, 26, 3597-3607.	3.2	26
6	Refining diffuse large B-cell lymphoma subgroups using integrated analysis of molecular profiles. EBioMedicine, 2019, 48, 58-69.	2.7	29
7	Identification of Recurrent Alternative RNA Splicing in Adverse-Risk Acute Myeloid Leukemia. Blood, 2019, 134, 457-457.	0.6	0
8	Authorsâ€™ Reply. Journal of Molecular Diagnostics, 2018, 20, 266.	1.2	0
9	Mediation analysis reveals common mechanisms of RUNX1 point mutations and RUNX1/RUNX1T1 fusions influencing survival of patients with acute myeloid leukemia. Scientific Reports, 2018, 8, 11293.	1.6	9
10	Identification of Somatic Mutations in Primary Cutaneous Diffuse Large B-Cell Lymphoma, Leg Type by Massive Parallel Sequencing. Journal of Investigative Dermatology, 2017, 137, 1984-1994.	0.3	93
11	Application of the cghRA framework to the genomic characterization of Diffuse Large B-Cell Lymphoma. Bioinformatics, 2017, 33, 2977-2985.	1.8	3
12	Biological and Clinical Relevance of Associated Genomic Alterations in MYD88 L265P and non-L265Pâ€“Mutated Diffuse Large B-Cell Lymphoma: Analysis of 361 Cases. Clinical Cancer Research, 2017, 23, 2232-2244.	3.2	82
13	Determination of Molecular Subtypes of Diffuse Large B-Cell Lymphoma Using a Reverse Transcriptase Multiplex Ligation-Dependent Probe Amplification Classifier. Journal of Molecular Diagnostics, 2017, 19, 892-904.	1.2	39
14	Oncogenic events rather than antigen selection pressure may be the main driving forces for relapse in diffuse large Bâ€¢cell lymphomas. American Journal of Hematology, 2017, 92, 68-76.	2.0	8
15	Non-invasive detection of somatic mutations using next-generation sequencing in primary central nervous system lymphoma. Oncotarget, 2017, 8, 48157-48168.	0.8	78
16	Whole exome sequencing of relapsed/refractory patients expands the repertoire of somatic mutations in diffuse large <scp>B</scp>â€¢cell lymphoma. Genes Chromosomes and Cancer, 2016, 55, 251-267.	1.5	75
17	Recurrent mutations of the exportin 1 gene (XPO1) and their impact on selective inhibitor of nuclear export compounds sensitivity in primary mediastinal Bâ€¢cell lymphoma. American Journal of Hematology, 2016, 91, 923-930.	2.0	79
18	Molecular Profile and FDG-PET Metabolic Volume at Staging in DLBCLâ€”Response. Clinical Cancer Research, 2016, 22, 3414-3415.	3.2	14

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19	Hypoalbuminemia and hypergammaglobulinemia are associated with an increased infection risk in patients with myeloid malignancies treated with azacitidine. A 3-year monocentric retrospective study. Leukemia and Lymphoma, 2016, 57, 1491-1493.	0.6	3
20	Detection and prognostic value of recurrent exportin 1 mutations in tumor and cell-free circulating DNA of patients with classical Hodgkin lymphoma. Haematologica, 2016, 101, 1094-1101.	1.7	97
21	HACE1 is a putative tumor suppressor gene in B-cell lymphomagenesis and is down-regulated by both deletion and epigenetic alterations. Leukemia Research, 2016, 45, 90-100.	0.4	9
22	Next-Generation Sequencing in Diffuse Large B-Cell Lymphoma Highlights Molecular Divergence and Therapeutic Opportunities: a LYSA Study. Clinical Cancer Research, 2016, 22, 2919-2928.	3.2	181
23	Digital PCR for quantification of recurrent and potentially actionable somatic mutations in circulating free DNA from patients with diffuse large B-cell lymphoma. Leukemia and Lymphoma, 2016, 57, 2171-2179.	0.6	69
24	Molecular Profile and FDG-PET/CT Total Metabolic Tumor Volume Improve Risk Classification at Diagnosis for Patients with Diffuse Large B-Cell Lymphoma. Clinical Cancer Research, 2016, 22, 3801-3809.	3.2	151
25	Integrated Analysis of IGHV Gene Status, Cell-of-Origin Signature and Genomic Features in Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 4118-4118.	0.6	0
26	EZH2-Activating Mutations in DLBCL Are Easily Predictable by Routine Immunohistochemistry Analysis: a Tool to More Efficiently Define EZH2 Inhibitor-Sensitive Patients?. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, S220.	0.2	0
27	Somatic mutations of cell-free circulating DNA detected by next-generation sequencing reflect the genetic changes in both germinal center B-cell-like and activated B-cell-like diffuse large B-cell lymphomas at the time of diagnosis. Haematologica, 2015, 100, e280-e284.	1.7	69
28	Outcome of patients older than 60Âyears with classical Hodgkin lymphoma treated with front line <scp>ABVD</scp> chemotherapy: frequent pulmonary events suggest limiting the use of bleomycin in the elderly. British Journal of Haematology, 2015, 170, 179-184.	1.2	69
29	Accurate Classification of Germinal Center B-Cellâ€“Like/Activated B-Cellâ€“Like Diffuse Large B-Cell Lymphoma Using a Simple and Rapid Reverse Transcriptaseâ€“Multiplex Ligation-Dependent Probe Amplification Assay. Journal of Molecular Diagnostics, 2015, 17, 273-283.	1.2	50
30	Genome-Wide Association Study of Event-Free Survival in Diffuse Large B-Cell Lymphoma Treated With Immunochemotherapy. Journal of Clinical Oncology, 2015, 33, 3930-3937.	0.8	24
31	Activating somatic mutations in diffuse large B-cell lymphomas: lessons from next generation sequencing and key elements in the precision medicine era. Leukemia and Lymphoma, 2015, 56, 1213-1222.	0.6	29
32	Recurrent Mutations of the Exportin 1 Gene (XPO1) in Primary Mediastinal B-Cell Lymphoma: A Lysa Study. Blood, 2015, 126, 129-129.	0.6	2
33	Somatic Mutations Detected in Plasma Cell-Free DNA By Targeted Sequencing: Assessment of Liquid Biopsy in Primary Central Nervous System Lymphoma. Blood, 2015, 126, 332-332.	0.6	8
34	Immunohistochemical and genomic profiles of diffuse large B-cell lymphomas: Implications for targeted EZH2 inhibitor therapy?. Oncotarget, 2015, 6, 16712-16724.	0.8	32
35	Integrative Analysis of Diffuse Large B Cell Lymphoma Mutational Landscape: A Lysa Study. Blood, 2015, 126, 1472-1472.	0.6	0
36	Sarcopenia is an independent prognostic factor in elderly patients with diffuse large B-cell lymphoma treated with immunochemotherapy. Leukemia and Lymphoma, 2014, 55, 817-823.	0.6	121

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37	Rgb: a scriptable genome browser for R. Bioinformatics, 2014, 30, 2204-2205.	1.8	2
38	Targetable activating mutations are very frequent in GCB and ABC diffuse large Bâ€cell lymphoma. Genes Chromosomes and Cancer, 2014, 53, 144-153.	1.5	76
39	Targeted EZH2 Inhibitors in Diffuse Large B-Cell Lymphoma (DLBCL): Immunohistochemical and Mutational Profiles of Patients May Determine Candidates for Treatment. Blood, 2014, 124, 1656-1656.	0.6	2
40	Highly Multiplexed Targeted Sequencing of Recurrent Fusion Genes in Acute Leukemia. Blood, 2014, 124, 2335-2335.	0.6	0
41	Immunoglobulin heavy chain/light chain pair measurement is associated with survival in diffuse large B-cell lymphoma. Leukemia and Lymphoma, 2013, 54, 1898-1907.	0.6	36
42	Accurate Classification Of GCB/ABC and MYC/BCL2 Diffuse Large B-Cell Lymphoma With a 14 Genes Expression Signature and a Simple and Robust RT-MLPA Assay. Blood, 2013, 122, 84-84.	0.6	3
43	Interim positron emission tomography scan associated with international prognostic index and germinal center B cell-like signature as prognostic index in diffuse large B-cell lymphoma. Leukemia and Lymphoma, 2012, 53, 34-42.	0.6	40
44	Several mechanisms lead to the inactivation of the CDKN2A (P16), P14ARF, or CDKN2B (P15) genes in the GCB and ABC molecular DLBCL subtypes. Genes Chromosomes and Cancer, 2012, 51, 858-867.	1.5	16
45	Integrated Analysis of High-Resolution Gene Expression and Copy Number Profiling Identified Biallelic Deletion of CDKN2A/2B Tumor Suppressor Locus As the Most Frequent and Unique Genomic Abnormality in Diffuse Large B-Cell Lymphoma (DLBCL) with Strong Prognostic Value in Both GCB and ABC Subtypes and Not Overcome by a Dose-Intensive Immunochemotherapy Regimen Plus Rituximab. Results of a Prospective GELA Clinical Trial Program. Blood, 2012, 120, 415-415.	0.6	6
46	Phylogenetic Evolution in Refractory/Relapsed Diffuse Large B-Cell Lymphoma. Blood, 2012, 120, 418-418.	0.6	0
47	The proportion of activated B-cell like subtype among de novo diffuse large B-cell lymphoma increases with age. Haematologica, 2011, 96, 1888-1890.	1.7	97