

Sylvain Mareschal

List of Publications by Year in descending order

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Version: 2024-02-01

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	Next-Generation Sequencing in Diffuse Large B-Cell Lymphoma Highlights Molecular Divergence and Therapeutic Opportunities: a LYSA Study. <i>Clinical Cancer Research</i> , 2016, 22, 2919-2928.	3.2	181
2	Molecular Profile and FDG-PET/CT Total Metabolic Tumor Volume Improve Risk Classification at Diagnosis for Patients with Diffuse Large B-Cell Lymphoma. <i>Clinical Cancer Research</i> , 2016, 22, 3801-3809.	3.2	151
3	Sarcopenia is an independent prognostic factor in elderly patients with diffuse large B-cell lymphoma treated with immunochemotherapy. <i>Leukemia and Lymphoma</i> , 2014, 55, 817-823.	0.6	121
4	The proportion of activated B-cell like subtype among de novo diffuse large B-cell lymphoma increases with age. <i>Haematologica</i> , 2011, 96, 1888-1890.	1.7	97
5	Detection and prognostic value of recurrent exportin 1 mutations in tumor and cell-free circulating DNA of patients with classical Hodgkin lymphoma. <i>Haematologica</i> , 2016, 101, 1094-1101.	1.7	97
6	Identification of Somatic Mutations in Primary Cutaneous Diffuse Large B-Cell Lymphoma, Leg Type by Massive Parallel Sequencing. <i>Journal of Investigative Dermatology</i> , 2017, 137, 1984-1994.	0.3	93
7	Biological and Clinical Relevance of Associated Genomic Alterations in MYD88 L265P and non-L265P Mutated Diffuse Large B-Cell Lymphoma: Analysis of 361 Cases. <i>Clinical Cancer Research</i> , 2017, 23, 2232-2244.	3.2	82
8	Recurrent mutations of the exportin 1 gene (XPO1) and their impact on selective inhibitor of nuclear export compounds sensitivity in primary mediastinal B-cell lymphoma. <i>American Journal of Hematology</i> , 2016, 91, 923-930.	2.0	79
9	Non-invasive detection of somatic mutations using next-generation sequencing in primary central nervous system lymphoma. <i>Oncotarget</i> , 2017, 8, 48157-48168.	0.8	78
10	Targetable activating mutations are very frequent in GCB and ABC diffuse large B-cell lymphoma. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 144-153.	1.5	76
11	Whole exome sequencing of relapsed/refractory patients expands the repertoire of somatic mutations in diffuse large B-cell lymphoma. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 251-267.	1.5	75
12	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. <i>Haematologica</i> , 2015, 100, e280-e284.	1.7	69
13	Outcome of patients older than 60 years with classical Hodgkin lymphoma treated with front line ABVD chemotherapy: frequent pulmonary events suggest limiting the use of bleomycin in the elderly. <i>British Journal of Haematology</i> , 2015, 170, 179-184.	1.2	69
14	Digital PCR for quantification of recurrent and potentially actionable somatic mutations in circulating free DNA from patients with diffuse large B-cell lymphoma. <i>Leukemia and Lymphoma</i> , 2016, 57, 2171-2179.	0.6	69
15	Accurate Classification of Germinal Center B-Cell-Like/Activated B-Cell-Like Diffuse Large B-Cell Lymphoma Using a Simple and Rapid Reverse Transcriptase-Multiplex Ligation-Dependent Probe Amplification Assay. <i>Journal of Molecular Diagnostics</i> , 2015, 17, 273-283.	1.2	50
16	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. <i>Leukemia and Lymphoma</i> , 2012, 53, 34-42.	0.6	40
17	Determination of Molecular Subtypes of Diffuse Large B-Cell Lymphoma Using a Reverse Transcriptase Multiplex Ligation-Dependent Probe Amplification Classifier. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 892-904.	1.2	39
18	Immunoglobulin heavy chain/light chain pair measurement is associated with survival in diffuse large B-cell lymphoma. <i>Leukemia and Lymphoma</i> , 2013, 54, 1898-1907.	0.6	36

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19	Immunohistochemical and genomic profiles of diffuse large B-cell lymphomas: Implications for targeted EZH2 inhibitor therapy?. <i>Oncotarget</i> , 2015, 6, 16712-16724.	0.8	32
20	Activating somatic mutations in diffuse large B-cell lymphomas: lessons from next generation sequencing and key elements in the precision medicine era. <i>Leukemia and Lymphoma</i> , 2015, 56, 1213-1222.	0.6	29
21	Refining diffuse large B-cell lymphoma subgroups using integrated analysis of molecular profiles. <i>EBioMedicine</i> , 2019, 48, 58-69.	2.7	29
22	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2020, 26, 3597-3607.	3.2	26
23	Genome-Wide Association Study of Event-Free Survival in Diffuse Large B-Cell Lymphoma Treated With Immunochemotherapy. <i>Journal of Clinical Oncology</i> , 2015, 33, 3930-3937.	0.8	24
24	Several mechanisms lead to the inactivation of the <i>CDKN2A</i> (<i>P16</i>), <i>P14ARF</i> , or <i>CDKN2B</i> (<i>P15</i>) genes in the GCB and ABC molecular DLBCL subtypes. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 858-867.	1.5	16
25	Molecular Profile and FDG-PET Metabolic Volume at Staging in DLBCL's Response. <i>Clinical Cancer Research</i> , 2016, 22, 3414-3415.	3.2	14
26	Challenging conventional karyotyping by next-generation karyotyping in 281 intensively treated patients with AML. <i>Blood Advances</i> , 2021, 5, 1003-1016.	2.5	12
27	HACE1 is a putative tumor suppressor gene in B-cell lymphomagenesis and is down-regulated by both deletion and epigenetic alterations. <i>Leukemia Research</i> , 2016, 45, 90-100.	0.4	9
28	Mediation analysis reveals common mechanisms of RUNX1 point mutations and RUNX1/RUNX1T1 fusions influencing survival of patients with acute myeloid leukemia. <i>Scientific Reports</i> , 2018, 8, 11293.	1.6	9
29	Oncogenic events rather than antigen selection pressure may be the main driving forces for relapse in diffuse large B-cell lymphomas. <i>American Journal of Hematology</i> , 2017, 92, 68-76.	2.0	8
30	Somatic Mutations Detected in Plasma Cell-Free DNA By Targeted Sequencing: Assessment of Liquid Biopsy in Primary Central Nervous System Lymphoma. <i>Blood</i> , 2015, 126, 332-332.	0.6	8
31	Integrated transcriptomic and genomic analysis improves prediction of complete remission and survival in elderly patients with acute myeloid leukemia. <i>Blood Cancer Journal</i> , 2020, 10, 67.	2.8	6
32	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. <i>Blood</i> , 2012, 120, 415-415.	0.6	6
33	Chronic T cell receptor stimulation unmasks NK receptor signaling in peripheral T cell lymphomas via epigenetic reprogramming. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	4
34	Hypoalbuminemia and hypergammaglobulinemia are associated with an increased infection risk in patients with myeloid malignancies treated with azacitidine. A 3-year monocentric retrospective study. <i>Leukemia and Lymphoma</i> , 2016, 57, 1491-1493.	0.6	3
35	Application of the cghRA framework to the genomic characterization of Diffuse Large B-Cell Lymphoma. <i>Bioinformatics</i> , 2017, 33, 2977-2985.	1.8	3
36	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. <i>Blood</i> , 2013, 122, 84-84.	0.6	3

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37	Rgb: a scriptable genome browser for R. <i>Bioinformatics</i> , 2014, 30, 2204-2205.	1.8	2
38	Targeted EZH2 Inhibitors in Diffuse Large B-Cell Lymphoma (DLBCL): Immunohistochemical and Mutational Profiles of Patients May Determine Candidates for Treatment. <i>Blood</i> , 2014, 124, 1656-1656.	0.6	2
39	Recurrent Mutations of the Exportin 1 Gene (XPO1) in Primary Mediastinal B-Cell Lymphoma: A Lysa Study. <i>Blood</i> , 2015, 126, 129-129.	0.6	2
40	Chromatin Accessibility Profiling to Increase Diagnostic Accuracy and Refine Cell-of-Origin Classification of Mature T-Cell Lymphomas. <i>Blood</i> , 2021, 138, 809-809.	0.6	1
41	EZH2-Activating Mutations in DLBCL Are Easily Predictable by Routine Immunohistochemistry Analysis: a Tool to More Efficiently Define EZH2 Inhibitor-Sensitive Patients?. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2015, 15, S220.	0.2	0
42	Authors'™ Reply. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 266.	1.2	0
43	Phylogenetic Evolution in Refractory/Relapsed Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2012, 120, 418-418.	0.6	0
44	Highly Multiplexed Targeted Sequencing of Recurrent Fusion Genes in Acute Leukemia. <i>Blood</i> , 2014, 124, 2335-2335.	0.6	0
45	Integrative Analysis of Diffuse Large B Cell Lymphoma Mutational Landscape: A Lysa Study. <i>Blood</i> , 2015, 126, 1472-1472.	0.6	0
46	Integrated Analysis of IGHV Gene Status, Cell-of-Origin Signature and Genomic Features in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016, 128, 4118-4118.	0.6	0
47	Identification of Recurrent Alternative RNA Splicing in Adverse-Risk Acute Myeloid Leukemia. <i>Blood</i> , 2019, 134, 457-457.	0.6	0