

Sofie Demeyer

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,499
citations

393982

19
h-index

414034

32
g-index

35
all docs

35
docs citations

35
times ranked

2507
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimizing the diagnostic workflow for acute lymphoblastic leukemia by optical genome mapping. <i>American Journal of Hematology</i> , 2022, 97, 548-561.	2.0	36
2	Monitoring of Leukemia Clones in B-cell Acute Lymphoblastic Leukemia at Diagnosis and During Treatment by Single-cell DNA Amplicon Sequencing. <i>HemaSphere</i> , 2022, 6, e700.	1.2	8
3	TAL1 cooperates with PI3K/AKT pathway activation in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2022, 107, 2304-2317.	1.7	5
4	PHGDH heterogeneity potentiates cancer cell dissemination and metastasis. <i>Nature</i> , 2022, 605, 747-753.	13.7	77
5	Single-cell DNA amplicon sequencing reveals clonal heterogeneity and evolution in T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2021, 137, 801-811.	0.6	43
6	Overexpression of wild-type IL-7R α promotes T-cell acute lymphoblastic leukemia/lymphoma. <i>Blood</i> , 2021, 138, 1040-1052.	0.6	28
7	Fusion transcripts FYN-TRAF3IP2 and KHDRBS1-LCK hijack T cell receptor signaling in peripheral T-cell lymphoma, not otherwise specified. <i>Nature Communications</i> , 2021, 12, 3705.	5.8	21
8	Oncogenic cooperation between TCF7-SPI1 and NRAS(G12D) requires β -catenin activity to drive T-cell acute lymphoblastic leukemia. <i>Nature Communications</i> , 2021, 12, 4164.	5.8	9
9	The XPO1 Inhibitor KPT-8602 Synergizes with Dexamethasone in Acute Lymphoblastic Leukemia. <i>Clinical Cancer Research</i> , 2020, 26, 5747-5758.	3.2	19
10	Suz12 inactivation cooperates with JAK3 mutant signaling in the development of T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2019, 134, 1323-1336.	0.6	37
11	Safe targeting of T cell acute lymphoblastic leukemia by pathology-specific NOTCH inhibition. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	74
12	Evolution of Clinically Relevant Subclones during Chemotherapy Treatment of ALL As Determined By Single-Cell DNA and RNA Sequencing. <i>Blood</i> , 2019, 134, 2749-2749.	0.6	0
13	HOXA9 Cooperates with Activated JAK/STAT Signaling to Drive Leukemia Development. <i>Cancer Discovery</i> , 2018, 8, 616-631.	7.7	76
14	Mutant JAK3 phosphoproteomic profiling predicts synergism between JAK3 inhibitors and MEK/BCL2 inhibitors for the treatment of T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2018, 32, 788-800.	3.3	75
15	Mutant JAK3 signaling is increased by loss of wild-type JAK3 or by acquisition of secondary JAK3 mutations in T-ALL. <i>Blood</i> , 2018, 131, 421-425.	0.6	30
16	Defining the molecular basis of oncogenic cooperation between TAL1 expression and Pten deletion in T-ALL using a novel pro-T-cell model system. <i>Leukemia</i> , 2018, 32, 941-951.	3.3	22
17	The Long Non-coding RNA Flutr Anticipates Foxp3 Expression in Regulatory T Cells. <i>Frontiers in Immunology</i> , 2018, 9, 1989.	2.2	36
18	Single-cell sequencing reveals the origin and the order of mutation acquisition in T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2018, 32, 1358-1369.	3.3	66

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19	The CCR4-NOT complex is a tumor suppressor in <i>Drosophila melanogaster</i> eye cancer models. <i>Journal of Hematology and Oncology</i> , 2018, 11, 108.	6.9	15
20	Cooperative Enhancer Activation by TLX1 and STAT5 Drives Development of NUP214-ABL1/TLX1-Positive T Cell Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2018, 34, 271-285.e7.	7.7	48
21	<i>c</i> BCR-ABL1 positive B-ALL can undergo T-cell lineage shift to become CD19-negative T-ALL. <i>HemaSphere</i> , 2018, 2, e42.	1.2	2
22	Hedgehog pathway activation in T-cell acute lymphoblastic leukemia predicts response to SMO and GLI1 inhibitors. <i>Blood</i> , 2016, 128, 2642-2654.	0.6	39
23	RNA sequencing unravels the genetics of refractory/relapsed T-cell acute lymphoblastic leukemia. Prognostic and therapeutic implications. <i>Haematologica</i> , 2016, 101, 941-950.	1.7	44
24	Deletions of the long arm of chromosome 5 define subgroups of T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2016, 101, 951-958.	1.7	18
25	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	9.4	88
26	Targeted sequencing identifies associations between IL7R-JAK mutations and epigenetic modulators in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2015, 100, 1301-1310.	1.7	151
27	The Index-Based Subgraph Matching Algorithm with General Symmetries (ISMAGS): Exploiting Symmetry for Faster Subgraph Enumeration. <i>PLoS ONE</i> , 2014, 9, e97896.	1.1	19
28	Dynamic and stochastic routing for multimodal transportation systems. <i>IET Intelligent Transport Systems</i> , 2014, 8, 112-123.	1.7	14
29	JAK3 mutants transform hematopoietic cells through JAK1 activation, causing T-cell acute lymphoblastic leukemia in a mouse model. <i>Blood</i> , 2014, 124, 3092-3100.	0.6	128
30	Fault tolerant network design inspired by <i>Physarum polycephalum</i> . <i>Natural Computing</i> , 2013, 12, 277-289.	1.8	17
31	Speeding up Martins's algorithm for multiple objective shortest path problems. <i>4or</i> , 2013, 11, 323-348.	1.0	22
32	The Index-Based Subgraph Matching Algorithm (ISMA): Fast Subgraph Enumeration in Large Networks Using Optimized Search Trees. <i>PLoS ONE</i> , 2013, 8, e61183.	1.1	17
33	Worldwide energy needs for ICT: The rise of power-aware networking. , 2008, , .		204
34	Ant colony optimization for the routing of jobs in optical grid networks. <i>Journal of Optical Networking</i> , 2008, 7, 160.	2.5	9