

Vincent-Philippe Lavalle

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

31
papers

811
citations

16
h-index

28
g-index

37
ext. papers

1,197
ext. citations

8.3
avg, IF

3.63
L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 31 | High frequency of germline RUNX1 mutations in patients with RUNX1-mutated AML. <i>Blood</i> , 2020 , 135, 1882-1886 | 2.2 | 19 |
| 30 | Regenerative lineages and immune-mediated pruning in lung cancer metastasis. <i>Nature Medicine</i> , 2020 , 26, 259-269 | 50.5 | 127 |
| 29 | Genetic characterization of ABT-199 sensitivity in human AML. <i>Leukemia</i> , 2020 , 34, 63-74 | 10.7 | 26 |
| 28 | Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML. <i>Blood</i> , 2019 , 134, 263-276 | 2.2 | 23 |
| 27 | Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of OXPHOS Dependency in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2019 , 36, 84-99.e8 | 24.3 | 75 |
| 26 | Targeted variant detection using unaligned RNA-Seq reads. <i>Life Science Alliance</i> , 2019 , 2, | 5.8 | 5 |
| 25 | Genetic mechanisms of primary chemotherapy resistance in pediatric acute myeloid leukemia. <i>Leukemia</i> , 2019 , 33, 1934-1943 | 10.7 | 26 |
| 24 | Complex karyotype AML displays G2/M signature and hypersensitivity to PLK1 inhibition. <i>Blood Advances</i> , 2019 , 3, 552-563 | 7.8 | 14 |
| 23 | Transcriptomic landscape of acute promyelocytic leukemia reveals aberrant surface expression of the platelet aggregation agonist Podoplanin. <i>Leukemia</i> , 2018 , 32, 1349-1357 | 10.7 | 17 |
| 22 | MEF2C Phosphorylation Is Required for Chemotherapy Resistance in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2018 , 8, 478-497 | 24.4 | 37 |
| 21 | High expression of HMGA2 independently predicts poor clinical outcomes in acute myeloid leukemia. <i>Blood Cancer Journal</i> , 2018 , 8, 68 | 7 | 23 |
| 20 | Chemogenomic Profiling of Complex Karyotype AML Reveals a Novel Susceptibility to G2/M Checkpoint Inhibition Mediated By HMGA2 Overexpression. <i>Blood</i> , 2018 , 132, 3925-3925 | 2.2 | 1 |
| 19 | Genetic Characterization of ABT-199 Sensitivity in Human AML. <i>Blood</i> , 2018 , 132, 283-283 | 2.2 | 1 |
| 18 | Chemogenomic Approach Unveils the Increased Susceptibility of RUNX1-Mutated AML to Glucocorticoids. <i>Blood</i> , 2018 , 132, 4675-4675 | 2.2 | |
| 17 | Comprehensive Single-Cell RNA-Sequencing Mapping of Primary Acute Myeloid Leukemias and Profiling of NPM1-Mutated Cells. <i>Blood</i> , 2018 , 132, 995-995 | 2.2 | 1 |
| 16 | MiSTIC, an integrated platform for the analysis of heterogeneity in large tumour transcriptome datasets. <i>Nucleic Acids Research</i> , 2017 , 45, e122 | 20.1 | 12 |
| 15 | Chemogenomic Landscape of -mutated AML Reveals Importance of Allele Dosage in Genetics and Glucocorticoid Sensitivity. <i>Clinical Cancer Research</i> , 2017 , 23, 6969-6981 | 12.9 | 26 |

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|----|--|------|----|
| 14 | mutations promote context-dependent transformation in acute myeloid leukemia with alterations. <i>Blood</i> , 2017 , 130, 2204-2214 | 2.2 | 38 |
| 13 | GPR56 identifies primary human acute myeloid leukemia cells with high repopulating potential in vivo. <i>Blood</i> , 2016 , 127, 2018-27 | 2.2 | 95 |
| 12 | RNA-sequencing analysis of core binding factor AML identifies recurrent ZBTB7A mutations and defines RUNX1-CBFA2T3 fusion signature. <i>Blood</i> , 2016 , 127, 2498-501 | 2.2 | 46 |
| 11 | Chemo-genomic interrogation of CEBPA mutated AML reveals recurrent CSF3R mutations and subgroup sensitivity to JAK inhibitors. <i>Blood</i> , 2016 , 127, 3054-61 | 2.2 | 55 |
| 10 | Chemo-Transcriptomic Analysis of Complex Karyotype AML Reveals Increased Expression of Cell Cycle Components and Exquisite Dependency on Polo-like Kinase 1. <i>Blood</i> , 2016 , 128, 769-769 | 2.2 | 1 |
| 9 | Transcriptional Landscape of APL Identifies Aberrant Podoplanin Expression As a Defining Feature and Missing Link for the Bleeding Disorder of This Disease. <i>Blood</i> , 2016 , 128, 1075-1075 | 2.2 | |
| 8 | The transcriptomic landscape and directed chemical interrogation of MLL-rearranged acute myeloid leukemias. <i>Nature Genetics</i> , 2015 , 47, 1030-7 | 36.3 | 95 |
| 7 | EV11-rearranged acute myeloid leukemias are characterized by distinct molecular alterations. <i>Blood</i> , 2015 , 125, 140-3 | 2.2 | 43 |
| 6 | Transcriptome Analysis Reveals That G Protein-Coupled Receptors Are Potential Diagnostic Markers or Therapeutic Targets in Acute Myeloid Leukemia. <i>Blood</i> , 2015 , 126, 3855-3855 | 2.2 | 2 |
| 5 | Mutational and Transcriptomic Landscape of AML with Core-Binding Factor Rearrangements. <i>Blood</i> , 2015 , 126, 802-802 | 2.2 | |
| 4 | Prospective Evaluation of Fetal Haemoglobin Induction in Maternal Erythrocytes: A Preliminary Analysis of a Cohort of 345 Parturients. <i>Blood</i> , 2015 , 126, 3370-3370 | 2.2 | |
| 3 | The Novel Leukemia Stem Cell Marker GPR56 Discriminates Leukemic Subclones with Divergent Stem Cell Properties in Human Acute Myeloid Leukemia. <i>Blood</i> , 2015 , 126, 1859-1859 | 2.2 | |
| 2 | NGS-Based Detection Of Multiple RAS-Mutated Clones In MLL-Rearranged Leukemias Suggests Strong Oncogenic Collaboration. <i>Blood</i> , 2013 , 122, 744-744 | 2.2 | |
| 1 | Target variant detection in leukemia using unaligned RNA-Seq reads | | 2 |