

Alexander V Penson

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

4,867
citations

516710

16
h-index

642732

23
g-index

25
all docs

25
docs citations

25
times ranked

11207
citing authors

#	ARTICLE	IF	CITATIONS
1	A randomized phase 3 trial of interferon- β vs hydroxyurea in polycythemia vera and essential thrombocythemia. <i>Blood</i> , 2022, 139, 2931-2941.	1.4	45
2	Mechanisms of Resistance to Noncovalent Bruton's Tyrosine Kinase Inhibitors. <i>New England Journal of Medicine</i> , 2022, 386, 735-743.	27.0	87
3	The context-specific role of germline pathogenicity in tumorigenesis. <i>Nature Genetics</i> , 2021, 53, 1577-1585.	21.4	44
4	SRSF2-P95H delays Myelofibrosis Development through Altered JAK/STAT Signaling in JAK2-V617F Megakaryocytes. <i>Blood</i> , 2021, 138, 2544-2544.	1.4	1
5	Modulation of RNA Splicing Enhances Response to BCL2 Inhibition in Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, 507-507.	1.4	5
6	Safety and activity of selinexor in patients with myelodysplastic syndromes or oligoblastic acute myeloid leukaemia refractory to hypomethylating agents: a single-centre, single-arm, phase 2 trial. <i>Lancet Haematology</i> , 2020, 7, e566-e574.	4.6	13
7	Phase and context shape the function of composite oncogenic mutations. <i>Nature</i> , 2020, 582, 100-103.	27.8	31
8	Altered RNA Splicing by Mutant p53 Activates Oncogenic RAS Signaling in Pancreatic Cancer. <i>Cancer Cell</i> , 2020, 38, 198-211.e8.	16.8	99
9	The Evolutionary Origins of Recurrent Pancreatic Cancer. <i>Cancer Discovery</i> , 2020, 10, 792-805.	9.4	71
10	Genetic basis for iMCD-TAFRO. <i>Oncogene</i> , 2020, 39, 3218-3225.	5.9	14
11	Modeling biological and genetic diversity in upper tract urothelial carcinoma with patient derived xenografts. <i>Nature Communications</i> , 2020, 11, 1975.	12.8	37
12	ZRSR2 Mutation Induced Minor Intron Retention Drives MDS and Diverse Cancer Predisposition Via Aberrant Splicing of LZTR1. <i>Blood</i> , 2020, 136, 10-11.	1.4	1
13	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. <i>Cancer Cell</i> , 2019, 36, 194-209.e9.	16.8	184
14	Nbn-Mre11 interaction is required for tumor suppression and genomic integrity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15178-15183.	7.1	8
15	Altered Nuclear Export Signal Recognition as a Driver of Oncogenesis. <i>Cancer Discovery</i> , 2019, 9, 1452-1467.	9.4	60
16	Spliceosomal disruption of the non-canonical BAF complex in cancer. <i>Nature</i> , 2019, 574, 432-436.	27.8	163
17	Aberrant RNA Splicing Contributes to the Pathogenesis of EVI-Rearranged Myeloid Leukemias. <i>Blood</i> , 2019, 134, 917-917.	1.4	0
18	Unifying cancer and normal RNA sequencing data from different sources. <i>Scientific Data</i> , 2018, 5, 180061.	5.3	152

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19	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	21.4	601
20	Widespread Selection for Oncogenic Mutant Allele Imbalance in Cancer. Cancer Cell, 2018, 34, 852-862.e4.	16.8	73
21	Genome doubling shapes the evolution and prognosis of advanced cancers. Nature Genetics, 2018, 50, 1189-1195.	21.4	411
22	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. Nature Medicine, 2017, 23, 703-713.	30.7	2,473
23	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. JCO Precision Oncology, 2017, 2017, 1-16.	3.0	286
24	Oncogenic Mutations in <i>XPO1</i> Promote Lymphoid Transformation By Altering Nuclear/Cytoplasmic Localization of NF κ B Signaling Intermediates. Blood, 2017, 130, 879-879.	1.4	0