

Pavel Sumazin

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

6,015
citations

136740

32
h-index

95083

68
g-index

103
all docs

103
docs citations

103
times ranked

12011
citing authors

#	ARTICLE	IF	CITATIONS
1	An Extensive MicroRNA-Mediated Network of RNA-RNA Interactions Regulates Established Oncogenic Pathways in Glioblastoma. <i>Cell</i> , 2011, 147, 370-381.	13.5	671
2	tRNA-derived microRNA modulates proliferation and the DNA damage response and is down-regulated in B cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1404-1409.	3.3	487
3	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
4	A human B cell interactome identifies MYB and FOXM1 as master regulators of proliferation in germinal centers. <i>Molecular Systems Biology</i> , 2010, 6, 377.	3.2	336
5	Whole Exome Sequencing to Identify a Novel Gene (Caveolin-1) Associated With Human Pulmonary Arterial Hypertension. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 336-343.	5.1	333
6	Trivalent CAR T cells overcome interpatient antigenic variability in glioblastoma. <i>Neuro-Oncology</i> , 2018, 20, 506-518.	0.6	306
7	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
8	Integrated biochemical and computational approach identifies BCL6 direct target genes controlling multiple pathways in normal germinal center B cells. <i>Blood</i> , 2010, 115, 975-984.	0.6	216
9	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	2.9	205
10	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. <i>Hepatology</i> , 2017, 65, 104-121.	3.6	192
11	BCL6 suppression of BCL2 via Miz1 and its disruption in diffuse large B cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11294-11299.	3.3	170
12	Lowest common ancestors in trees and directed acyclic graphs. <i>Journal of Algorithms</i> , 2005, 57, 75-94.	0.9	162
13	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. <i>Nature Communications</i> , 2015, 6, 8891.	5.8	126
14	Identification of the Human Mature B Cell miRNome. <i>Immunity</i> , 2009, 30, 744-752.	6.6	124
15	Reprogramming metabolic pathways in vivo with CRISPR/Cas9 genome editing to treat hereditary tyrosinaemia. <i>Nature Communications</i> , 2016, 7, 12642.	5.8	119
16	DNA motifs in human and mouse proximal promoters predict tissue-specific expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6275-6280.	3.3	114
17	A Molecular Signature Predictive of Indolent Prostate Cancer. <i>Science Translational Medicine</i> , 2013, 5, 202ra122.	5.8	114
18	Identifying tissue-selective transcription factor binding sites in vertebrate promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1560-1565.	3.3	113

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19	DWE: Discriminating Word Enumerator. <i>Bioinformatics</i> , 2005, 21, 31-38.	1.8	100
20	Similarity of position frequency matrices for transcription factor binding sites. <i>Bioinformatics</i> , 2005, 21, 307-313.	1.8	97
21	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. <i>Genome Research</i> , 2015, 25, 257-267.	2.4	94
22	LIN28 Selectively Modulates a Subclass of Let-7 MicroRNAs. <i>Molecular Cell</i> , 2018, 71, 271-283.e5.	4.5	89
23	Mining ChIP-chip data for transcription factor and cofactor binding sites. <i>Bioinformatics</i> , 2005, 21, i403-i412.	1.8	78
24	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	9.4	75
25	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 244-249.	3.3	74
26	MMTV-Espl1 transgenic mice develop aneuploid, estrogen receptor alpha (ER α)-positive mammary adenocarcinomas. <i>Oncogene</i> , 2014, 33, 5511-5522.	2.6	66
27	The <i>miR-424(322)/503</i> cluster orchestrates remodeling of the epithelium in the involuting mammary gland. <i>Genes and Development</i> , 2014, 28, 765-782.	2.7	66
28	Novel patient-derived xenograft and cell line models for therapeutic testing of pediatric liver cancer. <i>Journal of Hepatology</i> , 2016, 65, 325-333.	1.8	56
29	Tissue-specific regulatory elements in mammalian promoters. <i>Molecular Systems Biology</i> , 2007, 3, 73.	3.2	52
30	High-throughput validation of ceRNA regulatory networks. <i>BMC Genomics</i> , 2017, 18, 418.	1.2	46
31	Metformin induces FOXO3-dependent fetal hemoglobin production in human primary erythroid cells. <i>Blood</i> , 2018, 132, 321-333.	0.6	46
32	Genome-wide prediction and analysis of function-specific transcription factor binding sites. <i>In Silico Biology</i> , 2004, 4, 395-410.	0.4	43
33	Atovaquone is active against AML by upregulating the integrated stress pathway and suppressing oxidative phosphorylation. <i>Blood Advances</i> , 2019, 3, 4215-4227.	2.5	34
34	A novel humanized mouse lacking murine P450 oxidoreductase for studying human drug metabolism. <i>Nature Communications</i> , 2017, 8, 39.	5.8	33
35	Interrogation of a Context-Specific Transcription Factor Network Identifies Novel Regulators of Pluripotency. <i>Stem Cells</i> , 2015, 33, 367-377.	1.4	32
36	The number of titrated microRNA species dictates ceRNA regulation. <i>Nucleic Acids Research</i> , 2018, 46, 4354-4369.	6.5	32

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37	A Novel Cell Line Based Orthotopic Xenograft Mouse Model That Recapitulates Human Hepatoblastoma. <i>Scientific Reports</i> , 2017, 7, 17751.	1.6	29
38	A human liver chimeric mouse model for non-alcoholic fatty liver disease. <i>JHEP Reports</i> , 2021, 3, 100281.	2.6	27
39	MDM4 inhibition: a novel therapeutic strategy to reactivate p53 in hepatoblastoma. <i>Scientific Reports</i> , 2021, 11, 2967.	1.6	26
40	TEA Domain Transcription Factor 4 Is the Major Mediator of Yes-Associated Protein Oncogenic Activity in Mouse and Human Hepatoblastoma. <i>American Journal of Pathology</i> , 2019, 189, 1077-1090.	1.9	25
41	Pan-cancer clinical and molecular analysis of racial disparities. <i>Cancer</i> , 2020, 126, 800-807.	2.0	25
42	Overexpression and constitutive nuclear localization of cohesin protease Separase protein correlates with high incidence of relapse and reduced overall survival in glioblastoma multiforme. <i>Journal of Neuro-Oncology</i> , 2014, 119, 27-35.	1.4	24
43	Nonhomologous End Joining Is More Important Than Proton Linear Energy Transfer in Dictating Cell Death. <i>International Journal of Radiation Oncology Biology Physics</i> , 2019, 105, 1119-1125.	0.4	22
44	Restoration of the molecular clock is tumor suppressive in neuroblastoma. <i>Nature Communications</i> , 2021, 12, 4006.	5.8	22
45	Hepatoblastomas with carcinoma features represent a biological spectrum of aggressive neoplasms in children and young adults. <i>Journal of Hepatology</i> , 2022, 77, 1026-1037.	1.8	21
46	Increases in compulsivity, inflammation, and neural injury in HIV transgenic rats with escalated methamphetamine self-administration under extended-access conditions. <i>Brain Research</i> , 2020, 1726, 146502.	1.1	17
47	CHAF1A Blocks Neuronal Differentiation and Promotes Neuroblastoma Oncogenesis via Metabolic Reprogramming. <i>Advanced Science</i> , 2021, 8, e2005047.	5.6	17
48	Correlating measurements across samples improves accuracy of large-scale expression profile experiments. <i>Genome Biology</i> , 2009, 10, R143.	13.9	14
49	Integrative analysis identifies lincRNAs up- and downstream of neuroblastoma driver genes. <i>Scientific Reports</i> , 2019, 9, 5685.	1.6	14
50	A Systems Biology Approach to Transcription Factor Binding Site Prediction. <i>PLoS ONE</i> , 2010, 5, e9878.	1.1	11
51	An updated h-index measures both the primary and total scientific output of a researcher. <i>Discoveries</i> , 2015, 3, e50.	1.5	10
52	Epitranscriptomics: Correlation of N6-methyladenosine RNA methylation and pathway dysregulation in the hippocampus of HIV transgenic rats. <i>PLoS ONE</i> , 2019, 14, e0203566.	1.1	9
53	Direct ChIP-Seq significance analysis improves target prediction. <i>BMC Genomics</i> , 2015, 16, S4.	1.2	8
54	Cell lines of the same anatomic site and histologic type show large variability in intrinsic radiosensitivity and relative biological effectiveness to protons and carbon ions. <i>Medical Physics</i> , 2021, 48, 3243-3261.	1.6	7

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55	Deconvolving Sequence Variation in Mixed DNA Populations. <i>Journal of Computational Biology</i> , 2003, 10, 635-652.	0.8	6
56	Inferring clonal composition from multiple tumor biopsies. <i>Npj Systems Biology and Applications</i> , 2020, 6, 27.	1.4	5
57	Metformin Induces FOXO3-Dependent Fetal Hemoglobin Production in Primary Erythroid Cells. <i>Blood</i> , 2016, 128, 322-322.	0.6	4
58	Escalated (Dependent) Oxycodone Self-Administration Is Associated with Cognitive Impairment and Transcriptional Evidence of Neurodegeneration in Human Immunodeficiency Virus (HIV) Transgenic Rats. <i>Viruses</i> , 2022, 14, 669.	1.5	4
59	KrÄppel-like Factor 4 Supports the Expansion of Leukemia Stem Cells in MLL-AF9-driven Acute Myeloid Leukemia. <i>Stem Cells</i> , 2022, 40, 736-750.	1.4	4
60	A Model for Analyzing Black-Box Optimization. <i>Lecture Notes in Computer Science</i> , 2003, , 424-438.	1.0	3
61	Illuminating lncRNA Function Through Target Prediction. <i>Methods in Molecular Biology</i> , 2021, 2372, 263-295.	0.4	3
62	A Time-Sensitive System for Black-Box Combinatorial Optimization. <i>Lecture Notes in Computer Science</i> , 2002, , 16-28.	1.0	3
63	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. <i>Blood</i> , 2018, 132, 3641-3641.	0.6	3
64	HepT1-derived murine models of high-risk hepatoblastoma display vascular invasion, metastasis, and circulating tumor cells. <i>Biology Open</i> , 2022, 11, .	0.6	3
65	Abstract A33: Discovery of chimeric transcripts involving APC and TERT in pediatric HCC by RNA sequencing. , 2016, , .		2
66	CRLF2 overexpression results in reduced B-cell differentiation and upregulated E2F signaling in the Dp16 mouse model of Down syndrome. <i>Experimental Hematology</i> , 2022, 110, 34-38.	0.2	2
67	Editorial: The RNA Revolution in Embryonic Development and Cell Differentiation in Health and Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 715341.	1.8	1
68	Abstract 4186: An extensive microRNA-mediated network of RNA-RNA interactions regulates established oncogenic pathways in glioblastoma. , 2012, , .		1
69	Glypican-3-specific CAR-NKT cells overexpressing BATF3 mediate potent antitumor activity against hepatocellular carcinoma.. <i>Journal of Clinical Oncology</i> , 2022, 40, e14521-e14521.	0.8	1
70	Shift error detection in standardized exams. <i>Journal of Discrete Algorithms</i> , 2004, 2, 313-331.	0.7	0
71	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. <i>Nature Precedings</i> , 2007, , .	0.1	0
72	HG-108MULTISPECIFIC CHIMERIC ANTIGEN RECEPTOR (CAR) T-CELLS OVERCOME INTER-PATIENT TUMOR HETEROGENEITY AND EXHIBIT ENHANCED ANTITUMOR FUNCTIONALITY IN THE TREATMENT OF GLIOBLASTOMA. <i>Neuro-Oncology</i> , 2016, 18, iii73.3-iii73.	0.6	0

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73	Metabolic Pathway Reprogramming by CRISPR/CAS9 Genome Editing. Journal of Hepatology, 2016, 64, S216.	1.8	0
74	Abstract 2997: Novel orthotopic patient-derived xenograft mouse models of hepatoblastoma that replicate tumor heterogeneity, chemoresistance, and refractory disease. , 2021, , .		0
75	Integrated Biochemical and Computational Approach Identifies BCL6 Direct Target Genes Controlling Multiple Pathways in Normal Germinal-Center B Cells. Blood, 2008, 112, 2434-2434.	0.6	0
76	Abstract 4240: Transcription factor networks that regulate pluripotency and lineage differentiation in adult human male germ cell tumors. , 2010, , .		0
77	Identification of NOTCH1-Controlled Transcriptional Programs In Human T-Cell Development. Blood, 2010, 116, 2495-2495.	0.6	0
78	MIR-28 Silencing In Germinal Center-Derived Lymphomas. Blood, 2010, 116, 703-703.	0.6	0
79	Abstract LB-337: Post-transcriptional regulators of microRNA biogenesis drive glioblastoma-specific expression. , 2011, , .		0
80	Abstract LB-339: MicroRNA modulators regulate oncogenes and tumor suppressors in glioblastoma. , 2011, , .		0
81	Abstract 3410: Regulation of pluripotency and lineage differentiation in human male germ cell tumors. , 2011, , .		0
82	Abstract A14: microRNA-mediated interactions regulate established oncogenic pathways in cancer. Cancer Research, 2012, 72, A14-A14.	0.4	0
83	Abstract 2946: Post-transcriptional regulators of microRNA biogenesis regulate pathogenesis of cancer. , 2012, , .		0
84	Abstract 5231: Highly conserved ceRNA regulatory interactions cooperate with genomic variability to modulate drivers of tumorigenesis.. , 2013, , .		0
85	Abstract 2873: A molecular signature predictive of indolent prostate cancer. , 2014, , .		0
86	Abstract 4267: Integrated genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. , 2015, , .		0
87	Abstract IA14: Genomic alterations dysregulate cancer genes by modulating microRNA activity. , 2015, , .		0
88	Interleukin-6 Levels Predict Relapse Free Survival in Pediatric AML and Suggest a Mechanism of Chemotherapy Resistance. Blood, 2016, 128, 1724-1724.	0.6	0
89	Abstract 4877: Transcriptome sequencing of pediatric hepatocellular carcinoma reveals genomic events involvingAPCandTERT. , 2017, , .		0
90	Expression Differences Distinguish Pediatric Acute and Chronic ITP Using RNA Sequencing. Blood, 2018, 132, 127-127.	0.6	0

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91	Insulin-like Growth Factor Binding Protein-3 (IGFBP3) Induces Fetal Hemoglobin in Hematopoietic Stem and Progenitor Cells from Patients with Sickle Cell Anemia. Blood, 2018, 132, 722-722.	0.6	0
92	Abstract B76: Characterizing vascular invasion in hepatoblastoma. , 2020, , .		0
93	Cite-Seq Reveals Distinct Patterns and Potential Mechanisms of Relapse in Pediatric AML. Blood, 2021, 138, 3458-3458.	0.6	0
94	The KrÄppel-like Factor 4 Sustains a Leukemic Gene Expression Profile in MLL-AF9-Driven Acute Myeloid Leukemia. Blood, 2021, 138, 1143-1143.	0.6	0