Pavel Sumazin

List of Publications by Year
in descending order

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	Escalated (Dependent) Oxycodone Self-Administration Is Associated with Cognitive Impairment and Transcriptional Evidence of Neurodegeneration in Human Immunodeficiency Virus (HIV) Transgenic Rats. Viruses, 2022, 14, 669.	1.5	4
2	CRLF2 overexpression results in reduced B-cell differentiation and upregulated E2F signaling in the Dp16 mouse model of Down syndrome. Experimental Hematology, 2022, 110, 34-38.	0.2	2
3	HepT1-derived murine models of high-risk hepatoblastoma display vascular invasion, metastasis, and circulating tumor cells. Biology Open, 2022, 11, .	0.6	3
4	Krüppel-like Factor 4 Supports the Expansion of Leukemia Stem Cells in MLL-AF9-driven Acute Myeloid Leukemia. Stem Cells, 2022, 40, 736-750.	1.4	4
5	Hepatoblastomas with carcinoma features represent a biological spectrum of aggressive neoplasms in children and young adults. Journal of Hepatology, 2022, 77, 1026-1037.	1.8	21
6	Glypican-3-specific CAR-NKT cells overexpressing BATF3 mediate potent antitumor activity against hepatocellular carcinoma.. Journal of Clinical Oncology, 2022, 40, e14521-e14521.	0.8	1
7	Illuminating lncRNA Function Through Target Prediction. Methods in Molecular Biology, 2021, 2372, 263-295.	0.4	3
8	MDM4 inhibition: a novel therapeutic strategy to reactivate p53 in hepatoblastoma. Scientific Reports, 2021, 11, 2967.	1.6	26
9	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. Medical Physics, 2021, 48, 3243-3261.	1.6	7
10	The RNA Atlas expands the catalog of human non-coding RNAs. Nature Biotechnology, 2021, 39, 1453-1465.	9.4	75
11	Restoration of the molecular clock is tumor suppressive in neuroblastoma. Nature Communications, 2021, 12, 4006.	5.8	22
12	A human liver chimeric mouse model for non-alcoholic fatty liver disease. JHEP Reports, 2021, 3, 100281.	2.6	27
13	Abstract 2997: Novel orthotopic patient-derived xenograft mouse models of hepatoblastoma that replicate tumor heterogeneity, chemoresistance, and refractory disease. , 2021, , .		0
14	CHAF1A Blocks Neuronal Differentiation and Promotes Neuroblastoma Oncogenesis via Metabolic Reprogramming. Advanced Science, 2021, 8, e2005047.	5.6	17
15	Editorial: The RNA Revolution in Embryonic Development and Cell Differentiation in Health and Disease. Frontiers in Cell and Developmental Biology, 2021, 9, 715341.	1.8	1
16	Cite-Seq Reveals Distinct Patterns and Potential Mechanisms of Relapse in Pediatric AML. Blood, 2021, 138, 3458-3458.	0.6	0
17	The Krüppel-like Factor 4 Sustains a Leukemic Gene Expression Profile in MLL-AF9-Driven Acute Myeloid Leukemia. Blood, 2021, 138, 1143-1143.	0.6	0
18	Increases in compulsivity, inflammation, and neural injury in HIV transgenic rats with escalated methamphetamine self-administration under extended-access conditions. Brain Research, 2020, 1726, 146502.	1.1	17

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19	Pan‑cancer clinical and molecular analysis of racial disparities. Cancer, 2020, 126, 800-807.	2.0	25
20	Inferring clonal composition from multiple tumor biopsies. Npj Systems Biology and Applications, 2020, 6, 27.	1.4	5
21	Abstract B76: Characterizing vascular invasion in hepatoblastoma. , 2020, , .		0
22	Nonhomologous End Joining Is More Important Than Proton Linear Energy Transfer in Dictating Cell Death. International Journal of Radiation Oncology Biology Physics, 2019, 105, 1119-1125.	0.4	22
23	Integrative analysis identifies lincRNAs up- and downstream of neuroblastoma driver genes. Scientific Reports, 2019, 9, 5685.	1.6	14
24	TEA Domain Transcription Factor 4 Is the Major Mediator of Yes-Associated Protein Oncogenic Activity in Mouse and Human Hepatoblastoma. American Journal of Pathology, 2019, 189, 1077-1090.	1.9	25
25	Atovaquone is active against AML by upregulating the integrated stress pathway and suppressing oxidative phosphorylation. Blood Advances, 2019, 3, 4215-4227.	2.5	34
26	Epitranscriptomics: Correlation of N6-methyladenosine RNA methylation and pathway dysregulation in the hippocampus of HIV transgenic rats. PLoS ONE, 2019, 14, e0203566.	1.1	9
27	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
28	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205
29	The number of titrated microRNA species dictates ceRNA regulation. Nucleic Acids Research, 2018, 46, 4354-4369.	6.5	32
30	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
31	Trivalent CAR T cells overcome interpatient antigenic variability in glioblastoma. Neuro-Oncology, 2018, 20, 506-518.	0.6	306
32	LIN28 Selectively Modulates a Subclass of Let-7 MicroRNAs. Molecular Cell, 2018, 71, 271-283.e5.	4.5	89
33	Metformin induces FOXO3-dependent fetal hemoglobin production in human primary erythroid cells. Blood, 2018, 132, 321-333.	0.6	46
34	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. Blood, 2018, 132, 3641-3641.	0.6	3
35	Expression Differences Distinguish Pediatric Acute and Chronic ITP Using RNA Sequencing. Blood, 2018, 132, 127-127.	0.6	0
36	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

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37	A novel humanized mouse lacking murine P450 oxidoreductase for studying human drug metabolism. Nature Communications, 2017, 8, 39.	5.8	33
38	High-throughput validation of ceRNA regulatory networks. BMC Genomics, 2017, 18, 418.	1.2	46
39	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. Hepatology, 2017, 65, 104-121.	3.6	192
40	A Novel Cell Line Based Orthotopic Xenograft Mouse Model That Recapitulates Human Hepatoblastoma. Scientific Reports, 2017, 7, 17751.	1.6	29
41	Abstract 4877: Transcriptome sequencing of pediatric hepatocellular carcinoma reveals genomic events involvingAPCandTERT. , 2017, , .		0
42	HG-108MULTISPECIFIC CHIMERIC ANTIGEN RECEPTOR (CAR) T-CELLS OVERCOME INTER-PATIENT TUMOR HETEROGENEITY AND EXHIBIT ENHANCED ANTITUMOR FUNCTIONALITY IN THE TREATMENT OF GLIOBLASTOMA. Neuro-Oncology, 2016, 18, iii73.3-iii73.	0.6	0
43	Novel patient-derived xenograft and cell line models for therapeutic testing of pediatric liver cancer. Journal of Hepatology, 2016, 65, 325-333.	1.8	56
44	Metabolic Pathway Reprogramming by CRISPR/CAS9 Genome Editing. Journal of Hepatology, 2016, 64, S216.	1.8	0
45	Reprogramming metabolic pathways in vivo with CRISPR/Cas9 genome editing to treat hereditary tyrosinaemia. Nature Communications, 2016, 7, 12642.	5.8	119
46	Metformin Induces FOXO3-Dependent Fetal Hemoglobin Production in Primary Erythroid Cells. Blood, 2016, 128, 322-322.	0.6	4
47	Abstract A33: Discovery of chimeric transcripts involving APC and TERT in pediatric HCC by RNA sequencing. , 2016, , .		2
48	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
49	Direct ChIP-Seq significance analysis improves target prediction. BMC Genomics, 2015, 16, S4.	1.2	8
50	An updated h-index measures both the primary and total scientific output of a researcher. Discoveries, 2015, 3, e50.	1.5	10
51	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. Nature Communications, 2015, 6, 8891.	5.8	126
52	Interrogation of a Context-Specific Transcription Factor Network Identifies Novel Regulators of Pluripotency. Stem Cells, 2015, 33, 367-377.	1.4	32
53	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. Genome Research, 2015, 25, 257-267.	2.4	94
54	Abstract 4267: Integrated genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. , 2015, , .		0

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55	Abstract IA14: Genomic alterations dysregulate cancer genes by modulating microRNA activity. , 2015, , .		0
56	MMTV-Espl1 transgenic mice develop aneuploid, estrogen receptor alpha (ERÎ±)-positive mammary adenocarcinomas. Oncogene, 2014, 33, 5511-5522.	2.6	66
57	The <i>miR-424(322)/503</i> cluster orchestrates remodeling of the epithelium in the involuting mammary gland. Genes and Development, 2014, 28, 765-782.	2.7	66
58	Overexpression and constitutive nuclear localization of cohesin protease Separase protein correlates with high incidence of relapse and reduced overall survival in glioblastoma multiforme. Journal of Neuro-Oncology, 2014, 119, 27-35.	1.4	24
59	Abstract 2873: A molecular signature predictive of indolent prostate cancer. , 2014, , .		0
60	tRNA-derived microRNA modulates proliferation and the DNA damage response and is down-regulated in B cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1404-1409.	3.3	487
61	A Molecular Signature Predictive of Indolent Prostate Cancer. Science Translational Medicine, 2013, 5, 202ra122.	5.8	114
62	Abstract 5231: Highly conserved ceRNA regulatory interactions cooperate with genomic variability to modulate drivers of tumorigenesis.. , 2013, , .		0
63	Whole Exome Sequencing to Identify a Novel Gene (Caveolin-1) Associated With Human Pulmonary Arterial Hypertension. Circulation: Cardiovascular Genetics, 2012, 5, 336-343.	5.1	333
64	Abstract 4186: An extensive microRNA-mediated network of RNA-RNA interactions regulates established oncogenic pathways in glioblastoma. , 2012, , .		1
65	Abstract A14: microRNA-mediated interactions regulate established oncongenic pathways in cancer. Cancer Research, 2012, 72, A14-A14.	0.4	0
66	Abstract 2946: Post-transcriptional regulators of microRNA biogenesis regulate pathogenesis of cancer. , 2012, , .		0
67	An Extensive MicroRNA-Mediated Network of RNA-RNA Interactions Regulates Established Oncogenic Pathways in Glioblastoma. Cell, 2011, 147, 370-381.	13.5	671
68	Abstract LB-337: Post-transcriptional regulators of microRNA biogenesis drive glioblastoma-specific expression. , 2011, , .		0
69	Abstract LB-339: MicroRNA modulators regulate oncogenes and tumor suppressors in glioblastoma. , 2011, , .		0
70	Abstract 3410: Regulation of pluripotency and lineage differentiation in human male germ cell tumors. , 2011, , .		0
71	A human Bâ€cell interactome identifies MYB and FOXM1 as master regulators of proliferation in germinal centers. Molecular Systems Biology, 2010, 6, 377.	3.2	336
72	Integrated biochemical and computational approach identifies BCL6 direct target genes controlling multiple pathways in normal germinal center B cells. Blood, 2010, 115, 975-984.	0.6	216

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73	A Systems Biology Approach to Transcription Factor Binding Site Prediction. PLoS ONE, 2010, 5, e9878.	1.1	11
74	Abstract 4240: Transcription factor networks that regulate pluripotency and lineage differentiation in adult human male germ cell tumors. , 2010, , .		0
75	Identification of NOTCH1-Controlled Transcriptional Programs In Human T-Cell Development. Blood, 2010, 116, 2495-2495.	0.6	0
76	MiR-28 Silencing In Germinal Center-Derived Lymphomas. Blood, 2010, 116, 703-703.	0.6	0
77	BCL6 suppression of BCL2 via Miz1 and its disruption in diffuse large B cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11294-11299.	3.3	170
78	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 244-249.	3.3	74
79	Identification of the Human Mature B Cell miRNome. Immunity, 2009, 30, 744-752.	6.6	124
80	Correlating measurements across samples improves accuracy of large-scale expression profile experiments. Genome Biology, 2009, 10, R143.	13.9	14
81	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
82	Tissueâ€specific regulatory elements in mammalian promoters. Molecular Systems Biology, 2007, 3, 73.	3.2	52
83	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. Nature Precedings, 2007, , .	0.1	0
84	DNA motifs in human and mouse proximal promoters predict tissue-specific expression. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6275-6280.	3.3	114
85	Lowest common ancestors in trees and directed acyclic graphs. Journal of Algorithms, 2005, 57, 75-94.	0.9	162
86	Mining ChIP-chip data for transcription factor and cofactor binding sites. Bioinformatics, 2005, 21, i403-i412.	1.8	78
87	DWE: Discriminating Word Enumerator. Bioinformatics, 2005, 21, 31-38.	1.8	100
88	Identifying tissue-selective transcription factor binding sites in vertebrate promoters. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1560-1565.	3.3	113
89	Similarity of position frequency matrices for transcription factor binding sites. Bioinformatics, 2005, 21, 307-313.	1.8	97
90	Shift error detection in standardized exams. Journal of Discrete Algorithms, 2004, 2, 313-331.	0.7	0

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91	Genome-wide prediction and analysis of function-specific transcription factor binding sites. In Silico Biology, 2004, 4, 395-410.	0.4	43
92	Deconvolving Sequence Variation in Mixed DNA Populations. Journal of Computational Biology, 2003, 10, 635-652.	0.8	6
93	A Model for Analyzing Black-Box Optimization. Lecture Notes in Computer Science, 2003, , 424-438.	1.0	3
94	A Time-Sensitive System for Black-Box Combinatorial Optimization. Lecture Notes in Computer Science, 2002, , 16-28.	1.0	3