Ulf Schmitz

List of Publications by Year in descending order

62 papers	2,009 citations	236612 25 h-index	264894 42 g-index
74 all docs	74 docs citations	74 times ranked	3232 citing authors

#	Article	IF	Citations
1	Systems biology-based investigation of cooperating microRNAs as monotherapy or adjuvant therapy in cancer. Nucleic Acids Research, 2019, 47, 7753-7766.	6.5	126
2	A dynamic intron retention program in the mammalian megakaryocyte and erythrocyte lineages. Blood, 2016, 127, e24-e34.	0.6	94
3	The changing paradigm of intron retention: regulation, ramifications and recipes. Nucleic Acids Research, 2019, 47, 11497-11513.	6.5	90
4	Regulation of cell cycle checkpoint kinase WEE1 by miR-195 in malignant melanoma. Oncogene, 2013, 32, 3175-3183.	2.6	85
5	Unraveling a tumor type-specific regulatory core underlying E2F1-mediated epithelial-mesenchymal transition to predict receptor protein signatures. Nature Communications, 2017, 8, 198.	5.8	84
6	E2F1 confers anticancer drug resistance by targeting ABC transporter family members and Bcl-2 via the p73/DNp73-miR-205 circuitry. Cell Cycle, 2012, 11, 3067-3078.	1.3	82
7	Intron retention enhances gene regulatory complexity in vertebrates. Genome Biology, 2017, 18, 216.	3.8	79
8	E2F1 induces miRâ€224/452 expression to drive <scp>EMT</scp> through <scp>TXNIP</scp> downregulation. EMBO Reports, 2014, 15, 1315-1329.	2.0	78
9	Computational analysis of target hub gene repression regulated by multiple and cooperative miRNAs. Nucleic Acids Research, 2012, 40, 8818-8834.	6.5	77
10	Cooperative gene regulation by microRNA pairs and their identification using a computational workflow. Nucleic Acids Research, 2014, 42, 7539-7552.	6.5	72
11	miR-638 promotes melanoma metastasis and protects melanoma cells from apoptosis and autophagy. Oncotarget, 2015, 6, 2966-2980.	0.8	72
12	MicroRNAâ€"mRNA interactions in colorectal cancer and their role in tumor progression. Genes Chromosomes and Cancer, 2015, 54, 129-141.	1.5	70
13	MiR-205-5p and miR-342-3p cooperate in the repression of the E2F1 transcription factor in the context of anticancer chemotherapy resistance. Theranostics, 2018, 8, 1106-1120.	4.6	59
14	Kinetic Modelingâ€"Based Detection of Genetic Signatures That Provide Chemoresistance via the E2F1-p73/DNp73-miR-205 Network. Cancer Research, 2013, 73, 3511-3524.	0.4	56
15	Challenges in defining the role of intron retention in normal biology and disease. Seminars in Cell and Developmental Biology, 2018, 75, 40-49.	2.3	51
16	Exosomal lncRNAs and cancer: connecting the missing links. Bioinformatics, 2019, 35, 352-360.	1.8	51
17	MicroRNA-Regulated Networks: The Perfect Storm for Classical Molecular Biology, the Ideal Scenario for Systems Biology. Advances in Experimental Medicine and Biology, 2013, 774, 55-76.	0.8	50
18	RBM3 regulates temperature sensitive miR-142â€"5p and miR-143 (thermomiRs), which target immune genes and control fever. Nucleic Acids Research, 2016, 44, 2888-2897.	6.5	50

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19	CTCF genetic alterations in endometrial carcinoma are pro-tumorigenic. Oncogene, 2017, 36, 4100-4110.	2.6	50
20	Macrophage development and activation involve coordinated intron retention in key inflammatory regulators. Nucleic Acids Research, 2020, 48, 6513-6529.	6.5	45
21	MicroRNA and Transcription Factor Gene Regulatory Network Analysis Reveals Key Regulatory Elements Associated with Prostate Cancer Progression. PLoS ONE, 2016, 11, e0168760.	1.1	44
22	Tumor-promoting role of signal transducer and activator of transcription (Stat)1 in late-stage melanoma growth. Clinical and Experimental Metastasis, 2010, 27, 133-140.	1.7	40
23	TRAPLINE: a standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. BMC Bioinformatics, 2016, 17, 21.	1.2	35
24	A Systems' Biology Approach to Study MicroRNA-Mediated Gene Regulatory Networks. BioMed Research International, 2013, 2013, 1-15.	0.9	32
25	CTCF as a regulator of alternative splicing: new tricks for an old player. Nucleic Acids Research, 2021, 49, 7825-7838.	6.5	31
26	The Intricate Interplay between Epigenetic Events, Alternative Splicing and Noncoding RNA Deregulation in Colorectal Cancer. Cells, 2019, 8, 929.	1.8	28
27	2-DE profiling of GDNF overexpression-related proteome changes in differentiating ST14A rat progenitor cells. Proteomics, 2007, 7, 33-46.	1.3	25
28	Identification of immunogenic consensus T-cell epitopes in globally distributed influenza-A H1N1 neuraminidase. Infection, Genetics and Evolution, 2011, 11, 308-319.	1.0	23
29	Personalized cancer immunotherapy using Systems Medicine approaches. Briefings in Bioinformatics, 2016, 17, 453-467.	3.2	23
30	Naïve Bayes classifier predicts functional microRNA target interactions in colorectal cancer. Molecular BioSystems, 2015, 11, 2126-2134.	2.9	22
31	Hybrid modeling of the crosstalk between signaling and transcriptional networks using ordinary differential equations and multi-valued logic. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 289-298.	1.1	21
32	The RNA world in the 21st century—a systems approach to finding non-coding keys to clinical questions. Briefings in Bioinformatics, 2016, 17, 380-392.	3.2	19
33	Holding on to Junk Bonds: Intron Retention in Cancer and Therapy. Cancer Research, 2021, 81, 779-789.	0.4	19
34	A model-based strategy to investigate the role of microRNA regulation in cancer signalling networks. Theory in Biosciences, 2011, 130, 55-69.	0.6	18
35	Non-coding RNA detection methods combined to improve usability, reproducibility and precision. BMC Bioinformatics, 2010, 11, 491.	1.2	17
36	Analysis of cell adhesion during early stages of colon cancer based on an extended multi-valued logic approach. Molecular BioSystems, 2012, 8, 1230.	2.9	17

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37	MicroRNA Cancer Regulation. Advances in Experimental Medicine and Biology, 2013, , .	0.8	17
38	Web Resources for microRNA Research. Advances in Experimental Medicine and Biology, 2013, 774, 225-250.	0.8	16
39	Study of the Female Sex Survival Advantage in Melanomaâ€"A Focus on X-Linked Epigenetic Regulators and Immune Responses in Two Cohorts. Cancers, 2020, 12, 2082.	1.7	16
40	Intron retention: importance, challenges, and opportunities. Trends in Genetics, 2022, 38, 789-792.	2.9	16
41	Identifying microRNA determinants of human myelopoiesis. Scientific Reports, 2018, 8, 7264.	1.6	14
42	<i>Ctcf</i> haploinsufficiency mediates intron retention in a tissue-specific manner. RNA Biology, 2021, 18, 93-103.	1.5	12
43	A mutation in the NADH-dehydrogenase subunit 2 suppresses fibroblast aging. Oncotarget, 2015, 6, 8552-8566.	0.8	12
44	Structureâ€"function relationships explain CTCF zinc finger mutation phenotypes in cancer. Cellular and Molecular Life Sciences, 2021, 78, 7519-7536.	2.4	12
45	Widespread Aberrant Alternative Splicing despite Molecular Remission in Chronic Myeloid Leukaemia Patients. Cancers, 2020, 12, 3738.	1.7	10
46	Epithelial-to-mesenchymal transition and its association with PD-L1 and CD8 in thyroid cancer. Endocrine Connections, 2020, 9, 1028-1041.	0.8	9
47	Prospects and challenges of cancer systems medicine: from genes to disease networks. Briefings in Bioinformatics, 2022, 23, .	3.2	7
48	Computational and Experimental Identification of Tissue-Specific MicroRNA Targets. Methods in Molecular Biology, 2017, 1580, 127-147.	0.4	6
49	Computational analysis and modeling the effectiveness of â€˜Zanamivirâ€™ targeting neuraminidase protein in pandemic H1N1 strains. Infection, Genetics and Evolution, 2011, 11, 1072-1082.	1.0	4
50	The Fusion of CLEC12A and MIR223HG Arises from a trans-Splicing Event in Normal and Transformed Human Cells. International Journal of Molecular Sciences, 2021, 22, 12178.	1.8	4
51	Exploration of homodimer receptor: homodimer protein interactions. International Journal of Bioinformatics Research and Applications, 2009, 5, 447.	0.1	2
52	Computational Approaches in microRNA Biology. , 2019, , 317-330.		1
53	Computational microRNA Biology. , 2013, , 473-480.		1
54	RNA Systems Biology for Cancer: From Diagnosis to Therapy. Methods in Molecular Biology, 2016, 1386, 305-330.	0.4	1

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55	MicroRNA, Target Regulation. , 2013, , 1346-1350.		1
56	Computational Methods for Intron Retention Identification and Quantification. , 2021, , 63-74.		0
57	MiRBase. , 2013, , 1363-1366.		0
58	MicroRNA Web Resources. , 2013, , 1335-1337.		0
59	MicroRNA Biogenesis, Regulation. , 2013, , 1306-1310.		0
60	MicroRNA-embedding Regulation Networks, Logical Modeling. , 2013, , 1350-1354.		0
61	Target Site. , 2013, , 2142-2145.		0
62	Gene expression profiling of T-cell inflammation in small cell lung cancer.. Journal of Clinical Oncology, 2019, 37, e20097-e20097.	0.8	0