

# Ulf Schmitz

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Prospects and challenges of cancer systems medicine: from genes to disease networks. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
2	Intron retention: importance, challenges, and opportunities. <i>Trends in Genetics</i> , 2022, 38, 789-792.	2.9	16
3	Holding on to Junk Bonds: Intron Retention in Cancer and Therapy. <i>Cancer Research</i> , 2021, 81, 779-789.	0.4	19
4	<i>Ctcf</i> haploinsufficiency mediates intron retention in a tissue-specific manner. <i>RNA Biology</i> , 2021, 18, 93-103.	1.5	12
5	CTCF as a regulator of alternative splicing: new tricks for an old player. <i>Nucleic Acids Research</i> , 2021, 49, 7825-7838.	6.5	31
6	Computational Methods for Intron Retention Identification and Quantification. , 2021, , 63-74.		0
7	Structure–function relationships explain CTCF zinc finger mutation phenotypes in cancer. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 7519-7536.	2.4	12
8	The Fusion of CLEC12A and MIR223HG Arises from a trans-Splicing Event in Normal and Transformed Human Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12178.	1.8	4
9	Study of the Female Sex Survival Advantage in Melanoma—A Focus on X-Linked Epigenetic Regulators and Immune Responses in Two Cohorts. <i>Cancers</i> , 2020, 12, 2082.	1.7	16
10	Widespread Aberrant Alternative Splicing despite Molecular Remission in Chronic Myeloid Leukaemia Patients. <i>Cancers</i> , 2020, 12, 3738.	1.7	10
11	Macrophage development and activation involve coordinated intron retention in key inflammatory regulators. <i>Nucleic Acids Research</i> , 2020, 48, 6513-6529.	6.5	45
12	Epithelial-to-mesenchymal transition and its association with PD-L1 and CD8 in thyroid cancer. <i>Endocrine Connections</i> , 2020, 9, 1028-1041.	0.8	9
13	Exosomal lncRNAs and cancer: connecting the missing links. <i>Bioinformatics</i> , 2019, 35, 352-360.	1.8	51
14	The Intricate Interplay between Epigenetic Events, Alternative Splicing and Noncoding RNA Deregulation in Colorectal Cancer. <i>Cells</i> , 2019, 8, 929.	1.8	28
15	Systems biology-based investigation of cooperating microRNAs as monotherapy or adjuvant therapy in cancer. <i>Nucleic Acids Research</i> , 2019, 47, 7753-7766.	6.5	126
16	Computational Approaches in microRNA Biology. , 2019, , 317-330.		1
17	The changing paradigm of intron retention: regulation, ramifications and recipes. <i>Nucleic Acids Research</i> , 2019, 47, 11497-11513.	6.5	90
18	Gene expression profiling of T-cell inflammation in small cell lung cancer.. <i>Journal of Clinical Oncology</i> , 2019, 37, e20097-e20097.	0.8	0

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19	Challenges in defining the role of intron retention in normal biology and disease. <i>Seminars in Cell and Developmental Biology</i> , 2018, 75, 40-49.	2.3	51
20	MiR-205-5p and miR-342-3p cooperate in the repression of the E2F1 transcription factor in the context of anticancer chemotherapy resistance. <i>Theranostics</i> , 2018, 8, 1106-1120.	4.6	59
21	Identifying microRNA determinants of human myelopoiesis. <i>Scientific Reports</i> , 2018, 8, 7264.	1.6	14
22	Computational and Experimental Identification of Tissue-Specific MicroRNA Targets. <i>Methods in Molecular Biology</i> , 2017, 1580, 127-147.	0.4	6
23	CTCF genetic alterations in endometrial carcinoma are pro-tumorigenic. <i>Oncogene</i> , 2017, 36, 4100-4110.	2.6	50
24	Unraveling a tumor type-specific regulatory core underlying E2F1-mediated epithelial-mesenchymal transition to predict receptor protein signatures. <i>Nature Communications</i> , 2017, 8, 198.	5.8	84
25	Intron retention enhances gene regulatory complexity in vertebrates. <i>Genome Biology</i> , 2017, 18, 216.	3.8	79
26	A dynamic intron retention program in the mammalian megakaryocyte and erythrocyte lineages. <i>Blood</i> , 2016, 127, e24-e34.	0.6	94
27	TRAPLINE: a standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. <i>BMC Bioinformatics</i> , 2016, 17, 21.	1.2	35
28	RBM3 regulates temperature sensitive miR-142-5p and miR-143 (thermomiRs), which target immune genes and control fever. <i>Nucleic Acids Research</i> , 2016, 44, 2888-2897.	6.5	50
29	The RNA world in the 21st century—a systems approach to finding non-coding keys to clinical questions. <i>Briefings in Bioinformatics</i> , 2016, 17, 380-392.	3.2	19
30	Personalized cancer immunotherapy using Systems Medicine approaches. <i>Briefings in Bioinformatics</i> , 2016, 17, 453-467.	3.2	23
31	RNA Systems Biology for Cancer: From Diagnosis to Therapy. <i>Methods in Molecular Biology</i> , 2016, 1386, 305-330.	0.4	1
32	MicroRNA and Transcription Factor Gene Regulatory Network Analysis Reveals Key Regulatory Elements Associated with Prostate Cancer Progression. <i>PLoS ONE</i> , 2016, 11, e0168760.	1.1	44
33	MicroRNA-mRNA interactions in colorectal cancer and their role in tumor progression. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 129-141.	1.5	70
34	Naïve Bayes classifier predicts functional microRNA target interactions in colorectal cancer. <i>Molecular BioSystems</i> , 2015, 11, 2126-2134.	2.9	22
35	miR-638 promotes melanoma metastasis and protects melanoma cells from apoptosis and autophagy. <i>Oncotarget</i> , 2015, 6, 2966-2980.	0.8	72
36	A mutation in the NADH-dehydrogenase subunit 2 suppresses fibroblast aging. <i>Oncotarget</i> , 2015, 6, 8552-8566.	0.8	12

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37	Cooperative gene regulation by microRNA pairs and their identification using a computational workflow. <i>Nucleic Acids Research</i> , 2014, 42, 7539-7552.	6.5	72
38	Hybrid modeling of the crosstalk between signaling and transcriptional networks using ordinary differential equations and multi-valued logic. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 289-298.	1.1	21
39	E2F1 induces miR-224/452 expression to drive EMT through TXNIP downregulation. <i>EMBO Reports</i> , 2014, 15, 1315-1329.	2.0	78
40	MicroRNA Cancer Regulation. <i>Advances in Experimental Medicine and Biology</i> , 2013, , .	0.8	17
41	Web Resources for microRNA Research. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 225-250.	0.8	16
42	Kinetic Modeling-Based Detection of Genetic Signatures That Provide Chemoresistance via the E2F1-p73/DNp73-miR-205 Network. <i>Cancer Research</i> , 2013, 73, 3511-3524.	0.4	56
43	MicroRNA-Regulated Networks: The Perfect Storm for Classical Molecular Biology, the Ideal Scenario for Systems Biology. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 55-76.	0.8	50
44	A Systems Biology Approach to Study MicroRNA-Mediated Gene Regulatory Networks. <i>BioMed Research International</i> , 2013, 2013, 1-15.	0.9	32
45	Regulation of cell cycle checkpoint kinase WEE1 by miR-195 in malignant melanoma. <i>Oncogene</i> , 2013, 32, 3175-3183.	2.6	85
46	Computational microRNA Biology. , 2013, , 473-480.		1
47	MiRBase. , 2013, , 1363-1366.		0
48	MicroRNA Web Resources. , 2013, , 1335-1337.		0
49	MicroRNA Biogenesis, Regulation. , 2013, , 1306-1310.		0
50	MicroRNA-embedding Regulation Networks, Logical Modeling. , 2013, , 1350-1354.		0
51	Target Site. , 2013, , 2142-2145.		0
52	MicroRNA, Target Regulation. , 2013, , 1346-1350.		1
53	Computational analysis of target hub gene repression regulated by multiple and cooperative miRNAs. <i>Nucleic Acids Research</i> , 2012, 40, 8818-8834.	6.5	77
54	Analysis of cell adhesion during early stages of colon cancer based on an extended multi-valued logic approach. <i>Molecular BioSystems</i> , 2012, 8, 1230.	2.9	17

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55	E2F1 confers anticancer drug resistance by targeting ABC transporter family members and Bcl-2 via the p73/DNp73-miR-205 circuitry. <i>Cell Cycle</i> , 2012, 11, 3067-3078.	1.3	82
56	A model-based strategy to investigate the role of microRNA regulation in cancer signalling networks. <i>Theory in Biosciences</i> , 2011, 130, 55-69.	0.6	18
57	Identification of immunogenic consensus T-cell epitopes in globally distributed influenza-A H1N1 neuraminidase. <i>Infection, Genetics and Evolution</i> , 2011, 11, 308-319.	1.0	23
58	Computational analysis and modeling the effectiveness of Zanamivir™ targeting neuraminidase protein in pandemic H1N1 strains. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1072-1082.	1.0	4
59	Tumor-promoting role of signal transducer and activator of transcription (Stat)1 in late-stage melanoma growth. <i>Clinical and Experimental Metastasis</i> , 2010, 27, 133-140.	1.7	40
60	Non-coding RNA detection methods combined to improve usability, reproducibility and precision. <i>BMC Bioinformatics</i> , 2010, 11, 491.	1.2	17
61	Exploration of homodimer receptor: homodimer protein interactions. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 447.	0.1	2
62	2-DE profiling of GDNF overexpression-related proteome changes in differentiating ST14A rat progenitor cells. <i>Proteomics</i> , 2007, 7, 33-46.	1.3	25