

Reiner Schulz

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

2,386
citations

257450

24
h-index

276875

41
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43
all docs

43
docs citations

43
times ranked

4540
citing authors

#	ARTICLE	IF	CITATIONS
1	Imprinted Gene Expression and Function of the Dopa Decarboxylase Gene in the Developing Heart. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 676543.	3.7	9
2	HIV-1 Vpr Induces Widespread Transcriptomic Changes in CD4 ⁺ T Cells Early Postinfection. <i>MBio</i> , 2021, 12, e0136921.	4.1	12
3	Hydroxycarbamide effects on DNA methylation and gene expression in myeloproliferative neoplasms. <i>Genome Research</i> , 2021, 31, 1381-1394.	5.5	3
4	Extraction and high-throughput sequencing of oak heartwood DNA: Assessing the feasibility of genome-wide DNA methylation profiling. <i>PLoS ONE</i> , 2021, 16, e0254971.	2.5	1
5	Transcription of intragenic CpG islands influences spatiotemporal host gene pre-mRNA processing. <i>Nucleic Acids Research</i> , 2020, 48, 8349-8359.	14.5	10
6	CpG Dinucleotides Inhibit HIV-1 Replication through Zinc Finger Antiviral Protein (ZAP)-Dependent and -Independent Mechanisms. <i>Journal of Virology</i> , 2020, 94, .	3.4	54
7	Effects of maternal obesity on Wharton's Jelly mesenchymal stromal cells. <i>Scientific Reports</i> , 2017, 7, 17595.	3.3	8
8	Adjuvanted influenza-H1N1 vaccination reveals lymphoid signatures of age-dependent early responses and of clinical adverse events. <i>Nature Immunology</i> , 2016, 17, 204-213.	14.5	148
9	Network-Informed Gene Ranking Tackles Genetic Heterogeneity in Exome-Sequencing Studies of Monogenic Disease. <i>Human Mutation</i> , 2015, 36, 1135-1144.	2.5	7
10	Promiscuous RNA Binding Ensures Effective Encapsidation of APOBEC3 Proteins by HIV-1. <i>PLoS Pathogens</i> , 2015, 11, e1004609.	4.7	86
11	Protection of CpG islands against de novo DNA methylation during oogenesis is associated with the recognition site of E2f1 and E2f2. <i>Epigenetics and Chromatin</i> , 2014, 7, 26.	3.9	30
12	Human MX2 is an interferon-induced post-entry inhibitor of HIV-1 infection. <i>Nature</i> , 2013, 502, 559-562.	27.8	505
13	Genome-wide and parental allele-specific analysis of CTCF and cohesin DNA binding in mouse brain reveals a tissue-specific binding pattern and an association with imprinted differentially methylated regions. <i>Genome Research</i> , 2013, 23, 1624-1635.	5.5	55
14	Microarray Data Reveal Relationship between Jag1 and Ddr1 in Mouse Liver. <i>PLoS ONE</i> , 2013, 8, e84383.	2.5	4
15	Epigenetic control of alternative mRNA processing at the imprinted Herc3/Nap115 locus. <i>Nucleic Acids Research</i> , 2012, 40, 8917-8926.	14.5	44
16	Next generation sequencing in epigenetics: Insights and challenges. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 192-199.	5.0	83
17	Protection against De Novo Methylation Is Instrumental in Maintaining Parent-of-Origin Methylation Inherited from the Gametes. <i>Molecular Cell</i> , 2012, 47, 909-920.	9.7	118
18	Resources for methylome analysis suitable for gene knockout studies of potential epigenome modifiers. <i>GigaScience</i> , 2012, 1, 3.	6.4	39

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19	Gold nanoparticle-mediated gene delivery induces widespread changes in the expression of innate immunity genes. <i>Gene Therapy</i> , 2012, 19, 347-353.	4.5	53
20	The β -Globin Locus Control Region in Combination With the EF1 α Short Promoter Allows Enhanced Lentiviral Vector-mediated Erythroid Gene Expression With Conserved Multilineage Activity. <i>Molecular Therapy</i> , 2012, 20, 1400-1409.	8.2	31
21	Short Interspersed Element (SINE) Depletion and Long Interspersed Element (LINE) Abundance Are Not Features Universally Required for Imprinting. <i>PLoS ONE</i> , 2011, 6, e18953.	2.5	9
22	Transcriptional profiles underlying parent-of-origin effects in seeds of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2010, 10, 72.	3.6	71
23	Segmental paternal uniparental disomy (patUPD) of 14q32 with abnormal methylation elicits the characteristic features of complete patUPD14. <i>American Journal of Medical Genetics, Part A</i> , 2010, 152A, 1942-1950.	1.2	34
24	The Parental Non-Equivalence of Imprinting Control Regions during Mammalian Development and Evolution. <i>PLoS Genetics</i> , 2010, 6, e1001214.	3.5	61
25	The diagnosis of inherited metabolic diseases by microarray gene expression profiling. <i>Orphanet Journal of Rare Diseases</i> , 2010, 5, 34.	2.7	3
26	Transcript- and tissue-specific imprinting of a tumour suppressor gene. <i>Human Molecular Genetics</i> , 2009, 18, 118-127.	2.9	54
27	WAMIDEX: A web atlas of murine genomic imprinting and differential expression. <i>Epigenetics</i> , 2008, 3, 89-96.	2.7	51
28	G9a Histone Methyltransferase Contributes to Imprinting in the Mouse Placenta. <i>Molecular and Cellular Biology</i> , 2008, 28, 1104-1113.	2.3	172
29	Regulation of alternative polyadenylation by genomic imprinting. <i>Genes and Development</i> , 2008, 22, 1141-1146.	5.9	130
30	Genomic Imprinting of <i>Dopa decarboxylase</i> in Heart and Reciprocal Allelic Expression with Neighboring <i>Grb10</i> . <i>Molecular and Cellular Biology</i> , 2008, 28, 386-396.	2.3	40
31	<i>MATERNALLY EXPRESSED PAB C-TERMINAL</i> , a Novel Imprinted Gene in <i>Arabidopsis</i> , Encodes the Conserved C-Terminal Domain of Polyadenylate Binding Proteins. <i>Plant Cell</i> , 2008, 20, 2387-2398.	6.6	100
32	A Screen for Retrotransposed Imprinted Genes Reveals an Association between X Chromosome Homology and Maternal Germ-Line Methylation. <i>PLoS Genetics</i> , 2007, 3, e20.	3.5	103
33	Nondisjunction and transmission ratio distortion of Chromosome 2 in a (2.8) Robertsonian translocation mouse strain. <i>Mammalian Genome</i> , 2006, 17, 239-247.	2.2	8
34	Chromosome-wide identification of novel imprinted genes using microarrays and uniparental disomies. <i>Nucleic Acids Research</i> , 2006, 34, e88-e88.	14.5	61
35	Mirror Symmetric Topographic Maps Can Arise from Activity-Dependent Synaptic Changes. <i>Neural Computation</i> , 2005, 17, 1059-1083.	2.2	4
36	Temporally Asymmetric Learning Supports Sequence Processing in Multi-Winner Self-Organizing Maps. <i>Neural Computation</i> , 2004, 16, 535-561.	2.2	26

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37	Predicting Nearest Agent Distances in Artificial Worlds. <i>Artificial Life</i> , 2002, 8, 247-264.	1.3	3
38	The role of computational modeling in understanding hemispheric interactions and specialization. <i>Cognitive Systems Research</i> , 2002, 3, 87-94.	2.7	2
39	Conditions Enabling the Evolution of Inter-Agent Signaling in an Artificial World. <i>Artificial Life</i> , 2001, 7, 3-32.	1.3	17