## **Martin Simon**

List of Publications by Year in descending order

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623734 610901 37 709 14 24 h-index citations g-index papers 41 41 41 672 citing authors docs citations times ranked all docs

#	Article	IF	Citations
1	Oral Administration of Bacterially Expressed VP28dsRNA to Protect Penaeus monodon from White Spot Syndrome Virus. Marine Biotechnology, 2008, 10, 242-249.	2.4	116
2	Silencing VP28 Gene of White Spot Syndrome Virus of Shrimp by Bacterially Expressed dsRNA. Marine Biotechnology, 2008, 10, 198-206.	2.4	63
3	Distinct RNA-dependent RNA polymerases are required for RNAi triggered by double-stranded RNA versus truncated transgenes in Paramecium tetraurelia. Nucleic Acids Research, 2010, 38, 4092-4107.	14.5	48
4	Dysregulation of cholesterol homeostasis in human lung cancer tissue and tumour-associated macrophages. EBioMedicine, 2021, 72, 103578.	6.1	43
5	Selective and programmed cleavage of GPI-anchored proteins from the surface membrane by phospholipase C. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 117-124.	2.6	34
6	Unicellular Eukaryotes as Models in Cell and Molecular Biology. International Review of Cell and Molecular Biology, 2014, 309, 141-198.	3.2	34
7	Antigenic Variation in Ciliates: Antigen Structure, Function, Expression. Journal of Eukaryotic Microbiology, 2007, 54, 1-7.	1.7	31
8	More than the "Killer Trait― Infection with the Bacterial Endosymbiont Caedibacter taeniospiralis Causes Transcriptomic Modulation in Paramecium Host. Genome Biology and Evolution, 2018, 10, 646-656.	2.5	30
9	Primary and secondary siRNA synthesis triggered by RNAs from food bacteria in the ciliate Paramecium tetraurelia. Nucleic Acids Research, 2015, 43, 1818-1833.	14.5	27
10	Efficacy of bacterially expressed dsRNA specific to different structural genes of white spot syndrome virus (WSSV) in protection of shrimp from WSSV infection. Journal of Fish Diseases, 2010, 33, 603-607.	1.9	22
11	Exogenous RNAi mechanisms contribute to transcriptome adaptation by phased siRNA clusters in Paramecium. Nucleic Acids Research, 2019, 47, 8036-8049.	14.5	21
12	Two isoforms of eukaryotic phospholipase C in Paramecium affecting transport and release of GPI-anchored proteins in vivo. European Journal of Cell Biology, 2009, 88, 577-592.	3.6	19
13	Epigenetic regulation of serotype expression antagonizes transcriptome dynamics in <i>Paramecium tetraurelia </i> . DNA Research, 2015, 22, 293-305.	3.4	18
14	Communicative functions of GPI-anchored surface proteins in unicellular eukaryotes. Critical Reviews in Microbiology, 2013, 39, 70-78.	6.1	17
15	Two sets of RNAi components are required for heterochromatin formation (i) in trans (i) triggered by truncated transgenes. Nucleic Acids Research, 2016, 44, 5908-5923.	14.5	17
16	Genomic Characterization of Variable Surface Antigens Reveals a Telomere Position Effect as a Prerequisite for RNA Interference-Mediated Silencing in <i>Paramecium tetraurelia</i> i>NBio, 2014, 5, e01328.	4.1	13
17	Differential subcellular distribution of four phospholipase C isoforms and secretion of GPI-PLC activity. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 3157-3168.	2.6	13
18	Next Generation Sequencing Analysis of Total Small Noncoding RNAs from Low Input RNA from Dried Blood Sampling. Analytical Chemistry, 2018, 90, 11791-11796.	6.5	13

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19	Inefficient serotype knock down leads to stable coexistence of different surface antigens on the outer membrane in Paramecium tetraurelia. European Journal of Protistology, 2006, 42, 49-53.	1.5	12
20	Transgenic expression of the RNA binding protein IMP2 stabilizes miRNA targets in murine microsteatosis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 3099-3108.	3.8	10
21	The sncRNA Zoo: a repository for circulating small noncoding RNAs in animals. Nucleic Acids Research, 2019, 47, 4431-4441.	14.5	8
22	Yeast Viral Killer Toxin K1 Induces Specific Host Cell Adaptions via Intrinsic Selection Pressure. Applied and Environmental Microbiology, 2020, 86, .	3.1	8
23	Dual-Seq reveals genome and transcriptome of Caedibacter taeniospiralis, obligate endosymbiont of Paramecium. Scientific Reports, 2020, 10, 9727.	3.3	8
24	Automated analysis of small RNA datasets with RAPID. PeerJ, 2019, 7, e6710.	2.0	8
25	Environmental Temperature Controls Accumulation of Transacting siRNAs Involved in Heterochromatin Formation. Genes, 2018, 9, 117.	2.4	7
26	Transcriptomics of a KDELR1 knockout cell line reveals modulated cell adhesion properties. Scientific Reports, 2019, 9, 10611.	3.3	7
27	siRNA delivery to macrophages using aspherical, nanostructured microparticles as delivery system for pulmonary administration. European Journal of Pharmaceutics and Biopharmaceutics, 2021, 158, 284-293.	4.3	7
28	Broad domains of histone marks in the highly compact <i>Paramecium</i> macronuclear genome. Genome Research, 2022, 32, 710-725.	5.5	7
29	<i>Paramecium</i> epigenetics in development and proliferation. Journal of Eukaryotic Microbiology, 2022, 69, e12914.	1.7	7
30	Comparative Analysis of Biochemical Biases by Ligation- and Template-Switch-Based Small RNA Library Preparation Protocols. Clinical Chemistry, 2019, 65, 1581-1591.	3.2	5
31	Transcriptome Kinetics of Saccharomyces cerevisiae in Response to Viral Killer Toxin K1. Frontiers in Microbiology, 2019, 10, 1102.	3.5	5
32	Differential degradation of RNA species by autophagy-related pathways in Arabidopsis. Journal of Experimental Botany, 2021, 72, 6867-6881.	4.8	5
33	Two Piwis with Ago-like functions silence somatic genes at the chromatin level. RNA Biology, 2021, 18, 757-769.	3.1	5
34	Feeding exogenous dsRNA interferes with endogenous sRNA accumulation in Paramecium. DNA Research, 2020, 27, .	3.4	4
35	The complete mitochondrial genome of the photosymbiotic sea slug <i>Berghia stephanieae</i> (Valdés, 2005) (Gastropoda, Nudibranchia). Mitochondrial DNA Part B: Resources, 2021, 6, 2281-2284.	0.4	4
36	Dynamic chromatin remodelling of ciliate macronuclear DNA as determined by an optimized chromatin immunoprecipitation (ChIP) method for Paramecium tetraurelia. Applied Microbiology and Biotechnology, 2013, 97, 2661-2670.	3.6	3

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#	Article	IF	CITATIONS
37	Draft Genome Sequence and Annotation of the Obligate Bacterial Endosymbiont Caedibacter taeniospiralis , Causative Agent of the Killer Phenotype in Paramecium tetraurelia. Genome Announcements, $2018, 6, \ldots$	0.8	3