

# Kristin Reiche

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4527296/publications.pdf>

Version: 2024-02-01

30  
papers

2,319  
citations

567281

15  
h-index

454955

30  
g-index

33  
all docs

33  
docs citations

33  
times ranked

4048  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA sequencing of glioblastoma tissue slice cultures reveals the effects of treatment at the transcriptional level. <i>FEBS Open Bio</i> , 2022, 12, 480-493.	2.3	1
2	Time to evolve: predicting engineered T cell-associated toxicity with next-generation models. , 2022, 10, e003486.		21
3	Alzheimer-related genes show accelerated evolution. <i>Molecular Psychiatry</i> , 2021, 26, 5790-5796.	7.9	10
4	The noncoding RNA LINC00152 conveys contradicting effects in different glioblastoma cells. <i>Scientific Reports</i> , 2021, 11, 18499.	3.3	6
5	The Key Role of Patient Involvement in the Development of Core Outcome Sets in Prostate Cancer. <i>European Urology Focus</i> , 2021, 7, 943-946.	3.1	6
6	The Role of lncRNAs TAPIR-1 and -2 as Diagnostic Markers and Potential Therapeutic Targets in Prostate Cancer. <i>Cancers</i> , 2020, 12, 1122.	3.7	15
7	Introducing PIONEER: a project to harness big data in prostate cancer research. <i>Nature Reviews Urology</i> , 2020, 17, 351-362.	3.8	18
8	ProstaTrendâ€”A Multivariable Prognostic RNA Expression Score for Aggressive Prostate Cancer. <i>European Urology</i> , 2020, 78, 452-459.	1.9	15
9	Master and servant: LINC00152 â€” a STAT3-induced long noncoding RNA regulates STAT3 in a positive feedback in human multiple myeloma. <i>BMC Medical Genomics</i> , 2020, 13, 22.	1.5	11
10	Map and modelâ€”moving from observation to prediction in toxicogenomics. <i>GigaScience</i> , 2019, 8, .	6.4	14
11	Deep sequencing and automated histochemistry of human tissue slice cultures improve their usability as preclinical model for cancer research. <i>Scientific Reports</i> , 2019, 9, 19961.	3.3	6
12	uap: reproducible and robust HTS data analysis. <i>BMC Bioinformatics</i> , 2019, 20, 664.	2.6	14
13	Binding of NUFIP2 to Roquin promotes recognition and regulation of ICOS mRNA. <i>Nature Communications</i> , 2018, 9, 299.	12.8	27
14	Roquin targets mRNAs in a 3â€²-UTR-specific manner by different modes of regulation. <i>Nature Communications</i> , 2018, 9, 3810.	12.8	40
15	The Transcriptome of the Zebrafish Embryo After Chemical Exposure: A Meta-Analysis. <i>Toxicological Sciences</i> , 2017, 157, 291-304.	3.1	35
16	STAT3-induced long noncoding RNAs in multiple myeloma cells display different properties in cancer. <i>Scientific Reports</i> , 2017, 7, 7976.	3.3	26
17	Dissecting the genetics of the human transcriptome identifies novel trait-related <i>trans</i> -eQTLs and corroborates the regulatory relevance of non-protein coding loci. <i>Human Molecular Genetics</i> , 2015, 24, 4746-4763.	2.9	94
18	Comparison of splice sites reveals that long noncoding RNAs are evolutionarily well conserved. <i>Rna</i> , 2015, 21, 801-812.	3.5	83

#	ARTICLE	IF	CITATIONS
19	Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein-coding RNAs. <i>Genome Biology</i> , 2014, 15, R48.	9.6	37
20	CEM-Designer: Design of custom expression microarrays in the post-ENCODE Era. <i>Journal of Biotechnology</i> , 2014, 189, 154-156.	3.8	2
21	Long Non-Coding RNAs Differentially Expressed between Normal versus Primary Breast Tumor Tissues Disclose Converse Changes to Breast Cancer-Related Protein-Coding Genes. <i>PLoS ONE</i> , 2014, 9, e106076.	2.5	35
22	LocARNAscan: Incorporating thermodynamic stability in sequence and structure-based RNA homology search. <i>Algorithms for Molecular Biology</i> , 2013, 8, 14.	1.2	14
23	Bioinformatics for RNomics. <i>Methods in Molecular Biology</i> , 2011, 719, 299-330.	0.9	2
24	The primary transcriptome of the major human pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 2010, 464, 250-255.	27.8	1,115
25	DUPLICATED RNA GENES IN TELEOST FISH GENOMES. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 1157-1175.	0.8	10
26	NcDNAAlign: Plausible multiple alignments of non-protein-coding genomic sequences. <i>Genomics</i> , 2008, 92, 65-74.	2.9	18
27	Inferring Noncoding RNA Families and Classes by Means of Genome-Scale Structure-Based Clustering. <i>PLoS Computational Biology</i> , 2007, 3, e65.	3.2	424
28	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	5.5	150
29	RNAstrand: reading direction of structured RNAs in multiple sequence alignments. <i>Algorithms for Molecular Biology</i> , 2007, 2, 6.	1.2	26
30	Computational RNomics of <i>Drosophilids</i> . <i>BMC Genomics</i> , 2007, 8, 406.	2.8	38