Dietmar Rieder

List of Publications by Year
in descending order

47 papers	6,407 citations	257450 24 h-index	233421 45 g-index
51 all docs	51 docs citations	51 times ranked	10198 citing authors

#	Article	IF	Citations
1	Synthesis of 4-thiouridines with prodrug functionalization for RNA metabolic labeling. RSC Chemical Biology, 2022, 3, 447-455.	4.1	4
2	Comprehensive Analysis of R-Spondin Fusions and <i>RNF43</i> Mutations Implicate Novel Therapeutic Options in Colorectal Cancer. Clinical Cancer Research, 2022, 28, 1863-1870.	7.0	16
3	nextNEOpi: a comprehensive pipeline for computational neoantigen prediction. Bioinformatics, 2022, 38, 1131-1132.	4.1	17
4	MIO: microRNA target analysis system for immuno-oncology. Bioinformatics, 2022, 38, 3665-3667.	4.1	0
5	Cardiopulmonary recovery after COVID-19: an observational prospective multicentre trial. European Respiratory Journal, 2021, 57, 2003481.	6.7	313
6	CHD1 controls H3.3 incorporation in adult brain chromatin to maintain metabolic homeostasis and normal lifespan. Cell Reports, 2021, 37, 109769.	6.4	10
7	Computational cancer neoantigen prediction: current status and recent advances. Immuno-Oncology Technology, 2021, 12, 100052.	0.3	14
8	Deconvoluting tumor-infiltrating immune cells from RNA-seq data using quanTIseq. Methods in Enzymology, 2020, 636, 261-285.	1.0	141
9	NeoFuse: predicting fusion neoantigens from RNA sequencing data. Bioinformatics, 2020, 36, 2260-2261.	4.1	32
10	Scirpy: a Scanpy extension for analyzing single-cell T-cell receptor-sequencing data. Bioinformatics, 2020, 36, 4817-4818.	4.1	88
11	Thioguanosine Conversion Enables mRNA‐Lifetime Evaluation by RNA Sequencing Using Double Metabolic Labeling (TUC‐seq DUAL). Angewandte Chemie, 2020, 132, 6948-6953.	2.0	3
12	Thioguanosine Conversion Enables mRNA‐Lifetime Evaluation by RNA Sequencing Using Double Metabolic Labeling (TUC‐seq DUAL). Angewandte Chemie - International Edition, 2020, 59, 6881-6886.	13.8	26
13	Tumour-infiltrating lymphocytes (TILs) and BRCA-like status in stage III breast cancer patients randomised to adjuvant intensified platinum-based chemotherapy versus conventional chemotherapy. European Journal of Cancer, 2020, 127, 240-250.	2.8	21
14	Thiouridine-to-Cytidine Conversion Sequencing (TUC-Seq) to Measure mRNA Transcription and Degradation Rates. Methods in Molecular Biology, 2020, 2062, 191-211.	0.9	19
15	FoxH1 represses miR-430 during early embryonic development of zebrafish via non-canonical regulation. BMC Biology, 2019, 17, 61.	3.8	6
16	Next-generation computational tools for interrogating cancer immunity. Nature Reviews Genetics, 2019, 20, 724-746.	16.3	131
17	Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data. Genome Medicine, 2019, 11, 34.	8.2	732
18	A Variant of a Killer Cell Immunoglobulin-like Receptor Is Associated with Resistance to PD-1 Blockade in Lung Cancer. Clinical Cancer Research, 2019, 25, 3026-3034.	7.0	29

#	ARTICLE	IF	CITATIONS
19	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. Clinical Cancer Research, 2019, 25, 7351-7362.	7.0	61
20	Bisulfite Sequencing of RNA for Transcriptome-Wide Detection of 5-Methylcytosine. Methods in Molecular Biology, 2019, 1870, 1-21.	0.9	8
21	Safety and immunobiological activity of guadecitabine sequenced with ipilimumab in metastatic melanoma patients: The phase Ib NIBIT-M4 study.. Journal of Clinical Oncology, 2019, 37, 2549-2549.	1.6	0
22	Nuclear receptor NR2F6 inhibition potentiates responses to PD-L1/PD-1 cancer immune checkpoint blockade. Nature Communications, 2018, 9, 1538.	12.8	49
23	Targeting immune checkpoints potentiates immunoediting and changes the dynamics of tumor evolution. Nature Communications, 2018, 9, 32.	12.8	193
24	Adoptive T Cell Therapy: New Avenues Leading to Safe Targets and Powerful Allies. Trends in Immunology, 2018, 39, 921-936.	6.8	35
25	Genes regulated by SATB2 during neurodevelopment contribute to schizophrenia and educational attainment. PLoS Genetics, 2018, 14, e1007515.	3.5	29
26	Abstract CT059: Epigenetic tumor remodelling to improve the efficacy of immune checkpoint blockade: the NIBIT-M4 clinical trial. , 2018, , .		3
27	Distinct 5-methylcytosine profiles in poly(A) RNA from mouse embryonic stem cells and brain. Genome Biology, 2017, 18, 1.	8.8	587
28	Analysis of High-Throughput RNA Bisulfite Sequencing Data. Methods in Molecular Biology, 2017, 1562, 143-154.	0.9	2
29	Pan-cancer Immunogenomic Analyses Reveal Genotype-Immunophenotype Relationships and Predictors of Response to Checkpoint Blockade. Cell Reports, 2017, 18, 248-262.	6.4	2,953
30	Osmium–Mediated Transformation of 4–Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. Angewandte Chemie - International Edition, 2017, 56, 13479-13483.	13.8	73
31	Osmium–Mediated Transformation of 4–Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. Angewandte Chemie, 2017, 129, 13664-13668.	2.0	7
32	TIminer: NGS data mining pipeline for cancer immunology and immunotherapy. Bioinformatics, 2017, 33, 3140-3141.	4.1	68
33	Neoantigens Generated by Individual Mutations and Their Role in Cancer Immunity and Immunotherapy. Frontiers in Immunology, 2017, 8, 1679.	4.8	171
34	meRanTK: methylated RNA analysis ToolKit. Bioinformatics, 2016, 32, 782-785.	4.1	59
35	Satb2 determines miRNA expression and long-term memory in the adult central nervous system. ELife, 2016, 5, .	6.0	68
36	Impaired Contextual Fear Extinction Learning is Associated with Aberrant Regulation of CHD-Type Chromatin Remodeling Factors. Frontiers in Behavioral Neuroscience, 2015, 9, 313.	2.0	9

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37	Co-expressed genes prepositioned in spatial neighborhoods stochastically associate with SC35 speckles and RNA polymerase II factories. Cellular and Molecular Life Sciences, 2014, 71, 1741-1759.	5.4	40
38	Nr4a1 Is Required for Fasting-Induced Down-Regulation of PparÎ³2 in White Adipose Tissue. Molecular Endocrinology, 2013, 27, 135-149.	3.7	25
39	NAT8L (N-Acetyltransferase 8-Like) Accelerates Lipid Turnover and Increases Energy Expenditure in Brown Adipocytes. Journal of Biological Chemistry, 2013, 288, 36040-36051.	3.4	52
40	Transcription factories. Frontiers in Genetics, 2012, 3, 221.	2.3	83
41	Arxes: retrotransposed genes required for adipogenesis. Nucleic Acids Research, 2011, 39, 3224-3239.	14.5	15
42	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPARÎ³. Cellular and Molecular Life Sciences, 2010, 67, 4049-4064.	5.4	38
43	iLAP: a workflow-driven software for experimental protocol development, data acquisition and analysis. BMC Bioinformatics, 2009, 10, 390.	2.6	13
44	Organization of chromatin and histone modifications at a transcription site. Journal of Cell Biology, 2007, 177, 957-967.	5.2	29
45	A new platform linking chromosomal and sequence information. Chromosome Research, 2007, 15, 327-39.	2.2	7
46	Generic Features of Tertiary Chromatin Structure as Detected in Natural Chromosomes. Molecular and Cellular Biology, 2004, 24, 9359-9370.	2.3	52
47	ClusterControl: a web interface for distributing and monitoring bioinformatics applications on a Linux cluster. Bioinformatics, 2004, 20, 805-807.	4.1	15