

Dietmar Rieder

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

6,407
citations

257101

24
h-index

233125

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.	2.0	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.	3.2	16
3	nextNEOpI: a comprehensive pipeline for computational neoantigen prediction. Bioinformatics, 2022, 38, 1131-1132.	1.8	17
4	MIO: microRNA target analysis system for immuno-oncology. Bioinformatics, 2022, 38, 3665-3667.	1.8	0
5	Cardiopulmonary recovery after COVID-19: an observational prospective multicentre trial. European Respiratory Journal, 2021, 57, 2003481.	3.1	313
6	CHD1 controls H3.3 incorporation in adult brain chromatin to maintain metabolic homeostasis and normal lifespan. Cell Reports, 2021, 37, 109769.	2.9	10
7	Computational cancer neoantigen prediction: current status and recent advances. Immuno-Oncology Technology, 2021, 12, 100052.	0.2	14
8	Deconvoluting tumor-infiltrating immune cells from RNA-seq data using quanTIseq. Methods in Enzymology, 2020, 636, 261-285.	0.4	141
9	NeoFuse: predicting fusion neoantigens from RNA sequencing data. Bioinformatics, 2020, 36, 2260-2261.	1.8	32
10	Scirpy: a Scanpy extension for analyzing single-cell T-cell receptor-sequencing data. Bioinformatics, 2020, 36, 4817-4818.	1.8	88
11	Thioguanosine Conversion Enables mRNA Lifetime Evaluation by RNA Sequencing Using Double Metabolic Labeling (TUC-seq DUAL). Angewandte Chemie, 2020, 132, 6948-6953.	1.6	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.	7.2	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.	1.3	21
14	Thiouridine-to-Cytidine Conversion Sequencing (TUC-Seq) to Measure mRNA Transcription and Degradation Rates. Methods in Molecular Biology, 2020, 2062, 191-211.	0.4	19
15	FoxH1 represses miR-430 during early embryonic development of zebrafish via non-canonical regulation. BMC Biology, 2019, 17, 61.	1.7	6
16	Next-generation computational tools for interrogating cancer immunity. Nature Reviews Genetics, 2019, 20, 724-746.	7.7	131
17	Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data. Genome Medicine, 2019, 11, 34.	3.6	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.	3.2	29

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19	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. <i>Clinical Cancer Research</i> , 2019, 25, 7351-7362.	3.2	61
20	Bisulfite Sequencing of RNA for Transcriptome-Wide Detection of 5-Methylcytosine. <i>Methods in Molecular Biology</i> , 2019, 1870, 1-21.	0.4	8
21	Safety and immunobiological activity of guadecitabine sequenced with ipilimumab in metastatic melanoma patients: The phase Ib NIBIT-M4 study.. <i>Journal of Clinical Oncology</i> , 2019, 37, 2549-2549.	0.8	0
22	Nuclear receptor NR2F6 inhibition potentiates responses to PD-L1/PD-1 cancer immune checkpoint blockade. <i>Nature Communications</i> , 2018, 9, 1538.	5.8	49
23	Targeting immune checkpoints potentiates immunoediting and changes the dynamics of tumor evolution. <i>Nature Communications</i> , 2018, 9, 32.	5.8	193
24	Adoptive T Cell Therapy: New Avenues Leading to Safe Targets and Powerful Allies. <i>Trends in Immunology</i> , 2018, 39, 921-936.	2.9	35
25	Genes regulated by SATB2 during neurodevelopment contribute to schizophrenia and educational attainment. <i>PLoS Genetics</i> , 2018, 14, e1007515.	1.5	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. <i>Genome Biology</i> , 2017, 18, 1.	3.8	587
28	Analysis of High-Throughput RNA Bisulfite Sequencing Data. <i>Methods in Molecular Biology</i> , 2017, 1562, 143-154.	0.4	2
29	Pan-cancer Immunogenomic Analyses Reveal Genotype-Immunophenotype Relationships and Predictors of Response to Checkpoint Blockade. <i>Cell Reports</i> , 2017, 18, 248-262.	2.9	2,953
30	Osmium-Mediated Transformation of 4-Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 13479-13483.	7.2	73
31	Osmium-Mediated Transformation of 4-Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. <i>Angewandte Chemie</i> , 2017, 129, 13664-13668.	1.6	7
32	Tlminer: NGS data mining pipeline for cancer immunology and immunotherapy. <i>Bioinformatics</i> , 2017, 33, 3140-3141.	1.8	68
33	Neoantigens Generated by Individual Mutations and Their Role in Cancer Immunity and Immunotherapy. <i>Frontiers in Immunology</i> , 2017, 8, 1679.	2.2	171
34	meRanTK: methylated RNA analysis ToolKit. <i>Bioinformatics</i> , 2016, 32, 782-785.	1.8	59
35	Satb2 determines miRNA expression and long-term memory in the adult central nervous system. <i>ELife</i> , 2016, 5, .	2.8	68
36	Impaired Contextual Fear Extinction Learning is Associated with Aberrant Regulation of CHD-Type Chromatin Remodeling Factors. <i>Frontiers in Behavioral Neuroscience</i> , 2015, 9, 313.	1.0	9

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37	Co-expressed genes prepositioned in spatial neighborhoods stochastically associate with SC35 speckles and RNA polymerase II factories. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 1741-1759.	2.4	40
38	Nr4a1 Is Required for Fasting-Induced Down-Regulation of Ppar α in White Adipose Tissue. <i>Molecular Endocrinology</i> , 2013, 27, 135-149.	3.7	25
39	NAT8L (N-Acetyltransferase 8-Like) Accelerates Lipid Turnover and Increases Energy Expenditure in Brown Adipocytes. <i>Journal of Biological Chemistry</i> , 2013, 288, 36040-36051.	1.6	52
40	Transcription factories. <i>Frontiers in Genetics</i> , 2012, 3, 221.	1.1	83
41	Arxes: retrotransposed genes required for adipogenesis. <i>Nucleic Acids Research</i> , 2011, 39, 3224-3239.	6.5	15
42	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPAR α . <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 4049-4064.	2.4	38
43	iLAP: a workflow-driven software for experimental protocol development, data acquisition and analysis. <i>BMC Bioinformatics</i> , 2009, 10, 390.	1.2	13
44	Organization of chromatin and histone modifications at a transcription site. <i>Journal of Cell Biology</i> , 2007, 177, 957-967.	2.3	29
45	A new platform linking chromosomal and sequence information. <i>Chromosome Research</i> , 2007, 15, 327-39.	1.0	7
46	Generic Features of Tertiary Chromatin Structure as Detected in Natural Chromosomes. <i>Molecular and Cellular Biology</i> , 2004, 24, 9359-9370.	1.1	52
47	ClusterControl: a web interface for distributing and monitoring bioinformatics applications on a Linux cluster. <i>Bioinformatics</i> , 2004, 20, 805-807.	1.8	15