## Dietmar Rieder

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8021147/publications.pdf

Version: 2024-02-01

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	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
2	Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data. Genome Medicine, 2019, 11, 34.	8.2	732
3	Distinct 5-methylcytosine profiles in poly(A) RNA from mouse embryonic stem cells and brain. Genome Biology, 2017, 18, 1.	8.8	587
4	Cardiopulmonary recovery after COVID-19: an observational prospective multicentre trial. European Respiratory Journal, 2021, 57, 2003481.	6.7	313
5	Targeting immune checkpoints potentiates immunoediting and changes the dynamics of tumor evolution. Nature Communications, 2018, 9, 32.	12.8	193
6	Neoantigens Generated by Individual Mutations and Their Role in Cancer Immunity and Immunotherapy. Frontiers in Immunology, 2017, 8, 1679.	4.8	171
7	Deconvoluting tumor-infiltrating immune cells from RNA-seq data using quanTlseq. Methods in Enzymology, 2020, 636, 261-285.	1.0	141
8	Next-generation computational tools for interrogating cancer immunity. Nature Reviews Genetics, 2019, 20, 724-746.	16.3	131
9	Scirpy: a Scanpy extension for analyzing single-cell T-cell receptor-sequencing data. Bioinformatics, 2020, 36, 4817-4818.	4.1	88
10	Transcription factories. Frontiers in Genetics, 2012, 3, 221.	2.3	83
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11 12	Transcription factories. Frontiers in Genetics, 2012, 3, 221.  Osmiumâ€Mediated Transformation of 4â€Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. Angewandte Chemie - International Edition, 2017, 56, 13479-13483.  Tlminer: NGS data mining pipeline for cancer immunology and immunotherapy. Bioinformatics, 2017, 33, 3140-3141.  Satb2 determines miRNA expression and long-term memory in the adult central nervous system. ELife,	13.8	73 68
11 12 13	Transcription factories. Frontiers in Genetics, 2012, 3, 221.  Osmiumâ€Mediated Transformation of 4â€Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. Angewandte Chemie - International Edition, 2017, 56, 13479-13483.  Tlminer: NGS data mining pipeline for cancer immunology and immunotherapy. Bioinformatics, 2017, 33, 3140-3141.  Satb2 determines miRNA expression and long-term memory in the adult central nervous system. ELife, 2016, 5, .  Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. Clinical Cancer	13.8 4.1 6.0	<ul><li>73</li><li>68</li><li>68</li></ul>
11 12 13	Transcription factories. Frontiers in Genetics, 2012, 3, 221.  Osmiumâ€Mediated Transformation of 4â€Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. Angewandte Chemie - International Edition, 2017, 56, 13479-13483.  Tlminer: NGS data mining pipeline for cancer immunology and immunotherapy. Bioinformatics, 2017, 33, 3140-3141.  Satb2 determines miRNA expression and long-term memory in the adult central nervous system. ELife, 2016, 5, .  Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. Clinical Cancer Research, 2019, 25, 7351-7362.	13.8 4.1 6.0 7.0	73 68 68 61
11 12 13 14	Transcription factories. Frontiers in Genetics, 2012, 3, 221.  Osmiumâ€Mediated Transformation of 4â€Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. Angewandte Chemie - International Edition, 2017, 56, 13479-13483.  TIminer: NGS data mining pipeline for cancer immunology and immunotherapy. Bioinformatics, 2017, 33, 3140-3141.  Satb2 determines miRNA expression and long-term memory in the adult central nervous system. ELife, 2016, 5, .  Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. Clinical Cancer Research, 2019, 25, 7351-7362.  meRanTK: methylated RNA analysis ToolKit. Bioinformatics, 2016, 32, 782-785.  Generic Features of Tertiary Chromatin Structure as Detected in Natural Chromosomes. Molecular	13.8 4.1 6.0 7.0	73 68 68 61 59

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19	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
20	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPARγ. Cellular and Molecular Life Sciences, 2010, 67, 4049-4064.	5.4	38
21	Adoptive T Cell Therapy: New Avenues Leading to Safe Targets and Powerful Allies. Trends in Immunology, 2018, 39, 921-936.	6.8	35
22	NeoFuse: predicting fusion neoantigens from RNA sequencing data. Bioinformatics, 2020, 36, 2260-2261.	4.1	32
23	Organization of chromatin and histone modifications at a transcription site. Journal of Cell Biology, 2007, 177, 957-967.	5.2	29
24	Genes regulated by SATB2 during neurodevelopment contribute to schizophrenia and educational attainment. PLoS Genetics, 2018, 14, e1007515.	3.5	29
25	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
26	Thioguanosine Conversion Enables mRNAâ€Lifetime Evaluation by RNA Sequencing Using Double Metabolic Labeling (TUCâ€seq DUAL). Angewandte Chemie - International Edition, 2020, 59, 6881-6886.	13.8	26
27	Nr4a1 Is Required for Fasting-Induced Down-Regulation of PparÎ <sup>3</sup> 2 in White Adipose Tissue. Molecular Endocrinology, 2013, 27, 135-149.	3.7	25
28	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
29	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
30	nextNEOpi: a comprehensive pipeline for computational neoantigen prediction. Bioinformatics, 2022, 38, 1131-1132.	4.1	17
31	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
32	ClusterControl: a web interface for distributing and monitoring bioinformatics applications on a Linux cluster. Bioinformatics, 2004, 20, 805-807.	4.1	15
33	Arxes: retrotransposed genes required for adipogenesis. Nucleic Acids Research, 2011, 39, 3224-3239.	14.5	15
34	Computational cancer neoantigen prediction: current status and recent advances. Immuno-Oncology Technology, 2021, 12, 100052.	0.3	14
35	iLAP: a workflow-driven software for experimental protocol development, data acquisition and analysis. BMC Bioinformatics, 2009, 10, 390.	2.6	13
36	CHD1 controls H3.3 incorporation in adult brain chromatin to maintain metabolic homeostasis and normal lifespan. Cell Reports, 2021, 37, 109769.	6.4	10

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37	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
38	Bisulfite Sequencing of RNA for Transcriptome-Wide Detection of 5-Methylcytosine. Methods in Molecular Biology, 2019, 1870, 1-21.	0.9	8
39	A new platform linking chromosomal and sequence information. Chromosome Research, 2007, 15, 327-39.	2.2	7
40	Osmiumâ€Mediated Transformation of 4â€Thiouridine to Cytidine as Key To Study RNA Dynamics by Sequencing. Angewandte Chemie, 2017, 129, 13664-13668.	2.0	7
41	FoxH1 represses miR-430 during early embryonic development of zebrafish via non-canonical regulation. BMC Biology, 2019, 17, 61.	3.8	6
42	Synthesis of 4-thiouridines with prodrug functionalization for RNA metabolic labeling. RSC Chemical Biology, 2022, 3, 447-455.	4.1	4
43	Thioguanosine Conversion Enables mRNAâ€Lifetime Evaluation by RNA Sequencing Using Double Metabolic Labeling (TUCâ€seq DUAL). Angewandte Chemie, 2020, 132, 6948-6953.	2.0	3
44	Abstract CT059: Epigenetic tumor remodelling to improve the efficacy of immune checkpoint blockade: the NIBIT-M4 clinical trial. , 2018, , .		3
45	Analysis of High-Throughput RNA Bisulfite Sequencing Data. Methods in Molecular Biology, 2017, 1562, 143-154.	0.9	2
46	Safety and immunobiological activity of guadecitabine sequenced with ipilimumab in metastatic melanoma patients: The phase lb NIBIT-M4 study Journal of Clinical Oncology, 2019, 37, 2549-2549.	1.6	0
47	MIO: microRNA target analysis system for immuno-oncology. Bioinformatics, 2022, 38, 3665-3667.	4.1	O