

Matthias Lienhard

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3616271/publications.pdf>

Version: 2024-02-01

16
papers

15,103
citations

1039406

9
h-index

1058022

14
g-index

18
all docs

18
docs citations

18
times ranked

35860
citing authors

#	ARTICLE	IF	CITATIONS
1	Matching anticancer compounds and tumor cell lines by neural networks with ranking loss. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqab128.	1.5	2
2	A bioinformatics workflow to detect genes with DNA methylation alterations: a case study of analyzing MeDIP-seq data in cardiac microtissue exposed to epirubicin. , 2022, , .		0
3	Deregulation and epigenetic modification of BCL2-family genes cause resistance to venetoclax in hematologic malignancies. <i>Blood</i> , 2022, 140, 2113-2126.	0.6	24
4	PWD/Ph-Encoded Genetic Variants Modulate the Cellular Wnt/ β 2-Catenin Response to Suppress <i>ApC</i> Min-Triggered Intestinal Tumor Formation. <i>Cancer Research</i> , 2021, 81, 38-49.	0.4	0
5	Large-scale literature mining to assess the relation between anti-cancer drugs and cancer types. <i>Journal of Translational Medicine</i> , 2021, 19, 274.	1.8	4
6	Altered DNA Methylation Profiles in SF3B1 Mutated CLL Patients. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9337.	1.8	4
7	Network integration and modelling of dynamic drug responses at multi-omics levels. <i>Communications Biology</i> , 2020, 3, 573.	2.0	28
8	DMSO induces drastic changes in human cellular processes and epigenetic landscape in vitro. <i>Scientific Reports</i> , 2019, 9, 4641.	1.6	202
9	Combined Targeted Resequencing of Cytosine DNA Methylation and Mutations of DNA Repair Genes with Potential Use for Poly(ADP-Ribose) Polymerase 1 Inhibitor Sensitivity Testing. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 198-213.	1.2	2
10	Epigenomic profiling of non-small cell lung cancer xenografts uncover LRP12 DNA methylation as predictive biomarker for carboplatin resistance. <i>Genome Medicine</i> , 2018, 10, 55.	3.6	37
11	QSEA modelling of genome-wide DNA methylation from sequencing enrichment experiments. <i>Nucleic Acids Research</i> , 2017, 45, e44-e44.	6.5	39
12	Analyzing and interpreting genome data at the network level with ConsensusPathDB. <i>Nature Protocols</i> , 2016, 11, 1889-1907.	5.5	364
13	Quantitative Comparison of Large-Scale DNA Enrichment Sequencing Data. <i>Methods in Molecular Biology</i> , 2016, 1418, 191-208.	0.4	2
14	Simultaneous deletion of the methylcytosine oxidases Tet1 and Tet3 increases transcriptome variability in early embryogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4236-45.	3.3	87
15	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
16	MEDIPS: genome-wide differential coverage analysis of sequencing data derived from DNA enrichment experiments. <i>Bioinformatics</i> , 2014, 30, 284-286.	1.8	305