

# 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

1039880

9  
h-index

1058333

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. NAR Genomics and Bioinformatics, 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. Blood, 2022, 140, 2113-2126.	0.6	24
4	PWD/Ph-Encoded Genetic Variants Modulate the Cellular Wnt/ $\beta$ 2-Catenin Response to Suppress <i>Apc</i> Min-Triggered Intestinal Tumor Formation. Cancer Research, 2021, 81, 38-49.	0.4	0
5	Large-scale literature mining to assess the relation between anti-cancer drugs and cancer types. Journal of Translational Medicine, 2021, 19, 274.	1.8	4
6	Altered DNA Methylation Profiles in SF3B1 Mutated CLL Patients. International Journal of Molecular Sciences, 2021, 22, 9337.	1.8	4
7	Network integration and modelling of dynamic drug responses at multi-omics levels. Communications Biology, 2020, 3, 573.	2.0	28
8	DMSO induces drastic changes in human cellular processes and epigenetic landscape in vitro. Scientific Reports, 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. Journal of Molecular Diagnostics, 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. Genome Medicine, 2018, 10, 55.	3.6	37
11	QSEA—modelling of genome-wide DNA methylation from sequencing enrichment experiments. Nucleic Acids Research, 2017, 45, e44-e44.	6.5	39
12	Analyzing and interpreting genome data at the network level with ConsensusPathDB. Nature Protocols, 2016, 11, 1889-1907.	5.5	364
13	Quantitative Comparison of Large-Scale DNA Enrichment Sequencing Data. Methods in Molecular Biology, 2016, 1418, 191-208.	0.4	2
14	Simultaneous deletion of the methylcytosine oxidases Tet1 and Tet3 increases transcriptome variability in early embryogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4236-45.	3.3	87
15	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
16	MEDIPS: genome-wide differential coverage analysis of sequencing data derived from DNA enrichment experiments. Bioinformatics, 2014, 30, 284-286.	1.8	305