

Hinrich W GÃ¶hlmann

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5545682/publications.pdf>

Version: 2024-02-01

42
papers

3,470
citations

394390

19
h-index

302107

39
g-index

44
all docs

44
docs citations

44
times ranked

5227
citing authors

#	ARTICLE	IF	CITATIONS
1	A genetics-led approach defines the drug target landscape of 30 immune-related traits. <i>Nature Genetics</i> , 2019, 51, 1082-1091.	21.4	157
2	High-Throughput Gene Expression Profiles to Define Drug Similarity and Predict Compound Activity. <i>Assay and Drug Development Technologies</i> , 2018, 16, 162-176.	1.2	33
3	Progressive leukoencephalopathy impairs neurobehavioral development in sialin-deficient mice. <i>Experimental Neurology</i> , 2017, 291, 106-119.	4.1	10
4	Transcriptional Characterization of Compounds: Lessons Learned from the Public LINCS Data. <i>Assay and Drug Development Technologies</i> , 2016, 14, 252-260.	1.2	22
5	A joint modeling approach for uncovering associations between gene expression, bioactivity and chemical structure in early drug discovery to guide lead selection and genomic biomarker development. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2016, 15, 291-304.	0.6	5
6	Weighted similarity-based clustering of chemical structures and bioactivity data in early drug discovery. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1650018.	0.8	6
7	Translation of disease associated gene signatures across tissues. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 11, 301.	0.1	4
8	Using transcriptomics to guide lead optimization in drug discovery projects: Lessons learned from the QSTAR project. <i>Drug Discovery Today</i> , 2015, 20, 505-513.	6.4	80
9	Integrating High-Dimensional Transcriptomics and Image Analysis Tools into Early Safety Screening: Proof of Concept for a New Early Drug Development Strategy. <i>Chemical Research in Toxicology</i> , 2015, 28, 1914-1925.	3.3	10
10	Connecting gene expression data from connectivity map and in silico target predictions for small molecule mechanism-of-action analysis. <i>Molecular BioSystems</i> , 2015, 11, 86-96.	2.9	28
11	Dose-Response Modeling Under Simple Order Restrictions Using Bayesian Variable Selection Methods. <i>Statistics in Biopharmaceutical Research</i> , 2014, 6, 252-262.	0.8	6
12	Delayed bactericidal response of <i>Mycobacterium tuberculosis</i> to bedaquiline involves remodelling of bacterial metabolism. <i>Nature Communications</i> , 2014, 5, 3369.	12.8	219
13	Quality control of Platinum Spike dataset by probe-level mixed models. <i>Mathematical Biosciences</i> , 2014, 248, 1-10.	1.9	0
14	Increasing the discovery power of -omics studies. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 84-93.	0.7	2
15	Comparison of methods for the selection of genomic biomarkers. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 8, 24.	0.1	3
16	beadarrayFilter: An R Package to Filter Beads. <i>R Journal</i> , 2013, 5, 171.	1.8	1
17	Genomic Biomarkers for a Binary Clinical Outcome in Early Drug Development Microarray Experiments. <i>Journal of Biopharmaceutical Statistics</i> , 2012, 22, 72-92.	0.8	1
18	Gene Filtering in the Analysis of Illumina Microarray Experiments. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, .	0.6	3

#	ARTICLE	IF	CITATIONS
19	cn.FARMS: a latent variable model to detect copy number variations in microarray data with a low false discovery rate. <i>Nucleic Acids Research</i> , 2011, 39, e79-e79.	14.5	19
20	Microarray Profiling of DNA Extracted from FFPE Tissues Using SNP 6.0 Affymetrix Platform. <i>Methods in Molecular Biology</i> , 2011, 724, 147-160.	0.9	9
21	Informative or Noninformative Calls for Gene Expression: A Latent Variable Approach. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article 4.	0.6	8
22	Filtering data from high-throughput experiments based on measurement reliability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, E173-4; author reply E175.	7.1	21
23	Genomic Biomarkers for Depression: Feature-Specific and Joint Biomarkers. <i>Statistics in Biopharmaceutical Research</i> , 2010, 2, 419-434.	0.8	3
24	IsoGene: An R Package for Analyzing Dose-response Studies in Microarray Experiments. <i>R Journal</i> , 2010, 2, 5.	1.8	19
25	Abstract 115: An integrated framework of transcriptome analysis leads to mechanistic insights into the FTI/Taxol synergy. , 2010, , .		0
26	Response prediction to a multitargeted kinase inhibitor in cancer cell lines and xenograft tumors using high-content tyrosine peptide arrays with a kinetic readout. <i>Molecular Cancer Therapeutics</i> , 2009, 8, 1846-1855.	4.1	42
27	Genome-wide copy number alterations detection in fresh frozen and matched FFPE samples using SNP 6.0 arrays. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 957-964.	2.8	49
28	Alterations in Mucosal Immunity Identified in the Colon of Patients With Irritable Bowel Syndrome. <i>Clinical Gastroenterology and Hepatology</i> , 2008, 6, 194-205.	4.4	117
29	I/NI-calls for the exclusion of non-informative genes: a highly effective filtering tool for microarray data. <i>Bioinformatics</i> , 2007, 23, 2897-2902.	4.1	154
30	Testing for Trends in Dose-Response Microarray Experiments: A Comparison of Several Testing Procedures, Multiplicity and Resampling-Based Inference. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2007, 6, Article 26.	0.6	23
31	Alterations in Expression of p11 and SERT in Mucosal Biopsy Specimens of Patients With Irritable Bowel Syndrome. <i>Gastroenterology</i> , 2007, 132, 17-25.	1.3	116
32	Alterations in the Brain-Gut Axis Underlying Visceral Chemosensitivity in <i>Nippostrongylus brasiliensis</i> -Infected Mice. <i>Gastroenterology</i> , 2007, 132, 1375-1387.	1.3	35
33	Molecular profiling of murine sensory neurons in the nodose and dorsal root ganglia labeled from the peritoneal cavity. <i>Physiological Genomics</i> , 2006, 24, 252-263.	2.3	43
34	Analysis of Affymetrix GeneChip® data using amplified RNA. <i>BioTechniques</i> , 2006, 40, 165-170.	1.8	18
35	Rejoinder to Use of Principal Component Analysis and the GE -Biplot for the Graphical Exploration of Gene Expression Data. <i>Biometrics</i> , 2005, 61, 632-634.	1.4	1
36	A Diarylquinoline Drug Active on the ATP Synthase of <i>Mycobacterium tuberculosis</i> . <i>Science</i> , 2005, 307, 223-227.	12.6	1,907

#	ARTICLE	IF	CITATIONS
37	Transcriptional Response to Corticotropin-Releasing Factor in AtT-20 Cells. <i>Molecular Pharmacology</i> , 2004, 66, 1083-1092.	2.3	25
38	Graphical Exploration of Gene Expression Data: A Comparative Study of Three Multivariate Methods. <i>Biometrics</i> , 2003, 59, 1131-1139.	1.4	62
39	Transcription profiles of the bacterium <i>Mycoplasma pneumoniae</i> grown at different temperatures. <i>Nucleic Acids Research</i> , 2003, 31, 6306-6320.	14.5	78
40	Identification of a Small RNA within the <i>pdh</i> Gene Cluster of <i>Mycoplasma pneumoniae</i> and <i>Mycoplasma genitalium</i> . <i>Journal of Bacteriology</i> , 2000, 182, 3281-3284.	2.2	15
41	Cloning of a second gene encoding 6-phosphofructo-2-kinase in yeast, and characterization of mutant strains without fructose-2,6-bisphosphate. <i>Molecular Microbiology</i> , 1996, 20, 65-76.	2.5	84
42	cn.FARMS: a probabilistic model to detect DNA copy numbers. <i>Nature Precedings</i> , 0, , .	0.1	0