Florian Nigsch

List of Publications by Year
in descending order

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Version: 2024-02-01

43	3,013	236612	253896
papers	citations	25 h-index	43 g-index

48	48	48	5138
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Single-cell and bulk transcriptomics of the liver reveals potential targets of NASH with fibrosis. Scientific Reports, 2021, 11, 19396.	1.6	41
2	BET bromodomain inhibitors regulate keratinocyte plasticity. Nature Chemical Biology, 2021, 17, 280-290.	3.9	12
3	Genome-wide CRISPR-Cas9 screens identify mechanisms of BET bromodomain inhibitor sensitivity. IScience, 2021, 24, 103323.	1.9	5
4	Farnesoid X Receptor Agonism, Acetylâ€Coenzyme A Carboxylase Inhibition, and Back Translation of Clinically Observed Endpoints of De Novo Lipogenesis in a Murine NASH Model. Hepatology Communications, 2020, 4, 109-125.	2.0	16
5	Systematic Chemogenetic Library Assembly. Cell Chemical Biology, 2020, 27, 1124-1129.	2.5	37
6	Cell Types of the Human Retina and Its Organoids at Single-Cell Resolution. Cell, 2020, 182, 1623-1640.e34.	13.5	359
7	Proteomic identification of serum factors that correlate with reduction of HVPG following curative treatment for hepatitis C virus infection. Journal of Hepatology, 2020, 73, S786-S787.	1.8	0
8	CellSIUS provides sensitive and specific detection of rare cell populations from complex single-cell RNA-seq data. Genome Biology, 2019, 20, 142.	3.8	41
9	IRF2 is a master regulator of human keratinocyte stem cell fate. Nature Communications, 2019, 10, 4676.	5.8	25
10	YAP, but Not RSPO-LGR4/5, Signaling in Biliary Epithelial Cells Promotes a Ductular Reaction in Response to Liver Injury. Cell Stem Cell, 2019, 25, 39-53.e10.	5.2	150
11	Genome-wide CRISPR screen for PARKIN regulators reveals transcriptional repression as a determinant of mitophagy. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E180-E189.	3.3	73
12	Transcriptomic analysis reveals reduced transcriptional activity in the malaria parasite Plasmodium cynomolgi during progression into dormancy. ELife, 2018, 7, .	2.8	39
13	Screening of Intestinal Crypt Organoids: A Simple Readout for Complex Biology. SLAS Discovery, 2017, 22, 571-582.	1.4	16
14	Complementary activities of DOT1L and Menin inhibitors in MLL-rearranged leukemia. Leukemia, 2017, 31, 1269-1277.	3.3	76
15	A comparative transcriptomic analysis of replicating and dormant liver stages of the relapsing malaria parasite Plasmodium cynomolgi. ELife, 2017, 6, .	2.8	56
16	Multidimensional pooled shRNA screens in human THP-1 cells identify candidate modulators of macrophage polarization. PLoS ONE, 2017, 12, e0183679.	1.1	52
17	The RSPOâ€“LGR4/5â€“ZNRF3/RNF43 module controls liver zonation and size. Nature Cell Biology, 2016, 18, 467-479.	4.6	253
18	Data-Driven Derivation of an â€œInformer Compound Setâ€•for Improved Selection of Active Compounds in High-Throughput Screening. Journal of Chemical Information and Modeling, 2016, 56, 1622-1630.	2.5	14

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19	Evidence-Based and Quantitative Prioritization of Tool Compounds in Phenotypic Drug Discovery. Cell Chemical Biology, 2016, 23, 862-874.	2.5	52
20	Analysis of Iterative Screening with Stepwise Compound Selection Based on Novartis In-house HTS Data. ACS Chemical Biology, 2016, 11, 1255-1264.	1.6	42
21	High-resolution chemical dissection of a model eukaryote reveals targets, pathways and gene functions. Microbiological Research, 2014, 169, 107-120.	2.5	142
22	Causal Network Models for Predicting Compound Targets and Driving Pathways in Cancer. Journal of Biomolecular Screening, 2014, 19, 791-802.	2.6	23
23	The Multidimensional Perturbation Value: A Single Metric to Measure Similarity and Activity of Treatments in High-Throughput Multidimensional Screens. Journal of Biomolecular Screening, 2013, 18, 367-377.	2.6	30
24	Determination of minimal transcriptional signatures of compounds for target prediction. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 2.	1.4	7
25	Rethinking Molecular Similarity: Comparing Compounds on the Basis of Biological Activity. ACS Chemical Biology, 2012, 7, 1399-1409.	1.6	181
26	Predicting the mechanism of phospholipidosis. Journal of Cheminformatics, 2012, 4, 2.	2.8	49
27	Classifying Large Chemical Data Sets: Using A Regularized Potential Function Method. Journal of Chemical Information and Modeling, 2011, 51, 4-14.	2.5	11
28	Activity-Aware Clustering of High Throughput Screening Data and Elucidation of Orthogonal Structureâ€“Activity Relationships. Journal of Chemical Information and Modeling, 2011, 51, 3158-3168.	2.5	20
29	Computational methods for early predictive safety assessment from biological and chemical data. Expert Opinion on Drug Metabolism and Toxicology, 2011, 7, 1497-1511.	1.5	28
30	Online chemical modeling environment (OCHEM): web platform for data storage, model development and publishing of chemical information. Journal of Computer-Aided Molecular Design, 2011, 25, 533-554.	1.3	453
31	Recent trends and observations in the design of high-quality screening collections. Future Medicinal Chemistry, 2011, 3, 751-766.	1.1	55
32	A lead discovery strategy driven by a comprehensive analysis of proteases in the peptide substrate space. Protein Science, 2010, 19, 2096-2109.	3.1	7
33	Computational toxicology: an overview of the sources of data and of modelling methods. Expert Opinion on Drug Metabolism and Toxicology, 2009, 5, 1-14.	1.5	63
34	Simultaneous feature selection and parameter optimisation using an artificial ant colony: case study of melting point prediction. Chemistry Central Journal, 2008, 2, 21.	2.6	26
35	A novel hybrid ultrafast shape descriptor method for use in virtual screening. Chemistry Central Journal, 2008, 2, 3.	2.6	32
36	Toxicological relationships between proteins obtained from protein target predictions of large toxicity databases. Toxicology and Applied Pharmacology, 2008, 231, 225-234.	1.3	9

#	Article	IF	Citations
37	Why Are Some Properties More Difficult To Predict than Others? A Study of QSPR Models of Solubility, Melting Point, and Log P. Journal of Chemical Information and Modeling, 2008, 48, 220-232.	2.5	165
38	Ligand-Target Prediction Using Winnow and Naive Bayesian Algorithms and the Implications of Overall Performance Statistics. Journal of Chemical Information and Modeling, 2008, 48, 2313-2325.	2.5	92
39	How To Winnow Actives from Inactives:â€‰ Introducing Molecular Orthogonal Sparse Bigrams (MOSBs) and Multiclass Winnow. Journal of Chemical Information and Modeling, 2008, 48, 306-318.	2.5	17
40	In vitro models for processes involved in intestinal absorption. Expert Opinion on Drug Metabolism and Toxicology, 2007, 3, 545-556.	1.5	16
41	In vitro models for processes involved in intestinal absorption. Expert Opinion on Drug Metabolism and Toxicology, 2007, 3, 545-556.	1.5	3
42	Melting Point Prediction Employing k-Nearest Neighbor Algorithms and Genetic Parameter Optimization. Journal of Chemical Information and Modeling, 2006, 46, 2412-2422.	2.5	154
43	Total Synthesis of (+)-Crocacin Dâ€. Journal of Organic Chemistry, 2005, 70, 2225-2234.	1.7	58