Florian Nigsch

List of Publications by Year
in descending order

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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	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
2	Cell Types of the Human Retina and Its Organoids at Single-Cell Resolution. Cell, 2020, 182, 1623-1640.e34.	13.5	359
3	The RSPOâ€“LGR4/5â€“ZNRF3/RNF43 module controls liver zonation and size. Nature Cell Biology, 2016, 18, 467-479.	4.6	253
4	Rethinking Molecular Similarity: Comparing Compounds on the Basis of Biological Activity. ACS Chemical Biology, 2012, 7, 1399-1409.	1.6	181
5	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
6	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
7	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
8	High-resolution chemical dissection of a model eukaryote reveals targets, pathways and gene functions. Microbiological Research, 2014, 169, 107-120.	2.5	142
9	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
10	Complementary activities of DOT1L and Menin inhibitors in MLL-rearranged leukemia. Leukemia, 2017, 31, 1269-1277.	3.3	76
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	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
13	Total Synthesis of (+)-Crocacin Dâ€. Journal of Organic Chemistry, 2005, 70, 2225-2234.	1.7	58
14	A comparative transcriptomic analysis of replicating and dormant liver stages of the relapsing malaria parasite Plasmodium cynomolgi. ELife, 2017, 6, .	2.8	56
15	Recent trends and observations in the design of high-quality screening collections. Future Medicinal Chemistry, 2011, 3, 751-766.	1.1	55
16	Evidence-Based and Quantitative Prioritization of Tool Compounds in Phenotypic Drug Discovery. Cell Chemical Biology, 2016, 23, 862-874.	2.5	52
17	Multidimensional pooled shRNA screens in human THP-1 cells identify candidate modulators of macrophage polarization. PLoS ONE, 2017, 12, e0183679.	1.1	52
18	Predicting the mechanism of phospholipidosis. Journal of Cheminformatics, 2012, 4, 2.	2.8	49

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19	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
20	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
21	Single-cell and bulk transcriptomics of the liver reveals potential targets of NASH with fibrosis. Scientific Reports, 2021, 11, 19396.	1.6	41
22	Transcriptomic analysis reveals reduced transcriptional activity in the malaria parasite Plasmodium cynomolgi during progression into dormancy. ELife, 2018, 7, .	2.8	39
23	Systematic Chemogenetic Library Assembly. Cell Chemical Biology, 2020, 27, 1124-1129.	2.5	37
24	A novel hybrid ultrafast shape descriptor method for use in virtual screening. Chemistry Central Journal, 2008, 2, 3.	2.6	32
25	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
26	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
27	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
28	IRF2 is a master regulator of human keratinocyte stem cell fate. Nature Communications, 2019, 10, 4676.	5.8	25
29	Causal Network Models for Predicting Compound Targets and Driving Pathways in Cancer. Journal of Biomolecular Screening, 2014, 19, 791-802.	2.6	23
30	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
31	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
32	In vitro models for processes involved in intestinal absorption. Expert Opinion on Drug Metabolism and Toxicology, 2007, 3, 545-556.	1.5	16
33	Screening of Intestinal Crypt Organoids: A Simple Readout for Complex Biology. SLAS Discovery, 2017, 22, 571-582.	1.4	16
34	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
35	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
36	BET bromodomain inhibitors regulate keratinocyte plasticity. Nature Chemical Biology, 2021, 17, 280-290.	3.9	12

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37	Classifying Large Chemical Data Sets: Using A Regularized Potential Function Method. Journal of Chemical Information and Modeling, 2011, 51, 4-14.	2.5	11
38	Toxicological relationships between proteins obtained from protein target predictions of large toxicity databases. Toxicology and Applied Pharmacology, 2008, 231, 225-234.	1.3	9
39	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
40	Determination of minimal transcriptional signatures of compounds for target prediction. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 2.	1.4	7
41	Genome-wide CRISPR-Cas9 screens identify mechanisms of BET bromodomain inhibitor sensitivity. IScience, 2021, 24, 103323.	1.9	5
42	In vitro models for processes involved in intestinal absorption. Expert Opinion on Drug Metabolism and Toxicology, 2007, 3, 545-556.	1.5	3
43	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