Djork-Arné Clevert

List of Publications by Year
in descending order

28 papers	3,459 citations	471509 17 h-index	552781 26 g-index
33 all docs	33 docs citations	33 times ranked	6177 citing authors

#	Article	IF	Citations
1	A Fast and Interpretable Deep Learning Approach for Accurate Electrostatics-Driven pK_a Predictions in Proteins. Journal of Chemical Theory and Computation, 2022, 18, 5068-5078.	5.3	11
2	Self-supervised feature extraction from image time series in plant phenotyping using triplet networks. Bioinformatics, 2021, 37, 861-867.	4.1	14
3	Img2Mol â€" accurate SMILES recognition from molecular graphical depictions. Chemical Science, 2021, 12, 14174-14181.	7.4	32
4	Safer chemicals using less animals: kick-off of the European ONTOX project. Toxicology, 2021, 458, 152846.	4.2	33
5	pKPDB: a protein data bank extension database of pKa and pI theoretical values. Bioinformatics, 2021, 38, 297-298.	4.1	6
6	Parameterized Hypercomplex Graph Neural Networks for Graph Classification. Lecture Notes in Computer Science, 2021, , 204-216.	1.3	9
7	Unsupervised Representation Learning for Proteochemometric Modeling. International Journal of Molecular Sciences, 2021, 22, 12882.	4.1	5
8	De novo generation of hit-like molecules from gene expression signatures using artificial intelligence. Nature Communications, 2020, 11, 10.	12.8	253
9	Neuraldecipher â€" reverse-engineering extended-connectivity fingerprints (ECFPs) to their molecular structures. Chemical Science, 2020, 11, 10378-10389.	7.4	28
10	grünifai: interactive multiparameter optimization of molecules in a continuous vector space. Bioinformatics, 2020, 36, 4093-4094.	4.1	7
11	Modeling Physico-Chemical ADMET Endpoints with Multitask Graph Convolutional Networks. Molecules, 2020, 25, 44.	3.8	67
12	Efficient multi-objective molecular optimization in a continuous latent space. Chemical Science, 2019, 10, 8016-8024.	7.4	143
13	Learning continuous and data-driven molecular descriptors by translating equivalent chemical representations. Chemical Science, 2019, 10, 1692-1701.	7.4	293
14	Accurate Prediction of Biological Assays with High-Throughput Microscopy Images and Convolutional Networks. Journal of Chemical Information and Modeling, 2019, 59, 1163-1171.	5.4	69
15	Large-scale comparison of machine learning methods for drug target prediction on ChEMBL. Chemical Science, 2018, 9, 5441-5451.	7.4	357
16	Rectified factor networks for biclustering of omics data. Bioinformatics, 2017, 33, i59-i66.	4.1	7
17	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
18	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883

#	Article	IF	Citations
19	Increasing the discovery power of -omics studies. Systems Biomedicine (Austin, Tex), 2013, 1, 84-93.	0.7	2
20	cn.MOPS: mixture of Poissons for discovering copy number variations in next-generation sequencing data with a low false discovery rate. Nucleic Acids Research, 2012, 40, e69-e69.	14.5	394
21	Î´-Clustering of Monotone Profiles. , 2012, , 135-149.		0
22	cn.FARMS: a latent variable model to detect copy number variations in microarray data with a low false discovery rate. Nucleic Acids Research, 2011, 39, e79-e79.	14.5	19
23	Informative or Noninformative Calls for Gene Expression: A Latent Variable Approach. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 4.	0.6	8
24	FABIA: factor analysis for bicluster acquisition. Bioinformatics, 2010, 26, 1520-1527.	4.1	258
25	The Affymetrix GeneChipÂ® Microarray Platform. , 2009, , 251-261.		2
26	Genomeâ€wide copy number alterations detection in fresh frozen and matched FFPE samples using SNP 6.0 arrays. Genes Chromosomes and Cancer, 2008, 47, 957-964.	2.8	49
27	I/NI-calls for the exclusion of non-informative genes: a highly effective filtering tool for microarray data. Bioinformatics, 2007, 23, 2897-2902.	4.1	154
28	A new summarization method for affymetrix probe level data. Bioinformatics, 2006, 22, 943-949.	4.1	229