

Djork-ArnÃ© Clevert

List of Publications by Year in descending order

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Version: 2024-02-01

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 comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , 2014, 32, 903-914.	17.5	883
2	cn.MOPS: mixture of Poissons for discovering copy number variations in next-generation sequencing data with a low false discovery rate. <i>Nucleic Acids Research</i> , 2012, 40, e69-e69.	14.5	394
3	Large-scale comparison of machine learning methods for drug target prediction on ChEMBL. <i>Chemical Science</i> , 2018, 9, 5441-5451.	7.4	357
4	Learning continuous and data-driven molecular descriptors by translating equivalent chemical representations. <i>Chemical Science</i> , 2019, 10, 1692-1701.	7.4	293
5	FABIA: factor analysis for bicluster acquisition. <i>Bioinformatics</i> , 2010, 26, 1520-1527.	4.1	258
6	De novo generation of hit-like molecules from gene expression signatures using artificial intelligence. <i>Nature Communications</i> , 2020, 11, 10.	12.8	253
7	A new summarization method for affymetrix probe level data. <i>Bioinformatics</i> , 2006, 22, 943-949.	4.1	229
8	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
9	Efficient multi-objective molecular optimization in a continuous latent space. <i>Chemical Science</i> , 2019, 10, 8016-8024.	7.4	143
10	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	12.8	122
11	Accurate Prediction of Biological Assays with High-Throughput Microscopy Images and Convolutional Networks. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1163-1171.	5.4	69
12	Modeling Physico-Chemical ADMET Endpoints with Multitask Graph Convolutional Networks. <i>Molecules</i> , 2020, 25, 44.	3.8	67
13	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
14	Safer chemicals using less animals: kick-off of the European ONTOX project. <i>Toxicology</i> , 2021, 458, 152846.	4.2	33
15	Img2Mol â€œ accurate SMILES recognition from molecular graphical depictions. <i>Chemical Science</i> , 2021, 12, 14174-14181.	7.4	32
16	Neuraldecipher â€œ reverse-engineering extended-connectivity fingerprints (ECFPs) to their molecular structures. <i>Chemical Science</i> , 2020, 11, 10378-10389.	7.4	28
17	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
18	Self-supervised feature extraction from image time series in plant phenotyping using triplet networks. <i>Bioinformatics</i> , 2021, 37, 861-867.	4.1	14

#	ARTICLE	IF	CITATIONS
19	A Fast and Interpretable Deep Learning Approach for Accurate Electrostatics-Driven p <i>K</i> Predictions in Proteins. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 5068-5078.	5.3	11
20	Parameterized Hypercomplex Graph Neural Networks for Graph Classification. <i>Lecture Notes in Computer Science</i> , 2021, , 204-216.	1.3	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	Rectified factor networks for biclustering of omics data. <i>Bioinformatics</i> , 2017, 33, i59-i66.	4.1	7
23	gr4nifai: interactive multiparameter optimization of molecules in a continuous vector space. <i>Bioinformatics</i> , 2020, 36, 4093-4094.	4.1	7
24	pKPDB: a protein data bank extension database of p <i>K</i> and pI theoretical values. <i>Bioinformatics</i> , 2021, 38, 297-298.	4.1	6
25	Unsupervised Representation Learning for Proteochemometric Modeling. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12882.	4.1	5
26	Increasing the discovery power of -omics studies. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 84-93.	0.7	2
27	The Affymetrix GeneChip® Microarray Platform. , 2009, , 251-261.		2
28	Î-Clustering of Monotone Profiles. , 2012, , 135-149.		0