

Dominik Heider

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

99
papers

1,670
citations

24
h-index

37
g-index

119
ext. papers

2,198
ext. citations

5
avg, IF

5.1
L-index

#	Paper	IF	Citations
99	High-scale random access on DNA storage systems.. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqab126	3.7	1
98	sPLINK: a hybrid federated tool as a robust alternative to meta-analysis in genome-wide association studies.. <i>Genome Biology</i> , 2022 , 23, 32	18.3	1
97	Evaluation of machine learning strategies for imaging confirmed prostate cancer recurrence prediction on electronic health records.. <i>Computers in Biology and Medicine</i> , 2022 , 143, 105263	7	0
96	The relationship between land cover and microbial community composition in European lakes.. <i>Science of the Total Environment</i> , 2022 , 825, 153732	10.2	0
95	Multi-label classification for multi-drug resistance prediction of .. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 1264-1270	6.8	2
94	MOVIS: A multi-omics software solution for multi-modal time-series clustering, embedding, and visualizing tasks.. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 1044-1055	6.8	
93	Vision for Improving Pregnancy Health: Innovation and the Future of Pregnancy Research.. <i>Reproductive Sciences</i> , 2022 , 1	3	0
92	Design considerations for advancing data storage with synthetic DNA for long-term archiving. <i>Materials Today Bio</i> , 2022 , 100306	9.9	0
91	Transfer learning compensates limited data, batch effects and technological heterogeneity in single-cell sequencing. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab104	3.7	0
90	Gaussian noise up-sampling is better suited than SMOTE and ADASYN for clinical decision making. <i>BioData Mining</i> , 2021 , 14, 49	4.3	5
89	Chaos game representation and its applications in bioinformatics.. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 6263-6271	6.8	4
88	Machine learning with asymmetric abstention for biomedical decision-making. <i>BMC Medical Informatics and Decision Making</i> , 2021 , 21, 294	3.6	1
87	MOSGA: Modular Open-Source Genome Annotator. <i>Bioinformatics</i> , 2021 , 36, 5514-5515	7.2	1
86	Mushroom data creation, curation, and simulation to support classification tasks. <i>Scientific Reports</i> , 2021 , 11, 8134	4.9	1
85	A large-scale comparative study on peptide encodings for biomedical classification. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab039	3.7	6
84	Integrative Analysis of Next-Generation Sequencing for Next-Generation Cancer Research toward Artificial Intelligence. <i>Cancers</i> , 2021 , 13,	6.6	2
83	Fostering reproducibility, reusability, and technology transfer in health informatics. <i>IScience</i> , 2021 , 24, 102803	6.1	1

82	Identification of the most indicative and discriminative features from diagnostic instruments for children with autism. <i>JCPP Advances</i> , 2021 , 1, e12023		4
81	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021 , 22, 642-663	13.4	56
80	Prediction of antimicrobial resistance based on whole-genome sequencing and machine learning. <i>Bioinformatics</i> , 2021 ,	7.2	9
79	The visual story of data storage: From storage properties to user interfaces. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 4904-4918	6.8	2
78	Quantification of the covariation of lake microbiomes and environmental variables using a machine learning-based framework. <i>Molecular Ecology</i> , 2021 , 30, 2131-2144	5.7	5
77	Transaminase concentrations cannot separate NAFL and NASH in morbidly obese patients irrespective of histological algorithm. <i>Digestive Diseases</i> , 2021 ,	3.2	1
76	MOSGA 2: Comparative genomics and validation tools. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 5504-5509	6.8	0
75	A multi-omics study on quantifying antimicrobial resistance in European freshwater lakes. <i>Environment International</i> , 2021 , 157, 106821	12.9	0
74	Fractal construction of constrained code words for DNA storage systems.. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
73	gammaBORiS: Identification and Taxonomic Classification of Origins of Replication in Gammaproteobacteria using Motif-based Machine Learning. <i>Scientific Reports</i> , 2020 , 10, 6727	4.9	3
72	MESA: automated assessment of synthetic DNA fragments and simulation of DNA synthesis, storage, sequencing and PCR errors. <i>Bioinformatics</i> , 2020 , 36, 3322-3326	7.2	8
71	CORDITE: The Curated CORona Drug InTERactions Database for SARS-CoV-2. <i>IScience</i> , 2020 , 23, 101297	6.1	19
70	Four high-quality draft genome assemblies of the marine heterotrophic nanoflagellate Cafeteria roenbergensis. <i>Scientific Data</i> , 2020 , 7, 29	8.2	11
69	Comparative analyses of error handling strategies for next-generation sequencing in precision medicine. <i>Scientific Reports</i> , 2020 , 10, 5750	4.9	2
68	GALAD Score Detects Early Hepatocellular Carcinoma in an International Cohort of Patients With Nonalcoholic Steatohepatitis. <i>Clinical Gastroenterology and Hepatology</i> , 2020 , 18, 728-735.e4	6.9	73
67	Natrix: a Snakemake-based workflow for processing, clustering, and taxonomically assigning amplicon sequencing reads. <i>BMC Bioinformatics</i> , 2020 , 21, 526	3.6	5
66	Liver parameters as part of a non-invasive model for prediction of all-cause mortality after myocardial infarction. <i>Archives of Medical Science</i> , 2020 , 16, 71-80	2.9	5
65	Deep learning on chaos game representation for proteins. <i>Bioinformatics</i> , 2020 , 36, 272-279	7.2	17

64	Encodings and models for antimicrobial peptide classification for multi-resistant pathogens. <i>BioData Mining</i> , 2019 , 12, 7	4.3	40
63	Non-invasive assessment of NAFLD as systemic disease-A machine learning perspective. <i>PLoS ONE</i> , 2019 , 14, e0214436	3.7	30
62	The virtual doctor: An interactive clinical-decision-support system based on deep learning for non-invasive prediction of diabetes. <i>Artificial Intelligence in Medicine</i> , 2019 , 100, 101706	7.4	35
61	FRI-Feature Relevance Intervals for Interpretable and Interactive Data Exploration 2019 ,		1
60	NAFLD-Associated Comorbidities in Advanced Stage HCC Do Not Alter the Safety and Efficacy of Yttrium-90 Radioembolization. <i>Liver Cancer</i> , 2019 , 8, 491-504	9.1	6
59	GUESS: projecting machine learning scores to well-calibrated probability estimates for clinical decision-making. <i>Bioinformatics</i> , 2019 , 35, 2458-2465	7.2	15
58	SCOTCH: subtype A coreceptor tropism classification in HIV-1. <i>Bioinformatics</i> , 2018 , 34, 2575-2580	7.2	12
57	Phi-Delta-Diagrams: Software Implementation of a Visual Tool for Assessing Classifier and Feature Performance. <i>Machine Learning and Knowledge Extraction</i> , 2018 , 1, 121-137	3.1	2
56	SEDE-GPS: socio-economic data enrichment based on GPS information. <i>BMC Bioinformatics</i> , 2018 , 19, 440	3.6	3
55	Data Science for Molecular Diagnostics Applications: From Academia to Clinic to Industry. <i>Systems Medicine (New Rochelle, N Y)</i> , 2018 , 1, 13-17	1.6	4
54	Low transferrin and high ferritin concentrations are associated with worse outcome in acute liver failure. <i>Liver International</i> , 2017 , 37, 1032-1041	7.9	18
53	EFS: an ensemble feature selection tool implemented as R-package and web-application. <i>BioData Mining</i> , 2017 , 10, 21	4.3	49
52	eccCL: parallelized GPU implementation of Ensemble Classifier Chains. <i>BMC Bioinformatics</i> , 2017 , 18, 371	3.6	1
51	SHIVA - a web application for drug resistance and tropism testing in HIV. <i>BMC Bioinformatics</i> , 2016 , 17, 314	3.6	17
50	Protistan community analysis: key findings of a large-scale molecular sampling. <i>ISME Journal</i> , 2016 , 10, 2269-79	11.9	80
49	Genotypic Prediction of Co-receptor Tropism of HIV-1 Subtypes A and C. <i>Scientific Reports</i> , 2016 , 6, 24883	7.9	21
48	Exploiting HIV-1 protease and reverse transcriptase cross-resistance information for improved drug resistance prediction by means of multi-label classification. <i>BioData Mining</i> , 2016 , 9, 10	4.3	24
47	Current Approaches in Computational Drug Resistance Prediction in HIV. <i>Current HIV Research</i> , 2016 , 14, 307-15	1.3	11

46	Bacterial Glycosyltransferases: Challenges and Opportunities of a Highly Diverse Enzyme Class Toward Tailoring Natural Products. <i>Frontiers in Microbiology</i> , 2016 , 7, 182	5.7	49
45	Compensation of feature selection biases accompanied with improved predictive performance for binary classification by using a novel ensemble feature selection approach. <i>BioData Mining</i> , 2016 , 9, 36	4.3	30
44	In Acute Myocardial Infarction Liver Parameters Are Associated With Stenosis Diameter. <i>Medicine (United States)</i> , 2016 , 95, e2807	1.8	13
43	Normal liver enzymes are correlated with severity of metabolic syndrome in a large population based cohort. <i>Scientific Reports</i> , 2015 , 5, 13058	4.9	44
42	Parameters Influencing Baseline HIV-1 Genotypic Tropism Testing Related to Clinical Outcome in Patients on Maraviroc. <i>PLoS ONE</i> , 2015 , 10, e0125502	3.7	6
41	AmpliconDuo: A Split-Sample Filtering Protocol for High-Throughput Amplicon Sequencing of Microbial Communities. <i>PLoS ONE</i> , 2015 , 10, e0141590	3.7	29
40	A simple structure-based model for the prediction of HIV-1 co-receptor tropism. <i>BioData Mining</i> , 2014 , 7, 14	4.3	24
39	Endoscopic management is the treatment of choice for bile leaks after liver resection. <i>Gastrointestinal Endoscopy</i> , 2014 , 80, 626-633.e1	5.2	28
38	gCUP: rapid GPU-based HIV-1 co-receptor usage prediction for next-generation sequencing. <i>Bioinformatics</i> , 2014 , 30, 3272-3	7.2	7
37	Non-invasive separation of alcoholic and non-alcoholic liver disease with predictive modeling. <i>PLoS ONE</i> , 2014 , 9, e101444	3.7	32
36	Unsupervised Dimension Reduction Methods for Protein Sequence Classification. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2014 , 295-302	0.2	1
35	Baseline activity predicts working memory load of preceding task condition. <i>Human Brain Mapping</i> , 2013 , 34, 3010-22	5.9	17
34	Multilabel classification for exploiting cross-resistance information in HIV-1 drug resistance prediction. <i>Bioinformatics</i> , 2013 , 29, 1946-52	7.2	44
33	A new approach to inhibit human Eryptase by protein surface binding of four-armed peptide ligands with two different sets of arms. <i>Organic and Biomolecular Chemistry</i> , 2013 , 11, 1631-9	3.9	19
32	A combination of Efetoprotein and des-Ecarboxy prothrombin is superior in detection of hepatocellular carcinoma. <i>Digestion</i> , 2013 , 87, 121-31	3.6	76
31	On the Application of Supervised Machine Learning to Trustworthiness Assessment 2013 ,		7
30	Design of a modular protein-based MRI contrast agent for targeted application. <i>PLoS ONE</i> , 2013 , 8, e65346	3.9	11
29	A small set of succinct signature patterns distinguishes Chinese and non-Chinese HIV-1 genomes. <i>PLoS ONE</i> , 2013 , 8, e58804	3.7	7

28	Novel algorithm for non-invasive assessment of fibrosis in NAFLD. <i>PLoS ONE</i> , 2013 , 8, e62439	3.7	40
27	The action of small GTPases Rab11 and Rab25 in vesicle trafficking during cell migration. <i>Cellular Physiology and Biochemistry</i> , 2012 , 29, 647-56	3.9	29
26	Chemico-genetic strategies to inhibit the leukemic potential of threonine aspartase-1. <i>Blood Cancer Journal</i> , 2012 , 2, e77	7	15
25	3 γ Phosphoadenosine 5 γ phosphosulfate (PAPS) synthases, naturally fragile enzymes specifically stabilized by nucleotide binding. <i>Journal of Biological Chemistry</i> , 2012 , 287, 17645-17655	5.4	27
24	Machine learning on normalized protein sequences. <i>BMC Research Notes</i> , 2011 , 4, 94	2.3	11
23	Computational Design of a DNA- and Fc-Binding Fusion Protein. <i>Advances in Bioinformatics</i> , 2011 , 2011, 457578	5.5	1
22	DNA Watermarking: Challenging Perspectives for Biotechnological Applications. <i>Current Bioinformatics</i> , 2011 , 6, 375-382	4.7	19
21	Interpol: An R package for preprocessing of protein sequences. <i>BioData Mining</i> , 2011 , 4, 16	4.3	18
20	Improved Bevirimat resistance prediction by combination of structural and sequence-based classifiers. <i>BioData Mining</i> , 2011 , 4, 26	4.3	20
19	Dynamic causal modeling with genetic algorithms. <i>Journal of Neuroscience Methods</i> , 2011 , 194, 402-6	3	11
18	Single-domain parvulins constitute a specific marker for recently proposed deep-branching archaeal subgroups. <i>Evolutionary Bioinformatics</i> , 2011 , 7, 135-48	1.9	4
17	Group-Agreement as a Reliability Measure for Witness Recommendations in Reputation-Based Trust Protocols. <i>Lecture Notes in Computer Science</i> , 2011 , 231-255	0.9	
16	Insights into the classification of small GTPases. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2010 , 3, 15-24	1.5	16
15	Prediction of co-receptor usage of HIV-1 from genotype. <i>PLoS Computational Biology</i> , 2010 , 6, e10007435		44
14	fMRI data visualization with BrainBlend and Blender. <i>Neuroinformatics</i> , 2010 , 8, 21-31	3.2	10
13	Predicting Bevirimat resistance of HIV-1 from genotype. <i>BMC Bioinformatics</i> , 2010 , 11, 37	3.6	26
12	Structure of HIV-1 quasi-species as early indicator for switches of co-receptor tropism. <i>AIDS Research and Therapy</i> , 2010 , 7, 41	3	17
11	Reputation-Based Trust Diffusion in Complex Socio-Economic Networks. <i>Studies in Computational Intelligence</i> , 2010 , 21-40	0.8	1

10	Augmenting Reputation-Based Trust Metrics with Rumor-Like Dissemination of Reputation Information. <i>IFIP Advances in Information and Communication Technology</i> , 2010 , 136-147	0.5	2
9	Impact of working memory load on fMRI resting state pattern in subsequent resting phases. <i>PLoS ONE</i> , 2009 , 4, e7198	3.7	84
8	A computational approach for the identification of small GTPases based on preprocessed amino acid sequences. <i>Technology in Cancer Research and Treatment</i> , 2009 , 8, 333-41	2.7	17
7	DNA watermarks in non-coding regulatory sequences. <i>BMC Research Notes</i> , 2009 , 2, 125	2.3	23
6	Watermarking sexually reproducing diploid organisms. <i>Bioinformatics</i> , 2008 , 24, 1961-2	7.2	19
5	DNA watermarks: a proof of concept. <i>BMC Molecular Biology</i> , 2008 , 9, 40	4.5	38
4	DNA-based watermarks using the DNA-Crypt algorithm. <i>BMC Bioinformatics</i> , 2007 , 8, 176	3.6	89
3	sPLINK: A Federated, Privacy-Preserving Tool as a Robust Alternative to Meta-Analysis in Genome-Wide Association Studies		6
2	Deep Learning on Chaos Game Representation for Proteins		1
1	Four high-quality draft genome assemblies of the marine heterotrophic nanoflagellate <i>Cafeteria roenbergensis</i>		