Dirk Labudde

List of Publications by Year
in descending order

31 papers	**294** citations	1040056 **9** h-index	940533 **16** g-index
33 all docs	**33** docs citations	**33** times ranked	**428** citing authors

#	Article	IF	Citations
1	Iterative Named Entity Recognition with Conditional Random Fields. Applied Sciences (Switzerland), 2022, 12, 330.	2.5	4
2	A multiscale model of the regulation of aquaporin 2 recycling. Npj Systems Biology and Applications, 2022, 8, 16.	3.0	1
3	Analysis of the influence of EDTA-treated reference samples on forensic bloodstain age estimation. Forensic Science International, 2021, 325, 110876.	2.2	7
4	The structural basis of the genetic code: amino acid recognition by aminoacyl-tRNA synthetases. Scientific Reports, 2020, 10, 12647.	3.3	23
5	Structural change in GadD2 of Listeria monocytogenes field isolates supports nisin resistance. International Journal of Food Microbiology, 2019, 305, 108240.	4.7	22
6	Application of an interpretable classification model on Early Folding Residues during protein folding. BioData Mining, 2019, 12, 1.	4.0	27
7	StructureDistiller: Structural relevance scoring identifies the most informative entries of a contact map. Scientific Reports, 2019, 9, 18517.	3.3	3
8	Unsupervised Discovery of Geometrically Common Structural Motifs and Long-Range Contacts in Protein 3D Structures. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 671-680.	3.0	3
9	Pyridine Nucleotide Coenzyme Specificity of p-Hydroxybenzoate Hydroxylase and Related Flavoprotein Monooxygenases. Frontiers in Microbiology, 2018, 9, 3050.	3.5	17
10	Characterizing the relation of functional and Early Folding Residues in protein structures using the example of aminoacyl-tRNA synthetases. PLoS ONE, 2018, 13, e0206369.	2.5	4
11	Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases. PLoS Computational Biology, 2018, 14, e1006101.	3.2	17
12	Detailed Analysis of 17Î²-Estradiol-Aptamer Interactions: A Molecular Dynamics Simulation Study. Molecules, 2018, 23, 1690.	3.8	23
13	Towards substrate-independent age estimation of blood stains based on dimensionality reduction and k-nearest neighbor classification of absorbance spectroscopic data. Forensic Science International, 2017, 278, 1-8.	2.2	18
14	Simulation of diffusion using a modular cell dynamic simulation system. In Silico Biology, 2017, 12, 129-142.	0.9	4
15	Loss of heterozygosity in FANCG, FANCF and BRIP1 from head and neck squamous cell carcinoma of the oral cavity. International Journal of Oncology, 2017, 50, 2207-2220.	3.3	10
16	PIPINO: A Software Package to Facilitate the Identification of Protein-Protein Interactions from Affinity Purification Mass Spectrometry Data. BioMed Research International, 2016, 2016, 1-13.	1.9	0
17	OEZY: Optimising E n ZY me selection for best performing terminal restriction fragment length polymorphism analysis using ARB. Methods in Ecology and Evolution, 2016, 7, 242-248.	5.2	0
18	SequenceCEROSENE: a computational method and web server to visualize spatial residue neighborhoods at the sequence level. BioData Mining, 2016, 9, 6.	4.0	0

#	Article	IF	Citations
19	Numeric promoter description â€" A comparative view on concepts and general application. Journal of Molecular Graphics and Modelling, 2016, 63, 65-77.	2.4	0
20	Fit3D: a web application for highly accurate screening of spatial residue patterns in protein structure data. Bioinformatics, 2016, 32, 792-794.	4.1	10
21	Evolutionary Influenced Interaction Pattern as Indicator for the Investigation of Natural Variants Causing Nephrogenic Diabetes Insipidus. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-6.	1.3	0
22	A Novel Algorithm for Enhanced Structural Motif Matching in Proteins. Journal of Computational Biology, 2015, 22, 698-713.	1.6	8
23	The observation of evolutionary interaction pattern pairs in membrane proteins. BMC Structural Biology, 2015, 15, 6.	2.3	1
24	New Strategies for Evaluation and Analysis of SELEX Experiments. BioMed Research International, 2014, 2014, 1-12.	1.9	19
25	Selection of a DNA aptamer against norovirus capsid protein VP1. FEMS Microbiology Letters, 2014, 351, 162-169.	1.8	52
26	Scaffold preferences of mesenchymal stromal cells and adipose-derived stem cells from green fluorescent protein transgenic mice influence the tissue engineering of bone. British Journal of Oral and Maxillofacial Surgery, 2014, 52, 409-414.	0.8	9
27	Graph representation of high-dimensional alpha-helical membrane protein data. BioData Mining, 2013, 6, 21.	4.0	2
28	eProSâ€"a database and toolbox for investigating protein sequenceâ€"structureâ€"function relationships through energy profiles. Nucleic Acids Research, 2013, 41, D320-D326.	14.5	8
29	Structure Topology Prediction of Discriminative Sequence Motifs in Membrane Proteins with Domains of Unknown Functions. Structural Biology, 2013, 2013, 1-10.	0.0	2
30	Automatic Classification of Bloodstains with Deep Learning Methods. KI - Kunstliche Intelligenz, 0, , .	3.2	0
31	MoNA: A Forensic Analysis Platform for Mobile Communication. KI - Kunstliche Intelligenz, 0, , .	3.2	0