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	Selection of a DNA aptamer against norovirus capsid protein VP1. FEMS Microbiology Letters, 2014, 351, 162-169.	1.8	52
2	Application of an interpretable classification model on Early Folding Residues during protein folding. BioData Mining, 2019, 12, 1.	4.0	27
3	Detailed Analysis of 17Î²-Estradiol-Aptamer Interactions: A Molecular Dynamics Simulation Study. Molecules, 2018, 23, 1690.	3.8	23
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	New Strategies for Evaluation and Analysis of SELEX Experiments. BioMed Research International, 2014, 2014, 1-12.	1.9	19
7	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
8	Pyridine Nucleotide Coenzyme Specificity of p-Hydroxybenzoate Hydroxylase and Related Flavoprotein Monooxygenases. Frontiers in Microbiology, 2018, 9, 3050.	3.5	17
9	Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases. PLoS Computational Biology, 2018, 14, e1006101.	3.2	17
10	Fit3D: a web application for highly accurate screening of spatial residue patterns in protein structure data. Bioinformatics, 2016, 32, 792-794.	4.1	10
11	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
12	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
13	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
14	A Novel Algorithm for Enhanced Structural Motif Matching in Proteins. Journal of Computational Biology, 2015, 22, 698-713.	1.6	8
15	Analysis of the influence of EDTA-treated reference samples on forensic bloodstain age estimation. Forensic Science International, 2021, 325, 110876.	2.2	7
16	Simulation of diffusion using a modular cell dynamic simulation system. In Silico Biology, 2017, 12, 129-142.	0.9	4
17	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
18	Iterative Named Entity Recognition with Conditional Random Fields. Applied Sciences (Switzerland), 2022, 12, 330.	2.5	4

#	Article	IF	Citations
19	StructureDistiller: Structural relevance scoring identifies the most informative entries of a contact map. Scientific Reports, 2019, 9, 18517.	3.3	3
20	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
21	Graph representation of high-dimensional alpha-helical membrane protein data. BioData Mining, 2013, 6, 21.	4.0	2
22	Structure Topology Prediction of Discriminative Sequence Motifs in Membrane Proteins with Domains of Unknown Functions. Structural Biology, 2013, 2013, 1-10.	0.0	2
23	The observation of evolutionary interaction pattern pairs in membrane proteins. BMC Structural Biology, 2015, 15, 6.	2.3	1
24	A multiscale model of the regulation of aquaporin 2 recycling. Npj Systems Biology and Applications, 2022, 8, 16.	3.0	1
25	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
26	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
27	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
28	SequenceCEROSENE: a computational method and web server to visualize spatial residue neighborhoods at the sequence level. BioData Mining, 2016, 9, 6.	4.0	0
29	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
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