

# Mario Lebendiker

## List of Publications by Year in descending order

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28  
papers

1,524  
citations

430874

18  
h-index

501196

28  
g-index

29  
all docs

29  
docs citations

29  
times ranked

1663  
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein purification strategies must consider downstream applications and individual biological characteristics. <i>Microbial Cell Factories</i> , 2022, 21, 52.	4.0	5
2	Quality control of purified proteins to improve data quality and reproducibility: results from a large-scale survey. <i>European Biophysics Journal</i> , 2021, 50, 453-460.	2.2	6
3	Quality control of protein reagents for the improvement of research data reproducibility. <i>Nature Communications</i> , 2021, 12, 2795.	12.8	25
4	Expression, purification and crystallization of CLK1 kinase – A potential target for antiviral therapy. <i>Protein Expression and Purification</i> , 2020, 176, 105742.	1.3	6
5	Coupling Multi Angle Light Scattering to Ion Exchange chromatography (IEX-MALS) for protein characterization. <i>Scientific Reports</i> , 2018, 8, 6907.	3.3	39
6	Purification of Proteins Fused to Maltose-Binding Protein. <i>Methods in Molecular Biology</i> , 2017, 1485, 257-273.	0.9	13
7	The vapB–vapC Operon of <i>Acidovorax citrulli</i> Functions as a Bona-fide Toxin–Antitoxin Module. <i>Frontiers in Microbiology</i> , 2016, 6, 1499.	3.5	21
8	Differential effects of zinc binding on structured and disordered regions in the multidomain STIL protein. <i>Chemical Science</i> , 2016, 7, 4140-4147.	7.4	4
9	Highly homologous proteins exert opposite biological activities by using different interaction interfaces. <i>Scientific Reports</i> , 2015, 5, 11629.	3.3	10
10	Production of prone-to-aggregate proteins. <i>FEBS Letters</i> , 2014, 588, 236-246.	2.8	116
11	The STIL protein contains intrinsically disordered regions that mediate its protein–protein interactions. <i>Chemical Communications</i> , 2014, 50, 5245-5247.	4.1	10
12	The disordered region of Arabidopsis VIP1 binds the Agrobacterium VirE2 protein outside its DNA-binding site. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 439-446.	2.1	4
13	Specific Recognition of p53 Tetramers by Peptides Derived from p53 Interacting Proteins. <i>PLoS ONE</i> , 2012, 7, e38060.	2.5	21
14	Purification of Proteins Fused to Maltose-Binding Protein. <i>Methods in Molecular Biology</i> , 2011, 681, 281-293.	0.9	31
15	Mechanism of the Interaction between the Intrinsically Disordered C-Terminus of the Pro-Apoptotic ARTS Protein and the Bir3 Domain of XIAP. <i>PLoS ONE</i> , 2011, 6, e24655.	2.5	19
16	Chemical Synthesis and Expression of the HIV-1 Rev Protein. <i>ChemBioChem</i> , 2011, 12, 1097-1104.	2.6	68
17	The C-terminal domain of the HIV-1 Vif protein is natively unfolded in its unbound state. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 281-287.	2.1	29
18	A cyanobacterial Abr-like protein affects the apparent photosynthetic affinity for CO <sub>2</sub> by modulating low-CO <sub>2</sub> -induced gene expression. <i>Environmental Microbiology</i> , 2009, 11, 927-936.	3.8	80

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19	An AbrB-like protein might be involved in the regulation of cylindrospermopsin production by <i>Aphanizomenon ovalisporum</i> . <i>Environmental Microbiology</i> , 2008, 10, 988-999.	3.8	51
20	The Structure and Interactions of the Proline-rich Domain of ASPP2. <i>Journal of Biological Chemistry</i> , 2008, 283, 18990-18999.	3.4	40
21	Molecular basis of the interaction between the antiapoptotic Bcl-2 family proteins and the proapoptotic protein ASPP2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12277-12282.	7.1	49
22	Inhibiting HIV-1 integrase by shifting its oligomerization equilibrium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8316-8321.	7.1	177
23	Scanning Cysteine Accessibility of EmrE, an H <sup>+</sup> -coupled Multidrug Transporter from <i>Escherichia coli</i> , Reveals a Hydrophobic Pathway for Solutes. <i>Journal of Biological Chemistry</i> , 1999, 274, 19480-19486.	3.4	94
24	NMR investigation of the multidrug transporter EmrE, an integral membrane protein. <i>FEBS Journal</i> , 1998, 254, 610-619.	0.2	86
25	Determining the Secondary Structure and Orientation of EmrE, a Multi-Drug Transporter, Indicates a Transmembrane Four-Helix Bundle. <i>Biochemistry</i> , 1996, 35, 7233-7238.	2.5	101
26	Identification of Residues in the Translocation Pathway of EmrE, a Multidrug Antiporter from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1996, 271, 21193-21199.	3.4	27
27	Negative Dominance Studies Demonstrate the Oligomeric Structure of EmrE, a Multidrug Antiporter from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1996, 271, 31044-31048.	3.4	109
28	EmrE, an <i>Escherichia coli</i> 12-kDa Multidrug Transporter, Exchanges Toxic Cations and H <sup>+</sup> and Is Soluble in Organic Solvents. <i>Journal of Biological Chemistry</i> , 1995, 270, 6856-6863.	3.4	283