## Christof Lenz

## List of Publications by Year in descending order

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201674 182427 2,916 66 27 51 citations h-index g-index papers 73 73 73 5068 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Multiâ€omic landscaping of human midbrains identifies diseaseâ€relevant molecular targets and pathways in advancedâ€stage Parkinson's disease. Clinical and Translational Medicine, 2022, 12, e692.	4.0	22
2	Calpain cleavage of Junctophilin-2 generates a spectrum of calcium-dependent cleavage products and DNA-rich NT1-fragment domains in cardiomyocytes. Scientific Reports, 2022, 12, .	3.3	6
3	Caveolin3 Stabilizes McT1-Mediated Lactate/Proton Transport in Cardiomyocytes. Circulation Research, 2021, 128, e102-e120.	4.5	16
4	Translation error clusters induced by aminoglycoside antibiotics. Nature Communications, 2021, 12, 1830.	12.8	40
5	Calreticulin Deficiency Disturbs Ribosome Biogenesis and Results in Retardation in Embryonic Kidney Development. International Journal of Molecular Sciences, 2021, 22, 5858.	4.1	4
6	Enhancing the chondrogenic potential of chondrogenic progenitor cells by deleting RAB5C. IScience, 2021, 24, 102464.	4.1	1
7	Quantitative Analysis of the Cardiac Phosphoproteome in Response to Acute Î <sup>2</sup> -Adrenergic Receptor Stimulation In Vivo. International Journal of Molecular Sciences, 2021, 22, 12584.	4.1	4
8	Proteomic mapping of atrial and ventricular heart tissue in patients with aortic valve stenosis. Scientific Reports, 2021, 11, 24389.	3.3	3
9	Sequestosome 1 Is Part of the Interaction Network of VAPB. International Journal of Molecular Sciences, 2021, 22, 13271.	4.1	3
10	LEF1 supports metastatic brain colonization by regulating glutathione metabolism and increasing ROS resistance in breast cancer. International Journal of Cancer, 2020, 146, 3170-3183.	5.1	23
11	A streamlined pipeline for multiplexed quantitative site-specific N-glycoproteomics. Nature Communications, 2020, 11, 5268.	12.8	46
12	$14 ext{-}3 ext{-}3$ binding creates a memory of kinase action by stabilizing the modified state of phospholamban. Science Signaling, 2020, $13$ , .	3.6	19
13	The Archaeal Proteome Project advances knowledge about archaeal cell biology through comprehensive proteomics. Nature Communications, 2020, 11, 3145.	12.8	40
14	Probing the Environment of Emerin by Enhanced Ascorbate Peroxidase 2 (APEX2)-Mediated Proximity Labeling. Cells, 2020, 9, 605.	4.1	9
15	Intronic CRISPR Repair in a Preclinical Model of Noonan Syndrome–Associated Cardiomyopathy. Circulation, 2020, 142, 1059-1076.	1.6	43
16	How to Cope With Heavy Metal Ions: Cellular and Proteome-Level Stress Response to Divalent Copper and Nickel in Halobacterium salinarum R1 Planktonic and Biofilm Cells. Frontiers in Microbiology, 2020, 10, 3056.	3.5	15
17	Inhibition of the autophagic protein ULK1 attenuates axonal degeneration in vitro and in vivo, enhances translation, and modulates splicing. Cell Death and Differentiation, 2020, 27, 2810-2827.	11.2	25
18	The Response ofHaloferax volcaniito Salt and Temperature Stress: A Proteome Study by Labelâ€Free Mass Spectrometry. Proteomics, 2019, 19, 1800491.	2.2	28

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19	Proteomic mapping by rapamycin-dependent targeting of APEX2 identifies binding partners of VAPB at the inner nuclear membrane. Journal of Biological Chemistry, 2019, 294, 16241-16254.	3.4	30
20	The Core Proteome of Biofilm-Grown Clinical Pseudomonas aeruginosa Isolates. Cells, 2019, 8, 1129.	4.1	26
21	Loss of Protein Phosphatase 1 Regulatory Subunit PPP1R3A Promotes Atrial Fibrillation. Circulation, 2019, 140, 681-693.	1.6	47
22	A MICOS–TIM22 Association Promotes Carrier Import into Human Mitochondria. Journal of Molecular Biology, 2019, 431, 2835-2851.	4.2	43
23	Broad range of missense error frequencies in cellular proteins. Nucleic Acids Research, 2019, 47, 2932-2945.	14.5	27
24	A trap mutant reveals the physiological client spectrum of TRC40. Journal of Cell Science, 2019, 132, .	2.0	18
25	Proteome Profiling by Labelâ€Free Mass Spectrometry Reveals Differentiated Response ofCampylobacter jejuni81–176 to Sublethal Concentrations of Bile Acids. Proteomics - Clinical Applications, 2019, 13, 1800083.	1.6	5
26	A new albumin-depletion strategy improves proteomic research of gingival crevicular fluid from periodontitis patients. Clinical Oral Investigations, 2018, 22, 1375-1384.	3.0	10
27	Integrative omics - from data to biology. Expert Review of Proteomics, 2018, 15, 463-466.	3.0	20
28	Crohn's disease patient serum changes protein expression in a human mesenchymal stem cell model in a linear relationship to patients' disease stage and to bone mineral density. Journal of Clinical and Translational Endocrinology, 2018, 13, 26-38.	1.4	3
29	Comparative proteomics reveals a diagnostic signature for pulmonary headâ€andâ€neck cancerÂmetastasis. EMBO Molecular Medicine, 2018, 10, .	6.9	41
30	Deep phenotyping of human induced pluripotent stem cellâ $\in$ "derived atrial and ventricular cardiomyocytes. JCI Insight, 2018, 3, .	5.0	214
31	Mapping the secretome of human chondrogenic progenitor cells with mass spectrometry. Annals of Anatomy, 2017, 212, 4-10.	1.9	7
32	Human METTL16 is a <i>N</i> <sup>6</sup> â€methyladenosine (m <sup>6</sup> A) methyltransferase that targets preâ€mRNAs and various nonâ€coding RNAs. EMBO Reports, 2017, 18, 2004-2014.	4.5	481
33	Shedding light on biofilm formation of <i>Halobacterium salinarum</i> R1 by SWATH‣C/MS/MS analysis of planktonic and sessile cells. Proteomics, 2017, 17, 1600111.	2.2	22
34	DPP9 is a novel component of the N-end rule pathway targeting the tyrosine kinase Syk. ELife, 2016, 5, .	6.0	37
35	Active and Repressive Chromatin-Associated Proteome after MPA Treatment and the Role of Midkine in Epithelial Monolayer Permeability. International Journal of Molecular Sciences, 2016, 17, 597.	4.1	4
36	Elucidation of tonic and activated B-cell receptor signaling in Burkitt's lymphoma provides insights into regulation of cell survival. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5688-5693.	7.1	44

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37	TIM29 is a subunit of the human carrier translocase required for protein transport. FEBS Letters, 2016, 590, 4147-4158.	2.8	53
38	Hair cell synaptic dysfunction, auditory fatigue and thermal sensitivity in otoferlin Ile515Thr mutants. EMBO Journal, 2016, 35, 2519-2535.	7.8	70
39	Calpain-mediated cleavage of collapsin response mediator protein-2 drives acute axonal degeneration. Scientific Reports, 2016, 6, 37050.	3.3	27
40	Introduction to Proteomics Technologies. Methods in Molecular Biology, 2016, 1362, 3-27.	0.9	11
41	Quantitative Mass Spectrometric Profiling of Cancer-cell Proteomes Derived From Liquid and Solid Tumors. Journal of Visualized Experiments, 2015, , e52435.	0.3	5
42	A deep proteomics perspective on CRM1-mediated nuclear export and nucleocytoplasmic partitioning. ELife, 2015, 4, .	6.0	177
43	Dithiothreitol (DTT) Acts as a Specific, UV-inducible Cross-linker in Elucidation of Protein–RNA Interactions*. Molecular and Cellular Proteomics, 2015, 14, 3196-3210.	3.8	10
44	Studying macromolecular complex stoichiometries by peptideâ€based mass spectrometry. Proteomics, 2015, 15, 862-879.	2.2	19
45	Fourteen years of plant proteomics reflected in ⟨i⟩Proteomics⟨/i⟩: Moving from model species and 2DEâ€based approaches to orphan species and gelâ€free platforms. Proteomics, 2015, 15, 1089-1112.	2.2	91
46	A Complex of Cas Proteins 5, 6, and 7 Is Required for the Biogenesis and Stability of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-derived RNAs (crRNAs) in Haloferax volcanii. Journal of Biological Chemistry, 2014, 289, 7164-7177.	3.4	65
47	Effects of mycophenolate mofetil on kidney function and phosphorylation status of renal proteins in Alport COL4A3-deficient mice. Proteome Science, 2014, 12, 56.	1.7	6
48	Separation methodology to improve proteome coverage depth. Expert Review of Proteomics, 2014, 11, 409-414.	3.0	13
49	The SUMO1-E67 Interacting Loop Peptide Is an Allosteric Inhibitor of the Dipeptidyl Peptidases 8 and 9. Journal of Biological Chemistry, 2013, 288, 32787-32796.	3.4	22
50	Quantitative Clinical Chemistry Proteomics (qCCP) using mass spectrometry: general characteristics and application. Clinical Chemistry and Laboratory Medicine, 2013, 51, 919-35.	2.3	47
51	Quantitative analysis of erythropoietin in human plasma by tandem mass spectrometry. Analytical and Bioanalytical Chemistry, 2011, 400, 2073-2084.	3.7	12
52	Supramolecular structure of the OXPHOS system in highly thermogenic tissue of Arum maculatum. Plant Physiology and Biochemistry, 2010, 48, 265-272.	5.8	23
53	Mapping the binding site of snurportin 1 on native U1 snRNP by cross-linking and mass spectrometry. Nucleic Acids Research, 2010, 38, 5581-5593.	14.5	19
54	Determination of Protein Stoichiometry within Protein Complexes Using Absolute Quantification and Multiple Reaction Monitoring. Analytical Chemistry, 2010, 82, 2784-2796.	6.5	79

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55	Combined Proteomic and Transcriptomic Analysis Identifies Differentially Expressed Pathways Associated to <i>Pinus radiata</i> Needle Maturation. Journal of Proteome Research, 2010, 9, 3954-3979.	3.7	56
56	An ATM- and ATR-dependent checkpoint inactivates spindle assembly by targeting CEP63. Nature Cell Biology, 2009, $11,278-285$ .	10.3	67
57	Changes in the protein profile of Quercus ilex leaves in response to drought stress and recovery. Journal of Plant Physiology, 2009, 166, 233-245.	3.5	101
58	Proteomic Analysis of Pinus radiata Needles: 2-DE Map and Protein Identification by LC/MS/MS and Substitution-Tolerant Database Searching. Journal of Proteome Research, 2008, 7, 2616-2631.	3.7	48
59	Detection of protein-RNA crosslinks by nanoLC-ESI-MS/MS using precursor ion scanning and multiple reaction monitoring (MRM) experiments. Journal of the American Society for Mass Spectrometry, 2007, 18, 869-881.	2.8	28
60	The Holm Oak leaf proteome: Analytical and biological variability in the protein expression level assessed by 2-DE and protein identification tandem mass spectrometryde novosequencing and sequence similarity searching. Proteomics, 2005, 5, 222-234.	2.2	116
61	Proteome modifications of blue mussel (Mytilus edulisâ€L.) gills as an effect of water pollution. Proteomics, 2005, 5, 4958-4963.	2.2	52
62	Tyrosine 394 Is Phosphorylated in Alzheimer's Paired Helical Filament Tau and in Fetal Tau with c-Abl as the Candidate Tyrosine Kinase. Journal of Neuroscience, 2005, 25, 6584-6593.	3.6	168
63	Complete MALDI-ToF MS analysis of cross-linked peptide-RNA oligonucleotides derived from nonlabeled UV-irradiated ribonucleoprotein particles. Rna, 2005, 11, 1915-1930.	3.5	36
64	Towards a standardized human proteome database: Quantitative proteome profiling of living cells. Proteomics, 2004, 4, 1314-1323.	2.2	22
65	Further isoflavonoid metabolites from Millettia griffoniana (Bail). Phytochemistry, 2001, 56, 363-368.	2.9	31
66	Succinopyoverdins - a New Variety of the Pyoverdin Chromophore. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2000, 55, 146-152.	1.4	5