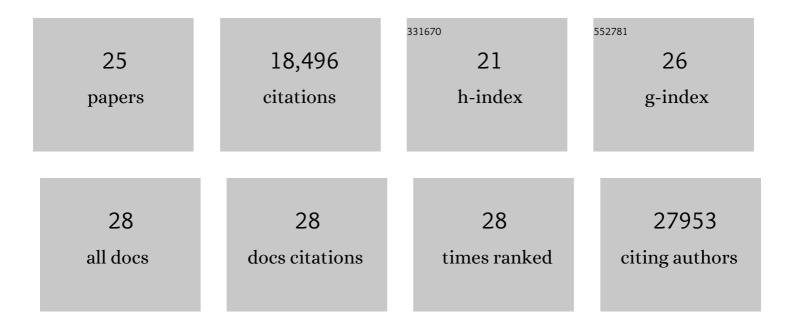
David Lyon

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/379921/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The STRING database in 2021: customizable protein–protein networks, and functional characterization of user-uploaded gene/measurement sets. Nucleic Acids Research, 2021, 49, D605-D612.	14.5	4,274
2	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	27.8	135
3	Analysis of human acetylation stoichiometry defines mechanistic constraints on protein regulation. Nature Communications, 2019, 10, 1055.	12.8	129
4	STRING v11: protein–protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	14.5	12,237
5	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. Angewandte Chemie, 2018, 130, 7491-7496.	2.0	1
6	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. Angewandte Chemie - International Edition, 2018, 57, 7369-7374.	13.8	76
7	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. Nature Communications, 2018, 9, 4744.	12.8	63
8	Systems-wide Analysis of Serine ADP-Ribosylation Reveals Widespread Occurrence and Site-Specific Overlap with Phosphorylation. Cell Reports, 2018, 24, 2493-2505.e4.	6.4	123
9	Site-specific characterization of endogenous SUMOylation across species and organs. Nature Communications, 2018, 9, 2456.	12.8	139
10	Site-specific mapping of the human SUMO proteome reveals co-modification with phosphorylation. Nature Structural and Molecular Biology, 2017, 24, 325-336.	8.2	283
11	Accurate Quantification of Site-specific Acetylation Stoichiometry Reveals the Impact of Sirtuin Deacetylase CobB on the E. coli Acetylome. Molecular and Cellular Proteomics, 2017, 16, 759-769.	3.8	80
12	Specifying RNA-Binding Regions in Proteins by Peptide Cross-Linking and Affinity Purification. Journal of Proteome Research, 2017, 16, 2762-2772.	3.7	37
13	Long-term iron deficiency: Tracing changes in the proteome of different pea (Pisum sativum L.) cultivars. Journal of Proteomics, 2016, 140, 13-23.	2.4	9
14	Drought and Recovery: Independently Regulated Processes Highlighting the Importance of Protein Turnover Dynamics and Translational Regulation in Medicago truncatula. Molecular and Cellular Proteomics, 2016, 15, 1921-1937.	3.8	50
15	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. Science Signaling, 2016, 9, rs9.	3.6	241
16	Comprehensive tissue-specific proteome analysis of drought stress responses in Pennisetum glaucum (L.) R. Br. (Pearl millet). Journal of Proteomics, 2016, 143, 122-135.	2.4	81
17	A Proteomic Workflow Using High-Throughput De Novo Sequencing Towards Complementation of Genome Information for Improved Comparative Crop Science. Methods in Molecular Biology, 2016, 1394, 233-243.	0.9	18
18	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. PeerJ, 2016, 4, e2433.	2.0	56

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#	Article	IF	CITATIONS
19	Avoiding abundance bias in the functional annotation of posttranslationally modified proteins. Nature Methods, 2015, 12, 1003-1004.	19.0	60
20	<i>Medicago truncatula</i> and <i>Glycine max</i> : Different Drought Tolerance and Similar Local Response of the Root Nodule Proteome. Journal of Proteome Research, 2015, 14, 5240-5251.	3.7	24
21	Targeted quantitative analysis of a diurnal RuBisCO subunit expression and translation profile in Chlamydomonas reinhardtii introducing a novel Mass Western approach. Journal of Proteomics, 2015, 113, 143-153.	2.4	34
22	Mass Western for Absolute Quantification of Target Proteins and Considerations About the Instrument of Choice. Methods in Molecular Biology, 2014, 1072, 199-208.	0.9	12
23	Automated Protein Turnover Calculations from 15N Partial Metabolic Labeling LC/MS Shotgun Proteomics Data. PLoS ONE, 2014, 9, e94692.	2.5	8
24	mzGroupAnalyzer-Predicting Pathways and Novel Chemical Structures from Untargeted High-Throughput Metabolomics Data. PLoS ONE, 2014, 9, e96188.	2.5	58
25	Possible Role of Nutritional Priming for Early Salt and Drought Stress Responses in Medicago truncatula. Frontiers in Plant Science, 2012, 3, 285.	3.6	28