

# David Lyon

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/379921/publications.pdf>

Version: 2024-02-01

25  
papers

18,496  
citations

331670

21  
h-index

552781

26  
g-index

28  
all docs

28  
docs citations

28  
times ranked

27953  
citing authors

#	ARTICLE	IF	CITATIONS
1	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , 2019, 47, D607-D613.	14.5	12,237
2	The STRING database in 2021: customizable protein-protein networks, and functional characterization of user-uploaded gene/measurement sets. <i>Nucleic Acids Research</i> , 2021, 49, D605-D612.	14.5	4,274
3	Site-specific mapping of the human SUMO proteome reveals co-modification with phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 325-336.	8.2	283
4	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. <i>Science Signaling</i> , 2016, 9, rs9.	3.6	241
5	Site-specific characterization of endogenous SUMOylation across species and organs. <i>Nature Communications</i> , 2018, 9, 2456.	12.8	139
6	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	27.8	135
7	Analysis of human acetylation stoichiometry defines mechanistic constraints on protein regulation. <i>Nature Communications</i> , 2019, 10, 1055.	12.8	129
8	Systems-wide Analysis of Serine ADP-Ribosylation Reveals Widespread Occurrence and Site-Specific Overlap with Phosphorylation. <i>Cell Reports</i> , 2018, 24, 2493-2505.e4.	6.4	123
9	Comprehensive tissue-specific proteome analysis of drought stress responses in <i>Pennisetum glaucum</i> (L.) R. Br. (Pearl millet). <i>Journal of Proteomics</i> , 2016, 143, 122-135.	2.4	81
10	Accurate Quantification of Site-specific Acetylation Stoichiometry Reveals the Impact of Sirtuin Deacetylase CobB on the <i>E. coli</i> Acetylome. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 759-769.	3.8	80
11	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7369-7374.	13.8	76
12	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744.	12.8	63
13	Avoiding abundance bias in the functional annotation of posttranslationally modified proteins. <i>Nature Methods</i> , 2015, 12, 1003-1004.	19.0	60
14	mzGroupAnalyzer-Predicting Pathways and Novel Chemical Structures from Untargeted High-Throughput Metabolomics Data. <i>PLoS ONE</i> , 2014, 9, e96188.	2.5	58
15	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. <i>PeerJ</i> , 2016, 4, e2433.	2.0	56
16	Drought and Recovery: Independently Regulated Processes Highlighting the Importance of Protein Turnover Dynamics and Translational Regulation in <i>Medicago truncatula</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1921-1937.	3.8	50
17	Specifying RNA-Binding Regions in Proteins by Peptide Cross-Linking and Affinity Purification. <i>Journal of Proteome Research</i> , 2017, 16, 2762-2772.	3.7	37
18	Targeted quantitative analysis of a diurnal RuBisCO subunit expression and translation profile in <i>Chlamydomonas reinhardtii</i> introducing a novel Mass Western approach. <i>Journal of Proteomics</i> , 2015, 113, 143-153.	2.4	34

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19	Possible Role of Nutritional Priming for Early Salt and Drought Stress Responses in <i>Medicago truncatula</i> . <i>Frontiers in Plant Science</i> , 2012, 3, 285.	3.6	28
20	<i>Medicago truncatula</i> and <i>Glycine max</i> : Different Drought Tolerance and Similar Local Response of the Root Nodule Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 5240-5251.	3.7	24
21	A Proteomic Workflow Using High-Throughput De Novo Sequencing Towards Complementation of Genome Information for Improved Comparative Crop Science. <i>Methods in Molecular Biology</i> , 2016, 1394, 233-243.	0.9	18
22	Mass Western for Absolute Quantification of Target Proteins and Considerations About the Instrument of Choice. <i>Methods in Molecular Biology</i> , 2014, 1072, 199-208.	0.9	12
23	Long-term iron deficiency: Tracing changes in the proteome of different pea ( <i>Pisum sativum</i> L.) cultivars. <i>Journal of Proteomics</i> , 2016, 140, 13-23.	2.4	9
24	Automated Protein Turnover Calculations from <sup>15</sup> N Partial Metabolic Labeling LC/MS Shotgun Proteomics Data. <i>PLoS ONE</i> , 2014, 9, e94692.	2.5	8
25	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie</i> , 2018, 130, 7491-7496.	2.0	1