

Michel Zivy

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/7092041/michel-zivy-publications-by-year.pdf>

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

110
papers

5,290
citations

38
h-index

71
g-index

115
ext. papers

6,206
ext. citations

4.9
avg. IF

5.25
L-index

#	Paper	IF	Citations
110	In vivo identification of putative CPK5 substrates in Arabidopsis thaliana.. <i>Plant Science</i> , 2022 , 314, 111123	3.3	1
109	The Nitrate Transporter MtNPF6.8 Is a Master Sensor of Nitrate Signal in the Primary Root Tip of .. <i>Frontiers in Plant Science</i> , 2022 , 13, 832246	6.2	0
108	The Cell Wall Proteome of Reveals Specificities Compared to Those of Flowering Plants.. <i>Frontiers in Plant Science</i> , 2021 , 12, 765846	6.2	1
107	Cell wall proteomic datasets of stems and leaves of. <i>Data in Brief</i> , 2021 , 35, 106818	1.2	1
106	Bradyrhizobium diazoefficiens USDA110 Nodulation of Aeschynomene afraspera Is Associated with Atypical Terminal Bacteroid Differentiation and Suboptimal Symbiotic Efficiency. <i>MSystems</i> , 2021 , 6,	7.6	1
105	Maize metabolome and proteome responses to controlled cold stress partly mimic early-sowing effects in the field and differ from those of Arabidopsis. <i>Plant, Cell and Environment</i> , 2021 , 44, 1504-1521	8.4	10
104	Proteomic data from leaves of twenty-four sunflower genotypes under water deficit. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2021 , 28, 12	1.5	3
103	Proteome adaptations under contrasting soil phosphate regimes of Rhizophagus irregularis engaged in a common mycorrhizal network. <i>Fungal Genetics and Biology</i> , 2021 , 147, 103517	3.9	2
102	Proteomics of developing pea seeds reveals a complex antioxidant network underlying the response to sulfur deficiency and water stress. <i>Journal of Experimental Botany</i> , 2021 , 72, 2611-2626	7	6
101	An integrative Study Showing the Adaptation to Sub-Optimal Growth Conditions of Natural Populations of : A Focus on Cell Wall Changes. <i>Cells</i> , 2020 , 9,	7.9	4
100	Metabolic leaf responses to potassium availability in oil palm (Elaeis guineensis Jacq.) trees grown in the field. <i>Environmental and Experimental Botany</i> , 2020 , 175, 104062	5.9	4
99	Comparative quantitative proteomics of osmotic signal transduction mutants in Botrytis cinerea explain mutant phenotypes and highlight interaction with cAMP and Ca signalling pathways. <i>Journal of Proteomics</i> , 2020 , 212, 103580	3.9	2
98	Transcriptomic and proteomic data in developing tomato fruit. <i>Data in Brief</i> , 2020 , 28, 105015	1.2	7
97	Protein synthesis increases with photosynthesis via the stimulation of translation initiation. <i>Plant Science</i> , 2020 , 291, 110352	5.3	5
96	A systems genetics approach reveals environment-dependent associations between SNPs, protein coexpression, and drought-related traits in maize. <i>Genome Research</i> , 2020 , 30, 1593-1604	9.7	3
95	Integrating multiple omics to identify common and specific molecular changes occurring in Arabidopsis under chronic nitrate and sulfate limitations. <i>Journal of Experimental Botany</i> , 2020 , 71, 6471-6490	7.4	4
94	Deciphering the Infectious Process of in Lupin through Transcriptomic and Proteomic Analysis. <i>Microorganisms</i> , 2020 , 8,	4.9	9

93	Proteomic and lipidomic analyses of the Arabidopsis atg5 autophagy mutant reveal major changes in endoplasmic reticulum and peroxisome metabolisms and in lipid composition. <i>New Phytologist</i> , 2019 , 223, 1461-1477	9.8	26
92	Modeling Protein Destiny in Developing Fruit. <i>Plant Physiology</i> , 2019 , 180, 1709-1724	6.6	15
91	Metabolic responses to potassium availability and waterlogging reshape respiration and carbon use efficiency in oil palm. <i>New Phytologist</i> , 2019 , 223, 310-322	9.8	25
90	Identification of Hanks-Type Kinase PknB-Specific Targets in the Phosphoproteome. <i>Frontiers in Microbiology</i> , 2019 , 10, 1329	5.7	7
89	Proteomic Data Integration Highlights Central Actors Involved in Einkorn (ssp.) Grain Filling in Relation to Grain Storage Protein Composition. <i>Frontiers in Plant Science</i> , 2019 , 10, 832	6.2	1
88	Peptide filtering differently affects the performances of XIC-based quantification methods. <i>Journal of Proteomics</i> , 2019 , 193, 131-141	3.9	6
87	Control of the ethylene signaling pathway prevents plant defenses during intracellular accommodation of the rhizobia. <i>New Phytologist</i> , 2018 , 219, 310-323	9.8	28
86	Increases in activity of proteasome and papain-like cysteine protease in Arabidopsis autophagy mutants: back-up compensatory effect or cell-death promoting effect?. <i>Journal of Experimental Botany</i> , 2018 , 69, 1369-1385	7	37
85	The plasma membrane proteome of Medicago truncatula roots as modified by arbuscular mycorrhizal symbiosis. <i>Mycorrhiza</i> , 2018 , 28, 1-16	3.9	32
84	Evaluation of Optimized Tube-Gel Methods of Sample Preparation for Large-Scale Plant Proteomics. <i>Proteomes</i> , 2018 , 6,	4.6	13
83	αAmylase Mediates Host Acceptance in the Braconid Parasitoid Cotesia flavipes. <i>Journal of Chemical Ecology</i> , 2018 , 44, 1030-1039	2.7	5
82	Cell wall proteome analysis of Arabidopsis thaliana mature stems. <i>Proteomics</i> , 2017 , 17, 1600449	4.8	22
81	Grain subproteome responses to nitrogen and sulfur supply in diploid wheat Triticum monococcum ssp. monococcum. <i>Plant Journal</i> , 2017 , 91, 894-910	6.9	22
80	XITandemPipeline: A Tool to Manage Sequence Redundancy for Protein Inference and Phosphosite Identification. <i>Journal of Proteome Research</i> , 2017 , 16, 494-503	5.6	98
79	Cell wall modifications of two Arabidopsis thaliana ecotypes, Col and Sha, in response to sub-optimal growth conditions: An integrative study. <i>Plant Science</i> , 2017 , 263, 183-193	5.3	12
78	Proline Hydroxylation in Cell Wall Proteins: Is It Yet Possible to Define Rules?. <i>Frontiers in Plant Science</i> , 2017 , 8, 1802	6.2	8
77	A Combination of Histological, Physiological, and Proteomic Approaches Shed Light on Seed Desiccation Tolerance of the Basal Angiosperm Amborella trichopoda. <i>Proteomes</i> , 2017 , 5,	4.6	5
76	Phosphoproteomic Analysis of Isolated Mitochondria in Yeast. <i>Methods in Molecular Biology</i> , 2017 , 1636, 283-299	1.4	5

75	An enlarged cell wall proteome of Arabidopsis thaliana rosettes. <i>Proteomics</i> , 2016 , 16, 3183-3187	4.8	22
74	The Arabidopsis TOR Kinase Specifically Regulates the Expression of Nuclear Genes Coding for Plastidic Ribosomal Proteins and the Phosphorylation of the Cytosolic Ribosomal Protein S6. <i>Frontiers in Plant Science</i> , 2016 , 7, 1611	6.2	70
73	Arabidopsis thaliana root cell wall proteomics: Increasing the proteome coverage using a combinatorial peptide ligand library and description of unexpected Hyp in peroxidase amino acid sequences. <i>Proteomics</i> , 2016 , 16, 491-503	4.8	38
72	Concerted Changes in the Phosphoproteome and Metabolome Under Different CO ₂ /O ₂ Gaseous Conditions in Arabidopsis Rosettes. <i>Plant and Cell Physiology</i> , 2016 , 57, 1544-1556	4.9	16
71	Thousand and one ways to quantify and compare protein abundances in label-free bottom-up proteomics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 883-95	4	48
70	A Systems Approach to Elucidate Heterosis of Protein Abundances in Yeast. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2056-71	7.6	27
69	The quest for tolerant varieties: the importance of integrating "omics" techniques to phenotyping. <i>Frontiers in Plant Science</i> , 2015 , 6, 448	6.2	56
68	The Amborella vacuolar processing enzyme family. <i>Frontiers in Plant Science</i> , 2015 , 6, 618	6.2	10
67	Differential Protein Phosphorylation Regulates Chloroplast Movement in Response to Strong Light and Darkness in Arabidopsis thaliana. <i>Plant Molecular Biology Reporter</i> , 2014 , 32, 987-1001	1.7	4
66	Quantitative variations of the mitochondrial proteome and phosphoproteome during fermentative and respiratory growth in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteomics</i> , 2014 , 106, 140-50	3.9	28
65	Phosphoproteome profiles of the phytopathogenic fungi <i>Alternaria brassicicola</i> and <i>Botrytis cinerea</i> during exponential growth in axenic cultures. <i>Proteomics</i> , 2014 , 14, 1639-45	4.8	12
64	Photosynthetic activity influences cellulose biosynthesis and phosphorylation of proteins involved therein in Arabidopsis leaves. <i>Journal of Experimental Botany</i> , 2014 , 65, 4997-5010	7	34
63	The membrane proteome of <i>Medicago truncatula</i> roots displays qualitative and quantitative changes in response to arbuscular mycorrhizal symbiosis. <i>Journal of Proteomics</i> , 2014 , 108, 354-68	3.9	35
62	An integrated "omics" approach to the characterization of maize (<i>Zea mays</i> L.) mutants deficient in the expression of two genes encoding cytosolic glutamine synthetase. <i>BMC Genomics</i> , 2014 , 15, 1005	4.5	14
61	Omics technologies provide new insights into the molecular physiopathology of equine osteochondrosis. <i>BMC Genomics</i> , 2014 , 15, 947	4.5	8
60	An extensive proteome map of tomato (<i>Solanum lycopersicum</i>) fruit pericarp. <i>Proteomics</i> , 2013 , 13, 3059-63	4.8	19
59	Yeast proteome variations reveal different adaptive responses to grape must fermentation. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1368-83	8.3	25
58	<i>Brachypodium distachyon</i> as a model plant toward improved biofuel crops: Search for secreted proteins involved in biogenesis and disassembly of cell wall polymers. <i>Proteomics</i> , 2013 , 13, 2438-54	4.8	41

57	Management and dissemination of MS proteomic data with PROTiCdb: example of a quantitative comparison between methods of protein extraction. <i>Proteomics</i> , 2013 , 13, 1457-66	4.8	20
56	Photosynthetic control of Arabidopsis leaf cytoplasmic translation initiation by protein phosphorylation. <i>PLoS ONE</i> , 2013 , 8, e70692	3.7	45
55	Phosphoproteome dynamics upon changes in plant water status reveal early events associated with rapid growth adjustment in maize leaves. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 957-72	7.6	84
54	The use of metabolomics integrated with transcriptomic and proteomic studies for identifying key steps involved in the control of nitrogen metabolism in crops such as maize. <i>Journal of Experimental Botany</i> , 2012 , 63, 5017-33	7	145
53	Including shared peptides for estimating protein abundances: a significant improvement for quantitative proteomics. <i>Proteomics</i> , 2012 , 12, 2797-801	4.8	18
52	A method for proteomic analysis of equine subchondral bone and epiphyseal cartilage. <i>Proteomics</i> , 2012 , 12, 1870-4	4.8	5
51	Oil body proteins sequentially accumulate throughout seed development in Brassica napus. <i>Journal of Plant Physiology</i> , 2011 , 168, 2015-20	3.6	39
50	Time to articulate a vision for the future of plant proteomics - A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO). <i>Proteomics</i> , 2011 , 11, 1559-68	4.8	24
49	Dynamics of post-translational modifications and protein stability in the stroma of Chlamydomonas reinhardtii chloroplasts. <i>Proteomics</i> , 2011 , 11, 1734-50	4.8	45
48	Analysis of the xylem sap proteome of Brassica oleracea reveals a high content in secreted proteins. <i>Proteomics</i> , 2011 , 11, 1798-813	4.8	71
47	MassChroQ: a versatile tool for mass spectrometry quantification. <i>Proteomics</i> , 2011 , 11, 3572-7	4.8	162
46	Combining various strategies to increase the coverage of the plant cell wall glycoproteome. <i>Phytochemistry</i> , 2011 , 72, 1109-23	4	60
45	The ZmASR1 protein influences branched-chain amino acid biosynthesis and maintains kernel yield in maize under water-limited conditions. <i>Plant Physiology</i> , 2011 , 157, 917-36	6.6	86
44	Phospho-site mapping, genetic and in planta activation studies reveal key aspects of the different phosphorylation mechanisms involved in activation of SnRK2s. <i>Plant Journal</i> , 2010 , 63, 778-90	6.9	59
43	The Arabidopsis ABA-activated kinase OST1 phosphorylates the bZIP transcription factor ABF3 and creates a 14-3-3 binding site involved in its turnover. <i>PLoS ONE</i> , 2010 , 5, e13935	3.7	147
42	Molecular and evolutionary bases of within-patient genotypic and phenotypic diversity in Escherichia coli extraintestinal infections. <i>PLoS Pathogens</i> , 2010 , 6, e1001125	7.6	55
41	Cotranslational proteolysis dominates glutathione homeostasis to support proper growth and development. <i>Plant Cell</i> , 2009 , 21, 3296-314	11.6	29
40	Phosphorylation of the Arabidopsis AtrbohF NADPH oxidase by OST1 protein kinase. <i>FEBS Letters</i> , 2009 , 583, 2982-6	3.8	317

39	Comparative proteomics of leaf, stem, and root tissues of synthetic Brassica napus. <i>Proteomics</i> , 2009 , 9, 793-9	4.8	28
38	Extent of N-terminal modifications in cytosolic proteins from eukaryotes. <i>Proteomics</i> , 2008 , 8, 2809-31	4.8	124
37	A method based on bead flows for spot detection on 2-D gel images. <i>Proteomics</i> , 2008 , 8, 4914-8	4.8	11
36	The PROTiCdb database for 2-DE proteomics. <i>Methods in Molecular Biology</i> , 2007 , 355, 279-303	1.4	10
35	A sub-proteome of Arabidopsis thaliana mature stems trapped on Concanavalin A is enriched in cell wall glycoside hydrolases. <i>Journal of Experimental Botany</i> , 2007 , 58, 2503-12	7	104
34	Quantitative analysis of 2D gels. <i>Methods in Molecular Biology</i> , 2007 , 355, 175-94	1.4	7
33	Total protein extraction with TCA-acetone. <i>Methods in Molecular Biology</i> , 2007 , 355, 1-8	1.4	84
32	Plant Proteome Responses to Abiotic Stress 2007 , 346-364		5
31	Proteomic analysis of different mutant genotypes of Arabidopsis led to the identification of 11 proteins correlating with adventitious root development. <i>Plant Physiology</i> , 2006 , 140, 349-64	6.6	91
30	Two cytosolic glutamine synthetase isoforms of maize are specifically involved in the control of grain production. <i>Plant Cell</i> , 2006 , 18, 3252-74	11.6	331
29	A mass spectrometric approach to identify arbuscular mycorrhiza-related proteins in root plasma membrane fractions. <i>Proteomics</i> , 2006 , 6 Suppl 1, S145-55	4.8	56
28	Maize cystatins respond to developmental cues, cold stress and drought. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005 , 1729, 186-99		62
27	PROTiCdb: a web-based application to store, track, query, and compare plant proteome data. <i>Proteomics</i> , 2005 , 5, 2069-81	4.8	39
26	Water deficits affect caffeate O-methyltransferase, lignification, and related enzymes in maize leaves. A proteomic investigation. <i>Plant Physiology</i> , 2005 , 137, 949-60	6.6	166
25	Protein composition of oil bodies in Arabidopsis thaliana ecotype WS. <i>Plant Physiology and Biochemistry</i> , 2004 , 42, 501-9	5.4	143
24	Deciphering genetic variations of proteome responses to water deficit in maize leaves. <i>Plant Physiology and Biochemistry</i> , 2004 , 42, 1003-11	5.4	74
23	A two-dimensional proteome map of maize endosperm. <i>Phytochemistry</i> , 2004 , 65, 1609-18	4	89
22	Combining proteomic and genetic studies in plants. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002 , 782, 137-49	3.2	48

21	Genetic variability of proteome expression and metabolic control. <i>Plant Physiology and Biochemistry</i> , 2001 , 39, 271-283	5.4	39
20	Comparative proteomics to establish genetic relationships in the Brassicaceae family. <i>Proteomics</i> , 2001 , 1, 1457-62	4.8	28
19	Proteomics: a link between genomics, genetics and physiology. <i>Plant Molecular Biology</i> , 2000 , 44, 575-80	4.6	90
18	Genetics of the Maize Proteome. <i>Stadler Genetics Symposia Series</i> , 2000 , 123-139		1
17	Proteomics for genetic and physiological studies in plants. <i>Electrophoresis</i> , 1999 , 20, 2013-26	3.6	185
16	Protein changes in response to progressive water deficit in maize . Quantitative variation and polypeptide identification. <i>Plant Physiology</i> , 1998 , 117, 1253-63	6.6	311
15	Potential of two-dimensional electrophoresis in routine identification of closely related durum wheat lines. <i>Electrophoresis</i> , 1997 , 18, 174-81	3.6	17
14	Amino acid analysis of proteins separated by two-dimensional electrophoresis in maize: isoform detection and function identification. <i>Electrophoresis</i> , 1996 , 17, 1393-401	3.6	18
13	Characterizing allelic proteins for genome mapping in maize. <i>Electrophoresis</i> , 1995 , 16, 1289-94	3.6	19
12	Distance indices in a comparison between the A, D, I and R genomes of the Triticeae tribe. <i>Electrophoresis</i> , 1995 , 16, 1295-300	3.6	13
11	Analysis of scaling methods to minimize experimental variations in two-dimensional electrophoresis quantitative data: application to the comparison of maize inbred lines. <i>Electrophoresis</i> , 1993 , 14, 1067-73	3.6	40
10	Study of Gene Expression During in Vitro Culture of Tobacco thin Cell Layers by two-Dimensional Electrophoresis of Proteins 1990 , 207-213		1
9	Homoeology and phylogeny of the A, S, and D genomes of the triticeae. <i>Journal of Molecular Evolution</i> , 1989 , 29, 89-94	3.1	20
8	Peptide mapping of polypeptides separated by two-dimensional electrophoresis: protease digestion directly on the two-dimensional gel followed by electrophoresis in reverse direction. <i>Electrophoresis</i> , 1988 , 9, 339-43	3.6	3
7	Genetic relationships in the Sitopsis section of Triticum and the origin of the B genome of polyploid wheats. <i>Heredity</i> , 1988 , 61, 473-480	3.6	32
6	Two-dimensional gel electrophoresis of proteins as a tool in wheat genetics. <i>Biochimie</i> , 1987 , 69, 781-7	4.6	7
5	Technical improvements in two-dimensional electrophoresis increase the level of genetic variation detected in wheat-seedling proteins. <i>Electrophoresis</i> , 1986 , 7, 52-54	3.6	623
4	Expression du g�nome du Bl tendre r�vis�e par l'�lectrophor�se bidimensionnelle des prot�ines � diff�rents stades de d�veloppement. <i>Bulletin De La Soci�t� Botanique De France Actualit�s Botaniques</i> , 1985 , 132, 97-101		

3	Proteomics for genetic and physiological studies in plants38-51	0
2	Comparative proteomics of osmotic signal transduction mutants in <i>Botrytis cinerea</i> explain loss of pathogenicity phenotypes and highlight interaction with cAMP and Ca ²⁺ -signalling pathways	1
1	Genetics of proteome variation for QTL characterization: application to drought-stress responses in maize	22