

Michel Zivy

List of Publications by Year in descending order

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110
papers

6,787
citations

70961

41
h-index

66788

78
g-index

115
all docs

115
docs citations

115
times ranked

8459
citing authors

#	ARTICLE	IF	CITATIONS
1	In vivo identification of putative CPK5 substrates in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2022, 314, 111121.	1.7	6
2	Comparison of Different Label-Free Techniques for the Semi-Absolute Quantification of Protein Abundance. <i>Proteomes</i> , 2022, 10, 2.	1.7	12
3	The Nitrate Transporter MtNPF6.8 Is a Master Sensor of Nitrate Signal in the Primary Root Tip of <i>Medicago truncatula</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 832246.	1.7	4
4	Dynamics of Protein Phosphorylation during <i>Arabidopsis</i> Seed Germination. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7059.	1.8	1
5	Maize metabolome and proteome responses to controlled cold stress partly mimic early sowing effects in the field and differ from those of <i>Arabidopsis</i> . <i>Plant, Cell and Environment</i> , 2021, 44, 1504-1521.	2.8	32
6	Proteomic data from leaves of twenty-four sunflower genotypes under water deficit. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2021, 28, 12.	0.6	6
7	Proteome adaptations under contrasting soil phosphate regimes of <i>Rhizophagus irregularis</i> engaged in a common mycorrhizal network. <i>Fungal Genetics and Biology</i> , 2021, 147, 103517.	0.9	2
8	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.	2.4	12
9	Cell wall proteomic datasets of stems and leaves of <i>Brachypodium distachyon</i> . <i>Data in Brief</i> , 2021, 35, 106818.	0.5	4
10	<i>Bradyrhizobium diazoefficiens</i> USDA110 Nodulation of <i>Aeschynomene afraspera</i> Is Associated with Atypical Terminal Bacteroid Differentiation and Suboptimal Symbiotic Efficiency. <i>MSystems</i> , 2021, 6, .	1.7	4
11	The Cell Wall Proteome of <i>Marchantia polymorpha</i> Reveals Specificities Compared to Those of Flowering Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 765846.	1.7	7
12	Comparative quantitative proteomics of osmotic signal transduction mutants in <i>Botrytis cinerea</i> explain mutant phenotypes and highlight interaction with cAMP and Ca ²⁺ signalling pathways. <i>Journal of Proteomics</i> , 2020, 212, 103580.	1.2	5
13	Transcriptomic and proteomic data in developing tomato fruit. <i>Data in Brief</i> , 2020, 28, 105015.	0.5	17
14	Protein synthesis increases with photosynthesis via the stimulation of translation initiation. <i>Plant Science</i> , 2020, 291, 110352.	1.7	10
15	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.	2.4	10
16	Integrating multiple omics to identify common and specific molecular changes occurring in <i>Arabidopsis</i> under chronic nitrate and sulfate limitations. <i>Journal of Experimental Botany</i> , 2020, 71, 6471-6490.	2.4	18
17	Deciphering the Infectious Process of <i>Colletotrichum lupini</i> in Lupin through Transcriptomic and Proteomic Analysis. <i>Microorganisms</i> , 2020, 8, 1621.	1.6	18
18	An Integrative Study Showing the Adaptation to Sub-Optimal Growth Conditions of Natural Populations of <i>Arabidopsis thaliana</i> : A Focus on Cell Wall Changes. <i>Cells</i> , 2020, 9, 2249.	1.8	7

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19	Metabolic leaf responses to potassium availability in oil palm (<i>Elaeis guineensis</i> Jacq.) trees grown in the field. <i>Environmental and Experimental Botany</i> , 2020, 175, 104062.	2.0	12
20	Identification of Hanks-Type Kinase PknB-Specific Targets in the <i>Streptococcus thermophilus</i> Phosphoproteome. <i>Frontiers in Microbiology</i> , 2019, 10, 1329.	1.5	15
21	Proteomic Data Integration Highlights Central Actors Involved in Einkorn (<i>Triticum monococcum</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Ov Science, 2019, 10, 832.	1.7	2
22	Proteomic and lipidomic analyses of the <i>Arabidopsis</i> <i>atg5</i> autophagy mutant reveal major changes in endoplasmic reticulum and peroxisome metabolisms and in lipid composition. <i>New Phytologist</i> , 2019, 223, 1461-1477.	3.5	54
23	Modeling Protein Destiny in Developing Fruit. <i>Plant Physiology</i> , 2019, 180, 1709-1724.	2.3	33
24	Metabolic responses to potassium availability and waterlogging reshape respiration and carbon use efficiency in oil palm. <i>New Phytologist</i> , 2019, 223, 310-322.	3.5	41
25	Peptide filtering differently affects the performances of XIC-based quantification methods. <i>Journal of Proteomics</i> , 2019, 193, 131-141.	1.2	9
26	Control of the ethylene signaling pathway prevents plant defenses during intracellular accommodation of the rhizobia. <i>New Phytologist</i> , 2018, 219, 310-323.	3.5	46
27	Increases in activity of proteasome and papain-like cysteine protease in <i>Arabidopsis</i> autophagy mutants: back-up compensatory effect or cell-death promoting effect?. <i>Journal of Experimental Botany</i> , 2018, 69, 1369-1385.	2.4	55
28	The plasma membrane proteome of <i>Medicago truncatula</i> roots as modified by arbuscular mycorrhizal symbiosis. <i>Mycorrhiza</i> , 2018, 28, 1-16.	1.3	44
29	Evaluation of Optimized Tube-Gel Methods of Sample Preparation for Large-Scale Plant Proteomics. <i>Proteomes</i> , 2018, 6, 6.	1.7	21
30	Î±-Amylase Mediates Host Acceptance in the Braconid Parasitoid <i>Cotesia flavipes</i> . <i>Journal of Chemical Ecology</i> , 2018, 44, 1030-1039.	0.9	9
31	Cell wall proteome analysis of <i>Arabidopsis thaliana</i> mature stems. <i>Proteomics</i> , 2017, 17, 1600449.	1.3	27
32	Grain subproteome responses to nitrogen and sulfur supply in diploid wheat (<i>Triticum monococcum</i> ssp. <i>monococcum</i>). <i>Plant Journal</i> , 2017, 91, 894-910.	2.8	54
33	X!TandemPipeline: A Tool to Manage Sequence Redundancy for Protein Inference and Phosphosite Identification. <i>Journal of Proteome Research</i> , 2017, 16, 494-503.	1.8	184
34	Cell wall modifications of two <i>Arabidopsis thaliana</i> ecotypes, Col and Sha, in response to sub-optimal growth conditions: An integrative study. <i>Plant Science</i> , 2017, 263, 183-193.	1.7	26
35	Proline Hydroxylation in Cell Wall Proteins: Is It Yet Possible to Define Rules?. <i>Frontiers in Plant Science</i> , 2017, 8, 1802.	1.7	34
36	A Combination of Histological, Physiological, and Proteomic Approaches Shed Light on Seed Desiccation Tolerance of the Basal Angiosperm <i>Amborella trichopoda</i> . <i>Proteomes</i> , 2017, 5, 19.	1.7	11

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37	Phosphoproteomic Analysis of Isolated Mitochondria in Yeast. <i>Methods in Molecular Biology</i> , 2017, 1636, 283-299.	0.4	8
38	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.	1.7	113
39	<i>Arabidopsis thaliana</i> 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.	1.3	45
40	Concerted changes in phosphoproteome and metabolome under different CO ₂ /O ₂ gaseous conditions in <i>Arabidopsis</i> rosettes. <i>Plant and Cell Physiology</i> , 2016, 57, pcw086.	1.5	19
41	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, 883-895.	1.1	66
42	An enlarged cell wall proteome of <i>Arabidopsis thaliana</i> rosettes. <i>Proteomics</i> , 2016, 16, 3183-3187.	1.3	31
43	The quest for tolerant varieties: the importance of integrating omics techniques to phenotyping. <i>Frontiers in Plant Science</i> , 2015, 6, 448.	1.7	67
44	The Amborella vacuolar processing enzyme family. <i>Frontiers in Plant Science</i> , 2015, 6, 618.	1.7	14
45	A Systems Approach to Elucidate Heterosis of Protein Abundances in Yeast. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2056-2071.	2.5	42
46	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.	1.2	15
47	Omics technologies provide new insights into the molecular physiopathology of equine osteochondrosis. <i>BMC Genomics</i> , 2014, 15, 947.	1.2	9
48	Differential Protein Phosphorylation Regulates Chloroplast Movement in Response to Strong Light and Darkness in <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology Reporter</i> , 2014, 32, 987-1001.	1.0	11
49	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, 140-150.	1.2	38
50	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, 1639-1645.	1.3	13
51	Photosynthetic activity influences cellulose biosynthesis and phosphorylation of proteins involved therein in <i>Arabidopsis</i> leaves. <i>Journal of Experimental Botany</i> , 2014, 65, 4997-5010.	2.4	41
52	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, 354-368.	1.2	49
53	An extensive proteome map of tomato (<i>Solanum lycopersicum</i>) fruit pericarp. <i>Proteomics</i> , 2013, 13, 3059-3063.	1.3	28
54	Yeast Proteome Variations Reveal Different Adaptive Responses to Grape Must Fermentation. <i>Molecular Biology and Evolution</i> , 2013, 30, 1368-1383.	3.5	36

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55	<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, 2438-2454.	1.3	46
56	Management and dissemination of MS proteomic data with PROTiCdb: Example of a quantitative comparison between methods of protein extraction. <i>Proteomics</i> , 2013, 13, 1457-1466.	1.3	25
57	Photosynthetic Control of Arabidopsis Leaf Cytoplasmic Translation Initiation by Protein Phosphorylation. <i>PLoS ONE</i> , 2013, 8, e70692.	1.1	55
58	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, 957-972.	2.5	100
59	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, 5017-5033.	2.4	175
60	Including shared peptides for estimating protein abundances: A significant improvement for quantitative proteomics. <i>Proteomics</i> , 2012, 12, 2797-2801.	1.3	27
61	A method for proteomic analysis of equine subchondral bone and epiphyseal cartilage. <i>Proteomics</i> , 2012, 12, 1870-1874.	1.3	7
62	Oil body proteins sequentially accumulate throughout seed development in <i>Brassica napus</i> . <i>Journal of Plant Physiology</i> , 2011, 168, 2015-2020.	1.6	49
63	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, 1559-1568.	1.3	31
64	Dynamics of post-translational modifications and protein stability in the stroma of <i>Chlamydomonas reinhardtii</i> chloroplasts. <i>Proteomics</i> , 2011, 11, 1734-1750.	1.3	51
65	Analysis of the xylem sap proteome of <i>Brassica oleracea</i> reveals a high content in secreted proteins. <i>Proteomics</i> , 2011, 11, 1798-1813.	1.3	94
66	MassChroQ: A versatile tool for mass spectrometry quantification. <i>Proteomics</i> , 2011, 11, 3572-3577.	1.3	255
67	Combining various strategies to increase the coverage of the plant cell wall glycoproteome. <i>Phytochemistry</i> , 2011, 72, 1109-1123.	1.4	66
68	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, 917-936.	2.3	108
69	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, 778-790.	2.8	69
70	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.	1.1	197
71	Molecular and Evolutionary Bases of Within-Patient Genotypic and Phenotypic Diversity in <i>Escherichia coli</i> Extraintestinal Infections. <i>PLoS Pathogens</i> , 2010, 6, e1001125.	2.1	68
72	Cotranslational Proteolysis Dominates Glutathione Homeostasis to Support Proper Growth and Development. <i>Plant Cell</i> , 2009, 21, 3296-3314.	3.1	38

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73	Phosphorylation of the Arabidopsis AtrbohF NADPH oxidase by OST1 protein kinase. FEBS Letters, 2009, 583, 2982-2986.	1.3	373
74	Comparative proteomics of leaf, stem, and root tissues of synthetic <i>Brassica napus</i> . Proteomics, 2009, 9, 793-799.	1.3	28
75	Extent of N-terminal modifications in cytosolic proteins from eukaryotes. Proteomics, 2008, 8, 2809-2831.	1.3	136
76	A method based on bead flows for spot detection on 2D gel images. Proteomics, 2008, 8, 4914-4918.	1.3	12
77	Quantitative Analysis of 2D Gels. , 2007, 355, 175-194.		8
78	Total Protein Extraction with TCA-Acetone. , 2007, 355, 1-8.		115
79	The PROTIcDb Database for 2-DE Proteomics. , 2007, 355, 279-304.		12
80	A sub-proteome of Arabidopsis thaliana mature stems trapped on Concanavalin A is enriched in cell wall glycoside hydrolases. Journal of Experimental Botany, 2007, 58, 2503-2512.	2.4	111
81	Plant Proteome Responses to Abiotic Stress. , 2007, , 346-364.		8
82	Two Cytosolic Glutamine Synthetase Isoforms of Maize Are Specifically Involved in the Control of Grain Production. Plant Cell, 2006, 18, 3252-3274.	3.1	416
83	A mass spectrometric approach to identify arbuscular mycorrhiza-related proteins in root plasma membrane fractions. Proteomics, 2006, 6, S145-S155.	1.3	71
84	Proteomic Analysis of Different Mutant Genotypes of Arabidopsis Led to the Identification of 11 Proteins Correlating with Adventitious Root Development. Plant Physiology, 2006, 140, 349-364.	2.3	104
85	Maize cystatins respond to developmental cues, cold stress and drought. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2005, 1729, 186-199.	2.4	73
86	PROTIcDb: A web-based application to store, track, query, and compare plant proteome data. Proteomics, 2005, 5, 2069-2081.	1.3	42
87	Water Deficits Affect Caffeate O-Methyltransferase, Lignification, and Related Enzymes in Maize Leaves. A Proteomic Investigation. Plant Physiology, 2005, 137, 949-960.	2.3	192
88	Protein composition of oil bodies in Arabidopsis thaliana ecotype WS. Plant Physiology and Biochemistry, 2004, 42, 501-509.	2.8	176
89	Deciphering genetic variations of proteome responses to water deficit in maize leaves. Plant Physiology and Biochemistry, 2004, 42, 1003-1011.	2.8	82
90	A two-dimensional proteome map of maize endosperm. Phytochemistry, 2004, 65, 1609-1618.	1.4	96

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91	Combining proteomic and genetic studies in plants. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002, 782, 137-149.	1.2	53
92	Genetic variability of proteome expression and metabolic control. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 271-283.	2.8	45
93	Comparative proteomics to establish genetic relationships in the Brassicaceae family. <i>Proteomics</i> , 2001, 1, 1457-1462.	1.3	32
94	Proteomics: a link between genomics, genetics and physiology. <i>Plant Molecular Biology</i> , 2000, 44, 575-580.	2.0	108
95	Genetics of the Maize Proteome. <i>Stadler Genetics Symposia Series</i> , 2000, , 123-139.	0.0	1
96	Proteomics for genetic and physiological studies in plants. <i>Electrophoresis</i> , 1999, 20, 2013-2026.	1.3	203
97	Protein Changes in Response to Progressive Water Deficit in Maize1. <i>Plant Physiology</i> , 1998, 117, 1253-1263.	2.3	350
98	Potential of two-dimensional electrophoresis in routine identification of closely related durum wheat lines. <i>Electrophoresis</i> , 1997, 18, 174-181.	1.3	23
99	Amino acid analysis of proteins separated by two-dimensional electrophoresis in maize: Isoform detection and function identification. <i>Electrophoresis</i> , 1996, 17, 1393-1401.	1.3	19
100	Characterizing allelic proteins for genome mapping in maize. <i>Electrophoresis</i> , 1995, 16, 1289-1294.	1.3	22
101	Distance indices in a comparison between the A, D, I and R genomes of the Triticeae tribe. <i>Electrophoresis</i> , 1995, 16, 1295-1300.	1.3	18
102	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, 1067-1073.	1.3	42
103	Study of Gene Expression During in Vitro Culture of Tobacco thin Cell Layers by two-Dimensional Electrophoresis of Proteins. , 1990, , 207-213.		1
104	Homoeology and phylogeny of the A, S, and D genomes of the triticeae. <i>Journal of Molecular Evolution</i> , 1989, 29, 89-94.	0.8	26
105	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, 339-343.	1.3	3
106	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.	1.2	66
107	Two-dimensional gel electrophoresis of proteins as a tool in wheat genetics. <i>Biochimie</i> , 1987, 69, 781-787.	1.3	7
108	Technical improvements in two-dimensional electrophoresis increase the level of genetic variation detected in wheat-seedling proteins. <i>Electrophoresis</i> , 1986, 7, 52-54.	1.3	728

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109	Expression du g�nome du Bl� tendre r�v�l�e par l�lectrophor�se bidimensionnelle des prot�ines � diff�rents stades de d�veloppement. Bulletin De La Soci�t� Botanique De France Actualit�s Botaniques.0 1985, 132, 97-101.		0
110	Genetics of proteome variation for QTL characterization: application to drought-stress responses in maize. , 0, .		24