

Michel Zivy

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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 | 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 |
| 109 | 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 |
| 108 | Phosphorylation of the Arabidopsis AtrbohF NADPH oxidase by OST1 protein kinase. <i>FEBS Letters</i> , 2009 , 583, 2982-6 | 3.8 | 317 |
| 107 | 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 |
| 106 | Proteomics for genetic and physiological studies in plants. <i>Electrophoresis</i> , 1999 , 20, 2013-26 | 3.6 | 185 |
| 105 | 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 |
| 104 | MassChroQ: a versatile tool for mass spectrometry quantification. <i>Proteomics</i> , 2011 , 11, 3572-7 | 4.8 | 162 |
| 103 | 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 |
| 102 | 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 |
| 101 | Protein composition of oil bodies in Arabidopsis thaliana ecotype WS. <i>Plant Physiology and Biochemistry</i> , 2004 , 42, 501-9 | 5.4 | 143 |
| 100 | Extent of N-terminal modifications in cytosolic proteins from eukaryotes. <i>Proteomics</i> , 2008 , 8, 2809-31 | 4.8 | 124 |
| 99 | 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 |
| 98 | X!TandemPipeline: 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 |
| 97 | 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 |
| 96 | Proteomics: a link between genomics, genetics and physiology. <i>Plant Molecular Biology</i> , 2000 , 44, 575-80 | 4.6 | 90 |
| 95 | A two-dimensional proteome map of maize endosperm. <i>Phytochemistry</i> , 2004 , 65, 1609-18 | 4 | 89 |
| 94 | 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 |

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|----|--|-----|----|
| 93 | 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 |
| 92 | Total protein extraction with TCA-acetone. <i>Methods in Molecular Biology</i> , 2007 , 355, 1-8 | 1.4 | 84 |
| 91 | 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 |
| 90 | 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 |
| 89 | 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 |
| 88 | Maize cystatins respond to developmental cues, cold stress and drought. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005 , 1729, 186-99 | | 62 |
| 87 | Combining various strategies to increase the coverage of the plant cell wall glycoproteome. <i>Phytochemistry</i> , 2011 , 72, 1109-23 | 4 | 60 |
| 86 | 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 |
| 85 | 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 |
| 84 | 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 |
| 83 | 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 |
| 82 | 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 |
| 81 | 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 |
| 80 | Photosynthetic control of Arabidopsis leaf cytoplasmic translation initiation by protein phosphorylation. <i>PLoS ONE</i> , 2013 , 8, e70692 | 3.7 | 45 |
| 79 | 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 |
| 78 | Brachypodium distachyon 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 |
| 77 | 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 |
| 76 | Oil body proteins sequentially accumulate throughout seed development in Brassica napus. <i>Journal of Plant Physiology</i> , 2011 , 168, 2015-20 | 3.6 | 39 |

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|----|---|------|----|
| 75 | PROTICdb: a web-based application to store, track, query, and compare plant proteome data. <i>Proteomics</i> , 2005 , 5, 2069-81 | 4.8 | 39 |
| 74 | Genetic variability of proteome expression and metabolic control. <i>Plant Physiology and Biochemistry</i> , 2001 , 39, 271-283 | 5.4 | 39 |
| 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 | 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 |
| 71 | The membrane proteome of Medicago truncatula roots displays qualitative and quantitative changes in response to arbuscular mycorrhizal symbiosis. <i>Journal of Proteomics</i> , 2014 , 108, 354-68 | 3.9 | 35 |
| 70 | 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 |
| 69 | The plasma membrane proteome of Medicago truncatula roots as modified by arbuscular mycorrhizal symbiosis. <i>Mycorrhiza</i> , 2018 , 28, 1-16 | 3.9 | 32 |
| 68 | 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 |
| 67 | Cotranslational proteolysis dominates glutathione homeostasis to support proper growth and development. <i>Plant Cell</i> , 2009 , 21, 3296-314 | 11.6 | 29 |
| 66 | 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 |
| 65 | Quantitative variations of the mitochondrial proteome and phosphoproteome during fermentative and respiratory growth in Saccharomyces cerevisiae. <i>Journal of Proteomics</i> , 2014 , 106, 140-50 | 3.9 | 28 |
| 64 | Comparative proteomics of leaf, stem, and root tissues of synthetic Brassica napus. <i>Proteomics</i> , 2009 , 9, 793-9 | 4.8 | 28 |
| 63 | Comparative proteomics to establish genetic relationships in the Brassicaceae family. <i>Proteomics</i> , 2001 , 1, 1457-62 | 4.8 | 28 |
| 62 | A Systems Approach to Elucidate Heterosis of Protein Abundances in Yeast. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2056-71 | 7.6 | 27 |
| 61 | 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 |
| 60 | 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 |
| 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 | 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 |

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| 57 | Cell wall proteome analysis of Arabidopsis thaliana mature stems. <i>Proteomics</i> , 2017 , 17, 1600449 | 4.8 | 22 |
| 56 | 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 |
| 55 | An enlarged cell wall proteome of Arabidopsis thaliana rosettes. <i>Proteomics</i> , 2016 , 16, 3183-3187 | 4.8 | 22 |
| 54 | Genetics of proteome variation for QTL characterization: application to drought-stress responses in maize | | 22 |
| 53 | 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 |
| 52 | 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 |
| 51 | An extensive proteome map of tomato (<i>Solanum lycopersicum</i>) fruit pericarp. <i>Proteomics</i> , 2013 , 13, 3059-63 | 4.63 | 19 |
| 50 | Characterizing allelic proteins for genome mapping in maize. <i>Electrophoresis</i> , 1995 , 16, 1289-94 | 3.6 | 19 |
| 49 | Including shared peptides for estimating protein abundances: a significant improvement for quantitative proteomics. <i>Proteomics</i> , 2012 , 12, 2797-801 | 4.8 | 18 |
| 48 | 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 |
| 47 | Potential of two-dimensional electrophoresis in routine identification of closely related durum wheat lines. <i>Electrophoresis</i> , 1997 , 18, 174-81 | 3.6 | 17 |
| 46 | 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 |
| 45 | Modeling Protein Destiny in Developing Fruit. <i>Plant Physiology</i> , 2019 , 180, 1709-1724 | 6.6 | 15 |
| 44 | 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 |
| 43 | Evaluation of Optimized Tube-Gel Methods of Sample Preparation for Large-Scale Plant Proteomics. <i>Proteomes</i> , 2018 , 6, | 4.6 | 13 |
| 42 | 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 |
| 41 | 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 |
| 40 | 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 |

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| 39 | A method based on bead flows for spot detection on 2-D gel images. <i>Proteomics</i> , 2008 , 8, 4914-8 | 4.8 | 11 |
| 38 | The Amborella vacuolar processing enzyme family. <i>Frontiers in Plant Science</i> , 2015 , 6, 618 | 6.2 | 10 |
| 37 | The PROTiCdb database for 2-DE proteomics. <i>Methods in Molecular Biology</i> , 2007 , 355, 279-303 | 1.4 | 10 |
| 36 | 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 |
| 35 | Deciphering the Infectious Process of in Lupin through Transcriptomic and Proteomic Analysis. <i>Microorganisms</i> , 2020 , 8, | 4.9 | 9 |
| 34 | 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 |
| 33 | Omics technologies provide new insights into the molecular physiopathology of equine osteochondrosis. <i>BMC Genomics</i> , 2014 , 15, 947 | 4.5 | 8 |
| 32 | Identification of Hanks-Type Kinase PknB-Specific Targets in the Phosphoproteome. <i>Frontiers in Microbiology</i> , 2019 , 10, 1329 | 5.7 | 7 |
| 31 | Quantitative analysis of 2D gels. <i>Methods in Molecular Biology</i> , 2007 , 355, 175-94 | 1.4 | 7 |
| 30 | Two-dimensional gel electrophoresis of proteins as a tool in wheat genetics. <i>Biochimie</i> , 1987 , 69, 781-7 | 4.6 | 7 |
| 29 | Transcriptomic and proteomic data in developing tomato fruit. <i>Data in Brief</i> , 2020 , 28, 105015 | 1.2 | 7 |
| 28 | Peptide filtering differently affects the performances of XIC-based quantification methods. <i>Journal of Proteomics</i> , 2019 , 193, 131-141 | 3.9 | 6 |
| 27 | 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 |
| 26 | αAmylase Mediates Host Acceptance in the Braconid Parasitoid Cotesia flavipes. <i>Journal of Chemical Ecology</i> , 2018 , 44, 1030-1039 | 2.7 | 5 |
| 25 | 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 |
| 24 | A method for proteomic analysis of equine subchondral bone and epiphyseal cartilage. <i>Proteomics</i> , 2012 , 12, 1870-4 | 4.8 | 5 |
| 23 | Phosphoproteomic Analysis of Isolated Mitochondria in Yeast. <i>Methods in Molecular Biology</i> , 2017 , 1636, 283-299 | 1.4 | 5 |
| 22 | Plant Proteome Responses to Abiotic Stress 2007 , 346-364 | | 5 |

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| 21 | Protein synthesis increases with photosynthesis via the stimulation of translation initiation. <i>Plant Science</i> , 2020 , 291, 110352 | 5.3 | 5 |
| 20 | 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 |
| 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 | 5.9 | 4 |
| 18 | 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 | 1.7 | 4 |
| 17 | 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 | 7.4 | 4 |
| 16 | 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 |
| 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 | 9.7 | 3 |
| 14 | 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 |
| 13 | Comparative quantitative proteomics of osmotic signal transduction mutants in <i>Botrytis cinerea</i> explain mutant phenotypes and highlight interaction with cAMP and Ca signalling pathways. <i>Journal of Proteomics</i> , 2020 , 212, 103580 | 3.9 | 2 |
| 12 | 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 | 3.9 | 2 |
| 11 | 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 |
| 10 | 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 |
| 9 | In vivo identification of putative CPK5 substrates in <i>Arabidopsis thaliana</i> .. <i>Plant Science</i> , 2022 , 314, 111133 | 3.3 | 1 |
| 8 | 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 |
| 7 | Study of Gene Expression During in Vitro Culture of Tobacco thin Cell Layers by two-Dimensional Electrophoresis of Proteins 1990 , 207-213 | | 1 |
| 6 | Cell wall proteomic datasets of stems and leaves of. <i>Data in Brief</i> , 2021 , 35, 106818 | 1.2 | 1 |
| 5 | <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, | 7.6 | 1 |
| 4 | Genetics of the Maize Proteome. <i>Stadler Genetics Symposia Series</i> , 2000 , 123-139 | | 1 |

- 3 Proteomics for genetic and physiological studies in plants 38-51 ○
- 2 The Nitrate Transporter MtNPF6.8 Is a Master Sensor of Nitrate Signal in the Primary Root Tip of ..
Frontiers in Plant Science, **2022**, 13, 832246 6.2 ○
- 1 Expression du g ome du Bl tendre r le 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, **1985**, 132, 97-101