

Jesus V Jorin Novo

List of Publications by Year in descending order

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144
papers

5,611
citations

61977

43
h-index

95259

68
g-index

146
all docs

146
docs citations

146
times ranked

5047
citing authors

#	ARTICLE	IF	CITATIONS
1	Plant proteome analysis. <i>Proteomics</i> , 2004, 4, 285-298.	2.2	264
2	Plant proteomics update (2007–2008): Second-generation proteomic techniques, an appropriate experimental design, and data analysis to fulfill MIAPE standards, increase plant proteome coverage and expand biological knowledge. <i>Journal of Proteomics</i> , 2009, 72, 285-314.	2.4	191
3	Vesicular fractions of sunflower apoplastic fluids are associated with potential exosome marker proteins. <i>FEBS Letters</i> , 2009, 583, 3363-3366.	2.8	161
4	Plant proteome analysis: A 2004–2006 update. <i>Proteomics</i> , 2006, 6, 5529-5548.	2.2	155
5	Proteomics study reveals the molecular mechanisms underlying water stress tolerance induced by <i>Piriformospora indica</i> in barley. <i>Journal of Proteomics</i> , 2013, 94, 289-301.	2.4	150
6	Back to the basics: Maximizing the information obtained by quantitative two dimensional gel electrophoresis analyses by an appropriate experimental design and statistical analyses. <i>Journal of Proteomics</i> , 2011, 74, 1-18.	2.4	148
7	Sunflower (<i>Helianthus annuus</i> L.) response to broomrape (<i>Orobanche cernua</i> Loefl.) parasitism: induced synthesis and excretion of 7-hydroxylated simple coumarins. <i>Journal of Experimental Botany</i> , 2001, 52, 2227-2234.	4.8	142
8	Proteomics of Plant Pathogenic Fungi. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-36.	3.0	127
9	The Holm Oak leaf proteome: Analytical and biological variability in the protein expression level assessed by 2-DE and protein identification tandem mass spectrometry de novo sequencing and sequence similarity searching. <i>Proteomics</i> , 2005, 5, 222-234.	2.2	116
10	Variation in the holm oak leaf proteome at different plant developmental stages, between provenances and in response to drought stress. <i>Proteomics</i> , 2006, 6, S207-S214.	2.2	110
11	Proteomics research on forest trees, the most recalcitrant and orphan plant species. <i>Phytochemistry</i> , 2011, 72, 1219-1242.	2.9	108
12	<i>Orobanche crenata</i> resistance and avoidance in pea (<i>Pisum</i> spp.) operate at different developmental stages of the parasite. <i>Weed Research</i> , 2005, 45, 379-387.	1.7	107
13	Changes in the protein profile of <i>Quercus ilex</i> leaves in response to drought stress and recovery. <i>Journal of Plant Physiology</i> , 2009, 166, 233-245.	3.5	101
14	Contribution of Proteomics to the Study of Plant Pathogenic Fungi. <i>Journal of Proteome Research</i> , 2012, 11, 3-16.	3.7	97
15	Fourteen years of plant proteomics reflected in <i>Proteomics</i> : Moving from model species and 2DE-based approaches to orphan species and gel-free platforms. <i>Proteomics</i> , 2015, 15, 1089-1112.	2.2	91
16	A proteomic approach to study pea (<i>Pisum sativum</i>) responses to powdery mildew (<i>Erysiphe pisi</i>). <i>Proteomics</i> , 2006, 6, S163-S174.	2.2	90
17	Plant resistance to parasitic plants: molecular approaches to an old foe. <i>New Phytologist</i> , 2007, 173, 703-712.	7.3	89
18	Stress Responses in Alfalfa (<i>Medicago sativa</i> L.). <i>Plant Physiology</i> , 1990, 92, 447-455.	4.8	87

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19	A proteomic approach to studying plant response to crenate broomrape (<i>Orobanche crenata</i>) in pea (<i>Pisum sativum</i>). <i>Phytochemistry</i> , 2004, 65, 1817-1828.	2.9	83
20	Evaluation of three different protocols of protein extraction for <i>Arabidopsis thaliana</i> leaf proteome analysis by two-dimensional electrophoresis. <i>Journal of Proteomics</i> , 2008, 71, 461-472.	2.4	82
21	Pre-haustorial resistance to broomrape (<i>Orobanche cumana</i>) in sunflower (<i>Helianthus annuus</i>): cytochemical studies. <i>Journal of Experimental Botany</i> , 2006, 57, 4189-4200.	4.8	81
22	Proteomic analysis of mycelium and secretome of different <i>Botrytis cinerea</i> wild-type strains. <i>Journal of Proteomics</i> , 2014, 97, 195-221.	2.4	74
23	Comparative 2-DE proteomic analysis of date palm (<i>Phoenix dactylifera</i> L.) somatic and zygotic embryos. <i>Journal of Proteomics</i> , 2009, 73, 161-177.	2.4	72
24	Abiotic elicitation of coumarin phytoalexins in sunflower. <i>Phytochemistry</i> , 1995, 38, 1185-1191.	2.9	70
25	Two-dimensional electrophoresis protein profile of the phytopathogenic fungus <i>Botrytis cinerea</i> . <i>Proteomics</i> , 2006, 6, S88-S96.	2.2	70
26	Proteomic analysis of phytopathogenic fungus <i>Botrytis cinerea</i> as a potential tool for identifying pathogenicity factors, therapeutic targets and for basic research. <i>Archives of Microbiology</i> , 2007, 187, 207-215.	2.2	70
27	Improving the quality of protein identification in non-model species. Characterization of <i>Quercus ilex</i> seed and <i>Pinus radiata</i> needle proteomes by using SEQUEST and custom databases. <i>Journal of Proteomics</i> , 2014, 105, 85-91.	2.4	69
28	Acibenzolar-S-methyl-induced resistance to sunflower rust (<i>Puccinia helianthi</i>) is associated with an enhancement of coumarins on foliar surface. <i>Physiological and Molecular Plant Pathology</i> , 2002, 60, 155-162.	2.5	65
29	Sunflower sesquiterpene lactone models induce <i>Orobanche cumana</i> seed germination. <i>Phytochemistry</i> , 2000, 53, 45-50.	2.9	64
30	Proteomic analysis of the development and germination of date palm (<i>Phoenix</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 Td (da	2.2	64
31	Population variability based on the morphometry and chemical composition of the acorn in Holm oak (<i>Quercus ilex</i> subsp. <i>ballota</i> [Desf.] Samp.). <i>European Journal of Forest Research</i> , 2012, 131, 893-904.	2.5	64
32	Studies of variability in Holm oak (<i>Quercus ilex</i> subsp. <i>ballota</i> [Desf.] Samp.) through acorn protein profile analysis. <i>Journal of Proteomics</i> , 2011, 74, 1244-1255.	2.4	63
33	2-DE proteomics analysis of drought treated seedlings of <i>Quercus ilex</i> supports a root active strategy for metabolic adaptation in response to water shortage. <i>Frontiers in Plant Science</i> , 2015, 6, 627.	3.6	63
34	Understanding <i>Orobanche</i> and <i>Phelipanche</i> "host plant interactions and developing resistance. <i>Weed Research</i> , 2009, 49, 8-22.	1.7	60
35	Combined Proteomic and Transcriptomic Analysis Identifies Differentially Expressed Pathways Associated to <i>Pinus radiata</i> Needle Maturation. <i>Journal of Proteome Research</i> , 2010, 9, 3954-3979.	3.7	56
36	Physiological and proteomics analyses of Holm oak (<i>Quercus ilex</i> subsp. <i>ballota</i> [Desf.] Samp.) responses to <i>Phytophthora cinnamomi</i> . <i>Plant Physiology and Biochemistry</i> , 2013, 71, 191-202.	5.8	56

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37	Proteomics: a promising approach to study biotic interaction in legumes. A review. <i>Euphytica</i> , 2006, 147, 37-47.	1.2	55
38	Physiological and Proteomic Analyses of Drought Stress Response in Holm Oak Provenances. <i>Journal of Proteome Research</i> , 2013, 12, 5110-5123.	3.7	53
39	Proteomic Analysis of <i>Pinus radiata</i> Needles: 2-DE Map and Protein Identification by LC/MS/MS and Substitution-Tolerant Database Searching. <i>Journal of Proteome Research</i> , 2008, 7, 2616-2631.	3.7	48
40	Unraveling the in vitro secretome of the phytopathogen <i>Botrytis cinerea</i> to understand the interaction with its hosts. <i>Frontiers in Plant Science</i> , 2015, 6, 839.	3.6	47
41	A multi-omics analysis of the grapevine pathogen <i>Lasiodiplodia theobromae</i> reveals that temperature affects the expression of virulence- and pathogenicity-related genes. <i>Scientific Reports</i> , 2019, 9, 13144.	3.3	47
42	Holm Oak (<i>Quercus ilex</i>) Transcriptome. De novo Sequencing and Assembly Analysis. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 70.	3.5	46
43	Gel electrophoresis-based plant proteomics: Past, present, and future. Happy 10th anniversary <i>Journal of Proteomics</i> !. <i>Journal of Proteomics</i> , 2019, 198, 1-10.	2.4	46
44	Fungitoxic effect of scopolin and related coumarins on <i>Sclerotinia sclerotiorum</i> . A way to overcome sunflower head rot. <i>Euphytica</i> , 2006, 147, 451-460.	1.2	44
45	Two-Dimensional Electrophoresis Based Proteomic Analysis of the Pea (<i>Pisum sativum</i>) in Response to <i>Mycosphaerella pinodes</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 12822-12832.	5.2	44
46	Extracellular Sunflower Proteins: Evidence on Non-classical Secretion of a Jacalin-Related Lectin. <i>Protein and Peptide Letters</i> , 2012, 19, 270-276.	0.9	44
47	Coumarins in <i>helianthus tuberosus</i> : characterization, induced accumulation and biosynthesis. <i>Phytochemistry</i> , 1998, 49, 1029-1036.	2.9	43
48	Differential expression proteomics to investigate responses and resistance to <i>Orobanche crenata</i> in <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2009, 10, 294.	2.8	42
49	Abscisic acid and sucrose increase the protein content in date palm somatic embryos, causing changes in 2-DE profile. <i>Phytochemistry</i> , 2010, 71, 1223-1236.	2.9	42
50	Proteomics for exploiting diversity of lupin seed storage proteins and their use as nutraceuticals for health and welfare. <i>Journal of Proteomics</i> , 2016, 143, 57-68.	2.4	42
51	Release of phytoalexins and related isoflavonoids from intact chickpea seedlings elicited with reduced glutathione at root level. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 785-795.	5.8	41
52	Plant Proteomics Methods and Protocols. <i>Methods in Molecular Biology</i> , 2014, 1072, 3-13.	0.9	41
53	Proteomic analysis of Holm oak (<i>Quercus ilex</i> subsp. <i>ballota</i> [Desf.] Samp.) pollen. <i>Journal of Proteomics</i> , 2012, 75, 2736-2744.	2.4	39
54	Crenate broomrape control in pea by foliar application of benzothiadiazole (BTH). <i>Phytoparasitica</i> , 2004, 32, 21-29.	1.2	37

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55	Proteomic analysis of Arabidopsis protein S-nitrosylation in response to inoculation with <i>Pseudomonas syringae</i> . <i>Acta Physiologiae Plantarum</i> , 2011, 33, 1493-1514.	2.1	37
56	A Multi-Omics Analysis Pipeline for the Metabolic Pathway Reconstruction in the Orphan Species <i>Quercus ilex</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 935.	3.6	37
57	The production of coumarin phytoalexins in different plant organs of sunflower (<i>Helianthus annuus</i>) Tj ETQq1 1 0.784314 rgBT /Overl	3.5	35
58	Constitutive Coumarin Accumulation on Sunflower Leaf Surface Prevents Rust Germ Tube Growth and Appressorium Differentiation. <i>Crop Science</i> , 2007, 47, 1119-1124.	1.8	33
59	Multiplex staining of 2-DE gels for an initial phosphoproteome analysis of germinating seeds and early grown seedlings from a non-orthodox specie: <i>Quercus ilex</i> L. subsp. <i>ballota</i> [Desf.] Samp.. <i>Frontiers in Plant Science</i> , 2015, 6, 620.	3.6	33
60	Title is missing!. <i>Euphytica</i> , 2003, 132, 321-329.	1.2	31
61	Application of proteomics to the assessment of the response to ionising radiation in <i>Arabidopsis thaliana</i> . <i>Journal of Proteomics</i> , 2011, 74, 1364-1377.	2.4	31
62	SAR Studies of Sesquiterpene Lactones as <i>Orobanche cumana</i> Seed Germination Stimulants. <i>Journal of Agricultural and Food Chemistry</i> , 2002, 50, 1911-1917.	5.2	30
63	Root-shoot signalling in sunflower plants with confined root systems. <i>Plant and Soil</i> , 1994, 166, 31-36.	3.7	29
64	Simple, rapid and reliable methods to obtain high quality RNA and genomic DNA from <i>Quercus ilex</i> L. leaves suitable for molecular biology studies. <i>Acta Physiologiae Plantarum</i> , 2012, 34, 793-805.	2.1	29
65	Application of Label-Free Shotgun nUPLC-MS ^E and 2-DE Approaches in the Study of <i>Botrytis cinerea</i> Mycelium. <i>Journal of Proteome Research</i> , 2013, 12, 3042-3056.	3.7	28
66	Ion Torrent and Illumina, two complementary RNA-seq platforms for constructing the holm oak (<i>Quercus ilex</i>) transcriptome. <i>PLoS ONE</i> , 2019, 14, e0210356.	2.5	28
67	Production of toxic metabolites by two strains of <i>Lasiodiplodia theobromae</i> , isolated from a coconut tree and a human patient. <i>Mycologia</i> , 2018, 110, 642-653.	1.9	27
68	Standardization of Data Processing and Statistical Analysis in Comparative Plant Proteomics Experiment. <i>Methods in Molecular Biology</i> , 2014, 1072, 51-60.	0.9	27
69	Phytochemical composition and variability in <i>Quercus ilex</i> acorn morphotypes as determined by NIRS and MS-based approaches. <i>Food Chemistry</i> , 2021, 338, 127803.	8.2	25
70	Antifungal Activity of a New Phenolic Compound from Capitulum of a Head Rot-resistant Sunflower Genotype. <i>Journal of Chemical Ecology</i> , 2007, 33, 2245-2253.	1.8	24
71	Stress responses in alfalfa (<i>Medicago sativa</i> L.) VII. Induction of defence related mRNAs in elicitor-treated cell suspension cultures. <i>Physiological and Molecular Plant Pathology</i> , 1990, 37, 293-307.	2.5	23
72	Protein profile of cotyledon, tegument, and embryonic axis of mature acorns from a non-orthodox plant species: <i>Quercus ilex</i> . <i>Planta</i> , 2016, 243, 369-396.	3.2	23

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73	Germination and Early Seedling Development in <i>Quercus ilex</i> Recalcitrant and Non-dormant Seeds: Targeted Transcriptional, Hormonal, and Sugar Analysis. <i>Frontiers in Plant Science</i> , 2018, 9, 1508.	3.6	23
74	Effect and Response of <i>Quercus ilex</i> subsp. <i>ballota</i> [Desf.] Samp. Seedlings From Three Contrasting Andalusian Populations to Individual and Combined <i>Phytophthora cinnamomi</i> and Drought Stresses. <i>Frontiers in Plant Science</i> , 2021, 12, 722802.	3.6	23
75	Population Genetic Diversity of <i>Quercus ilex</i> subsp. <i>ballota</i> (Desf.) Samp. Reveals Divergence in Recent and Evolutionary Migration Rates in the Spanish Dehesas. <i>Forests</i> , 2018, 9, 337.	2.1	22
76	Effect of ABA, arginine and sucrose on protein content of date palm somatic embryos. <i>Scientia Horticulturae</i> , 2009, 120, 379-385.	3.6	21
77	Chitinase and beta-1,3-glucanase activities in chickpea (<i>Cicer arietinum</i>). Induction of different isoenzymes in response to wounding and ethephon. <i>Physiologia Plantarum</i> , 1994, 92, 654-660.	5.2	20
78	Characterization and inducibility of a scopoletin-degrading enzyme from sunflower. <i>Phytochemistry</i> , 1997, 45, 1109-1114.	2.9	20
79	Proteomics, Holm Oak (<i>Quercus ilex</i> L.) and Other Recalcitrant and Orphan Forest Tree Species: How do They See Each Other?. <i>International Journal of Molecular Sciences</i> , 2019, 20, 692.	4.1	20
80	<i>Quercus ilex</i> pollen allergen, Que i 1, responsible for pollen food allergy syndrome caused by fruits in Spanish allergic patients. <i>Clinical and Experimental Allergy</i> , 2020, 50, 815-823.	2.9	20
81	Purification and properties of phenylalanine ammonia-lyase from sunflower (<i>Helianthus annuus</i> L.) hypocotyls. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1988, 964, 73-82.	2.4	19
82	Two-dimensional gel electrophoresis-based proteomic analysis of the <i>Medicago truncatula</i> "rust (<i>Uromyces striatus</i>) interaction. <i>Annals of Applied Biology</i> , 2010, 157, 243-257.	2.5	19
83	What proteomic analysis of the apoplast tells us about plant-pathogen interactions. <i>Plant Pathology</i> , 2018, 67, 1647-1668.	2.4	19
84	Responses and Differences in Tolerance to Water Shortage under Climatic Dryness Conditions in Seedlings from <i>Quercus</i> spp. and Andalusian <i>Q. ilex</i> Populations. <i>Forests</i> , 2020, 11, 707.	2.1	19
85	Toward characterizing germination and early growth in the non-orthodox forest tree species <i>Quercus ilex</i> through complementary gel and gel-free proteomic analysis of embryo and seedlings. <i>Journal of Proteomics</i> , 2019, 197, 60-70.	2.4	18
86	Molecular Research on Stress Responses in <i>Quercus</i> spp.: From Classical Biochemistry to Systems Biology through Omics Analysis. <i>Forests</i> , 2021, 12, 364.	2.1	18
87	Induction of different chitinase and β -1,3-glucanase isoenzymes in sunflower (<i>Helianthus annuus</i> L.) seedlings in response to infection by <i>Plasmopara halstedii</i> . <i>European Journal of Plant Pathology</i> , 1996, 102, 401-405.	1.7	17
88	Metabolite and proteome changes during the ripening of Syrah and Cabernet Sauvignon grape varieties cultured in a nontraditional wine region in Brazil. <i>Journal of Proteomics</i> , 2015, 113, 206-225.	2.4	16
89	Plant responses to tomato chlorotic mottle virus: Proteomic view of the resistance mechanisms to a bipartite begomovirus in tomato. <i>Journal of Proteomics</i> , 2017, 151, 284-292.	2.4	16
90	Holm oak proteomic response to water limitation at seedling establishment stage reveals specific changes in different plant parts as well as interaction between roots and cotyledons. <i>Plant Science</i> , 2018, 276, 1-13.	3.6	16

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91	2-DE based proteomic analysis of <i>Saccharomyces cerevisiae</i> wild and K ⁺ transport-affected mutant (trk1,2) strains at the growth exponential and stationary phases. <i>Journal of Proteomics</i> , 2010, 73, 2316-2335.	2.4	15
92	Dissecting the Seed Maturation and Germination Processes in the Non-Orthodox <i>Quercus ilex</i> Species Based on Protein Signatures as Revealed by 2-DE Coupled to MALDI-TOF/TOF Proteomics Strategy. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4870.	4.1	15
93	Induction of phenylalanine ammonia-lyase in hypocotyls of sunflower seedlings by light, excision and sucrose. <i>Physiologia Plantarum</i> , 1984, 60, 159-165.	5.2	14
94	Differences in the Triticale (X <i>Triticosecale</i> Wittmack) Flag Leaf 2-DE Protein Profile between Varieties and Nitrogen Fertilization Levels. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 5698-5707.	5.2	14
95	Proteomics and plant biology: contributions to date and a look towards the next decade. <i>Expert Review of Proteomics</i> , 2021, 18, 93-103.	3.0	14
96	Substantial equivalence analysis in fruits from three <i>Theobroma</i> species through chemical composition and protein profiling. <i>Food Chemistry</i> , 2018, 240, 496-504.	8.2	13
97	Proteomic Analysis and Functional Validation of a <i>Brassica oleracea</i> Endochitinase Involved in Resistance to <i>Xanthomonas campestris</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 414.	3.6	13
98	Proteomics Data Analysis for the Identification of Proteins and Derived Proteotypic Peptides of Potential Use as Putative Drought Tolerance Markers for <i>Quercus ilex</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 3191.	4.1	13
99	Untargeted MS-Based Metabolomics Analysis of the Responses to Drought Stress in <i>Quercus ilex</i> L. Leaf Seedlings and the Identification of Putative Compounds Related to Tolerance. <i>Forests</i> , 2022, 13, 551.	2.1	13
100	Back to Osborne. Sequential Protein Extraction and LC-MS Analysis for the Characterization of the Holm Oak Seed Proteome. <i>Methods in Molecular Biology</i> , 2014, 1072, 379-389.	0.9	12
101	Combining P and Zn fertilization to enhance yield and grain quality in maize grown on Mediterranean soils. <i>Scientific Reports</i> , 2021, 11, 7427.	3.3	12
102	Towards a global analysis of porcine alveolar macrophages proteins through two-dimensional electrophoresis and mass spectrometry. <i>Developmental and Comparative Immunology</i> , 2007, 31, 1220-1232.	2.3	11
103	Proteomics analysis of date palm leaves affected at three characteristic stages of brittle leaf disease. <i>Planta</i> , 2012, 236, 1599-1613.	3.2	11
104	GeLC-Orbitrap/MS and 2-DE-MALDI-TOF/TOF comparative proteomics analysis of seed cotyledons from the non-orthodox <i>Quercus ilex</i> tree species. <i>Journal of Proteomics</i> , 2021, 233, 104087.	2.4	11
105	Plant Proteomics. <i>Journal of Proteomics</i> , 2009, 72, 283-284.	2.4	10
106	Characterization of the orthodox <i>Pinus occidentalis</i> seed and pollen proteomes by using complementary gel-based and gel-free approaches. <i>Journal of Proteomics</i> , 2016, 143, 382-389.	2.4	10
107	Translational Proteomics Special Issue. <i>Journal of Proteomics</i> , 2013, 93, 1-4.	2.4	9
108	A year (2014-2015) of plants in <i>Proteomics</i> journal. Progress in wet and dry methodologies, moving from protein catalogs, and the view of classic plant biochemists. <i>Proteomics</i> , 2016, 16, 866-876.	2.2	9

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109	Facing challenges in Proteomics today and in the coming decade: Report of Roundtable Discussions at the 4th EuPA Scientific Meeting, Portugal, Estoril 2010. <i>Journal of Proteomics</i> , 2011, 75, 4-17.	2.4	8
110	A proteomic approach analysing the <i>Arabidopsis thaliana</i> response to virulent and avirulent <i>Pseudomonas syringae</i> strains. <i>Acta Physiologiae Plantarum</i> , 2012, 34, 905-922.	2.1	8
111	Proteomic Protocols for the Study of Filamentous Fungi. , 2013, , 299-308.		8
112	Protein Carbonylation As a Biomarker of Heavy Metal, Cd and Pb, Damage in <i>Paspalum fasciculatum</i> Willd. ex Fl. <i>Plants</i> , 2019, 8, 513.	3.5	8
113	L-Phenylalanine Ammonia-Lyase from Sunflower Hypocotyls: Modulation by Cinnamic Acids. <i>Journal of Plant Physiology</i> , 1990, 136, 415-420.	3.5	7
114	Adaptation to potassium starvation of wild-type and K ⁺ transport mutant (<i>trk1,2</i>) of <i>Saccharomyces cerevisiae</i> : 2-dimensional gel electrophoresis-based proteomic approach. <i>MicrobiologyOpen</i> , 2012, 1, 182-193.	3.0	7
115	Scientific standards and MIAPEs in plant proteomics research and publications. <i>Frontiers in Plant Science</i> , 2015, 6, 473.	3.6	7
116	A physiological, biochemical and proteomic characterization of <i>Saccharomyces cerevisiae</i> <i>trk1,2</i> transport mutants grown under limiting potassium conditions. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1260-1270.	1.8	7
117	Plant Proteomic Research 3.0: Challenges and Perspectives. <i>International Journal of Molecular Sciences</i> , 2021, 22, 766.	4.1	7
118	What Is New in (Plant) Proteomics Methods and Protocols: The 2015–2019 Quinquennium. <i>Methods in Molecular Biology</i> , 2020, 2139, 1-10.	0.9	7
119	AGRONOMIC ASPECTS OF THE SUNFLOWER 7-HYDROXYLATED SIMPLE COUMARINS / ASPECTOS AGRONÓMICOS DE LAS CUMARINAS SIMPLES 7- HIDROXILADAS EN GIRASOL / ASPECTS AGRONOMIQUES DE 7 COUMARINES HYDROXYLES SIMPLES CHEZ LE TOURNESOL. <i>Helia</i> , 2000, 23, 105-112.	0.4	7
120	Recent Advances in MS-Based Plant Proteomics: Proteomics Data Validation Through Integration with Other Classic and -Omics Approaches. <i>Progress in Botany Fortschritte Der Botanik</i> , 2019, , 77-101.	0.3	6
121	Application and optimization of label-free shotgun approaches in the study of <i>Quercus ilex</i> . <i>Journal of Proteomics</i> , 2021, 233, 104082.	2.4	6
122	Diverse facets of plant proteomics. <i>Phytochemistry</i> , 2011, 72, 961-962.	2.9	5
123	Phosphorylated 11S globulins in sunflower seeds. <i>Seed Science Research</i> , 2013, 23, 199-204.	1.7	5
124	Food and Crop Proteomics. <i>Journal of Proteomics</i> , 2016, 143, 1-2.	2.4	5
125	Variability studies of allochthonous stone pine (<i>Pinus pinea</i> L.) plantations in Chile through nut protein profiling. <i>Journal of Proteomics</i> , 2018, 175, 95-104.	2.4	5
126	Why Consumers Prefer Green Friariello Pepper: Changes in the Protein and Metabolite Profiles Along the Ripening. <i>Frontiers in Plant Science</i> , 2021, 12, 668562.	3.6	5

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127	EuPA achieves visibility “ An activity report on the first three years. Journal of Proteomics, 2008, 71, 11-18.	2.4	4
128	Making a Protein Extract from Plant Pathogenic Fungi for Gel- and LC-Based Proteomics. Methods in Molecular Biology, 2014, 1072, 93-109.	0.9	4
129	Sunflower Coumarin Phytoalexins Inhibit the Growth of the Virulent Pathogen Sclerotinia sclerotiorum. Journal of Phytopathology, 1999, 147, 441-443.	1.0	3
130	Proteotyping of Holm Oak (<i>Quercus ilex</i> subsp. <i>ballota</i>) Provenances Through Proteomic Analysis of Acorn Flour. Methods in Molecular Biology, 2014, 1072, 709-723.	0.9	3
131	Identification of Proteases and Protease Inhibitors in Seeds of the Recalcitrant Forest Tree Species <i>Quercus ilex</i> . Frontiers in Plant Science, 0, 13, .	3.6	3
132	Purification and partial characterization of soluble α -mannosidase isoforms from sunflower (<i>Helianthus annuus</i> L.) hypocotyls. Plant Science, 1989, 62, 11-19.	3.6	2
133	Effects of actinomycin D, cordycepin and cycloheximide on phenylalanine ammonia-lyase turnover in sunflower hypocotyls. Journal of Plant Physiology, 1990, 137, 252-255.	3.5	2
134	OUT OF CÃ“RDOBA. Proteomics, 2006, 6, S1-S3.	2.2	2
135	Plant proteomics in Europe “ COST action FA0603. Journal of Proteomics, 2011, 74, 1161-1164.	2.4	2
136	Editorial: International Plant Proteomics Organization (INPPO) World Congress 2014. Frontiers in Plant Science, 2016, 7, 1190.	3.6	2
137	Interspecific Variation between the American <i>Quercus virginiana</i> and Mediterranean <i>Quercus</i> Species in Terms of Seed Nutritional Composition, Phytochemical Content, and Antioxidant Activity. Molecules, 2021, 26, 2351.	3.8	2
138	Electrophoresis-Based Proteomics to Study Development and Germination of Date Palm Zygotic Embryos. Methods in Molecular Biology, 2017, 1638, 365-380.	0.9	1
139	Proteomics Analysis of Plant Tissues Based on Two-Dimensional Gel Electrophoresis. , 2018, , 309-322.		1
140	Proteomic Insights of Date Palm Embryogenesis and Responses to Environmental Stress. Compendium of Plant Genomes, 2021, , 85-99.	0.5	1
141	Mike Dunn: Proteomics in Spain, and the field of plant proteomics. Proteomics, 2016, 16, 2842-2844.	2.2	0
142	Can the increment of temperature associated to climate change alter the olive oil chemical composition and its nutritional and nutraceutical properties?. , 0, ,		0
143	A Pipeline for Metabolic Pathway Reconstruction in Plant Orphan Species. Methods in Molecular Biology, 2020, 2139, 367-380.	0.9	0
144	Population genetic structure and dispersal of <i>Pinus occidentalis</i> in the Dominican Republic by chloroplastic SSR, with implications for its conservation, management, and reforestation. Canadian Journal of Forest Research, 2022, 52, 553-560.	1.7	0