Hans-Peter Braun

List of Publications by Year
in descending order

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184
papers

13,575
citations

23567
58
h-index

25787
108
g-index

200
all docs

200
docs citations

200
times ranked

12227
citing authors

#	ARTICLE	IF	CITATIONS
1	Blue native PAGE. Nature Protocols, 2006, 1, 418-428.	12.0	1,502
2	Amino Acid Catabolism in Plants. Molecular Plant, 2015, 8, 1563-1579.	8.3	898
3	Proteomic Approach to Identify Novel Mitochondrial Proteins in Arabidopsis. Plant Physiology, 2001, 127, 1694-1710.	4.8	369
4	New Insights into the Respiratory Chain of Plant Mitochondria. Supercomplexes and a Unique Composition of Complex II. Plant Physiology, 2003, 133, 274-286.	4.8	333
5	Structure of a mitochondrial supercomplex formed by respiratory-chain complexes I and III. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3225-3229.	7.1	311
6	The role of amino acid metabolism during abiotic stress release. Plant, Cell and Environment, 2019, 42, 1630-1644.	5.7	278
7	New insights into the composition, molecular mass and stoichiometry of the protein complexes of plant mitochondria. Plant Journal, 1996, 9, 357-368.	5.7	219
8	Respiratory electron transfer pathways in plant mitochondria. Frontiers in Plant Science, 2014, 5, 163.	3.6	209
9	Supramolecular Structure of the Mitochondrial Oxidative Phosphorylation System. Journal of Biological Chemistry, 2007, 282, 1-4.	3.4	195
10	Purification and Characterization of the Preprotein Translocase of the Outer Mitochondrial Membrane from Arabidopsis. Identification of Multiple Forms of TOM20. Plant Physiology, 2001, 125, 943-954.	4.8	192
11	The mitochondrial complexome of <i>Arabidopsis thaliana</i>. Plant Journal, 2017, 89, 1079-1092.	5.7	192
12	The plant mitochondrial proteome. Trends in Plant Science, 2005, 10, 36-43.	8.8	188
13	Internal Architecture of Mitochondrial Complex I from <i>Arabidopsis thaliana</i>. Plant Cell, 2010, 22, 797-810.	6.6	187
14	Mitochondrial cytochrome c oxidase and succinate dehydrogenase complexes contain plant specific subunits. Plant Molecular Biology, 2004, 56, 77-90.	3.9	184
15	Effect of Manganese Toxicity on the Proteome of the Leaf Apoplast in Cowpea. Plant Physiology, 2003, 133, 1935-1946.	4.8	183
16	Structure and function of mitochondrial supercomplexes. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 664-670.	1.0	177
17	Structure of dimeric ATP synthase from mitochondria: An angular association of monomers induces the strong curvature of the inner membrane. FEBS Letters, 2005, 579, 5769-5772.	2.8	175
18	Disruption of a Nuclear Gene Encoding a Mitochondrial Gamma Carbonic Anhydrase Reduces Complex I and Supercomplex I+III2 Levels and Alters Mitochondrial Physiology in Arabidopsis. Journal of Molecular Biology, 2005, 350, 263-277.	4.2	174

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19	Carbonic Anhydrase Subunits Form a Matrix-exposed Domain Attached to the Membrane Arm of Mitochondrial Complex I in Plants. Journal of Biological Chemistry, 2006, 281, 6482-6488.	3.4	169
20	Identification and Characterization of Respirasomes in Potato Mitochondria. Plant Physiology, 2004, 134, 1450-1459.	4.8	166
21	Defining the<i>Protein Complex Proteome</i>of Plant Mitochondria Â. Plant Physiology, 2011, 157, 587-598.	4.8	164
22	Title is missing!. Photosynthesis Research, 1997, 53, 35-44.	2.9	158
23	Single organelle function and organization as estimated from Arabidopsis mitochondrial proteomics. Plant Journal, 2020, 101, 420-441.	5.7	152
24	Biochemical dissection of the mitochondrial proteome fromArabidopsis thaliana by three-dimensional gel electrophoresis. Electrophoresis, 2002, 23, 640-646.	2.4	151
25	Arabidopsisphosphatidylglycerophosphate synthase 1 is essential for chloroplast differentiation, but is dispensable for mitochondrial function. Plant Journal, 2003, 33, 899-909.	5.7	147
26	A Structural Model of the Cytochrome c Reductase/Oxidase Supercomplex from Yeast Mitochondria. Journal of Biological Chemistry, 2007, 282, 12240-12248.	3.4	145
27	Blue-native PAGE in plants: a tool in analysis of protein-protein interactions. Plant Methods, 2005, 1, 11.	4.3	144
28	Are the â€˜coreâ€™ proteins of the mitochondrial bc1 complex evolutionary relics of a processing protease?. Trends in Biochemical Sciences, 1995, 20, 171-175.	7.5	140
29	Characterization of dimeric ATP synthase and cristae membrane ultrastructure fromSaccharomycesandPolytomellamitochondria. FEBS Letters, 2006, 580, 3427-3432.	2.8	139
30	Analysis of the <i>Aspergillus fumigatus</i> Proteome Reveals Metabolic Changes and the Activation of the Pseurotin A Biosynthesis Gene Cluster in Response to Hypoxia. Journal of Proteome Research, 2011, 10, 2508-2524.	3.7	135
31	Respiratory chain supercomplexes in plant mitochondria. Plant Physiology and Biochemistry, 2004, 42, 937-942.	5.8	126
32	Proteomic approach: Identification of Medicago truncatula proteins induced in roots after infection with the pathogenic oomycete Aphanomyces euteiches. Plant Molecular Biology, 2004, 55, 109-120.	3.9	126
33	Proteomic approach to characterize the supramolecular organization of photosystems in higher plants. Phytochemistry, 2004, 65, 1683-1692.	2.9	117
34	Nuclear Photosynthetic Gene Expression Is Synergistically Modulated by Rates of Protein Synthesis in Chloroplasts and Mitochondria. Plant Cell, 2006, 18, 970-991.	6.6	117
35	Megacomplex organization of the oxidative phosphorylation system by structural analysis of respiratory supercomplexes from potato. Biochimica Et Biophysica Acta - Bioenergetics, 2009, 1787, 60-67.	1.0	117
36	Respiratory chain supercomplexes in the plant mitochondrial membrane. Trends in Plant Science, 2006, 11, 232-240.	8.8	116

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37	Seed Architecture Shapes Embryo Metabolism in Oilseed Rape Â. Plant Cell, 2013, 25, 1625-1640.	6.6	109
38	The life of plant mitochondrial complex I. Mitochondrion, 2014, 19, 295-313.	3.4	103
39	The Role of Hydrogen Peroxide-Producing and Hydrogen Peroxide-Consuming Peroxidases in the Leaf Apoplast of Cowpea in Manganese Tolerance. Plant Physiology, 2006, 140, 1451-1463.	4.8	102
40	The Arabidopsis Class II Sirtuin Is a Lysine Deacetylase and Interacts with Mitochondrial Energy Metabolism Â Â Â. Plant Physiology, 2014, 164, 1401-1414.	4.8	96
41	Life without complex I: proteome analyses of an Arabidopsis mutant lacking the mitochondrial NADH dehydrogenase complex. Journal of Experimental Botany, 2016, 67, 3079-3093.	4.8	91
42	Row-like organization of ATP synthase in intact mitochondria determined by cryo-electron tomography. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 272-277.	1.0	90
43	Early manganeseâ€toxicity response in <i>Vigna unguiculata</i> L. â€“ a proteomic and transcriptomic study. Proteomics, 2008, 8, 149-159.	2.2	88
44	Proteomic analyses of somatic and zygotic embryos of Cyclamen persicum Mill. reveal new insights into seed and germination physiology. Planta, 2006, 224, 508-519.	3.2	86
45	The higher level of organization of the oxidative phosphorylation system: mitochondrial supercomplexes. Journal of Bioenergetics and Biomembranes, 2008, 40, 419-424.	2.3	83
46	l-Galactono-1,4-lactone dehydrogenase (GLDH) Forms Part of Three Subcomplexes of Mitochondrial Complex I in Arabidopsis thaliana. Journal of Biological Chemistry, 2012, 287, 14412-14419.	3.4	80
47	A basal carbon concentrating mechanism in plants?. Plant Science, 2012, 187, 97-104.	3.6	79
48	The Oxidative Phosphorylation system of the mitochondria in plants. Mitochondrion, 2020, 53, 66-75.	3.4	78
49	Unique Composition of the Preprotein Translocase of the Outer Mitochondrial Membrane from Plants. Journal of Biological Chemistry, 1998, 273, 17251-17257.	3.4	76
50	Impaired expression of the plastidic ferrochelatase by antisense RNA synthesis leads to a necrotic phenotype of transformed tobacco plants. Plant Journal, 2001, 28, 41-50.	5.7	76
51	Physiological and proteomic characterization of manganese sensitivity and tolerance in rice (Oryza) Tj ETQq1 1 0.784314 rgBT /Overl	2.9	76
52	Aluminum resistance in common bean (<i>Phaseolus vulgaris</i>) involves induction and maintenance of citrate exudation from root apices. Physiologia Plantarum, 2010, 138, 176-190.	5.2	73
53	Characterization of leaf apoplastic peroxidases and metabolites in Vigna unguiculata in response to toxic manganese supply and silicon. Journal of Experimental Botany, 2009, 60, 1663-1678.	4.8	72
54	Quantitative Multilevel Analysis of Central Metabolism in Developing Oilseeds of Oilseed Rape during in Vitro Culture. Plant Physiology, 2015, 168, 828-848.	4.8	71

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55	Proteomic Profiling Unravels Insights into the Molecular Background Underlying Increased Aphanomyces euteiches-Tolerance of Medicago truncatula. Plant Molecular Biology, 2005, 59, 387-406.	3.9	69
56	Absence of Complex I Implicates Rearrangement of the Respiratory Chain in European Mistletoe. Current Biology, 2018, 28, 1606-1613.e4.	3.9	68
57	Mitochondrial gamma carbonic anhydrases are required for complex <scp>I</scp> assembly and plant reproductive development. New Phytologist, 2016, 211, 194-207.	7.3	67
58	Gamma carbonic anhydrase like complex interact with plant mitochondrial complex I. Plant Molecular Biology, 2004, 56, 947-957.	3.9	66
59	Carbonic anhydrase subunits of the mitochondrial NADH dehydrogenase complex (complex I) in plants. Physiologia Plantarum, 2007, 129, 114-122.	5.2	64
60	Fatty Acid Biosynthesis in Mitochondria of Grasses: Malonyl-Coenzyme A Is Generated by a MitochondrialLocalized Acetyl-Coenzyme A Carboxylase. Plant Physiology, 2003, 133, 875-884.	4.8	62
61	Analysis of cell wall proteins regulated in stem of susceptible and resistant tomato species after inoculation with Ralstonia solanacearum: a proteomic approach. Plant Molecular Biology, 2010, 73, 643-658.	3.9	59
62	The protein-import apparatus of plant mitochondria. Planta, 1999, 209, 267-274.	3.2	58
63	Alloplasmic male sterility in Brassica napus (CMS 'Tournefortii-Stiewe') is associated with a special gene arrangement around a novel atp9 gene. Molecular Genetics and Genomics, 2003, 269, 723-731.	2.1	58
64	3D Gel Map of Arabidopsis Complex I. Frontiers in Plant Science, 2013, 4, 153.	3.6	58
65	A structural investigation of complex I and I+III2 supercomplex from Zea mays at 11â€“13ÂÃ… resolution: Assignment of the carbonic anhydrase domain and evidence for structural heterogeneity within complex I. Biochimica Et Biophysica Acta - Bioenergetics, 2008, 1777, 84-93.	1.0	57
66	Engineering photorespiration: current state and future possibilities. Plant Biology, 2013, 15, 754-758.	3.8	57
67	The Mitochondrial Sulfur Dioxygenase ETHYLMALONIC ENCEPHALOPATHY PROTEIN1 Is Required for Amino Acid Catabolism during Carbohydrate Starvation and Embryo Development in Arabidopsis Â Â. Plant Physiology, 2014, 165, 92-104.	4.8	57
68	Cytochrome c1 from potato: a protein with a presequence for targeting to the mitochondrial intermembrane space. Molecular Genetics and Genomics, 1992, 231, 217-225.	2.4	55
69	The bifunctional cytochromec reductase/processing peptidase complex from plant mitochondria. Journal of Bioenergetics and Biomembranes, 1995, 27, 423-436.	2.3	55
70	Biochemical characterization of proline dehydrogenase in Arabidopsis mitochondria. FEBS Journal, 2014, 281, 2794-2804.	4.7	54
71	Affinity purification of cytochrome c reductase from potato mitochondria. FEBS Journal, 1992, 208, 761-767.	0.2	53
72	Mitochondrial complex <scp>II</scp> of plants: subunit composition, assembly, and function in respiration and signaling. Plant Journal, 2019, 98, 405-417.	5.7	52

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73	A ferredoxin bridge connects the two arms of plant mitochondrial complex I. Plant Cell, 2021, 33, 2072-2091.	6.6	52
74	HSP68 â€” a DnaK-like heat-stress protein of plant mitochondria. Planta, 1993, 190, 32-43.	3.2	50
75	The general mitochondrial processing peptidase from wheat is integrated into the cytochrome bc 1-complex of the respiratory chain. Planta, 1995, 195, 396-402.	3.2	50
76	Blue native DIGE as a tool for comparative analyses of protein complexes. Journal of Proteomics, 2009, 72, 539-544.	2.4	50
77	Lack of cytochrome c in Arabidopsis decreases stability of Complex IV and modifies redox metabolism without affecting Complexes I and III. Biochimica Et Biophysica Acta - Bioenergetics, 2012, 1817, 990-1001.	1.0	50
78	Analysis of membraneâ€“protein complexes of the marine sulfate reducer <i>Desulfobacula toluolica</i> Tol2 by 1D blue nativeâ€PAGE complexome profiling and 2D blue nativeâ€/SDSâ€PAGE. Proteomics, 2016, 16, 973-988.	2.2	49
79	Proteomic Approach to Identify Novel Mitochondrial Proteins in Arabidopsis. Plant Physiology, 2001, 127, 1694-1710.	4.8	48
80	Proteomic and functional analysis of proline dehydrogenase 1 link proline catabolism to mitochondrial electron transport in <i>Arabidopsis thaliana</i>. Biochemical Journal, 2016, 473, 2623-2634.	3.7	47
81	Proline oxidation fuels mitochondrial respiration during dark-induced leaf senescence in Arabidopsis thaliana. Journal of Experimental Botany, 2019, 70, 6203-6214.	4.8	47
82	New Insights into the Co-evolution of Cytochrome cReductase and the Mitochondrial Processing Peptidase. Journal of Biological Chemistry, 1998, 273, 13143-13149.	3.4	46
83	Proteomic approach to characterize mitochondrial complex I from plants. Phytochemistry, 2011, 72, 1071-1080.	2.9	46
84	Comparative proteomic analysis of early somatic and zygotic embryogenesis in Theobroma cacao L.. Journal of Proteomics, 2013, 78, 123-133.	2.4	46
85	Functional characterization of mutants affected in the carbonic anhydrase domain of the respiratory complexÂI in <i><scp>A</scp>rabidopsis thaliana</i>. Plant Journal, 2015, 83, 831-844.	5.7	46
86	Complex Iâ€“complex II ratio strongly differs in various organs of Arabidopsis thaliana. Plant Molecular Biology, 2012, 79, 273-284.	3.9	45
87	The ADP/ATP translocator from potato has a long amino-terminal extension. Current Genetics, 1991, 20, 405-410.	1.7	44
88	From callus to embryo: a proteomic view on the development and maturation of somatic embryos in Cyclamen persicum. Planta, 2012, 235, 995-1011.	3.2	44
89	Identification of novel subunits of the TOM complex from Arabidopsis thaliana. Plant Physiology and Biochemistry, 2003, 41, 407-416.	5.8	43
90	D-Lactate dehydrogenase links methylglyoxal degradation and electron transport through cytochrome C. Plant Physiology, 2016, 172, pp.01174.2016.	4.8	42

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91	Proteomic and physiological responses of the halophyte Cakile maritima to moderate salinity at the germinative and vegetative stages. Journal of Proteomics, 2012, 75, 5667-5694.	2.4	41
92	Pathogenesis and stress related, as well as metabolic proteins are regulated in tomato stems infected with Ralstonia solanacearum. Plant Physiology and Biochemistry, 2009, 47, 838-846.	5.8	39
93	The enigmatic mitochondrial ORF ymf39 codes for ATP synthase chain b. Nucleic Acids Research, 2003, 31, 2353-2360.	14.5	38
94	Ectopic expression of mitochondrial gamma carbonic anhydrase 2 causes male sterility by anther indehiscence. Plant Molecular Biology, 2009, 70, 471-485.	3.9	38
95	Proteomic and phosphoproteomic analysis of polyethylene glycol-induced osmotic stress in root tips of common bean (Phaseolus vulgaris L.). Journal of Experimental Botany, 2013, 64, 5569-5586.	4.8	38
96	Complexome Profiling Reveals Association of PPR Proteins with Ribosomes in the Mitochondria of Plants. Molecular and Cellular Proteomics, 2019, 18, 1345-1362.	3.8	38
97	Proteomic approach for investigation of cytoplasmic male sterility (CMS) in Brassica. Journal of Plant Physiology, 2001, 158, 787-794.	3.5	37
98	The mitochondrial processing peptidase. International Journal of Biochemistry and Cell Biology, 1997, 29, 1043-1045.	2.8	36
99	Enolases: storage compounds in seeds? Evidence from a proteomic comparison of zygotic and somatic embryos of Cyclamen persicum Mill.. Plant Molecular Biology, 2011, 75, 305-319.	3.9	36
100	<scp>RNA PROCESSING FACTOR</scp> 5 is required for efficient 5â€² cleavage at a processing site conserved in <scp>RNA</scp>s of three different mitochondrial genes in <i><scp>A</scp>rabidopsis thaliana</i>. Plant Journal, 2013, 74, 593-604.	5.7	35
101	High salinity impacts germination of the halophyte <scp><i>Cakile maritima</i></scp> but primes seeds for rapid germination upon stress release. Physiologia Plantarum, 2018, 164, 134-144.	5.2	35
102	The mitochondrial processing peptidase from potato: a self-processing enzyme encoded by two differentially expressed genes. Molecular Genetics and Genomics, 1994, 245, 237-245.	2.4	34
103	Depletion of the â€œgamma-type carbonic anhydrase-likeâ€•subunits of complex I affects central mitochondrial metabolism in Arabidopsis thaliana. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 60-71.	1.0	34
104	3-Hydroxyisobutyrate Dehydrogenase Is Involved in Both, Valine and Isoleucine Degradation in <i>Arabidopsis thaliana</i>. Plant Physiology, 2017, 175, 51-61.	4.8	33
105	Molecular features, processing and import of the Rieske iron-sulfur protein from potato mitochondria. Plant Molecular Biology, 1994, 25, 271-281.	3.9	32
106	AtFer4 ferritin is a determinant of iron homeostasis in Arabidopsis thaliana heterotrophic cells. Journal of Plant Physiology, 2010, 167, 1598-1605.	3.5	31
107	Proteome adaptations in Ethe1-deficient mice indicate a role in lipid catabolism and cytoskeleton organization via post-translational protein modifications. Bioscience Reports, 2013, 33, .	2.4	31
108	Structure and function of complex I in animals and plantsÂâ€"Âa comparative view. Physiologia Plantarum, 2017, 161, 6-15.	5.2	31

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109	SDH6 and SDH7 Contribute to Anchoring Succinate Dehydrogenase to the Inner Mitochondrial Membrane in <i>Arabidopsis thaliana</i>. Plant Physiology, 2017, 173, 1094-1108.	4.8	30
110	Molecular identification of the ten subunits of cytochrome-c reductase from potato mitochondria. Planta, 1994, 193, 99-106.	3.2	29
111	The carbonic anhydrase domain of plant mitochondrial complex I. Physiologia Plantarum, 2016, 157, 289-296.	5.2	29
112	Purification and sequencing of cytochromebfrom potato reveals methionine cleavage of a mitochondriallly encoded protein. FEBS Letters, 1993, 316, 128-132.	2.8	28
113	Medicago truncatula proteomics. Journal of Proteomics, 2010, 73, 1974-1985.	2.4	28
114	GelMapâ€"A novel software tool for building and presenting proteome reference maps. Journal of Proteomics, 2011, 74, 2214-2219.	2.4	28
115	Mitochondria in parasitic plants. Mitochondrion, 2020, 52, 173-182.	3.4	28
116	Cardiolipin Supports Respiratory Enzymes in Plants in Different Ways. Frontiers in Plant Science, 2017, 08, 72.	3.6	27
117	CEDAR, an online resource for the reporting and exploration of complexome profiling data. Biochimica Et Biophysica Acta - Bioenergetics, 2021, 1862, 148411.	1.0	27
118	Cytochrome c Reductase from Potato Does not Comprise Three Core Proteins but Contains an Additional Low-Molecular-Mass Subunit. FEBS Journal, 1995, 228, 878-885.	0.2	27
119	Two-Dimensional Blue Native/Blue Native Polyacrylamide Gel Electrophoresis for the Characterization of Mitochondrial Protein Complexes and Supercomplexes. Methods in Molecular Biology, 2007, 372, 315-324.	0.9	26
120	Extended darkness induces internal turnover of glucosinolates in Arabidopsis thaliana leaves. PLoS ONE, 2018, 13, e0202153.	2.5	24
121	Supramolecular structure of the OXPHOS system in highly thermogenic tissue of Arum maculatum. Plant Physiology and Biochemistry, 2010, 48, 265-272.	5.8	23
122	The mitochondrial proteome of the model legume Medicago truncatula. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1658-1668.	2.3	23
123	The â€˜protein complex proteomeâ€™ of chloroplasts in Arabidopsis thaliana. Journal of Proteomics, 2013, 91, 73-83.	2.4	23
124	The â€˜Hingeâ€™ protein of cytochrome c reductase from potato lacks the acidic domain and has no cleavable presequence. FEBS Letters, 1994, 347, 90-94.	2.8	22
125	Estimating the number of protein molecules in a plant cell: protein and amino acid homeostasis during drought. Plant Physiology, 2021, 185, 385-404.	4.8	21
126	The Native Structure and Composition of the Cruciferin Complex in Brassica napus. Journal of Biological Chemistry, 2013, 288, 2238-2245.	3.4	20

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127	Dealing with the sulfur part of cysteine: four enzymatic steps degrade <scp>l</scp>â€cysteine to pyruvate and thiosulfate in Arabidopsis mitochondria. Physiologia Plantarum, 2016, 157, 352-366.	5.2	20
128	Primary structure and expression of a gene encoding the cytosolic ribosomal protein S4 from potato. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1994, 1218, 435-438.	2.4	19
129	Functional Annotation of 2D Protein Maps: The GelMap Portal. Frontiers in Plant Science, 2012, 3, 87.	3.6	19
130	Proteomic analysis dissects the impact of nodulation and biological nitrogen fixation on Vicia faba root nodule physiology. Plant Molecular Biology, 2018, 97, 233-251.	3.9	19
131	Cellular Plasticity in Response to Suppression of Storage Proteins in the Brassica napus Embryo. Plant Cell, 2020, 32, 2383-2401.	6.6	19
132	A possible role for the chloroplast pyruvate dehydrogenase complex in plant glycolate and glyoxylate metabolism. Phytochemistry, 2013, 95, 168-176.	2.9	18
133	Activity Measurements of Mitochondrial Enzymes in Native Gels. Methods in Molecular Biology, 2015, 1305, 131-138.	0.9	18
134	One C-to-U RNA Editing Site and Two Independently Evolved Editing Factors: Testing Reciprocal Complementation with DYW-Type PPR Proteins from the Moss <i>Physcomitrium</i> (<i>Physcomitrella</i>) <i>patens</i> and the Flowering Plants <i>Macadamia integrifolia</i> and Arabidopsis. Plant Cell, 2020, 32, 2997-3018.	6.6	18
135	Brassica napus seed endosperm â€" Metabolism and signaling in a dead end tissue. Journal of Proteomics, 2014, 108, 382-426.	2.4	17
136	The 23-kDa light-stress-regulated heat-shock protein of Chenopodium rubrum L. is located in the mitochondria. Planta, 1997, 201, 326-333.	3.2	16
137	Blue-Native Gel Electrophoresis for the Characterization of Protein Complexes in Plants. , 2007, 355, 343-352.		16
138	Differential impact of amino acids on OXPHOS system activity following carbohydrate starvation in Arabidopsis cell suspensions. Physiologia Plantarum, 2017, 161, 451-467.	5.2	16
139	Comparative analysis of salt-induced changes in the root proteome of two accessions of the halophyte Cakile maritima. Plant Physiology and Biochemistry, 2018, 130, 20-29.	5.8	16
140	Cytochrome c Reductase from Potato Does not Comprise Three Core Proteins but Contains an Additional Low-Molecular-Mass Subunit. FEBS Journal, 1995, 228, 878-885.	0.2	14
141	Effects of Clostridium difficile Toxin A on the proteome of colonocytes studied by differential 2D electrophoresis. Journal of Proteomics, 2011, 75, 469-479.	2.4	13
142	The Mitochondrial Complexome of Medicago truncatula. Frontiers in Plant Science, 2013, 4, 84.	3.6	13
143	Primary structure, cell-free synthesis and mitochondrial targeting of the 8.2 kDa protein of cytochrome c reductase from potato. Biochimica Et Biophysica Acta - Bioenergetics, 1994, 1188, 367-372.	1.0	12
144	Molecular structure of the 8.0 kDa subunit of cytochrome-c reductase from potato and its Î”Ïˆ-dependent import into isolated mitochondria. Biochimica Et Biophysica Acta - Bioenergetics, 1995, 1229, 181-186.	1.0	12

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145	Proteomic and histological analyses of endosperm development in Cyclamen persicum as a basis for optimization of somatic embryogenesis. Plant Science, 2013, 201-202, 52-65.	3.6	12
146	Differential proteomics analysis of Frankliniella occidentalis immune response after infection with Tomato spotted wilt virus (Tospovirus). Developmental and Comparative Immunology, 2017, 67, 1-7.	2.3	12
147	The two high molecular weight subunits of cytochrome c reductase from potato are immunologically related to the mitochondrial processing enhancing protein. Biochimica Et Biophysica Acta - Bioenergetics, 1993, 1142, 306-310.	1.0	11
148	Molecular Features and Mitochondrial Import Pathway of the 14-Kilodalton Subunit of Cytochrome c Reductase from Potato. Plant Physiology, 1995, 107, 1217-1223.	4.8	11
149	Lowâ€SDS Blue native PAGE. Proteomics, 2011, 11, 1834-1839.	2.2	11
150	Composition and Stability of the Oxidative Phosphorylation System in the Halophile Plant Cakile maritima. Frontiers in Plant Science, 2019, 10, 1010.	3.6	11
151	Protein interaction patterns in Arabidopsis thaliana leaf mitochondria change in dependence to light. Biochimica Et Biophysica Acta - Bioenergetics, 2021, 1862, 148443.	1.0	11
152	Structure of the bc1 Complex from Seculamonas ecuadoriensis, a Jakobid Flagellate with an Ancestral Mitochondrial Genome. Molecular Biology and Evolution, 2003, 20, 145-153.	8.9	10
153	Recovery aptitude of the halophyte Cakile maritima upon water deficit stress release is sustained by extensive modulation of the leaf proteome. Ecotoxicology and Environmental Safety, 2019, 179, 198-211.	6.0	9
154	The gene space of European mistletoe (Viscum album). Plant Journal, 2021, , .	5.7	9
155	Characterization of the PetM subunit of the b6f complex from higher plants. Journal of Plant Physiology, 1998, 153, 581-586.	3.5	8
156	Identification of regulated proteins in naked barley grains (Hordeum vulgare nudum) after Fusarium graminearum infection at different grain ripening stages. Journal of Proteomics, 2016, 133, 86-92.	2.4	8
157	The Role of Persulfide Metabolism During Arabidopsis Seed Development Under Light and Dark Conditions. Frontiers in Plant Science, 2018, 9, 1381.	3.6	8
158	Stability of thylakoid protein complexes and preserving photosynthetic efficiency are crucial for the successful recovery of the halophyte Cakile maritima from high salinity. Plant Physiology and Biochemistry, 2021, 166, 177-190.	5.8	8
159	Proteomic approach to characterize the supramolecular organization of photosystems in higher plants. Phytochemistry, 2004, 65, 1683-1683.	2.9	7
160	Chapter 10 Purification of the Cytochrome c Reductase/Cytochrome c Oxidase Super Complex of Yeast Mitochondria. Methods in Enzymology, 2009, 456, 183-190.	1.0	7
161	Approximate calculation and experimental derivation of native isoelectric points of membrane protein complexes of Arabidopsis chloroplasts and mitochondria. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 1036-1046.	2.6	7
162	Sample Preparation for Analysis of the Plant Mitochondrial Membrane Proteome. Methods in Molecular Biology, 2018, 1696, 163-183.	0.9	7

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163	The Role of the Leaf Apoplast in Manganese Toxicity and Tolerance in Cowpea (Vigna Unguiculata L.) Tj ETQq1 1 0.784314 rgBT /Overlo		7
164	[6] Cytochrome-c reductase/processing peptidase complex from potato mitochondria. Methods in Enzymology, 1995, 260, 70-82.	1.0	6
165	Comparative Analyses of Protein Complexes by Blue Native DIGE. Methods in Molecular Biology, 2012, 854, 145-154.	0.9	6
166	Proteomics in Plant Biology. , 2003, , 409-416.		6
167	Subunit VII of ubiquinol:cytochrome-c oxidoreductase from Neurospora crassa is functional in yeast and has an N-terminal extension that is not essential for mitochondrial targeting. Biochemical Journal, 1996, 320, 769-775.	3.7	4
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