## Hans-Peter Braun

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Complexome Profiling of Plant Mitochondrial Fractions. Methods in Molecular Biology, 2022, 2363, 101-110.	0.9	3
2	The role of the electronâ€ŧransfer flavoprotein: ubiquinone oxidoreductase following carbohydrate starvation in Arabidopsis cell cultures. Plant Cell Reports, 2022, 41, 431-446.	5.6	3
3	Changes in leaf ecophysiological traits and proteome profile provide new insights into variability of salt response in the succulent halophyte Cakile maritima. Functional Plant Biology, 2022, , .	2.1	4
4	The complexome profiling approach for direct biochemical analysis of multiprotein assemblies. Biochimica Et Biophysica Acta - Bioenergetics, 2022, 1863, 148522.	1.0	2
5	A ferredoxin bridge connects the two arms of plant mitochondrial complex I. Plant Cell, 2021, 33, 2072-2091.	6.6	52
6	CEDAR, an online resource for the reporting and exploration of complexome profiling data. Biochimica Et Biophysica Acta - Bioenergetics, 2021, 1862, 148411.	1.0	27
7	Protein interaction patterns in Arabidopsis thaliana leaf mitochondria change in dependence to light. Biochimica Et Biophysica Acta - Bioenergetics, 2021, 1862, 148443.	1.0	11
8	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
9	The two roles of complex III in plants. ELife, 2021, 10, .	6.0	4
10	The gene space of European mistletoe ( Viscum album ). Plant Journal, 2021, , .	5.7	9
11	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
12	Single organelle function and organization as estimated from Arabidopsis mitochondrial proteomics. Plant Journal, 2020, 101, 420-441.	5.7	152
13	Cellular Plasticity in Response to Suppression of Storage Proteins in the Brassica napus Embryo. Plant Cell, 2020, 32, 2383-2401.	6.6	19
14	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
15	Mitochondria in parasitic plants. Mitochondrion, 2020, 52, 173-182.	3.4	28
16	The Oxidative Phosphorylation system of the mitochondria in plants. Mitochondrion, 2020, 53, 66-75.	3.4	78
17	Composition and Stability of the Oxidative Phosphorylation System in the Halophile Plant Cakile maritima. Frontiers in Plant Science, 2019, 10, 1010.	3.6	11
18	Proline oxidation fuels mitochondrial respiration during dark-induced leaf senescence in Arabidopsis thaliana. Journal of Experimental Botany, 2019, 70, 6203-6214.	4.8	47

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19	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
20	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
21	The role of amino acid metabolism during abiotic stress release. Plant, Cell and Environment, 2019, 42, 1630-1644.	5.7	278
22	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
23	Absence of Complex I Implicates Rearrangement of the Respiratory Chain in European Mistletoe. Current Biology, 2018, 28, 1606-1613.e4.	3.9	68
24	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
25	Sample Preparation for Analysis of the Plant Mitochondrial Membrane Proteome. Methods in Molecular Biology, 2018, 1696, 163-183.	0.9	7
26	The Role of Persulfide Metabolism During Arabidopsis Seed Development Under Light and Dark Conditions. Frontiers in Plant Science, 2018, 9, 1381.	3.6	8
27	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
28	Extended darkness induces internal turnover of glucosinolates in Arabidopsis thaliana leaves. PLoS ONE, 2018, 13, e0202153.	2.5	24
29	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
30	Structure and function of complex I in animals and plants–Âa comparative view. Physiologia Plantarum, 2017, 161, 6-15.	5.2	31
31	The mitochondrial complexome of <i>Arabidopsis thaliana</i> . Plant Journal, 2017, 89, 1079-1092.	5.7	192
32	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
33	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
34	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
35	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
36	Cardiolipin Supports Respiratory Enzymes in Plants in Different Ways. Frontiers in Plant Science, 2017, 08, 72.	3.6	27

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37	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
38	The carbonic anhydrase domain of plant mitochondrial complex I. Physiologia Plantarum, 2016, 157, 289-296.	5.2	29
39	Dealing with the sulfur part of cysteine: four enzymatic steps degrade <scp>l</scp> ysteine to pyruvate and thiosulfate in Arabidopsis mitochondria. Physiologia Plantarum, 2016, 157, 352-366.	5.2	20
40	Analysis of membrane–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
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	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
43	D-Lactate dehydrogenase links methylglyoxal degradation and electron transport through cytochrome C. Plant Physiology, 2016, 172, pp.01174.2016.	4.8	42
44	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
45	Depletion of the "gamma-type carbonic anhydrase-like―subunits of complex I affects central mitochondrial metabolism in Arabidopsis thaliana. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 60-71.	1.0	34
46	Functional characterization of mutants affected in the carbonic anhydrase domain of the respiratory complexÂl in <i><scp>A</scp>rabidopsis thaliana</i> . Plant Journal, 2015, 83, 831-844.	5.7	46
47	Activity Measurements of Mitochondrial Enzymes in Native Gels. Methods in Molecular Biology, 2015, 1305, 131-138.	0.9	18
48	Amino Acid Catabolism in Plants. Molecular Plant, 2015, 8, 1563-1579.	8.3	898
49	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
50	Identification of Differently Regulated Proteins after Fusarium graminearum Infection of Emmer (Triticum dicoccum) at Several Grain Ripening Stages. Food Technology and Biotechnology, 2015, 53, 261-268.	2.1	2
51	The Arabidopsis Class II Sirtuin Is a Lysine Deacetylase and Interacts with Mitochondrial Energy Metabolism   Â. Plant Physiology, 2014, 164, 1401-1414.	4.8	96
52	Respiratory electron transfer pathways in plant mitochondria. Frontiers in Plant Science, 2014, 5, 163.	3.6	209
53	The Mitochondrial Sulfur Dioxygenase ETHYLMALONIC ENCEPHALOPATHY PROTEIN1 Is Required for Amino Acid Catabolism during Carbohydrate Starvation and Embryo Development in Arabidopsis  Â. Plant Physiology, 2014, 165, 92-104.	4.8	57
54	Biochemical characterization of proline dehydrogenase in Arabidopsis mitochondria. FEBS Journal, 2014, 281, 2794-2804.	4.7	54

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55	The life of plant mitochondrial complex I. Mitochondrion, 2014, 19, 295-313.	3.4	103
56	Brassica napus seed endosperm — Metabolism and signaling in a dead end tissue. Journal of Proteomics, 2014, 108, 382-426.	2.4	17
57	Respiratory Chain Supercomplexes in Mitochondria. Advances in Photosynthesis and Respiration, 2014, , 217-229.	1.0	2
58	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
59	The â€~protein complex proteome' of chloroplasts in Arabidopsis thaliana. Journal of Proteomics, 2013, 91, 73-83.	2.4	23
60	A possible role for the chloroplast pyruvate dehydrogenase complex in plant glycolate and glyoxylate metabolism. Phytochemistry, 2013, 95, 168-176.	2.9	18
61	The Native Structure and Composition of the Cruciferin Complex in Brassica napus. Journal of Biological Chemistry, 2013, 288, 2238-2245.	3.4	20
62	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
63	Engineering photorespiration: current state and future possibilities. Plant Biology, 2013, 15, 754-758.	3.8	57
64	Comparative proteomic analysis of early somatic and zygotic embryogenesis in Theobroma cacao L Journal of Proteomics, 2013, 78, 123-133.	2.4	46
65	<pre><scp>RNA PROCESSING FACTOR</scp> 5 is required for efficient 5′ 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.</pre>	5.7	35
66	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
67	Seed Architecture Shapes Embryo Metabolism in Oilseed Rape Â. Plant Cell, 2013, 25, 1625-1640.	6.6	109
68	3D Gel Map of Arabidopsis Complex I. Frontiers in Plant Science, 2013, 4, 153.	3.6	58
69	The Mitochondrial Complexome of Medicago truncatula. Frontiers in Plant Science, 2013, 4, 84.	3.6	13
70	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
71	Functional Annotation of 2D Protein Maps: The GelMap Portal. Frontiers in Plant Science, 2012, 3, 87.	3.6	19
72	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

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73	Organellar Proteomics: Close Insights into the Spatial Breakdown and Functional Dynamics of Plant Primary Metabolism. Advances in Photosynthesis and Respiration, 2012, , 357-378.	1.0	1
74	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
75	A basal carbon concentrating mechanism in plants?. Plant Science, 2012, 187, 97-104.	3.6	79
76	Comparative Analyses of Protein Complexes by Blue Native DIGE. Methods in Molecular Biology, 2012, 854, 145-154.	0.9	6
77	DIGE Analysis of Plant Tissue Proteomes Using a Phenolic Protein Extraction Method. Methods in Molecular Biology, 2012, 854, 335-342.	0.9	2
78	Complex l–complex II ratio strongly differs in various organs of Arabidopsis thaliana. Plant Molecular Biology, 2012, 79, 273-284.	3.9	45
79	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
80	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
81	Defining the <i>Protein Complex Proteome</i> of Plant Mitochondria Â. Plant Physiology, 2011, 157, 587-598.	4.8	164
82	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
83	The mitochondrial proteome of the model legume Medicago truncatula. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1658-1668.	2.3	23
84	Biogenesis and Supramolecular Organization of the Oxidative Phosphorylation System in Plants. , 2011, , 327-355.		3
85	GelMap—A novel software tool for building and presenting proteome reference maps. Journal of Proteomics, 2011, 74, 2214-2219.	2.4	28
86	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
87	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
88	Lowâ€ <b>S</b> DS Blue native PAGE. Proteomics, 2011, 11, 1834-1839.	2.2	11
89	Proteomic approach to characterize mitochondrial complex I from plants. Phytochemistry, 2011, 72, 1071-1080.	2.9	46
90	Supramolecular structure of the OXPHOS system in highly thermogenic tissue of Arum maculatum. Plant Physiology and Biochemistry, 2010, 48, 265-272.	5.8	23

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91	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
92	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
93	Structure and function of mitochondrial supercomplexes. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 664-670.	1.0	177
94	Medicago truncatula proteomics. Journal of Proteomics, 2010, 73, 1974-1985.	2.4	28
95	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
96	ESTABLISHMENT OF PROTEOME REFERENCE MAPS FOR SOMATIC AND ZYGOTIC EMBRYOS OF CYCLAMEN PERSICUM MILL Acta Horticulturae, 2010, , 239-242.	0.2	1
97	Internal Architecture of Mitochondrial Complex I from <i>Arabidopsis thaliana</i> . Plant Cell, 2010, 22, 797-810.	6.6	187
98	Physiological and proteomic characterization of manganese sensitivity and tolerance in rice (Oryza) Tj ETQq0 0 0	rgBT /Ove	erlock 10 Tf S
99	AtFer4 ferritin is a determinant of iron homeostasis in Arabidopsis thaliana heterotrophic cells. Journal of Plant Physiology, 2010, 167, 1598-1605.	3.5	31
100	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

101	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
102	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
103	Ectopic expression of mitochondrial gamma carbonic anhydrase 2 causes male sterility by anther indehiscence. Plant Molecular Biology, 2009, 70, 471-485.	3.9	38
104	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
105	Blue native DIGE as a tool for comparative analyses of protein complexes. Journal of Proteomics, 2009, 72, 539-544.	2.4	50
106	The higher level of organization of the oxidative phosphorylation system: mitochondrial supercomplexes. Journal of Bioenergetics and Biomembranes, 2008, 40, 419-424.	2.3	83
107	Early manganeseâ€ŧoxicity response in <b><i>Vigna unguiculata</i></b> L. – a proteomic and transcriptomic study. Proteomics, 2008, 8, 149-159.	2.2	88
108	A structural investigation of complex I and I+III2 supercomplex from Zea mays at 11–13Âà 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

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109	Blue-Native Gel Electrophoresis for the Characterization of Protein Complexes in Plants. , 2007, 355, 343-352.		16
110	A Structural Model of the Cytochrome c Reductase/Oxidase Supercomplex from Yeast Mitochondria. Journal of Biological Chemistry, 2007, 282, 12240-12248.	3.4	145
111	Supramolecular Structure of the Mitochondrial Oxidative Phosphorylation System. Journal of Biological Chemistry, 2007, 282, 1-4.	3.4	195
112	Carbonic anhydrase subunits of the mitochondrial NADH dehydrogenase complex (complex I) in plants. Physiologia Plantarum, 2007, 129, 114-122.	5.2	64
113	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
114	The Role of the Leaf Apoplast in Manganese Toxicity and Tolerance in Cowpea (Vigna Unguiculata L.) Tj ETQq0 0	0 rgBT /Oי	verlock 10 Tf
115	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
116	Characterization of dimeric ATP synthase and cristae membrane ultrastructure fromSaccharomycesandPolytomellamitochondria. FEBS Letters, 2006, 580, 3427-3432.	2.8	139
117	Respiratory chain supercomplexes in the plant mitochondrial membrane. Trends in Plant Science, 2006, 11, 232-240.	8.8	116
118	Blue native PAGE. Nature Protocols, 2006, 1, 418-428.	12.0	1,502
119	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
120	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
121	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
122	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
123	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
124	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
125	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
126	The plant mitochondrial proteome. Trends in Plant Science, 2005, 10, 36-43.	8.8	188

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127	Blue-native PAGE in plants: a tool in analysis of protein-protein interactions. Plant Methods, 2005, 1, 11.	4.3	144
128	Identification and Characterization of Respirasomes in Potato Mitochondria. Plant Physiology, 2004, 134, 1450-1459.	4.8	166
129	Respiratory chain supercomplexes in plant mitochondria. Plant Physiology and Biochemistry, 2004, 42, 937-942.	5.8	126
130	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
131	Mitochondrial cytochrome c oxidase and succinate dehydrogenase complexes contain plant specific subunits. Plant Molecular Biology, 2004, 56, 77-90.	3.9	184
132	Gamma carbonic anhydrase like complex interact with plant mitochondrial complex I. Plant Molecular Biology, 2004, 56, 947-957.	3.9	66
133	Proteomic approach to characterize the supramolecular organization of photosystems in higher plants. Phytochemistry, 2004, 65, 1683-1692.	2.9	117
134	Proteomic approach to characterize the supramolecular organization of photosystems in higher plants. Phytochemistry, 2004, 65, 1683-1683.	2.9	7
135	Proteome Analyses for Characterization of Plant Mitochondria. Advances in Photosynthesis and Respiration, 2004, , 143-162.	1.0	2
136	Mitochondrial processing peptidase. , 2004, , 882-886.		0
137	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
138	Identification of novel subunits of the TOM complex from Arabidopsis thaliana. Plant Physiology and Biochemistry, 2003, 41, 407-416.	5.8	43
139	Arabidopsisphosphatidylglycerophosphate synthase 1 is essential for chloroplast differentiation, but is dispensable for mitochondrial function. Plant Journal, 2003, 33, 899-909.	5.7	147
140	Effect of Manganese Toxicity on the Proteome of the Leaf Apoplast in Cowpea. Plant Physiology, 2003, 133, 1935-1946.	4.8	183
141	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
142	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
143	The enigmatic mitochondrial ORF ymf39 codes for ATP synthase chain b. Nucleic Acids Research, 2003, 31, 2353-2360.	14.5	38
144	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

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145	Proteomics in Plant Biology. , 2003, , 409-416.		6
146	Biochemical dissection of the mitochondrial proteome fromArabidopsis thaliana by three-dimensional gel electrophoresis. Electrophoresis, 2002, 23, 640-646.	2.4	151
147	Proteomic approach for investigation of cytoplasmic male sterility (CMS) in Brassica. Journal of Plant Physiology, 2001, 158, 787-794.	3.5	37
148	Proteomic Approach to Identify Novel Mitochondrial Proteins in Arabidopsis. Plant Physiology, 2001, 127, 1694-1710.	4.8	48
149	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
150	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
151	Proteomic Approach to Identify Novel Mitochondrial Proteins in Arabidopsis. Plant Physiology, 2001, 127, 1694-1710.	4.8	369
152	The protein-import apparatus of plant mitochondria. Planta, 1999, 209, 267-274.	3.2	58
153	Characterization of the PetM subunit of the b6f complex from higher plants. Journal of Plant Physiology, 1998, 153, 581-586.	3.5	8
154	Unique Composition of the Preprotein Translocase of the Outer Mitochondrial Membrane from Plants. Journal of Biological Chemistry, 1998, 273, 17251-17257.	3.4	76
155	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
156	The mitochondrial processing peptidase. International Journal of Biochemistry and Cell Biology, 1997, 29, 1043-1045.	2.8	36
157	Title is missing!. Photosynthesis Research, 1997, 53, 35-44.	2.9	158
158	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
159	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
160	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
161	Identification of novel homologues of three low molecular weight subunits of the mitochondrial bc1 complex. Molecular Biology Reports, 1996, 23, 71-77.	2.3	1
162	[6] Cytochrome-c reductase/processing peptidase complex from potato mitochondria. Methods in Enzymology, 1995, 260, 70-82.	1.0	6

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163	Are the â€~core' proteins of the mitochondrial bc1 complex evolutionary relics of a processing protease?. Trends in Biochemical Sciences, 1995, 20, 171-175.	7.5	140
164	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
165	The bifunctional cytochromec reductase/processing peptidase complex from plant mitochondria. Journal of Bioenergetics and Biomembranes, 1995, 27, 423-436.	2.3	55
166	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
167	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
168	Molecular structure of the 8.0 kDa subunit of cytochrome-c reductase from potato and its ΔĨ^-dependent import into isolated mitochondria. Biochimica Et Biophysica Acta - Bioenergetics, 1995, 1229, 181-186.	1.0	12
169	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
170	Molecular identification of the ten subunits of cytochrome-c reductase from potato mitochondria. Planta, 1994, 193, 99-106.	3.2	29
171	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
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