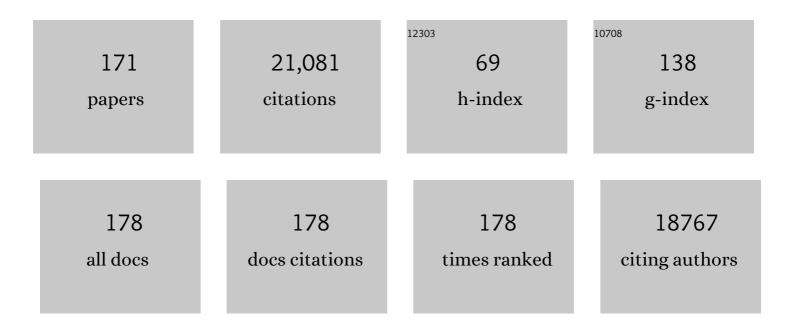
Lee J Sweetlove

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3574066/publications.pdf Version: 2024-02-01



#	Article	lF	CITATIONS
1	A hybrid kinetic and constraintâ€based model of leaf metabolism allows predictions of metabolic fluxes in different environments. Plant Journal, 2022, 109, 295-313.	2.8	9
2	Genomeâ€wide association study reveals that the cupin domain protein OsCDP3.10 regulates seed vigour in rice. Plant Biotechnology Journal, 2022, 20, 485-498.	4.1	26
3	Suppression of metabolite shuttles for export of chloroplast and mitochondrial ATP and NADPH increases the cytosolic NADH:NAD+ ratio in tobacco leaves in the dark. Journal of Plant Physiology, 2022, 268, 153578.	1.6	4
4	The metabolic changes that effect fruit quality during tomato fruit ripening. Molecular Horticulture, 2022, 2, .	2.3	15
5	The Bacillus subtilis glutamate anti-metabolon. Nature Metabolism, 2022, 4, 161-162.	5.1	3
6	Advances in the Understanding of Reactive Oxygen Species-Dependent Regulation on Seed Dormancy, Germination, and Deterioration in Crops. Frontiers in Plant Science, 2022, 13, 826809.	1.7	22
7	Plant metabolic gene clusters in the multi-omics era. Trends in Plant Science, 2022, 27, 981-1001.	4.3	41
8	Ultraviolet-B Radiation Represses Primary Root Elongation by Inhibiting Cell Proliferation in the Meristematic Zone of Arabidopsis Seedlings. Frontiers in Plant Science, 2022, 13, 829336.	1.7	8
9	A <i>Solanum lycopersicoides</i> reference genome facilitates insights into tomato specialized metabolism and immunity. Plant Journal, 2022, 110, 1791-1810.	2.8	16
10	Leaf Mutant 7 Encoding Heat Shock Protein OsHSP40 Regulates Leaf Size in Rice. International Journal of Molecular Sciences, 2022, 23, 4446.	1.8	7
11	Stable and Temporary Enzyme Complexes and Metabolons Involved in Energy and Redox Metabolism. Antioxidants and Redox Signaling, 2021, 35, 788-807.	2.5	14
12	Metabolons, enzyme–enzyme assemblies that mediate substrate channeling, and their roles in plant metabolism. Plant Communications, 2021, 2, 100081.	3.6	78
13	Integrating multi-omics data for crop improvement. Journal of Plant Physiology, 2021, 257, 153352.	1.6	78
14	A genome-wide association study reveals that the glucosyltransferase OsIAGLU regulates root growth in rice. Journal of Experimental Botany, 2021, 72, 1119-1134.	2.4	12
15	IntEResting structures: formation and applications of organized smooth endoplasmic reticulum in plant cells. Plant Physiology, 2021, 185, 550-561.	2.3	7
16	Cytochrome c Deficiency Differentially Affects the In Vivo Mitochondrial Electron Partitioning and Primary Metabolism Depending on the Photoperiod. Plants, 2021, 10, 444.	1.6	3
17	The Rice Small Auxin-Up RNA Gene OsSAUR33 Regulates Seed Vigor via Sugar Pathway during Early Seed Germination. International Journal of Molecular Sciences, 2021, 22, 1562.	1.8	25
18	Evolutionary History of Plant Metabolism. Annual Review of Plant Biology, 2021, 72, 185-216.	8.6	48

#	Article	IF	CITATIONS
19	Plant biotechnology for sustainable agriculture and food safety. Journal of Plant Physiology, 2021, 261, 153416.	1.6	7
20	Advances in the Identification of Quantitative Trait Loci and Genes Involved in Seed Vigor in Rice. Frontiers in Plant Science, 2021, 12, 659307.	1.7	22
21	Return of the Lemnaceae: duckweed as a model plant system in the genomics and postgenomics era. Plant Cell, 2021, 33, 3207-3234.	3.1	111
22	Genome-wide association studies: assessing trait characteristics in model and crop plants. Cellular and Molecular Life Sciences, 2021, 78, 5743-5754.	2.4	54
23	From Affinity to Proximity Techniques to Investigate Protein Complexes in Plants. International Journal of Molecular Sciences, 2021, 22, 7101.	1.8	10
24	A genomeâ€wide association study reveals that the 2â€oxoglutarate/malate translocator mediates seed vigor in rice. Plant Journal, 2021, 108, 478-491.	2.8	13
25	A genome-wide association study reveals that the cytochrome b5 involved in seed reserve mobilization during seed germination in rice. Theoretical and Applied Genetics, 2021, 134, 4067-4076.	1.8	7
26	Plant cell cultures as heterologous bio-factories for secondary metabolite production. Plant Communications, 2021, 2, 100235.	3.6	40
27	The knowns and unknowns of intracellular partitioning of carbon and nitrogen, with focus on the organic acid-mediated interplay between mitochondrion and chloroplast. Journal of Plant Physiology, 2021, 266, 153521.	1.6	13
28	Genome and time-of-day transcriptome of <i>Wolffia australiana</i> link morphological minimization with gene loss and less growth control. Genome Research, 2021, 31, 225-238.	2.4	56
29	E2Fb and E2Fa transcription factors independently regulate the DNA damage response after UVâ€B exposure in Arabidopsis. Plant Journal, 2021, , .	2.8	7
30	The Assembly of Super-Complexes in the Plant Chloroplast. Biomolecules, 2021, 11, 1839.	1.8	5
31	Does the alternative respiratory pathway offer protection against the adverse effects resulting from climate change?. Journal of Experimental Botany, 2020, 71, 465-469.	2.4	23
32	Modelâ€assisted identification of metabolic engineering strategies for <i>Jatropha curcas</i> lipid pathways. Plant Journal, 2020, 104, 76-95.	2.8	11
33	Alternative Crassulacean Acid Metabolism Modes Provide Environment-Specific Water-Saving Benefits in a Leaf Metabolic Model. Plant Cell, 2020, 32, 3689-3705.	3.1	48
34	Multi-gene metabolic engineering of tomato plants results in increased fruit yield up to 23%. Scientific Reports, 2020, 10, 17219.	1.6	15
35	A moonlighting role for enzymes of glycolysis in the co-localization of mitochondria and chloroplasts. Nature Communications, 2020, 11, 4509.	5.8	47
36	The Cassava Source–Sink project: opportunities and challenges for crop improvement by metabolic engineering. Plant Journal, 2020, 103, 1655-1665.	2.8	33

#	Article	IF	CITATIONS
37	Journal Flexibility in the Troubling Times of COVID-19. Plant Physiology, 2020, 182, 1795-1795.	2.3	0
38	Journal Flexibility in the Troubling Times of COVID-19. Plant Cell, 2020, 32, 1337-1337.	3.1	0
39	Towards model-driven characterization and manipulation of plant lipid metabolism. Progress in Lipid Research, 2020, 80, 101051.	5.3	28
40	A Highly Efficient Agrobacterium-Mediated Method for Transient Gene Expression and Functional Studies in Multiple Plant Species. Plant Communications, 2020, 1, 100028.	3.6	85
41	Synchronization of developmental, molecular and metabolic aspects of source–sink interactions. Nature Plants, 2020, 6, 55-66.	4.7	107
42	Multiscale computational models can guide experimentation and targeted measurements for crop improvement. Plant Journal, 2020, 103, 21-31.	2.8	36
43	Flux balance analysis of metabolism during growth by osmotic cell expansion and its application to to tomato fruits. Plant Journal, 2020, 103, 68-82.	2.8	26
44	Indoleâ€3â€acetate betaâ€glucosyltransferase <i>OsIAGLU</i> regulates seed vigour through mediating crosstalk between auxin and abscisic acid in rice. Plant Biotechnology Journal, 2020, 18, 1933-1945.	4.1	44
45	Multiple Metabolic Innovations and Losses Are Associated with Major Transitions in Land Plant Evolution. Current Biology, 2020, 30, 1783-1800.e11.	1.8	42
46	<i>Cis</i> â€regulated alternative splicing divergence and its potential contribution to environmental responses in Arabidopsis. Plant Journal, 2019, 97, 555-570.	2.8	33
47	Influence of isopropylmalate synthase <i>Os<scp>IPMS</scp>1</i> on seed vigour associated with amino acid and energy metabolism in rice. Plant Biotechnology Journal, 2019, 17, 322-337.	4.1	69
48	Physiological characteristics of cold stratification on seed dormancy release in rice. Plant Growth Regulation, 2019, 89, 131-141.	1.8	18
49	SEB â€Wiley―TPJ awards for outstanding papers published in TPJ in 2018. Plant Journal, 2019, 97, 1001-1002.	2.8	0
50	Rapid Identification of Proteinâ€Protein Interactions in Plants. Current Protocols in Plant Biology, 2019, 4, e20099.	2.8	22
51	Editorial: Introducing TPJ Fellowships for early stage Principal Investigators. Plant Journal, 2019, 100, 435-435.	2.8	0
52	Engineering Strategies to Boost Crop Productivity by Cutting Respiratory Carbon Loss. Plant Cell, 2019, 31, 297-314.	3.1	86
53	Metabolomics for understanding stomatal movements. Theoretical and Experimental Plant Physiology, 2019, 31, 91-102.	1.1	18
54	Leaf Energy Balance Requires Mitochondrial Respiration and Export of Chloroplast NADPH in the Light. Plant Physiology, 2019, 180, 1947-1961.	2.3	80

#	Article	IF	CITATIONS
55	AtCAFâ€1 mutants show different DNA damage responses after ultravioletâ€B than those activated by other genotoxic agents in leaves. Plant, Cell and Environment, 2019, 42, 2730-2745.	2.8	10
56	De Novo Domestication: An Alternative Route toward New Crops for the Future. Molecular Plant, 2019, 12, 615-631.	3.9	267
57	A Subsidiary Cell-Localized Glucose Transporter Promotes Stomatal Conductance and Photosynthesis. Plant Cell, 2019, 31, 1328-1343.	3.1	63
58	Metabolite profiles reveal interspecific variation in operation of the Calvin–Benson cycle in both C4 and C3 plants. Journal of Experimental Botany, 2019, 70, 1843-1858.	2.4	47
59	Arabidopsis E2Fc is required for the <scp>DNA</scp> damage response under <scp>UV</scp> â€B radiation epistatically over the micro <scp>RNA</scp> 396 and independently of E2Fe. Plant Journal, 2019, 97, 749-764.	2.8	18
60	A quantitative trait locus, <i><scp>qSE</scp>3</i> , promotes seed germination and seedling establishment under salinity stress in rice. Plant Journal, 2019, 97, 1089-1104.	2.8	107
61	A <i>Solanum neorickii</i> introgression population providing a powerful complement to the extensively characterized <i>Solanum pennellii</i> population. Plant Journal, 2019, 97, 391-403.	2.8	18
62	Editorial. Plant Journal, 2018, 94, 3-5.	2.8	2
63	Computational analysis of the productivity potential of CAM. Nature Plants, 2018, 4, 165-171.	4.7	83
64	Next-generation strategies for understanding and influencing source–sink relations in crop plants. Current Opinion in Plant Biology, 2018, 43, 63-70.	3.5	119
65	Phosphoglycerate Kinases Are Co-Regulated to Adjust Metabolism and to Optimize Growth. Plant Physiology, 2018, 176, 1182-1198.	2.3	62
66	Advances in metabolic flux analysis toward genome-scale profiling of higher organisms. Bioscience Reports, 2018, 38, .	1.1	36
67	Extending the cascade: identification of a mitogenâ€activated protein kinase phosphatase playing a key role in rice yield. Plant Journal, 2018, 95, 935-936.	2.8	1
68	The intertwined metabolism during symbiotic nitrogen fixation elucidated by metabolic modelling. Scientific Reports, 2018, 8, 12504.	1.6	45
69	The role of dynamic enzyme assemblies and substrate channelling in metabolic regulation. Nature Communications, 2018, 9, 2136.	5.8	290
70	The Extra-Pathway Interactome of the TCA Cycle: Expected and Unexpected Metabolic Interactions. Plant Physiology, 2018, 177, 966-979.	2.3	81
71	Generating a highâ€confidence reference genome map of the Greater Duckweed by integration of cytogenomic, optical mapping, and Oxford Nanopore technologies. Plant Journal, 2018, 96, 670-684.	2.8	64
72	Passing the Baton: Substrate Channelling in Respiratory Metabolism. Research, 2018, 2018, 1539325.	2.8	22

#	Article	IF	CITATIONS
73	Growth rate correlates negatively with protein turnover in Arabidopsis accessions. Plant Journal, 2017, 91, 416-429.	2.8	58
74	Protein-protein interactions and metabolite channelling in the plant tricarboxylic acid cycle. Nature Communications, 2017, 8, 15212.	5.8	103
75	UV-B Inhibits Leaf Growth through Changes in Growth Regulating Factors and Gibberellin Levels. Plant Physiology, 2017, 174, 1110-1126.	2.3	79
76	Engineering central metabolism – a grand challenge for plant biologists. Plant Journal, 2017, 90, 749-763.	2.8	78
77	Canalization of Tomato Fruit Metabolism. Plant Cell, 2017, 29, 2753-2765.	3.1	47
78	Developmental reprogramming by UV-B radiation in plants. Plant Science, 2017, 264, 96-101.	1.7	62
79	The Genetics of Plant Metabolism. Annual Review of Genetics, 2017, 51, 287-310.	3.2	118
80	Editorial. Plant Journal, 2017, 91, 359-360.	2.8	0
81	Microcompartmentation of cytosolic aldolase by interaction with the actin cytoskeleton in Arabidopsis. Journal of Experimental Botany, 2017, 68, 885-898.	2.4	16
82	Comprehensive definition of genome features in <i>Spirodela polyrhiza</i> by highâ€depth physical mapping and shortâ€read <scp>DNA</scp> sequencing strategies. Plant Journal, 2017, 89, 617-635.	2.8	115
83	HAC1 and HAF1 Histone Acetyltransferases Have Different Roles in UV-B Responses in Arabidopsis. Frontiers in Plant Science, 2017, 8, 1179.	1.7	24
84	Identification and Characterization of Quantitative Trait Loci for Shattering in Japonica Rice Landrace Jiucaiqing from Taihu Lake Valley, China. Plant Genome, 2016, 9, plantgenome2016.03.0034.	1.6	11
85	Natural variation of H3K27me3 modification in two <i>Arabidopsis</i> accessions and their hybrid. Journal of Integrative Plant Biology, 2016, 58, 466-474.	4.1	17
86	iReMet-flux: constraint-based approach for integrating relative metabolite levels into a stoichiometric metabolic models. Bioinformatics, 2016, 32, i755-i762.	1.8	30
87	Characterization of a recently evolved flavonol-phenylacyltransferase gene provides signatures of natural light selection in Brassicaceae. Nature Communications, 2016, 7, 12399.	5.8	145
88	Acquisition of desiccation tolerance during seed development is associated with oxidative processes in rice. Botany, 2016, 94, 91-101.	0.5	9
89	AtPDCD5 Plays a Role in Programmed Cell Death after UV-B Exposure in Arabidopsis. Plant Physiology, 2016, 170, 2444-2460.	2.3	24
90	Synthetic biology for basic and applied plant research. Plant Journal, 2016, 87, 3-4.	2.8	6

#	Article	IF	CITATIONS
91	<scp>MSL</scp> 1 is a mechanosensitive ion channel that dissipates mitochondrial membrane potential and maintains redox homeostasis in mitochondria during abiotic stress. Plant Journal, 2016, 88, 809-825.	2.8	82
92	The regulatory interplay between photorespiration and photosynthesis. Journal of Experimental Botany, 2016, 67, 2923-2929.	2.4	74
93	Identification of QTLs with Additive, Epistatic, and QTL × Seed Maturity Interaction Effects for Seed Vigor in Rice. Plant Molecular Biology Reporter, 2016, 34, 160-171.	1.0	9
94	Proteomic Analysis Reveals Proteins Involved in Seed Imbibition under Salt Stress in Rice. Frontiers in Plant Science, 2016, 7, 2006.	1.7	32
95	A tonoplast Glu/Asp/ <scp>GABA</scp> exchanger that affects tomato fruit amino acid composition. Plant Journal, 2015, 81, 651-660.	2.8	73
96	Association mapping of seed germination and seedling growth at three conditions in indica rice (Oryza sativa L.). Euphytica, 2015, 206, 103-115.	0.6	29
97	Quantifying Protein Synthesis and Degradation in Arabidopsis by Dynamic ¹³ CO ₂ Labeling and Analysis of Enrichment in Individual Amino Acids in Their Free Pools and in Protein. Plant Physiology, 2015, 168, 74-93.	2.3	132
98	A Method of Accounting for Enzyme Costs in Flux Balance Analysis Reveals Alternative Pathways and Metabolite Stores in an Illuminated Arabidopsis Leaf Â. Plant Physiology, 2015, 169, 1671-1682.	2.3	53
99	Physiological characteristics of seed reserve utilization during the early seedling growth in rice. Revista Brasileira De Botanica, 2015, 38, 751-759.	0.5	18
100	Genetic Determinants of the Network of Primary Metabolism and Their Relationships to Plant Performance in a Maize Recombinant Inbred Line Population. Plant Cell, 2015, 27, 1839-1856.	3.1	149
101	Natural variance in salt tolerance and induction of starch accumulation in duckweeds. Planta, 2015, 241, 1395-1404.	1.6	61
102	Inference and prediction of metabolic network fluxes. Plant Physiology, 2015, 169, pp.01082.2015.	2.3	46
103	Dynamic Quantitative Trait Locus Analysis of Seed Vigor at Three Maturity Stages in Rice. PLoS ONE, 2014, 9, e115732.	1.1	39
104	Silencing of the tomato Sugar Partitioning Affecting protein (<scp>SPA</scp>) modifies sink strength through a shift in leaf sugar metabolism. Plant Journal, 2014, 77, 676-687.	2.8	28
105	Metabolic flux phenotype of tobacco hairy roots engineered for increased geraniol production. Phytochemistry, 2014, 99, 73-85.	1.4	33
106	Dynamic quantitative trait locus analysis of seed dormancy at three development stages in rice. Molecular Breeding, 2014, 34, 501-510.	1.0	25
107	Remarkable Reproducibility of Enzyme Activity Profiles in Tomato Fruits Grown under Contrasting Environments Provides a Roadmap for Studies of Fruit Metabolism Â. Plant Physiology, 2014, 164, 1204-1221.	2.3	119
108	The genome of the stress-tolerant wild tomato species Solanum pennellii. Nature Genetics, 2014, 46, 1034-1038.	9.4	391

#	Article	IF	CITATIONS
109	Genome-Wide Association in Tomato Reveals 44 Candidate Loci for Fruit Metabolic Traits Â. Plant Physiology, 2014, 165, 1120-1132.	2.3	187
110	Systems analysis of metabolic phenotypes: what have we learnt?. Trends in Plant Science, 2014, 19, 222-230.	4.3	40
111	A Diel Flux Balance Model Captures Interactions between Light and Dark Metabolism during Day-Night Cycles in C3 and Crassulacean Acid Metabolism Leaves A. Plant Physiology, 2014, 165, 917-929.	2.3	181
112	A method for accounting for maintenance costs in flux balance analysis improves the prediction of plant cell metabolic phenotypes under stress conditions. Plant Journal, 2013, 75, 1050-1061.	2.8	121
113	Modelling metabolic <scp><co>CO₂</co></scp> evolution – a fresh perspective on respiration. Plant, Cell and Environment, 2013, 36, 1631-1640.	2.8	59
114	Repression of Growth Regulating Factors by the MicroRNA396 Inhibits Cell Proliferation by UV-B Radiation in <i>Arabidopsis</i> Leaves. Plant Cell, 2013, 25, 3570-3583.	3.1	124
115	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2655-62.	3.3	325
116	On the regulation and function of secondary metabolism during fruit development and ripening. Journal of Experimental Botany, 2013, 65, 4599-4611.	2.4	92
117	Resolution by recombination: breaking up Solanum pennellii introgressions. Trends in Plant Science, 2013, 18, 536-538.	4.3	74
118	The Spatial Organization of Metabolism Within the Plant Cell. Annual Review of Plant Biology, 2013, 64, 723-746.	8.6	191
119	Plant Abiotic Stress. Scientific World Journal, The, 2013, 2013, 1-2.	0.8	22
120	QTL Analysis of Na+ and K+ Concentrations in Roots and Shoots under Different Levels of NaCl Stress in Rice (Oryza sativa L.). PLoS ONE, 2012, 7, e51202.	1.1	85
121	Integrative Comparative Analyses of Transcript and Metabolite Profiles from Pepper and Tomato Ripening and Development Stages Uncovers Species-Specific Patterns of Network Regulatory Behavior Â. Plant Physiology, 2012, 159, 1713-1729.	2.3	174
122	Identification of QTLs with main, epistatic and QTLÂ×Âenvironment interaction effects for salt tolerance in rice seedlings under different salinity conditions. Theoretical and Applied Genetics, 2012, 125, 807-815.	1.8	122
123	Sucrose Efflux Mediated by SWEET Proteins as a Key Step for Phloem Transport. Science, 2012, 335, 207-211.	6.0	1,085
124	Molecular regulation of seed and fruit set. Trends in Plant Science, 2012, 17, 656-665.	4.3	331
125	Metabolic control and regulation of the tricarboxylic acid cycle in photosynthetic and heterotrophic plant tissues. Plant, Cell and Environment, 2012, 35, 1-21.	2.8	267
126	Recommendations for Reporting Metabolite Data. Plant Cell, 2011, 23, 2477-2482.	3.1	326

#	Article	IF	CITATIONS
127	Antisense Inhibition of the Iron-Sulphur Subunit of Succinate Dehydrogenase Enhances Photosynthesis and Growth in Tomato via an Organic Acid–Mediated Effect on Stomatal Aperture Â. Plant Cell, 2011, 23, 600-627.	3.1	221
128	Flux-Balance Modeling of Plant Metabolism. Frontiers in Plant Science, 2011, 2, 38.	1.7	124
129	Quantitative trait loci controlling rice seed germination under salt stress. Euphytica, 2011, 178, 297-307.	0.6	139
130	Identification of quantitative trait loci for cold tolerance during the germination and seedling stages in rice (Oryza sativa L.). Euphytica, 2011, 181, 405.	0.6	42
131	The genetic architecture of branched-chain amino acid accumulation in tomato fruits. Journal of Experimental Botany, 2011, 62, 3895-3906.	2.4	31
132	A Deficiency in the Flavoprotein of Arabidopsis Mitochondrial Complex II Results in Elevated Photosynthesis and Better Growth in Nitrogen-Limiting Conditions Â. Plant Physiology, 2011, 157, 1114-1127.	2.3	57
133	Profiling Primary Metabolites of Tomato Fruit with Gas Chromatography/Mass Spectrometry. Methods in Molecular Biology, 2011, 860, 101-109.	0.4	40
134	hi2-1, A QTL which improves harvest index, earliness and alters metabolite accumulation of processing tomatoes. Theoretical and Applied Genetics, 2010, 121, 1587-1599.	1.8	41
135	A Genome-Scale Metabolic Model Accurately Predicts Fluxes in Central Carbon Metabolism under Stress Conditions Â. Plant Physiology, 2010, 154, 311-323.	2.3	124
136	Characterization of the Branched-Chain Amino Acid Aminotransferase Enzyme Family in Tomato Â. Plant Physiology, 2010, 153, 925-936.	2.3	80
137	The Influence of Fruit Load on the Tomato Pericarp Metabolome in a <i>Solanum chmielewskii</i> Introgression Line Population. Plant Physiology, 2010, 154, 1128-1142.	2.3	80
138	Photorespiration: players, partners and origin. Trends in Plant Science, 2010, 15, 330-336.	4.3	540
139	Not just a circle: flux modes in the plant TCA cycle. Trends in Plant Science, 2010, 15, 462-470.	4.3	713
140	Metabolic and Signaling Aspects Underpinning the Regulation of Plant Carbon Nitrogen Interactions. Molecular Plant, 2010, 3, 973-996.	3.9	616
141	A Genome-Scale Metabolic Model of Arabidopsis and Some of Its Properties Â. Plant Physiology, 2009, 151, 1570-1581.	2.3	273
142	Monitoring the in vivo redox state of plant mitochondria: Effect of respiratory inhibitors, abiotic stress and assessment of recovery from oxidative challenge. Biochimica Et Biophysica Acta - Bioenergetics, 2009, 1787, 468-475.	0.5	137
143	Chapter 1 Oxidation of Proteins in Plants—Mechanisms and Consequences. Advances in Botanical Research, 2009, 52, 1-23.	0.5	29
144	RNA Interference of LIN5 in Tomato Confirms Its Role in Controlling Brix Content, Uncovers the Influence of Sugars on the Levels of Fruit Hormones, and Demonstrates the Importance of Sucrose Cleavage for Normal Fruit Development and Fertility Â. Plant Physiology, 2009, 150, 1204-1218.	2.3	226

#	Article	IF	CITATIONS
145	Mode of Inheritance of Primary Metabolic Traits in Tomato Â. Plant Cell, 2008, 20, 509-523.	3.1	208
146	Characterization of Arabidopsis Lines Deficient in GAPC-1, a Cytosolic NAD-Dependent Glyceraldehyde-3-Phosphate Dehydrogenase. Plant Physiology, 2008, 148, 1655-1667.	2.3	115
147	Metabolic Network Fluxes in Heterotrophic Arabidopsis Cells: Stability of the Flux Distribution under Different Oxygenation Conditions Â. Plant Physiology, 2008, 148, 704-718.	2.3	119
148	Getting to grips with the plant metabolic network. Biochemical Journal, 2008, 409, 27-41.	1.7	84
149	The enigmatic contribution of mitochondrial function in photosynthesis. Journal of Experimental Botany, 2007, 59, 1675-1684.	2.4	104
150	Glycolytic Enzymes Associate Dynamically with Mitochondria in Response to Respiratory Demand and Support Substrate Channeling. Plant Cell, 2007, 19, 3723-3738.	3.1	249
151	Deficiency of mitochondrial fumarase activity in tomato plants impairs photosynthesis via an effect on stomatal function. Plant Journal, 2007, 50, 1093-1106.	2.8	294
152	Operation and function of the tricarboxylic acid cycle in the illuminated leaf. Physiologia Plantarum, 2007, 129, 45-56.	2.6	77
153	The Mitochondrion: An Integration Point of Cellular Metabolism and Signalling. Critical Reviews in Plant Sciences, 2007, 26, 17-43.	2.7	102
154	Integrated Analysis of Metabolite and Transcript Levels Reveals the Metabolic Shifts That Underlie Tomato Fruit Development and Highlight Regulatory Aspects of Metabolic Network Behavior. Plant Physiology, 2006, 142, 1380-1396.	2.3	432
155	Metabolic regulation underlying tomato fruit development. Journal of Experimental Botany, 2006, 57, 1883-1897.	2.4	308
156	Gas chromatography mass spectrometry–based metabolite profiling in plants. Nature Protocols, 2006, 1, 387-396.	5.5	1,808
157	Comprehensive metabolic profiling and phenotyping of interspecific introgression lines for tomato improvement. Nature Biotechnology, 2006, 24, 447-454.	9.4	707
158	Characterization of an Arabidopsis thaliana mutant lacking a cytosolic non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase. Plant Molecular Biology, 2006, 61, 945-957.	2.0	82
159	Mitochondrial uncoupling protein is required for efficient photosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19587-19592.	3.3	226
160	Regulation of metabolic networks: understanding metabolic complexity in the systems biology era. New Phytologist, 2005, 168, 9-24.	3.5	149
161	Inhibition of de Novo Pyrimidine Synthesis in Growing Potato Tubers Leads to a Compensatory Stimulation of the Pyrimidine Salvage Pathway and a Subsequent Increase in Biosynthetic Performance. Plant Cell, 2005, 17, 2077-2088.	3.1	86
162	Enhanced Photosynthetic Performance and Growth as a Consequence of Decreasing Mitochondrial Malate Dehydrogenase Activity in Transgenic Tomato Plants. Plant Physiology, 2005, 137, 611-622.	2.3	335

#	Article	IF	CITATIONS
163	GMD@CSB.DB: the Golm Metabolome Database. Bioinformatics, 2005, 21, 1635-1638.	1.8	1,247
164	Zooming In on a Quantitative Trait for Tomato Yield Using Interspecific Introgressions. Science, 2004, 305, 1786-1789.	6.0	452
165	A proteomic analysis of plant programmed cell death. Phytochemistry, 2004, 65, 1829-1838.	1.4	81
166	Metabolic profiling of leaves and fruit of wild species tomato: a survey of the Solanum lycopersicum complex. Journal of Experimental Botany, 2004, 56, 297-307.	2.4	240
167	Reduced Expression of Aconitase Results in an Enhanced Rate of Photosynthesis and Marked Shifts in Carbon Partitioning in Illuminated Leaves of Wild Species Tomato. Plant Physiology, 2003, 133, 1322-1335.	2.3	210
168	Enzymes of Glycolysis Are Functionally Associated with the Mitochondrion in Arabidopsis Cells. Plant Cell, 2003, 15, 2140-2151.	3.1	345
169	A Bypass of Sucrose Synthase Leads to Low Internal Oxygen and Impaired Metabolic Performance in Growing Potato Tubers. Plant Physiology, 2003, 132, 2058-2072.	2.3	135
170	Starch content and yield increase as a result of altering adenylate pools in transgenic plants. Nature Biotechnology, 2002, 20, 1256-1260.	9.4	176
171	Starch synthesis in transgenic potato tubers with increased 3-phosphoglyceric acid content as a consequence of increased 6-phosphofructokinase activity. Planta, 2001, 213, 478-482.	1.6	9