Basil J Nikolau

List of Publications by Year
in descending order

96 papers	5,268 citations	71102 41 h-index	91884 69 g-index
103 all docs	103 docs citations	103 times ranked	6485 citing authors

#	Article	IF	Citations
1	Complex Changes in Membrane Lipids Associated with the Modification of Autophagy in Arabidopsis. Metabolites, 2022, 12, 190.	2.9	7
2	The Effects of Carbon Source and Growth Temperature on the Fatty Acid Profiles of Thermobifida fusca. Frontiers in Molecular Biosciences, 2022, 9, .	3.5	0
3	Heterologous Expression and Characterization of Plant Wax Ester Producing Enzymes. Metabolites, 2022, 12, 577.	2.9	1
4	High spatial resolution imaging of the dynamics of cuticular lipid deposition during Arabidopsis flower development. Plant Direct, 2021, 5, e00322.	1.9	3
5	Nectar biosynthesis is conserved among floral and extrafloral nectaries. Plant Physiology, 2021, 185, 1595-1616.	4.8	15
6	Dual-Localized Enzymatic Components Constitute the Fatty Acid Synthase Systems in Mitochondria and Plastids. Plant Physiology, 2020, 183, 517-529.	4.8	20
7	Mitochondrial Fatty Acid Synthase Utilizes Multiple Acyl Carrier Protein Isoforms. Plant Physiology, 2020, 183, 547-557.	4.8	18
8	Maize <i>Glossy2</i> and <i>Glossy2-like</i> Genes Have Overlapping and Distinct Functions in Cuticular Lipid Deposition. Plant Physiology, 2020, 183, 840-853.	4.8	14
9	Non-Catalytic Subunits Facilitate Quaternary Organization of Plastidic Acetyl-CoA Carboxylase. Plant Physiology, 2020, 182, 756-775.	4.8	14
10	Metabolomic Profiling of Nicotiana Spp. Nectars Indicate That Pollinator Feeding Preference Is a Stronger Determinant Than Plant Phylogenetics in Shaping Nectar Diversity. Metabolites, 2020, 10, 214.	2.9	8
11	Failure to Maintain Acetate Homeostasis by Acetate-Activating Enzymes Impacts Plant Development. Plant Physiology, 2020, 182, 1256-1271.	4.8	23
12	Kinetic, Structural, and Mutational Analysis of Acyl-CoA Carboxylase From Thermobifida fusca YX. Frontiers in Molecular Biosciences, 2020, 7, 615614.	3.5	3
13	Genetic and environmental variation impact the cuticular hydrocarbon metabolome on the stigmatic surfaces of maize. BMC Plant Biology, 2019, 19, 430.	3.6	11
14	Altering the Substrate Specificity of Acetyl-CoA Synthetase by Rational Mutagenesis of the Carboxylate Binding Pocket. ACS Synthetic Biology, 2019, 8, 1325-1336.	3.8	27
15	An integrated transcriptomics and metabolomics analysis of the <i>Cucurbita pepo</i> nectary implicates key modules of primary metabolism involved in nectar synthesis and secretion. Plant Direct, 2019, 3, e00120.	1.9	25
16	A single-cell platform for reconstituting and characterizing fatty acid elongase component enzymes. PLoS ONE, 2019, 14, e0213620.	2.5	14
17	Two distinct domains contribute to the substrate acyl chain length selectivity of plant acyl-ACP thioesterase. Nature Communications, 2018, 9, 860.	12.8	28
18	Combined use of cutinase and high-resolution mass-spectrometry to query the molecular architecture of cutin. Plant Methods, 2018, 14, 117.	4.3	9

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19	Heterotrimeric Gâ€Proteinâ€Dependent Proteome and Phosphoproteome in Unstimulated Arabidopsis Roots. Proteomics, 2018, 18, e1800323.	2.2	26
20	Identification of active site residues implies a two-step catalytic mechanism for acyl-ACP thioesterase. Biochemical Journal, 2018, 475, 3861-3873.	3.7	4
21	Light-Dependent Changes in the Spatial Localization of Metabolites in Solenostemon scutellarioides (Coleus Henna) Visualized by Matrix-Free Atmospheric Pressure Electrospray Laser Desorption Ionization Mass Spectrometry Imaging. Frontiers in Plant Science, 2018, 9, 1348.	3.6	11
22	Characterizing virus-induced gene silencing at the cellular level with in situ multimodal imaging. Plant Methods, 2018, 14, 37.	4.3	12
23	Sex-Dependent Variation of Pumpkin (Cucurbita maxima cv. Big Max) Nectar and Nectaries as Determined by Proteomics and Metabolomics. Frontiers in Plant Science, 2018, 9, 860.	3.6	17
24	Discovery and Characterization of the 3-Hydroxyacyl-ACP Dehydratase Component of the Plant Mitochondrial Fatty Acid Synthase System. Plant Physiology, 2017, 173, 2010-2028.	4.8	21
25	Spatial Mapping and Profiling of Metabolite Distributions during Germination. Plant Physiology, 2017, 174, 2532-2548.	4.8	50
26	Lubricant Properties of Ï‰Ââˆ'Â1 Hydroxy Branched Fatty Acid-Containing Natural and Synthetic Lipids. Tribology Letters, 2017, 65, 1.	2.6	6
27	High spatial resolution mass spectrometry imaging reveals the genetically programmed, developmental modification of the distribution of thylakoid membrane lipids among individual cells of maize leaf. Plant Journal, 2017, 89, 825-838.	5.7	52
28	A robust and efficientÂmethod for the extraction of plant extracellular surface lipids as applied to the analysis of silks and seedling leaves of maize. PLoS ONE, 2017, 12, e0180850.	2.5	19
29	Haploid differentiation in maize kernels based on fluorescence imaging. Plant Breeding, 2016, 135, 439-445.	1.9	37
30	<i><scp>AAE</scp>13</i> encodes a dualâ€localized malonylâ€CoA synthetase that is crucial for mitochondrial fatty acid biosynthesis. Plant Journal, 2016, 85, 581-593.	5.7	31
31	Integrating metabolomics and transcriptomics data to discover a biocatalyst that can generate the amine precursors for alkamide biosynthesis. Plant Journal, 2016, 88, 775-793.	5.7	17
32	Microbial production of bi-functional molecules by diversification of the fatty acid pathway. Metabolic Engineering, 2016, 35, 9-20.	7.0	12
33	A Role for GIBBERELLIN 2-OXIDASE6 and Gibberellins in Regulating Nectar Production. Molecular Plant, 2016, 9, 753-756.	8.3	24
34	A phosphopantetheinyl transferase that is essential for mitochondrial fatty acid biosynthesis. Plant Journal, 2015, 84, 718-732.	5.7	21
35	Subcellular-level resolution MALDI-MS imaging of maize leaf metabolites by MALDI-linear ion trap-Orbitrap mass spectrometer. Analytical and Bioanalytical Chemistry, 2015, 407, 2301-2309.	3.7	113
36	Modern plant metabolomics: advanced natural product gene discoveries, improved technologies, and future prospects. Natural Product Reports, 2015, 32, 212-229.	10.3	190

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37	Metabolomic Profiling of the Nectars of Aquilegia pubescens and A. Canadensis. PLoS ONE, 2015, 10, e0124501.	2.5	44
38	Proposed quantitative and alphanumeric metabolite identification metrics. Metabolomics, 2014, 10, 1047-1049.	3.0	91
39	Evaluating PHA Productivity of Bioengineered Rhodosprillum rubrum. PLoS ONE, 2014, 9, e96621.	2.5	14
40	Metabolomic Characterization of Knockout Mutants in Arabidopsis: Development of a Metabolite Profiling Database for Knockout Mutants in Arabidopsis Â Â. Plant Physiology, 2014, 165, 948-961.	4.8	49
41	A global approach to analysis and interpretation of metabolic data for plant natural product discovery. Natural Product Reports, 2013, 30, 565.	10.3	104
42	<i>PIN6</i> is required for nectary auxin response and short stamen development. Plant Journal, 2013, 74, 893-904.	5.7	81
43	Substrate promiscuity of Î²â€Ketoacyl ACP Synthase III (KASIII): Understanding the structural basis for functional diversity of KASIII enzymes. FASEB Journal, 2013, 27, 559.4.	0.5	0
44	Role of Genetic Redundancy in Polyhydroxyalkanoate (PHA) Polymerases in PHA Biosynthesis in Rhodospirillum rubrum. Journal of Bacteriology, 2012, 194, 5522-5529.	2.2	28
45	Role of Genetic Redundancy in Polyhydroxyalkanoate (PHA) Polymerases in PHA Biosynthesis in Rhodospirillum rubrum. Journal of Bacteriology, 2012, 194, 6699-6699.	2.2	0
46	Functional genomics of nectar production in the Brassicaceae. Flora: Morphology, Distribution, Functional Ecology of Plants, 2012, 207, 491-496.	1.2	26
47	Medicinal Plants: A Public Resource for Metabolomics and Hypothesis Development. Metabolites, 2012, 2, 1031-1059.	2.9	32
48	Mass spectrometric imaging as a high-spatial resolution tool for functional genomics: Tissue-specific gene expression of TT7 inferred from heterogeneous distribution of metabolites in Arabidopsis flowers. Analytical Methods, 2012, 4, 474-481.	2.7	19
49	Metabolomics as a Hypothesis-Generating Functional Genomics Tool for the Annotation of Arabidopsis thaliana Genes of â€œUnknown Functionâ€ Frontiers in Plant Science, 2012, 3, 15.	3.6	82
50	The inhibition of lipopolysaccharide-induced macrophage inflammation by 4 compounds in Hypericum perforatum extract is partially dependent on the activation of SOCS3. Phytochemistry, 2012, 76, 106-116.	2.9	35
51	Genetic dissection of methylcrotonyl CoA carboxylase indicates a complex role for mitochondrial leucine catabolism during seed development and germination. Plant Journal, 2012, 70, 562-577.	5.7	60
52	Use of mass spectrometry for imaging metabolites in plants. Plant Journal, 2012, 70, 81-95.	5.7	193
53	Reverse genetic characterization of two paralogous acetoacetyl CoA thiolase genes in Arabidopsis reveals their importance in plant growth and development. Plant Journal, 2012, 70, 1015-1032.	5.7	59
54	Identification of anti-inflammatory constituents in Hypericum perforatum and Hypericum gentianoides extracts using RAW 264.7 mouse macrophages. Phytochemistry, 2011, 72, 2015-2023.	2.9	54

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55	Phylogenetic and experimental characterization of an acyl-ACP thioesterase family reveals significant diversity in enzymatic specificity and activity. BMC Biochemistry, 2011, 12, 44.	4.4	142
56	Silencing of Soybean Seed Storage Proteins Results in a Rebalanced Protein Composition Preserving Seed Protein Content without Major Collateral Changes in the Metabolome and Transcriptome Â. Plant Physiology, 2011, 156, 330-345.	4.8	135
57	Reverse-Genetic Analysis of the Two Biotin-Containing Subunit Genes of the Heteromeric Acetyl-Coenzyme A Carboxylase in Arabidopsis Indicates a Unidirectional Functional Redundancy Â Â Â. Plant Physiology, 2011, 155, 293-314.	4.8	62
58	Biological origins of normal-chain hydrocarbons: a pathway model based on cuticular wax analyses of maize silks. Plant Journal, 2010, 64, 618-632.	5.7	40
59	Enrichment of Echinacea angustifolia with Bauer Alkylamide 11 and Bauer Ketone 23 Increased Anti-inflammatory Potential through Interference with COX-2 Enzyme Activity. Journal of Agricultural and Food Chemistry, 2010, 58, 8573-8584.	5.2	11
60	High-Spatial and High-Mass Resolution Imaging of Surface Metabolites of <i>Arabidopsis thaliana</i> by Laser Desorption-Ionization Mass Spectrometry Using Colloidal Silver. Analytical Chemistry, 2010, 82, 3255-3265.	6.5	145
61	PlantMetabolomics.org: A Web Portal for Plant Metabolomics Experiments. Plant Physiology, 2010, 152, 1807-1816.	4.8	93
62	Identification of antiâ€inflammatory constituents in Hypericum perforatum and Hypericum gentianoides extracts using mouse macrophages. FASEB Journal, 2010, 24, 321.8.	0.5	0
63	Metabolic Profiling ofEchinaceaGenotypes and a Test of Alternative Taxonomic Treatments. Planta Medica, 2009, 75, 178-183.	1.3	19
64	Quantitative analysis of short-chain acyl-coenzymeAs in plant tissues by LCâ€"MSâ€"MS electrospray ionization method. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 482-488.	2.3	36
65	Rosmarinic Acid in Prunella vulgaris Ethanol Extract Inhibits Lipopolysaccharide-Induced Prostaglandin E2 and Nitric Oxide in RAW 264.7 Mouse Macrophages. Journal of Agricultural and Food Chemistry, 2009, 57, 10579-10589.	5.2	96
66	Acetyl-CoAâ€"Life at the metabolic nexus. Plant Science, 2009, 176, 597-601.	3.6	102
67	Direct Profiling and Imaging of Epicuticular Waxes on Arabidopsis thaliana by Laser Desorption/Ionization Mass Spectrometry Using Silver Colloid as a Matrix. Analytical Chemistry, 2009, 81, 2991-3000.	6.5	77
68	Platform biochemicals for a biorenewable chemical industry. Plant Journal, 2008, 54, 536-545.	5.7	165
69	Direct profiling and imaging of plant metabolites in intact tissues by using colloidal graphiteâ€assisted laser desorption ionization mass spectrometry. Plant Journal, 2008, 55, 348-360.	5.7	138
70	Articulation of three core metabolic processes in Arabidopsis: Fatty acid biosynthesis, leucine catabolism and starch metabolism. BMC Plant Biology, 2008, 8, 76.	3.6	83
71	A Bifunctional Locus (<i>BIO3</i>-<i>BIO1</i>) Required for Biotin Biosynthesis in Arabidopsis. Plant Physiology, 2008, 146, 60-73.	4.8	45
72	MetNet: Systems Biology Tools for Arabidopsis. , 2007, , 145-157.		24

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73	Effects of trans-acting Genetic Modifiers on Meiotic Recombination Across the a1â€“sh2 Interval of Maize. Genetics, 2006, 174, 101-112.	2.9	27
74	In-situ probing of the biotic-abiotic boundary of plants by laser desorption/ionization time-of-flight mass spectrometry. Journal of the American Society for Mass Spectrometry, 2005, 16, 107-115.	2.8	20
75	Characterization of two GL8 paralogs reveals that the 3-ketoacyl reductase component of fatty acid elongase is essential for maize (Zea mays L.) development. Plant Journal, 2005, 42, 844-861.	5.7	82
76	MuDR Transposase Increases the Frequency of Meiotic Crossovers in the Vicinity of a Mu Insertion in the Maize a1 Gene. Genetics, 2005, 169, 917-929.	2.9	28
77	Reverse Genetic Characterization of Cytosolic Acetyl-CoA Generation by ATP-Citrate Lyase in Arabidopsis. Plant Cell, 2005, 17, 182-203.	6.6	185
78	Plant biotin-containing carboxylases. Archives of Biochemistry and Biophysics, 2003, 414, 211-222.	3.0	208
79	The Role of Biotin in Regulating 3-Methylcrotonyl-Coenzyme A Carboxylase Expression in Arabidopsis. Plant Physiology, 2003, 131, 1479-1486.	4.8	29
80	Molecular characterization of meiotic recombination across the 140-kb multigenic a1-sh2 interval of maize. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6157-6162.	7.1	120
81	Metabolic and Environmental Regulation of 3-Methylcrotonyl-Coenzyme A Carboxylase Expression in Arabidopsis. Plant Physiology, 2002, 129, 625-637.	4.8	49
82	The Endoplasmic Reticulum-Associated Maize GL8 Protein Is a Component of the Acyl-Coenzyme A Elongase Involved in the Production of Cuticular Waxes. Plant Physiology, 2002, 128, 924-934.	4.8	67
83	Molecular Characterization of a Heteromeric ATP-Citrate Lyase That Generates Cytosolic Acetyl-Coenzyme A in Arabidopsis,. Plant Physiology, 2002, 130, 740-756.	4.8	183
84	Maize <i>Mu</i> Transposons Are Targeted to the 5â€² Untranslated Region of the <i>gl8</i> Gene and Sequences Flanking <i>Mu</i> Target-Site Duplications Exhibit Nonrandom Nucleotide Composition Throughout the Genome. Genetics, 2002, 160, 697-716.	2.9	108
85	Characterization of 3-Methylcrotonyl-CoA Carboxylase from Plants. Methods in Enzymology, 2000, 324, 280-292.	1.0	9
86	The Role of Pyruvate Dehydrogenase and Acetyl-Coenzyme A Synthetase in Fatty Acid Synthesis in Developing Arabidopsis Seeds. Plant Physiology, 2000, 123, 497-508.	4.8	147
87	Coordinate Regulation of the Nuclear and Plastidic Genes Coding for the Subunits of the Heteromeric Acetyl-Coenzyme A Carboxylase. Plant Physiology, 2000, 122, 1057-1072.	4.8	99
88	Molecular Characterization of the Non-biotin-containing Subunit of 3-Methylcrotonyl-CoA Carboxylase. Journal of Biological Chemistry, 2000, 275, 5582-5590.	3.4	29
89	Geranoyl-CoA Carboxylase: A Novel Biotin-Containing Enzyme in Plants. Archives of Biochemistry and Biophysics, 1999, 362, 12-21.	3.0	30
90	Genetic recombination in plants. Current Opinion in Plant Biology, 1998, 1, 123-129.	7.1	102

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91	3-Methylcrotonyl-Coenzyme A Carboxylase Is a Component of the Mitochondrial Leucine Catabolic Pathway in Plants. Plant Physiology, 1998, 118, 1127-1138.	4.8	99
92	Genomic Organization of 251 kDa Acetyl-CoA Carboxylase Genes in Arabidopsis: Tandem Gene Duplication has Made Two Differentially Expressed Isozymes. Plant and Cell Physiology, 1995, 36, 779-787.	3.1	59
93	Differential Accumulation of Biotin Enzymes during Carrot Somatic Embryogenesis. Plant Physiology, 1992, 99, 1699-1703.	4.8	37
94	Plants contain multiple biotin enzymes: Discovery of 3-methylcrotonyl-CoA carboxylase, propionyl-CoA carboxylase and pyruvate carboxylase in the plant kingdom. Archives of Biochemistry and Biophysics, 1990, 278, 179-186.	3.0	99
95	Use of streptavidin to detect biotin-containing proteins in plants. Analytical Biochemistry, 1985, 149, 448-453.	2.4	64
96	Purification and characterization of maize leaf acetyl-coenzyme a carboxylase. Archives of Biochemistry and Biophysics, 1984, 228, 86-96.	3.0	81