# Wolfram Weckwerth

## List of Publications by Year in Descending Order



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|---|---|---|---|
| 244 papers | 12,438 citations | 58 h-index | 104 g-index |
| 271 ext. papers | 15,950 ext. citations | 6.6 avg, IF | 6.62 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 244 | Functional Traits 2.0: The power of the metabolome for ecology. *Journal of Ecology*, **2022**, 110, 4-20 | 6 | 5 |
| 243 | Proteomics for abiotic stresses in legumes: present status and future directions.. *Critical Reviews in Biotechnology*, **2022**, 1-20 | 9.4 | 0 |
| 242 | Root exudation of contrasting drought-stressed pearl millet genotypes conveys varying biological nitrification inhibition (BNI) activity.. *Biology and Fertility of Soils*, **2022**, 58, 291-306 | 6.1 | 5 |
| 241 | Linear Predictive Modeling for Immune Metabolites Related to Other Metabolites. *Lecture Notes in Computer Science*, **2022**, 16-27 | 0.9 | |
| 240 | The Quest for System-Theoretical Medicine in the COVID-19 Era. *Frontiers in Medicine*, **2021**, 8, 640974 | 4.9 | 4 |
| 239 | Heat stress response mechanisms in pollen development. *New Phytologist*, **2021**, 231, 571-585 | 9.8 | 15 |
| 238 | Systems biology for crop improvement. *Plant Genome*, **2021**, 14, e20098 | 4.4 | 15 |
| 237 | Metabolite Profiling in with Moderately Impaired Photorespiration Reveals Novel Metabolic Links and Compensatory Mechanisms of Photorespiration. *Metabolites*, **2021**, 11, | 5.6 | 2 |
| 236 | Dissecting Metabolism of Leaf Nodules in and. *Frontiers in Molecular Biosciences*, **2021**, 8, 683671 | 5.6 | 2 |
| 235 | The TOR-Auxin Connection Upstream of Root Hair Growth. *Plants*, **2021**, 10, | 4.5 | 6 |
| 234 | Magnetic Field Induced Changes in the Shoot and Root Proteome of Barley ( L.). *Frontiers in Plant Science*, **2021**, 12, 622795 | 6.2 | 5 |
| 233 | Spatial distribution of proteins and metabolites in developing wheat grain and their differential regulatory response during the grain filling process. *Plant Journal*, **2021**, 107, 669-687 | 6.9 | 5 |
| 232 | Exogenous carbon source supplementation counteracts root and hypocotyl growth limitations under increased cotyledon shading, with glucose and sucrose differentially modulating growth curves. *Plant Signaling and Behavior*, **2021**, 16, 1969818 | 2.5 | 0 |
| 231 | Rapid delivery systems for future food security. *Nature Biotechnology*, **2021**, 39, 1179-1181 | 44.5 | 4 |
| 230 | Fast-forward breeding for a food-secure world. *Trends in Genetics*, **2021**, 37, 1124-1136 | 8.5 | 15 |
| 229 | An Innovative Perspective on Metabolomics Data Analysis in Biomedical Research Using Concept Drift Detection **2021**, | | 1 |
| 228 | In Vitro Evaluation of Pro- and Antioxidant Effects of Flavonoid Tricetin in Comparison to Myricetin. *Molecules*, **2020**, 25, | 4.8 | 2 |

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| 227 | Molecular Mechanisms of Microbial Survivability in Outer Space: A Systems Biology Approach. *Frontiers in Microbiology*, **2020**, 11, 923 | 5.7 | 10 |
| 226 | Structural and Functional Heat Stress Responses of Chloroplasts of. *Genes*, **2020**, 11, | 4.2 | 7 |
| 225 | Adjustment of photosynthetic activity to drought and fluctuating light in wheat. *Plant, Cell and Environment*, **2020**, 43, 1484-1500 | 8.4 | 18 |
| 224 | PANOMICS meets germplasm. *Plant Biotechnology Journal*, **2020**, 18, 1507-1525 | 11.6 | 39 |
| 223 | Multiomics approach unravels fertility transition in a pigeonpea line for a two-line hybrid system. *Plant Genome*, **2020**, 13, e20028 | 4.4 | 10 |
| 222 | Mexicanolide-type limonoids from the twigs and leaves of Cipadessa baccifera. *Phytochemistry*, **2020**, 177, 112449 | 4 | 3 |
| 221 | Mass Spectrometry Untangles Plant Membrane Protein Signaling Networks. *Trends in Plant Science*, **2020**, 25, 930-944 | 13.1 | 12 |
| 220 | The Potato Yam Phyllosphere Ectosymbiont sp. Msb3 Is a Potent Growth Promotor in Tomato. *Frontiers in Microbiology*, **2020**, 11, 581 | 5.7 | 5 |
| 219 | Inverse Data-Driven Modeling and Multiomics Analysis Reveals Phgdh as a Metabolic Checkpoint of Macrophage Polarization and Proliferation. *Cell Reports*, **2020**, 30, 1542-1552.e7 | 10.6 | 17 |
| 218 | Genomic footprints of repeated evolution of CAM photosynthesis in a Neotropical species radiation. *Plant, Cell and Environment*, **2020**, 43, 2987-3001 | 8.4 | 3 |
| 217 | Current status of the multinational Arabidopsis community. *Plant Direct*, **2020**, 4, e00248 | 3.3 | 4 |
| 216 | Biological nitrification inhibition in the rhizosphere: determining interactions and impact on microbially mediated processes and potential applications. *FEMS Microbiology Reviews*, **2020**, 44, 874-908 | 15.1 | 21 |
| 215 | Molecular repertoire of Deinococcus radiodurans after 1 year of exposure outside the International Space Station within the Tanpopo mission. *Microbiome*, **2020**, 8, 150 | 16.6 | 10 |
| 214 | Physiological and Proteomic Signatures Reveal Mechanisms of Superior Drought Resilience in Pearl Millet Compared to Wheat. *Frontiers in Plant Science*, **2020**, 11, 600278 | 6.2 | 16 |
| 213 | Coordination Complex Formation and Redox Properties of Kynurenic and Xanthurenic Acid Can Affect Brain Tissue Homeodynamics. *Antioxidants*, **2019**, 8, | 7.1 | 13 |
| 212 | Current research in biotechnology: Exploring the biotech forefront. *Current Research in Biotechnology*, **2019**, 1, 34-40 | 4.8 | 9 |
| 211 | The High Light Response in Arabidopsis Requires the Calcium Sensor Protein CAS, a Target of STN7- and STN8-Mediated Phosphorylation. *Frontiers in Plant Science*, **2019**, 10, 974 | 6.2 | 17 |
| 210 | Proteomic and Metabolomic Profiling of Recovering After Exposure to Simulated Low Earth Orbit Vacuum Conditions. *Frontiers in Microbiology*, **2019**, 10, 909 | 5.7 | 12 |

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| 209 | Combination of Hypoglycemia and Metformin Impairs Tumor Metabolic Plasticity and Growth by Modulating the PP2A-GSK3MCL-1 Axis. *Cancer Cell*, **2019**, 35, 798-815.e5 | 24.3 | 108 |
| 208 | Molecular Mechanisms of Tungsten Toxicity Differ for Depending on Nitrogen Regime. *Frontiers in Plant Science*, **2019**, 10, 367 | 6.2 | 4 |
| 207 | Subcellular dynamics of proteins and metabolites under abiotic stress reveal deferred response of the Arabidopsis thaliana hexokinase-1 mutant gin2-1 to high light. *Plant Journal*, **2019**, 100, 456-472 | 6.9 | 7 |
| 206 | Male Sterility in Maize after Transient Heat Stress during the Tetrad Stage of Pollen Development. *Plant Physiology*, **2019**, 181, 683-700 | 6.6 | 57 |
| 205 | Resolving subcellular plant metabolism. *Plant Journal*, **2019**, 100, 438-455 | 6.9 | 23 |
| 204 | Dynamics of Plant Metabolism during Cold Acclimation. *International Journal of Molecular Sciences*, **2019**, 20, | 6.3 | 41 |
| 203 | Toward a Unification of System-Theoretical Principles in Biology and Ecology the Stochastic Lyapunov Matrix Equation and Its Inverse Application. *Frontiers in Applied Mathematics and Statistics*, **2019**, 5, | 2.2 | 14 |
| 202 | Molecular response of Deinococcus radiodurans to simulated microgravity explored by proteometabolomic approach. *Scientific Reports*, **2019**, 9, 18462 | 4.9 | 8 |
| 201 | Deciphering key proteins of oil palm (Elaeis guineensis Jacq.) fruit mesocarp development by proteomics and chemometrics. *Electrophoresis*, **2019**, 40, 254-265 | 3.6 | 6 |
| 200 | Plastic and genetic responses of a common sedge to warming have contrasting effects on carbon cycle processes. *Ecology Letters*, **2019**, 22, 159-169 | 10 | 15 |
| 199 | Metabolomics in Plant Stress Physiology. *Advances in Biochemical Engineering/Biotechnology*, **2018**, 164, 187-236 | 1.7 | 38 |
| 198 | Studying AMPK in an Evolutionary Context. *Methods in Molecular Biology*, **2018**, 1732, 111-142 | 1.4 | 1 |
| 197 | Snf1-RELATED KINASE1-Controlled C/S-bZIP Signaling Activates Alternative Mitochondrial Metabolic Pathways to Ensure Plant Survival in Extended Darkness. *Plant Cell*, **2018**, 30, 495-509 | 11.6 | 70 |
| 196 | The SnRK1 Kinase as Central Mediator of Energy Signaling between Different Organelles. *Plant Physiology*, **2018**, 176, 1085-1094 | 6.6 | 77 |
| 195 | Using RT-qPCR, Proteomics, and Microscopy to Unravel the Spatio-Temporal Expression and Subcellular Localization of Hordoindolines Across Development in Barley Endosperm. *Frontiers in Plant Science*, **2018**, 9, 775 | 6.2 | 9 |
| 194 | Antioxidant Properties and the Formation of Iron Coordination Complexes of 8-Hydroxyquinoline. *International Journal of Molecular Sciences*, **2018**, 19, | 6.3 | 17 |
| 193 | Combined multivariate analysis and machine learning reveals a predictive module of metabolic stress response in Arabidopsis thaliana. *Molecular Omics*, **2018**, 14, 437-449 | 4.4 | 8 |
| 192 | Metabolomics: Integrating the Metabolome and the Proteome for Systems Biology **2018**, 258-289 | | 1 |

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| 191 | Quantitative Phosphoproteomic and System-Level Analysis of TOR Inhibition Unravel Distinct Organellar Acclimation in. *Frontiers in Plant Science*, **2018**, 9, 1590 | 6.2 | 25 |
| 190 | Proteomics of Heat-Stress and Ethylene-Mediated Thermotolerance Mechanisms in Tomato Pollen Grains. *Frontiers in Plant Science*, **2018**, 9, 1558 | 6.2 | 38 |
| 189 | Microscopic and Proteomic Analysis of Dissected Developing Barley Endosperm Layers Reveals the Starchy Endosperm as Prominent Storage Tissue for ER-Derived Hordeins Alongside the Accumulation of Barley Protein Disulfide Isomerase (HvPDIL1-1). *Frontiers in Plant Science*, **2018**, 9, 1248 | 6.2 | 11 |
| 188 | Eco-Metabolomics and Metabolic Modeling: Making the Leap From Model Systems in the Lab to Native Populations in the Field. *Frontiers in Plant Science*, **2018**, 9, 1556 | 6.2 | 19 |
| 187 | Vacuolar sucrose cleavage prevents limitation of cytosolic carbohydrate metabolism and stabilizes photosynthesis under abiotic stress. *FEBS Journal*, **2018**, 285, 4082-4098 | 5.7 | 32 |
| 186 | Sumoylation and phosphorylation: hidden and overt links. *Journal of Experimental Botany*, **2018**, 69, 4583-4590 | 7 | 13 |
| 185 | Glycolate Induces Redox Tuning Of Photosystem II in Vivo: Study of a Photorespiration Mutant. *Plant Physiology*, **2018**, 177, 1277-1285 | 6.6 | 16 |
| 184 | Mathematical Modeling Approaches in Plant Metabolomics. *Methods in Molecular Biology*, **2018**, 1778, 329-347 | 1.4 | 3 |
| 183 | Integrated Physiological, Proteomic, and Metabolomic Analysis of Ultra Violet (UV) Stress Responses and Adaptation Mechanisms in. *Molecular and Cellular Proteomics*, **2017**, 16, 485-501 | 7.6 | 28 |
| 182 | Chronic signaling via the metabolic checkpoint kinase mTORC1 induces macrophage granuloma formation and marks sarcoidosis progression. *Nature Immunology*, **2017**, 18, 293-302 | 19.1 | 117 |
| 181 | Protein sumoylation and phosphorylation intersect in Arabidopsis signaling. *Plant Journal*, **2017**, 91, 505-517 | 6.1 | 21 |
| 180 | Proteomics survey of Solanaceae family: Current status and challenges ahead. *Journal of Proteomics*, **2017**, 169, 41-57 | 3.9 | 28 |
| 179 | Proteometabolomic response of Deinococcus radiodurans exposed to UVC and vacuum conditions: Initial studies prior to the Tanpopo space mission. *PLoS ONE*, **2017**, 12, e0189381 | 3.7 | 16 |
| 178 | Quantitative in vivo phosphoproteomics reveals reversible signaling processes during nitrogen starvation and recovery in the biofuel model organism. *Biotechnology for Biofuels*, **2017**, 10, 280 | 7.8 | 34 |
| 177 | Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. *Nature Biotechnology*, **2017**, 35, 969-976 | 44.5 | 197 |
| 176 | Redox state-dependent modulation of plant SnRK1 kinase activity differs from AMPK regulation in animals. *FEBS Letters*, **2017**, 591, 3625-3636 | 3.8 | 27 |
| 175 | Subcellular reprogramming of metabolism during cold acclimation in Arabidopsis thaliana. *Plant, Cell and Environment*, **2017**, 40, 602-610 | 8.4 | 66 |
| 174 | Lichen secondary metabolites affect growth of Physcomitrella patens by allelopathy. *Protoplasma*, **2017**, 254, 1307-1315 | 3.4 | 16 |

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| 173 | Cereal Crop Proteomics: Systemic Analysis of Crop Drought Stress Responses Towards Marker-Assisted Selection Breeding. *Frontiers in Plant Science*, **2017**, 8, 757 | 6.2 | 71 |
| 172 | System-Level and Granger Network Analysis of Integrated Proteomic and Metabolomic Dynamics Identifies Key Points of Grape Berry Development at the Interface of Primary and Secondary Metabolism. *Frontiers in Plant Science*, **2017**, 8, 1066 | 6.2 | 37 |
| 171 | Comparison between Proteome and Transcriptome Response in Potato (Solanum tuberosum L.) Leaves Following Potato Virus Y (PVY) Infection. *Proteomes*, **2017**, 5, | 4.6 | 25 |
| 170 | Combined Metabolomic Analysis of Plasma and Urine Reveals AHBA, Tryptophan and Serotonin Metabolism as Potential Risk Factors in Gestational Diabetes Mellitus (GDM). *Frontiers in Molecular Biosciences*, **2017**, 4, 84 | 5.6 | 30 |
| 169 | Protocol for Enrichment of the Membrane Proteome of Mature Tomato Pollen. *Bio-protocol*, **2017**, 7, e2315 | 0.9 | 2 |
| 168 | Pollen Metabolome Dynamics: Biochemistry, Regulation and Analysis **2017**, 319-336 | | 2 |
| 167 | The membrane proteome of male gametophyte in Solanum lycopersicum. *Journal of Proteomics*, **2016**, 131, 48-60 | 3.9 | 22 |
| 166 | Girdling interruption between source and sink in Quercus pubescens does not trigger leaf senescence. *Photosynthetica*, **2016**, 54, 589-597 | 2.2 | 4 |
| 165 | Biodiesel and poly-unsaturated fatty acids production from algae and crop plants - a rapid and comprehensive workflow for lipid analysis. *Biotechnology Journal*, **2016**, 11, 1262-1267 | 5.6 | 10 |
| 164 | Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. *Cell*, **2016**, 166, 492-505 | 56.2 | 353 |
| 163 | Proteomics and comparative genomics of Nitrososphaera viennensis reveal the core genome and adaptations of archaeal ammonia oxidizers. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E7937-E7946 | 11.5 | 103 |
| 162 | Quantitative phosphoproteomics reveals the role of the AMPK plant ortholog SnRK1 as a metabolic master regulator under energy deprivation. *Scientific Reports*, **2016**, 6, 31697 | 4.9 | 164 |
| 161 | An evolutionary perspective of AMPK-TOR signaling in the three domains of life. *Journal of Experimental Botany*, **2016**, 67, 3897-907 | 7 | 41 |
| 160 | Pollen proteomics: from stress physiology to developmental priming. *Plant Reproduction*, **2016**, 29, 119-32 | 3.9 | 31 |
| 159 | 1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. *Cell*, **2016**, 166, 481-491 | 56.2 | 620 |
| 158 | Comprehensive tissue-specific proteome analysis of drought stress responses in Pennisetum glaucum (L.) R. Br. (Pearl millet). *Journal of Proteomics*, **2016**, 143, 122-135 | 3.9 | 32 |
| 157 | The variations in the nuclear proteome reveal new transcription factors and mechanisms involved in UV stress response in Pinus radiata. *Journal of Proteomics*, **2016**, 143, 390-400 | 3.9 | 14 |
| 156 | Induction and quantitative proteomic analysis of cell dedifferentiation during callus formation of lotus (Nelumbo nucifera Gaertn.spp. baijianlian). *Journal of Proteomics*, **2016**, 131, 61-70 | 3.9 | 19 |

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| 155 | Primary Metabolism, Phenylpropanoids and Antioxidant Pathways Are Regulated in Potato as a Response to Potato virus Y Infection. *PLoS ONE*, **2016**, 11, e0146135 | 3.7 | 34 |
| 154 | A Strategy for Functional Interpretation of Metabolomic Time Series Data in Context of Metabolic Network Information. *Frontiers in Molecular Biosciences*, **2016**, 3, 6 | 5.6 | 11 |
| 153 | Pro- and Antioxidant Activity of Three Selected Flavan Type Flavonoids: Catechin, Eriodictyol and Taxifolin. *International Journal of Molecular Sciences*, **2016**, 17, | 6.3 | 25 |
| 152 | Metabolic Consequences of Infection of Grapevine (Vitis vinifera L.) cv. "Modra frankinja" with Flavescence Dorée Phytoplasma. *Frontiers in Plant Science*, **2016**, 7, 711 | 6.2 | 40 |
| 151 | Metabolomic and Proteomic Profiles Reveal the Dynamics of Primary Metabolism during Seed Development of Lotus (Nelumbo nucifera). *Frontiers in Plant Science*, **2016**, 7, 750 | 6.2 | 28 |
| 150 | A Benchtop Fractionation Procedure for Subcellular Analysis of the Plant Metabolome. *Frontiers in Plant Science*, **2016**, 7, 1912 | 6.2 | 28 |
| 149 | Exploring natural variation of Pinus pinaster Aiton using metabolomics: Is it possible to identify the region of origin of a pine from its metabolites?. *Molecular Ecology*, **2016**, 25, 959-76 | 5.7 | 42 |
| 148 | System level analysis of cacao seed ripening reveals a sequential interplay of primary and secondary metabolism leading to polyphenol accumulation and preparation of stress resistance. *Plant Journal*, **2016**, 87, 318-32 | 6.9 | 39 |
| 147 | Longer telomeres in chronic, moderate, unconjugated hyperbilirubinaemia: insights from a human study on Gilbert's Syndrome. *Scientific Reports*, **2016**, 6, 22300 | 4.9 | 14 |
| 146 | Dataset of UV induced changes in nuclear proteome obtained by GeLC-Orbitrap/MS in Pinus radiata needles. *Data in Brief*, **2016**, 7, 1477-82 | 1.2 | 4 |
| 145 | Cajanus cajan- a source of PPARγ activators leading to anti-inflammatory and cytotoxic effects. *Food and Function*, **2016**, 7, 3798-806 | 6.1 | 18 |
| 144 | Iron chelation and redox chemistry of anthranilic acid and 3-hydroxyanthranilic acid: A comparison of two structurally related kynurenine pathway metabolites to obtain improved insights into their potential role in neurological disease development. *Journal of Organometallic Chemistry*, **2015**, 782, 103-110 | 2.3 | 24 |
| 143 | Diurnal effects of anoxia on the metabolome of the seagrass Zostera marina. *Metabolomics*, **2015**, 11, 1208-1218 | 4.7 | 27 |
| 142 | Altitudinal patterns of diversity and functional traits of metabolically active microorganisms in stream biofilms. *ISME Journal*, **2015**, 9, 2454-64 | 11.9 | 33 |
| 141 | Heat-Treatment-Responsive Proteins in Different Developmental Stages of Tomato Pollen Detected by Targeted Mass Accuracy Precursor Alignment (tMAPA). *Journal of Proteome Research*, **2015**, 14, 4463-71 | 5.6 | 27 |
| 140 | Ectopic overexpression of the cell wall invertase gene CIN1 leads to dehydration avoidance in tomato. *Journal of Experimental Botany*, **2015**, 66, 863-78 | 7 | 53 |
| 139 | Targeted quantitative analysis of a diurnal RuBisCO subunit expression and translation profile in Chlamydomonas reinhardtii introducing a novel Mass Western approach. *Journal of Proteomics*, **2015**, 113, 143-53 | 3.9 | 20 |
| 138 | Integrative molecular profiling indicates a central role of transitory starch breakdown in establishing a stable C/N homeostasis during cold acclimation in two natural accessions of Arabidopsis thaliana. *BMC Plant Biology*, **2015**, 15, 284 | 5.3 | 22 |

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| 137 | Challenges of Inversely Estimating Jacobian from Metabolomics Data. *Frontiers in Bioengineering and Biotechnology*, **2015**, 3, 188 | 5.8 | 6 |
| 136 | Proteomics and Metabolomics: Two Emerging Areas for Legume Improvement. *Frontiers in Plant Science*, **2015**, 6, 1116 | 6.2 | 72 |
| 135 | Bimodal dynamics of primary metabolism-related responses in tolerant potato-Potato virus Y interaction. *BMC Genomics*, **2015**, 16, 716 | 4.5 | 35 |
| 134 | Fragmentation patterns of methyloxime-trimethylsilyl derivatives of constitutive mono- and disaccharide isomers analyzed by gas chromatography/field ionization mass spectrometry. *Rapid Communications in Mass Spectrometry*, **2015**, 29, 238-46 | 2.2 | 7 |
| 133 | Effects of endogenous neurotoxin quinolinic acid on reactive oxygen species production by Fenton reaction catalyzed by iron or copper. *Journal of Organometallic Chemistry*, **2015**, 782, 111-115 | 2.3 | 12 |
| 132 | SnRK1-triggered switch of bZIP63 dimerization mediates the low-energy response in plants. *ELife*, **2015**, 4, | 8.9 | 132 |
| 131 | A universal protocol for the combined isolation of metabolites, DNA, long RNAs, small RNAs, and proteins from plants and microorganisms. *Plant Journal*, **2014**, 79, 173-80 | 6.9 | 66 |
| 130 | A specialized bird pollination system with a bellows mechanism for pollen transfer and staminal food body rewards. *Current Biology*, **2014**, 24, 1615-1619 | 6.3 | 35 |
| 129 | Solving the differential biochemical Jacobian from metabolomics covariance data. *PLoS ONE*, **2014**, 9, e92299 | 3.7 | 27 |
| 128 | System-level network analysis of nitrogen starvation and recovery in Chlamydomonas reinhardtii reveals potential new targets for increased lipid accumulation. *Biotechnology for Biofuels*, **2014**, 7, 171 | 7.8 | 72 |
| 127 | A tandem affinity purification tag of TGA2 for isolation of interacting proteins in Arabidopsis thaliana. *Plant Signaling and Behavior*, **2014**, 9, e972794 | 2.5 | 4 |
| 126 | Mathematical modeling reveals that metabolic feedback regulation of SnRK1 and hexokinase is sufficient to control sugar homeostasis from energy depletion to full recovery. *Frontiers in Plant Science*, **2014**, 5, 365 | 6.2 | 21 |
| 125 | Field-omics-understanding large-scale molecular data from field crops. *Frontiers in Plant Science*, **2014**, 5, 286 | 6.2 | 32 |
| 124 | Comprehensive cell-specific protein analysis in early and late pollen development from diploid microsporocytes to pollen tube growth. *Molecular and Cellular Proteomics*, **2014**, 13, 295-310 | 7.6 | 44 |
| 123 | Draft Genome Sequence of the Growth-Promoting Endophyte Paenibacillus sp. P22, Isolated from Populus. *Genome Announcements*, **2014**, 2, | | 3 |
| 122 | Myo-inositol oxygenase is important for the removal of excess myo-inositol from syncytia induced by Heterodera schachtii in Arabidopsis roots. *New Phytologist*, **2014**, 201, 476-485 | 9.8 | 26 |
| 121 | Metabolism and development - integration of micro computed tomography data and metabolite profiling reveals metabolic reprogramming from floral initiation to silique development. *New Phytologist*, **2014**, 202, 322-335 | 9.8 | 32 |
| 120 | Boron nitride as desalting material in combination with phosphopeptide enrichment in shotgun proteomics. *Analytical Biochemistry*, **2014**, 452, 16-8 | 3.1 | 7 |

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| 119 | Automated protein turnover calculations from 15N partial metabolic labeling LC/MS shotgun proteomics data. *PLoS ONE*, **2014**, 9, e94692 | 3.7 | 5 |
| 118 | mzGroupAnalyzer--predicting pathways and novel chemical structures from untargeted high-throughput metabolomics data. *PLoS ONE*, **2014**, 9, e96188 | 3.7 | 30 |
| 117 | Mass Western for absolute quantification of target proteins and considerations about the instrument of choice. *Methods in Molecular Biology*, **2014**, 1072, 199-208 | 1.4 | 2 |
| 116 | From proteomics to systems biology: MAPA, MASS WESTERN, PROMEX, and COVAIN as a user-oriented platform. *Methods in Molecular Biology*, **2014**, 1072, 15-27 | 1.4 | 8 |
| 115 | An improved detergent-compatible gel-fractionation LC-LTQ-Orbitrap-MS workflow for plant and microbial proteomics. *Methods in Molecular Biology*, **2014**, 1072, 347-58 | 1.4 | 29 |
| 114 | Tandem metal-oxide affinity chromatography for enhanced depth of phosphoproteome analysis. *Methods in Molecular Biology*, **2014**, 1072, 621-32 | 1.4 | 10 |
| 113 | Gas Chromatography Coupled to Mass Spectrometry for Metabolomics Research **2014**, 783-797 | | 1 |
| 112 | Using COVAIN to Analyze Metabolomics Data **2013**, 305-320 | | 5 |
| 111 | Metabolite Clustering and Visualization of Mass Spectrometry Data Using One-Dimensional Self-Organizing Maps **2013**, 273-287 | | |
| 110 | Cell-specific analysis of the tomato pollen proteome from pollen mother cell to mature pollen provides evidence for developmental priming. *Journal of Proteome Research*, **2013**, 12, 4892-903 | 5.6 | 64 |
| 109 | Granger causality in integrated GC-MS and LC-MS metabolomics data reveals the interface of primary and secondary metabolism. *Metabolomics*, **2013**, 9, 564-574 | 4.7 | 81 |
| 108 | Medicago Truncatula Root and Shoot Metabolomics: Protocol for the Investigation of the Primary Carbon and Nitrogen Metabolism Based on GC-MS **2013**, 111-123 | | 3 |
| 107 | Study of the Volatile Metabolome in Plant-Insect Interactions **2013**, 125-153 | | 1 |
| 106 | Metabolomics in Herbal Medicine Research **2013**, 155-174 | | 5 |
| 105 | Integrative Analysis of Secondary Metabolism and Transcript Regulation in Arabidopsis Thaliana **2013**, 175-195 | | |
| 104 | Metabolomics-Assisted Plant Breeding **2013**, 245-254 | | 8 |
| 103 | Using ProtMAX to create high-mass-accuracy precursor alignments from label-free quantitative mass spectrometry data generated in shotgun proteomics experiments. *Nature Protocols*, **2013**, 8, 595-601 | 18.8 | 22 |
| 102 | Metabolomics and Its Role in the Study of Mammalian Systems **2013**, 345-377 | | 1 |

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| 101 | Metabolic Profiling of Plants by GC–MS **2013**, 1-23 | | 11 |
| 100 | Isotopologue Profiling – Toward a Better Understanding of Metabolic Pathways **2013**, 25-56 | | 5 |
| 99 | Nuclear Magnetic Resonance Spectroscopy for Plant Metabolite Profiling **2013**, 57-76 | | 7 |
| 98 | Comprehensive Two-Dimensional Gas Chromatography for Metabolomics **2013**, 77-91 | | 2 |
| 97 | MALDI Mass Spectrometric Imaging of Plants **2013**, 93-110 | | 6 |
| 96 | Liquid Chromatographic–Mass Spectrometric Analysis of Flavonoids **2013**, 197-213 | | 5 |
| 95 | Introduction to Lipid (FAME) Analysis in Algae Using Gas Chromatography–Mass Spectrometry **2013**, 215-225 | | 9 |
| 94 | Multi-Gene Transformation for Pathway Engineering of Secondary Metabolites **2013**, 227-244 | | |
| 93 | Metabolite Identification and Computational Mass Spectrometry **2013**, 289-303 | | |
| 92 | Mass Spectral Search and Analysis Using the Golm Metabolome Database **2013**, 321-343 | | 23 |
| 91 | Conducting Genome-Wide Association Mapping of Metabolites **2013**, 255-271 | | |
| 90 | Phytochemical composition of L. analyzed by an integrative GC-MS and LC-MS metabolomics platform. *Metabolomics*, **2013**, 9, 599-607 | 4.7 | 55 |
| 89 | Identification of novel in vivo MAP kinase substrates in Arabidopsis thaliana through use of tandem metal oxide affinity chromatography. *Molecular and Cellular Proteomics*, **2013**, 12, 369-80 | 7.6 | 97 |
| 88 | A workflow for mathematical modeling of subcellular metabolic pathways in leaf metabolism of Arabidopsis thaliana. *Frontiers in Plant Science*, **2013**, 4, 541 | 6.2 | 12 |
| 87 | Dynamic adaption of metabolic pathways during germination and growth of lily pollen tubes after inhibition of the electron transport chain. *Plant Physiology*, **2013**, 162, 1822-33 | 6.6 | 50 |
| 86 | Systemic cold stress adaptation of Chlamydomonas reinhardtii. *Molecular and Cellular Proteomics*, **2013**, 12, 2032-47 | 7.6 | 87 |
| 85 | Proteome and metabolome profiling of cytokinin action in Arabidopsis identifying both distinct and similar responses to cytokinin down- and up-regulation. *Journal of Experimental Botany*, **2013**, 64, 4193-206 | 7 | 47 |
| 84 | INPPO Actions and Recognition as a Driving Force for Progress in Plant Proteomics: Change of Guard, INPPO Update, and Upcoming Activities. *Proteomics*, **2013**, 13, 3093-3100 | 4.8 | |

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|---|---|---|---|
| 83 | Methylotrophic methanogenic Thermoplasmata implicated in reduced methane emissions from bovine rumen. *Nature Communications*, **2013**, 4, 1428 | 17.4 | 215 |
| 82 | Pepino mosaic virus infection of tomato affects allergen expression, but not the allergenic potential of fruits. *PLoS ONE*, **2013**, 8, e65116 | 3.7 | 17 |
| 81 | Eigenvalues of Jacobian Matrices Report on Steps of Metabolic Reprogramming in a Complex Plant-Environment Interaction. *Applied Mathematics*, **2013**, 04, 44-49 | 0.4 | 3 |
| 80 | The different proteomes of Chlamydomonas reinhardtii. *Journal of Proteomics*, **2012**, 75, 5883-7 | 3.9 | 14 |
| 79 | Mathematical modeling of plant metabolism-from reconstruction to prediction. *Metabolites*, **2012**, 2, 553-66 | 5.6 | 11 |
| 78 | Boosting the globalization of plant proteomics through INPPO: current developments and future prospects. *Proteomics*, **2012**, 12, 359-68 | 4.8 | 9 |
| 77 | COVAIN: a toolbox for uni- and multivariate statistics, time-series and correlation network analysis and inverse estimation of the differential Jacobian from metabolomics covariance data. *Metabolomics*, **2012**, 8, 81-93 | 4.7 | 98 |
| 76 | Metabolite changes with induction of Cuscuta haustorium and translocation from host plants. *Journal of Plant Interactions*, **2012**, 7, 84-93 | 3.8 | 21 |
| 75 | ProMEX - a mass spectral reference database for plant proteomics. *Frontiers in Plant Science*, **2012**, 3, 125 | 6.2 | 34 |
| 74 | From bench to bountiful harvests: a road map for the next decade of Arabidopsis research. *Plant Cell*, **2012**, 24, 2240-7 | 11.6 | 7 |
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