

Martin Hajduch

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,673
citations

394421

19
h-index

477307

29
g-index

31
all docs

31
docs citations

31
times ranked

1863
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomics study of silver nanoparticles on Caco-2 cells. <i>Toxicology in Vitro</i> , 2018, 50, 347-372.	2.4	20
2	DNA damage, repair monitoring and epigenetic DNA methylation changes in seedlings of Chernobyl soybeans. <i>DNA Repair</i> , 2017, 50, 14-21.	2.8	40
3	Using 7 cm immobilized pH gradient strips to determine levels of clinically relevant proteins in wheat grain extracts. <i>Frontiers in Plant Science</i> , 2015, 6, 433.	3.6	5
4	Chernobyl seed project. Advances in the identification of differentially abundant proteins in a radio-contaminated environment. <i>Frontiers in Plant Science</i> , 2015, 6, 493.	3.6	14
5	Do Cupins Have a Function Beyond Being Seed Storage Proteins?. <i>Frontiers in Plant Science</i> , 2015, 6, 1215.	3.6	19
6	Comparative quantitative proteomic analysis of embryogenic and non-embryogenic calli in maize suggests the role of oxylipins in plant totipotency. <i>Journal of Proteomics</i> , 2014, 104, 57-65.	2.4	43
7	Establishing a Leaf Proteome Reference Map for <i>Ginkgo biloba</i> Provides Insight into Potential Ethnobotanical Uses. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 11547-11556.	5.2	2
8	Proteomics of Field Samples in Radioactive Chernobyl Area. <i>Methods in Molecular Biology</i> , 2014, 1072, 555-561.	0.9	0
9	MS ^E Based Multiplex Protein Analysis Quantified Important Allergenic Proteins and Detected Relevant Peptides Carrying Known Epitopes in Wheat Grain Extracts. <i>Journal of Proteome Research</i> , 2013, 12, 4862-4869.	3.7	47
10	The MSE-proteomic analysis of gliadins and glutenins in wheat grain identifies and quantifies proteins associated with celiac disease and baker's asthma. <i>Journal of Proteomics</i> , 2013, 93, 65-73.	2.4	25
11	Radioactive Chernobyl Environment Has Produced High-Oil Flax Seeds That Show Proteome Alterations Related to Carbon Metabolism during Seed Development. <i>Journal of Proteome Research</i> , 2013, 12, 4799-4806.	3.7	13
12	Seeds in Chernobyl: the database on proteome response on radioactive environment. <i>Frontiers in Plant Science</i> , 2012, 3, 231.	3.6	11
13	Soybeans Grown in the Chernobyl Area Produce Fertile Seeds that Have Increased Heavy Metal Resistance and Modified Carbon Metabolism. <i>PLoS ONE</i> , 2012, 7, e48169.	2.5	22
14	Using proteomics to study sexual reproduction in angiosperms. <i>Sexual Plant Reproduction</i> , 2011, 24, 9-22.	2.2	23
15	Comparative proteomics of seed maturation in oilseeds reveals differences in intermediary metabolism. <i>Proteomics</i> , 2011, 11, 1619-1629.	2.2	36
16	Seed proteomics. <i>Journal of Proteomics</i> , 2011, 74, 389-400.	2.4	79
17	Agricultural recovery of a formerly radioactive area: II. Systematic proteomic characterization of flax seed development in the remediated Chernobyl area. <i>Journal of Proteomics</i> , 2011, 74, 1378-1384.	2.4	14
18	Agricultural recovery of a formerly radioactive area: I. Establishment of high-resolution quantitative protein map of mature flax seeds harvested from the remediated Chernobyl area. <i>Phytochemistry</i> , 2011, 72, 1308-1315.	2.9	12

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19	Systems Analysis of Seed Filling in Arabidopsis: Using General Linear Modeling to Assess Concordance of Transcript and Protein Expression. <i>Plant Physiology</i> , 2010, 152, 2078-2087.	4.8	126
20	Proteomics Analysis of Flax Grown in Chernobyl Area Suggests Limited Effect of Contaminated Environment on Seed Proteome. <i>Environmental Science & Technology</i> , 2010, 44, 6940-6946.	10.0	33
21	Techniques in Plant Proteomics. , 2010, , 469-491.		0
22	System Analysis of an Arabidopsis Mutant Altered in de Novo Fatty Acid Synthesis Reveals Diverse Changes in Seed Composition and Metabolism. <i>Plant Physiology</i> , 2009, 150, 27-41.	4.8	63
23	Quantitative Proteomics of Seed Filling in Castor: Comparison with Soybean and Rapeseed Reveals Differences between Photosynthetic and Nonphotosynthetic Seed Metabolism. <i>Plant Physiology</i> , 2009, 151, 857-868.	4.8	95
24	Proteomic Analysis of Mature Soybean Seeds from the Chernobyl Area Suggests Plant Adaptation to the Contaminated Environment. <i>Journal of Proteome Research</i> , 2009, 8, 2915-2922.	3.7	61
25	Reduction of IgE Binding and Nonpromotion of <i>Aspergillus flavus</i> Fungal Growth by Simultaneously Silencing Ara h 2 and Ara h 6 in Peanut. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 11225-11233.	5.2	68
26	In-Depth Investigation of the Soybean Seed-Filling Proteome and Comparison with a Parallel Study of Rapeseed. <i>Plant Physiology</i> , 2008, 148, 504-518.	4.8	106
27	Proteomic Analysis of Near-Isogenic Sunflower Varieties Differing in Seed Oil Traits. <i>Journal of Proteome Research</i> , 2007, 6, 3232-3241.	3.7	59
28	Protein and lipid composition analysis of oil bodies from two <i>Brassica napus</i> cultivars. <i>Proteomics</i> , 2006, 6, 4586-4598.	2.2	127
29	Proteomic Analysis of Seed Filling in <i>Brassica napus</i> . Developmental Characterization of Metabolic Isozymes Using High-Resolution Two-Dimensional Gel Electrophoresis. <i>Plant Physiology</i> , 2006, 141, 32-46.	4.8	173
30	A Systematic Proteomic Study of Seed Filling in Soybean. Establishment of High-Resolution Two-Dimensional Reference Maps, Expression Profiles, and an Interactive Proteome Database. <i>Plant Physiology</i> , 2005, 137, 1397-1419.	4.8	333
31	Total protein and isozyme characterization in the flax zygotic embryo during development. <i>Sexual Plant Reproduction</i> , 2001, 13, 329-334.	2.2	4