

# Martin Hajduch

## List of Publications by Year in descending order

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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	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
2	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
3	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
4	Systems Analysis of Seed Filling in <i>Arabidopsis</i> : Using General Linear Modeling to Assess Concordance of Transcript and Protein Expression. <i>Plant Physiology</i> , 2010, 152, 2078-2087.	4.8	126
5	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
6	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
7	Seed proteomics. <i>Journal of Proteomics</i> , 2011, 74, 389-400.	2.4	79
8	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
9	System Analysis of an <i>Arabidopsis</i> 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
10	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
11	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
12	MS <sup>E</sup> 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
13	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
14	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
15	Comparative proteomics of seed maturation in oilseeds reveals differences in intermediary metabolism. <i>Proteomics</i> , 2011, 11, 1619-1629.	2.2	36
16	Proteomics Analysis of Flax Grown in Chernobyl Area Suggests Limited Effect of Contaminated Environment on Seed Proteome. <i>Environmental Science &amp; Technology</i> , 2010, 44, 6940-6946.	10.0	33
17	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
18	Using proteomics to study sexual reproduction in angiosperms. <i>Sexual Plant Reproduction</i> , 2011, 24, 9-22.	2.2	23

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19	Soybeans Grown in the Chernobyl Area Produce Fertile Seeds that Have Increased Heavy Metal Resistance and Modified Carbon Metabolism. PLoS ONE, 2012, 7, e48169.	2.5	22
20	Proteomics study of silver nanoparticles on Caco-2 cells. Toxicology in Vitro, 2018, 50, 347-372.	2.4	20
21	Do Cupins Have a Function Beyond Being Seed Storage Proteins?. Frontiers in Plant Science, 2015, 6, 1215.	3.6	19
22	Agricultural recovery of a formerly radioactive area: II. Systematic proteomic characterization of flax seed development in the remediated Chernobyl area. Journal of Proteomics, 2011, 74, 1378-1384.	2.4	14
23	Chernobyl seed project. Advances in the identification of differentially abundant proteins in a radio-contaminated environment. Frontiers in Plant Science, 2015, 6, 493.	3.6	14
24	Radioactive Chernobyl Environment Has Produced High-Oil Flax Seeds That Show Proteome Alterations Related to Carbon Metabolism during Seed Development. Journal of Proteome Research, 2013, 12, 4799-4806.	3.7	13
25	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. Phytochemistry, 2011, 72, 1308-1315.	2.9	12
26	Seeds in Chernobyl: the database on proteome response on radioactive environment. Frontiers in Plant Science, 2012, 3, 231.	3.6	11
27	Using 7 cm immobilized pH gradient strips to determine levels of clinically relevant proteins in wheat grain extracts. Frontiers in Plant Science, 2015, 6, 433.	3.6	5
28	Total protein and isozyme characterization in the flax zygotic embryo during development. Sexual Plant Reproduction, 2001, 13, 329-334.	2.2	4
29	Establishing a Leaf Proteome Reference Map for <i>Ginkgo biloba</i> Provides Insight into Potential Ethnobotanical Uses. Journal of Agricultural and Food Chemistry, 2014, 62, 11547-11556.	5.2	2
30	Techniques in Plant Proteomics. , 2010, , 469-491.		0
31	Proteomics of Field Samples in Radioactive Chernobyl Area. Methods in Molecular Biology, 2014, 1072, 555-561.	0.9	0