

Janusz DÄbski

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2476937/publications.pdf>

Version: 2024-02-01

43
papers

1,645
citations

331670

21
h-index

302126

39
g-index

44
all docs

44
docs citations

44
times ranked

2917
citing authors

#	ARTICLE	IF	CITATIONS
1	CENP-C Is a Structural Platform for Kinetochore Assembly. <i>Current Biology</i> , 2011, 21, 399-405.	3.9	233
2	The Role of Annexin 1 in Drought Stress in Arabidopsis Å. <i>Plant Physiology</i> , 2009, 150, 1394-1410.	4.8	220
3	Plk4 Phosphorylates Ana2 to Trigger Sas6 Recruitment and Procentriole Formation. <i>Current Biology</i> , 2014, 24, 2526-2532.	3.9	152
4	Regulation of Autophosphorylation Controls PLK4 Self-Destruction and Centriole Number. <i>Current Biology</i> , 2013, 23, 2245-2254.	3.9	110
5	A Complex Containing the CPSF73 Endonuclease and Other Polyadenylation Factors Associates with U7 snRNP and Is Recruited to Histone Pre-mRNA for 3â€™-End Processing. <i>Molecular and Cellular Biology</i> , 2013, 33, 28-37.	2.3	67
6	Phosphoproteomic analysis reveals that dehydrins ERD10 and ERD14 are phosphorylated by SNF1â€™related protein kinase 2.10 in response to osmotic stress. <i>Plant, Cell and Environment</i> , 2019, 42, 931-946.	5.7	63
7	Proteomic analysis of the palmitoyl protein thioesterase 1 interactome in SH-SY5Y human neuroblastoma cells. <i>Journal of Proteomics</i> , 2015, 123, 42-53.	2.4	62
8	Global proteomic approach unmask involvement of keratins 8 and 18 in the delivery of cystic fibrosis transmembrane conductance regulator (CFTR)/F508-CFTR to the plasma membrane. <i>Proteomics</i> , 2004, 4, 3833-3844.	2.2	55
9	Casein kinase II-mediated phosphorylation of general repressor Maf1 triggers RNA polymerase III activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4926-4931.	7.1	55
10	Suppression of Scant Identifies Endos as a Substrate of Greatwall Kinase and a Negative Regulator of Protein Phosphatase 2A in Mitosis. <i>PLoS Genetics</i> , 2011, 7, e1002225.	3.5	55
11	Drafting the CLN3 Protein Interactome in SH-SY5Y Human Neuroblastoma Cells: A Label-free Quantitative Proteomics Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2101-2115.	3.7	42
12	Cross-regulation between Aurora B and Citron kinase controls midbody architecture in cytokinesis. <i>Open Biology</i> , 2016, 6, 160019.	3.6	39
13	Application of a new procedure for liquid chromatography/mass spectrometry profiling of plasma amino acid-related metabolites and untargeted shotgun proteomics to identify mechanisms and biomarkers of calcific aortic stenosis. <i>Journal of Chromatography A</i> , 2017, 1517, 66-78.	3.7	35
14	Keratinous waste decomposition and peptide production by keratinase from <i>Geobacillus stearothermophilus</i> AD-11. <i>International Journal of Biological Macromolecules</i> , 2015, 75, 158-165.	7.5	33
15	Phosphatase ABI1 and okadaic acid-sensitive phosphoprotein phosphatases inhibit salt stress-activated SnRK2.4 kinase. <i>BMC Plant Biology</i> , 2016, 16, 136.	3.6	32
16	Structure of Î³-conglutin: insight into the quaternary structure of 7S basic globulins from legumes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 224-238.	2.5	31
17	The Pentameric Nucleoplasmin Fold Is Present in <i>Drosophila</i> FKBP39 and a Large Number of Chromatin-Related Proteins. <i>Journal of Molecular Biology</i> , 2015, 427, 1949-1963.	4.2	29
18	Effect of chronic mild stress and imipramine on the proteome of the rat dentate gyrus. <i>Journal of Neurochemistry</i> , 2010, 113, 848-859.	3.9	28

#	ARTICLE	IF	CITATIONS
19	Positions of disulfide bonds and N-glycosylation site in juvenile hormone binding protein. Archives of Biochemistry and Biophysics, 2004, 421, 260-266.	3.0	25
20	Impact of <i>OmpR</i> on the membrane proteome of <i>Yersinia enterocolitica</i> in different environments: repression of major adhesin <i>YadA</i> and heme receptor <i>HemR</i> . Environmental Microbiology, 2016, 18, 997-1021.	3.8	25
21	Peroxiredoxin 6 Fails to Limit Phospholipid Peroxidation in Lung from Cftr-Knockout Mice Subjected to Oxidative Challenge. PLoS ONE, 2009, 4, e6075.	2.5	24
22	The Ability of Lytic Staphylococcal Podovirus vB_SauP_phiAGO1.3 to Coexist in Equilibrium With Its Host Facilitates the Selection of Host Mutants of Attenuated Virulence but Does Not Preclude the Phage Antistaphylococcal Activity in a Nematode Infection Model. Frontiers in Microbiology, 2018, 9, 3227.	3.5	24
23	Novel perspectives of target-binding by the evolutionarily conserved PP4 phosphatase. Open Biology, 2020, 10, 200343.	3.6	19
24	A Strong Neutrophil Elastase Proteolytic Fingerprint Marks the Carcinoma Tumor Proteome. Molecular and Cellular Proteomics, 2017, 16, 213-227.	3.8	17
25	Molecular Signatures Associated with Treatment of Triple-Negative MDA-MB231 Breast Cancer Cells with Histone Deacetylase Inhibitors JAHA and SAHA. Chemical Research in Toxicology, 2017, 30, 2187-2196.	3.3	16
26	Characterization of the cofactor-binding site in the SPOUT-fold methyltransferases by computational docking of S-adenosylmethionine to three crystal structures. BMC Bioinformatics, 2003, 4, 9.	2.6	15
27	Mass spectrometry identification of granins and other proteins secreted by neuroblastoma cells. Tumor Biology, 2013, 34, 1773-1781.	1.8	13
28	Catalytic activities of Werner protein are affected by adduction with 4-hydroxy-2-nonenal. Nucleic Acids Research, 2014, 42, 11119-11135.	14.5	13
29	Quantitative proteomic analysis of differentially expressed proteins in tubers of potato plants differing in resistance to <i>Dickeya solani</i> . Plant and Soil, 2019, 441, 317-329.	3.7	13
30	Evaluation of Anti-cancer Activity of Stilbene and Methoxydibenzo[b,f] oxepin Derivatives. Current Cancer Drug Targets, 2018, 18, 706-717.	1.6	12
31	Influence of Environmental and Genetic Factors on Proteomic Profiling of Outer Membrane Vesicles from <i>Campylobacter jejuni</i> . Polish Journal of Microbiology, 2019, 68, 255-261.	1.7	12
32	Protein kinase C beta in postischemic brain mitochondria. Mitochondrion, 2012, 12, 138-143.	3.4	11
33	Quantitative analysis of PPT1 interactome in human neuroblastoma cells. Data in Brief, 2015, 4, 207-216.	1.0	11
34	Enhanced cardiac hypoxic injury in atherogenic dyslipidaemia results from alterations in the energy metabolism pattern. Metabolism: Clinical and Experimental, 2021, 114, 154400.	3.4	9
35	Multi-omic signatures of atherogenic dyslipidaemia: pre-clinical target identification and validation in humans. Journal of Translational Medicine, 2021, 19, 6.	4.4	8
36	Overexpression of juvenile hormone binding protein in bacteria and <i>Pichia pastoris</i> . Protein Expression and Purification, 2003, 31, 173-180.	1.3	6

#	ARTICLE	IF	CITATIONS
37	N-linked glycosylation of G. mellonella juvenile hormone binding protein – Comparison of recombinant mutants expressed in P. pastoris cells with native protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 610-621.	2.3	6
38	Proteomic Profiling of Secreted Proteins for the Hematopoietic Support of Interleukin-Stimulated Human Umbilical Vein Endothelial Cells. <i>Cell Transplantation</i> , 2013, 22, 1185-1199.	2.5	6
39	New Candidates for Biomarkers and Drug Targets of Ischemic Stroke – A First Dynamic LC-MS Human Serum Proteomic Study. <i>Journal of Clinical Medicine</i> , 2022, 11, 339.	2.4	6
40	Platelet-Derived Drug Targets and Biomarkers of Ischemic Stroke – The First Dynamic Human LC-MS Proteomic Study. <i>Journal of Clinical Medicine</i> , 2022, 11, 1198.	2.4	5
41	Ribosomal DNA status inferred from DNA cloud assays and mass spectrometry identification of agarose-squeezed proteins interacting with chromatin (ASPIC-MS). <i>Oncotarget</i> , 2017, 8, 24988-25004.	1.8	4
42	Effect of Posttranslational Modifications on the Structure and Activity of FTO Demethylase. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4512.	4.1	3
43	Identification of proteins involved in starch and polygalacturonic acid degradation using LC/MS. <i>Open Life Sciences</i> , 2014, 9, 708-716.	1.4	1