

# Pitter F Huesgen

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

2,409  
citations

218592

26  
h-index

223716

46  
g-index

75  
all docs

75  
docs citations

75  
times ranked

3212  
citing authors

#	ARTICLE	IF	CITATIONS
1	Omics approaches to determine protease degradomes in complex biological matrices. , 2022, , 209-228.		0
2	An advanced method for the release, enrichment and purification of high-quality <i>Arabidopsis thaliana</i> rosette leaf trichomes enables profound insights into the trichome proteome. <i>Plant Methods</i> , 2022, 18, 12.	1.9	5
3	A bipartite chromatophore transit peptide and N-terminal protein processing in the <i>Paulinella</i> chromatophore. <i>Plant Physiology</i> , 2022, 189, 152-164.	2.3	7
4	Sensitive Plant N-Terminome Profiling with HUNTER. <i>Methods in Molecular Biology</i> , 2022, 2447, 139-158.	0.4	2
5	Profiling Sequence Specificity of Proteolytic Activities Using Proteome-Derived Peptide Libraries. <i>Methods in Molecular Biology</i> , 2022, 2447, 159-174.	0.4	0
6	A User Guide to Validation, Annotation, and Evaluation of N-Terminome Datasets with MANTI. <i>Methods in Molecular Biology</i> , 2022, 2447, 271-283.	0.4	1
7	Abundance of metalloprotease FtsH12 modulates chloroplast development in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 3455-3473.	2.4	19
8	A 9-kDa matricellular SPARC fragment released by cathepsin D exhibits pro-tumor activity in the triple-negative breast cancer microenvironment. <i>Theranostics</i> , 2021, 11, 6173-6192.	4.6	27
9	Multistep optimization of a cell-penetrating peptide towards its antimicrobial activity. <i>Biochemical Journal</i> , 2021, 478, 63-78.	1.7	12
10	Cutting the line: manipulation of plant immunity by bacterial type III effector proteases. <i>Journal of Experimental Botany</i> , 2021, 72, 3395-3409.	2.4	6
11	Host apoplastic cysteine protease activity is suppressed during the mutualistic association of <i>Lolium perenne</i> and <i>Epichloa festucae</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 3410-3426.	2.4	6
12	MANTI: Automated Annotation of Protein N-Termini for Rapid Interpretation of N-Terminome Data Sets. <i>Analytical Chemistry</i> , 2021, 93, 5596-5605.	3.2	9
13	Proteolysis and inflammation of the kidney glomerulus. <i>Cell and Tissue Research</i> , 2021, 385, 489-500.	1.5	4
14	Overexpression of human BAG3P209L in mice causes restrictive cardiomyopathy. <i>Nature Communications</i> , 2021, 12, 3575.	5.8	17
15	Maintaining proteostasis under mechanical stress. <i>EMBO Reports</i> , 2021, 22, e52507.	2.0	28
16	The Peptide Ligase Activity of Human Legumain Depends on Fold Stabilization and Balanced Substrate Affinities. <i>ACS Catalysis</i> , 2021, 11, 11885-11896.	5.5	15
17	Identification of Putative Mitochondrial Protease Substrates. <i>Methods in Molecular Biology</i> , 2021, 2192, 313-329.	0.4	1
18	Structural and functional studies of <i>Arabidopsis thaliana</i> legumain beta reveal isoform specific mechanisms of activation and substrate recognition. <i>Journal of Biological Chemistry</i> , 2020, 295, 13047-13064.	1.6	24

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19	The Mouse Heart Mitochondria N Terminome Provides Insights into ClpXP-Mediated Proteolysis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1330-1345.	2.5	20
20	Photoprotective Acclimation of the <i>Arabidopsis thaliana</i> Leaf Proteome to Fluctuating Light. <i>Frontiers in Genetics</i> , 2020, 11, 154.	1.1	24
21	Extending Proteome Coverage with Legumain as a Highly Specific Digestion Protease. <i>Analytical Chemistry</i> , 2020, 92, 2961-2971.	3.2	17
22	Deep Profiling of the Cleavage Specificity and Human Substrates of Snake Venom Metalloprotease HF3 by Proteomic Identification of Cleavage Site Specificity (PICS) Using Proteome Derived Peptide Libraries and Terminal Amine Isotopic Labeling of Substrates (TAILS) N-Terminomics. <i>Journal of Proteome Research</i> , 2019, 18, 3419-3428.	1.8	15
23	Solution structure of the autophagy-related protein LC3C reveals a polyproline II motif on a mobile tether with phosphorylation site. <i>Scientific Reports</i> , 2019, 9, 14167.	1.6	15
24	DEG10 contributes to mitochondrial proteostasis, root growth, and seed yield in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 5423-5436.	2.4	13
25	The Influence of Different Fat Sources on Steatohepatitis and Fibrosis Development in the Western Diet Mouse Model of Non-alcoholic Steatohepatitis (NASH). <i>Frontiers in Physiology</i> , 2019, 10, 770.	1.3	27
26	New beginnings and new ends: methods for large-scale characterization of protein termini and their use in plant biology. <i>Journal of Experimental Botany</i> , 2019, 70, 2021-2038.	2.4	37
27	A fungal substrate mimicking molecule suppresses plant immunity via an inter-kingdom conserved motif. <i>Nature Communications</i> , 2019, 10, 1576.	5.8	55
28	Metabolic resistance of the D-peptide RD2 developed for direct elimination of amyloid- $\beta$ oligomers. <i>Scientific Reports</i> , 2019, 9, 5715.	1.6	25
29	An atypical aspartic protease modulates lateral root development in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 2157-2171.	2.4	24
30	Sensitive Determination of Proteolytic Proteoforms in Limited Microscale Proteome Samples. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2335-2347.	2.5	74
31	Sirtilins - the new old members of the vitamin K-dependent coagulation factor family. <i>Journal of Thrombosis and Haemostasis</i> , 2019, 17, 470-481.	1.9	8
32	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. <i>Kidney International</i> , 2019, 95, 333-349.	2.6	55
33	Positional proteomics for identification of secreted proteoforms released by site-specific processing of membrane proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 140138.	1.1	23
34	Molecular composition of the human primary visual cortex profiled by multimodal mass spectrometry imaging. <i>Brain Structure and Function</i> , 2018, 223, 2767-2783.	1.2	18
35	Quantitative proteomics in plant protease substrate identification. <i>New Phytologist</i> , 2018, 218, 936-943.	3.5	26
36	Heterologous expression and characterization of a novel serine protease from <i>Daphnia magna</i> : A possible role in susceptibility to toxic cyanobacteria. <i>Aquatic Toxicology</i> , 2018, 205, 140-147.	1.9	7

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37	The podocyte protease web: uncovering the gatekeepers of glomerular disease. <i>American Journal of Physiology - Renal Physiology</i> , 2018, 315, F1812-F1816.	1.3	17
38	Dual function of a secreted fungalsin metalloprotease in <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2018, 220, 249-261.	3.5	82
39	Profiling of Protein N-Termini and Their Modifications in Complex Samples. <i>Methods in Molecular Biology</i> , 2017, 1574, 35-50.	0.4	24
40	N-Degradomic Analysis Reveals a Proteolytic Network Processing the Podocyte Cytoskeleton. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 2867-2878.	3.0	41
41	Enzymatic properties, evidence for in vivo expression, and intracellular localization of shewasin D, the pepsin homolog from <i>Shewanella denitrificans</i> . <i>Scientific Reports</i> , 2016, 6, 23869.	1.6	6
42	Identification of Protease Specificity by Combining Proteome-Derived Peptide Libraries and Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2515-2524.	2.5	43
43	Active site specificity profiling datasets of matrix metalloproteinases (MMPs) 1, 2, 3, 7, 8, 9, 12, 13 and 14. <i>Data in Brief</i> , 2016, 7, 299-310.	0.5	21
44	Active site specificity profiling of the matrix metalloproteinase family: Proteomic identification of 4300 cleavage sites by nine MMPs explored with structural and synthetic peptide cleavage analyses. <i>Matrix Biology</i> , 2016, 49, 37-60.	1.5	177
45	LysargiNase mirrors trypsin for protein C-terminal and methylation-site identification. <i>Nature Methods</i> , 2015, 12, 55-58.	9.0	128
46	Snake venom serine proteinases specificity mapping by proteomic identification of cleavage sites. <i>Journal of Proteomics</i> , 2015, 113, 260-267.	1.2	23
47	RC1339/APRc from <i>Rickettsia conorii</i> Is a Novel Aspartic Protease with Properties of Retropepsin-Like Enzymes. <i>PLoS Pathogens</i> , 2014, 10, e1004324.	2.1	17
48	Family-wide characterization of matrix metalloproteinases from <i>Arabidopsis thaliana</i> reveals their distinct proteolytic activity and cleavage site specificity. <i>Biochemical Journal</i> , 2014, 457, 335-346.	1.7	33
49	Ensembles of protein termini and specific proteolytic signatures as candidate biomarkers of disease. <i>Proteomics - Clinical Applications</i> , 2014, 8, 338-350.	0.8	28
50	Proteomic protease specificity profiling of clostridial collagenases reveals their intrinsic nature as dedicated degraders of collagen. <i>Journal of Proteomics</i> , 2014, 100, 102-114.	1.2	60
51	Annotating N Termini for the Human Proteome Project: N Termini and N <sup>ε</sup> -Acetylation Status Differentiate Stable Cleaved Protein Species from Degradation Remnants in the Human Erythrocyte Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 2028-2044.	1.8	95
52	Structure of the Mycosin-1 Protease from the Mycobacterial ESX-1 Protein Type VII Secretion System. <i>Journal of Biological Chemistry</i> , 2013, 288, 17782-17790.	1.6	48
53	Proteomic Amino-Termini Profiling Reveals Targeting Information for Protein Import into Complex Plastids. <i>PLoS ONE</i> , 2013, 8, e74483.	1.1	41
54	Proteolysis of cystatin C by cathepsin D in the breast cancer microenvironment. <i>FASEB Journal</i> , 2012, 26, 5172-5181.	0.2	58

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55	TopFIND 2.0-linking protein termini with proteolytic processing and modifications altering protein function. <i>Nucleic Acids Research</i> , 2012, 40, D351-D361.	6.5	54
56	The family of Deg/HtrA proteases in plants. <i>BMC Plant Biology</i> , 2012, 12, 52.	1.6	37
57	N- and C-terminal degradomics: new approaches to reveal biological roles for plant proteases from substrate identification. <i>Physiologia Plantarum</i> , 2012, 145, 5-17.	2.6	45
58	Development of Soluble Ester-Linked Aldehyde Polymers for Proteomics. <i>Analytical Chemistry</i> , 2011, 83, 6500-6510.	3.2	9
59	Recombinant Deg/HtrA proteases from <i>Synechocystis</i> sp. PCC 6803 differ in substrate specificity, biochemical characteristics and mechanism. <i>Biochemical Journal</i> , 2011, 435, 733-742.	1.7	28
60	Characterization of the prime and non-prime active site specificities of proteases by proteome-derived peptide libraries and tandem mass spectrometry. <i>Nature Protocols</i> , 2011, 6, 111-120.	5.5	97
61	Identification and Relative Quantification of Native and Proteolytically Generated Protein C-Termini from Complex Proteomes: C-Terminome Analysis. <i>Methods in Molecular Biology</i> , 2011, 781, 59-69.	0.4	23
62	Proteome-wide analysis of protein carboxy termini: C terminomics. <i>Nature Methods</i> , 2010, 7, 508-511.	9.0	144
63	Deg/HtrA proteases as components of a network for photosystem II quality control in chloroplasts and cyanobacteria. <i>Research in Microbiology</i> , 2009, 160, 726-732.	1.0	48
64	Eukaryotic GCP1 is a conserved mitochondrial protein required for progression of embryo development beyond the globular stage in <i>Arabidopsis thaliana</i> . <i>Biochemical Journal</i> , 2009, 423, 333-341.	1.7	12
65	The DEG15 Serine Protease Cleaves Peroxisomal Targeting Signal 2-Containing Proteins in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2008, 148, 1847-1856.	2.3	77
66	Dual specificities of the glyoxysomal/peroxisomal processing protease Deg15 in higher plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11501-11506.	3.3	84
67	The Serine Protease HhoA from <i>Synechocystis</i> sp. Strain PCC 6803: Substrate Specificity and Formation of a Hexameric Complex Are Regulated by the PDZ Domain. <i>Journal of Bacteriology</i> , 2007, 189, 6611-6618.	1.0	17
68	Photodamaged D1 protein is degraded in <i>Arabidopsis</i> mutants lacking the Deg2 protease. <i>FEBS Letters</i> , 2006, 580, 6929-6932.	1.3	56
69	The family of Deg proteases in cyanobacteria and chloroplasts of higher plants. <i>Physiologia Plantarum</i> , 2005, 123, 413-420.	2.6	65
70	ENRICHMENT OF NATURAL AND PROTEOLYTICALLY GENERATED PROTEIN C-TERMINI ON A PROTEOME-WIDE SCALE. <i>Protocol Exchange</i> , 0, , .	0.3	0