

# Pitter F Huesgen

## List of Publications by Year in descending order

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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	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
2	Proteome-wide analysis of protein carboxy termini: C terminomics. <i>Nature Methods</i> , 2010, 7, 508-511.	9.0	144
3	LysargiNase mirrors trypsin for protein C-terminal and methylation-site identification. <i>Nature Methods</i> , 2015, 12, 55-58.	9.0	128
4	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
5	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
6	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
7	Dual function of a secreted fungalysin metalloprotease in <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2018, 220, 249-261.	3.5	82
8	The DEG15 Serine Protease Cleaves Peroxisomal Targeting Signal 2-Containing Proteins in Arabidopsis. <i>Plant Physiology</i> , 2008, 148, 1847-1856.	2.3	77
9	Sensitive Determination of Proteolytic Proteoforms in Limited Microscale Proteome Samples. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2335-2347.	2.5	74
10	The family of Deg proteases in cyanobacteria and chloroplasts of higher plants. <i>Physiologia Plantarum</i> , 2005, 123, 413-420.	2.6	65
11	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
12	Proteolysis of cystatin C by cathepsin D in the breast cancer microenvironment. <i>FASEB Journal</i> , 2012, 26, 5172-5181.	0.2	58
13	Photodamaged D1 protein is degraded in Arabidopsis mutants lacking the Deg2 protease. <i>FEBS Letters</i> , 2006, 580, 6929-6932.	1.3	56
14	A fungal substrate mimicking molecule suppresses plant immunity via an inter-kingdom conserved motif. <i>Nature Communications</i> , 2019, 10, 1576.	5.8	55
15	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
16	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
17	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
18	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

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19	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
20	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
21	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
22	Proteomic Amino-Termini Profiling Reveals Targeting Information for Protein Import into Complex Plastids. <i>PLoS ONE</i> , 2013, 8, e74483.	1.1	41
23	The family of Deg/HtrA proteases in plants. <i>BMC Plant Biology</i> , 2012, 12, 52.	1.6	37
24	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
25	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
26	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
27	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
28	Maintaining proteostasis under mechanical stress. <i>EMBO Reports</i> , 2021, 22, e52507.	2.0	28
29	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
30	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
31	Quantitative proteomics in plant protease substrate identification. <i>New Phytologist</i> , 2018, 218, 936-943.	3.5	26
32	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
33	Profiling of Protein N-Termini and Their Modifications in Complex Samples. <i>Methods in Molecular Biology</i> , 2017, 1574, 35-50.	0.4	24
34	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
35	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
36	Photoprotective Acclimation of the <i>Arabidopsis thaliana</i> Leaf Proteome to Fluctuating Light. <i>Frontiers in Genetics</i> , 2020, 11, 154.	1.1	24

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37	Snake venom serine proteinases specificity mapping by proteomic identification of cleavage sites. <i>Journal of Proteomics</i> , 2015, 113, 260-267.	1.2	23
38	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
39	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
40	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
41	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
42	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
43	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
44	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
45	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
46	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
47	ExteNDing Proteome Coverage with Legumain as a Highly Specific Digestion Protease. <i>Analytical Chemistry</i> , 2020, 92, 2961-2971.	3.2	17
48	Overexpression of human BAG3P209L in mice causes restrictive cardiomyopathy. <i>Nature Communications</i> , 2021, 12, 3575.	5.8	17
49	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
50	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
51	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
52	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
53	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
54	Multistep optimization of a cell-penetrating peptide towards its antimicrobial activity. <i>Biochemical Journal</i> , 2021, 478, 63-78.	1.7	12

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55	Development of Soluble Ester-Linked Aldehyde Polymers for Proteomics. <i>Analytical Chemistry</i> , 2011, 83, 6500-6510.	3.2	9
56	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
57	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
58	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
59	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
60	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
61	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
62	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
63	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
64	Proteolysis and inflammation of the kidney glomerulus. <i>Cell and Tissue Research</i> , 2021, 385, 489-500.	1.5	4
65	Sensitive Plant N-Terminome Profiling with HUNTER. <i>Methods in Molecular Biology</i> , 2022, 2447, 139-158.	0.4	2
66	Identification of Putative Mitochondrial Protease Substrates. <i>Methods in Molecular Biology</i> , 2021, 2192, 313-329.	0.4	1
67	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
68	ENRICHMENT OF NATURAL AND PROTEOLYTICALLY GENERATED PROTEIN C-TERMINI ON A PROTEOME-WIDE SCALE. <i>Protocol Exchange</i> , 0, , .	0.3	0
69	Omics approaches to determine protease degradomes in complex biological matrices. , 2022, , 209-228.		0
70	Profiling Sequence Specificity of Proteolytic Activities Using Proteome-Derived Peptide Libraries. <i>Methods in Molecular Biology</i> , 2022, 2447, 159-174.	0.4	0