Christopher M Overall

List of Publications by Year
in descending order

276 papers	29,041 citations	3531 90 h-index	5988 160 g-index
283 all docs	283 docs citations	283 times ranked	25153 citing authors

#	Article	IF	Citations
1	A 9-kDa matricellular SPARC fragment released by cathepsin D exhibits pro-tumor activity in the triple-negative breast cancer microenvironment. Theranostics, 2021, 11, 6173-6192.	10.0	27
2	Mechanistic understanding of the combined immunodeficiency in complete human CARD11 deficiency. Journal of Allergy and Clinical Immunology, 2021, 148, 1559-1574.e13.	2.9	22
3	MMP8 increases tongue carcinoma cellâ€“cell adhesion and diminishes migration via cleavage of anti-adhesive FXYD5. Oncogenesis, 2021, 10, 44.	4.9	11
4	Enzymatically releasable polyethylene glycol â€“ host defense peptide conjugates with improved activity and biocompatibility. Journal of Controlled Release, 2021, 339, 220-231.	9.9	8
5	MALT1-Dependent Cleavage of HOIL1 Modulates Canonical NF-Î°B Signaling and Inflammatory Responsiveness. Frontiers in Immunology, 2021, 12, 749794.	4.8	9
6	Mechanistic insights into COVID-19 by global analysis of the SARS-CoV-2 3CLpro substrate degradome. Cell Reports, 2021, 37, 109892.	6.4	60
7	Progress Identifying and Analyzing the Human Proteome: 2021ÂMetrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2021, 20, 5227-5240.	3.7	30
8	A Flickering Light at the End of the Pandemic Tunnel. Journal of Proteome Research, 2021, 20, 5223-5226.	3.7	0
9	Moonlighting matrix metalloproteinase substrates: Enhancement of proinflammatory functions of extracellular tyrosyl-tRNA synthetase upon cleavage. Journal of Biological Chemistry, 2020, 295, 2186-2202.	3.4	17
10	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	12.8	152
11	The HUPO High-Stringency Inventory of Humanityâ€™s Shared Human Proteome Revealed. Journal of Proteome Research, 2020, 19, 4211-4214.	3.7	3
12	The Human Proteome: 90% in the Light, 10% on the Dark Side. Journal of Proteome Research, 2020, 19, 4731-4734.	3.7	6
13	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. Journal of Proteome Research, 2020, 19, 4735-4746.	3.7	38
14	Classification and Nomenclature of Metacaspases and Paracaspases: No More Confusion with Caspases. Molecular Cell, 2020, 77, 927-929.	9.7	71
15	Kallikrein-Related Peptidase 14 Activates Zymogens of Membrane Type Matrix Metalloproteinases (MT-MMPs)â€”A CleavEx Based Analysis. International Journal of Molecular Sciences, 2020, 21, 4383.	4.1	5
16	Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. MSystems, 2020, 5, .	3.8	3
17	DIPPER, a spatiotemporal proteomics atlas of human intervertebral discs for exploring ageing and degeneration dynamics. ELife, 2020, 9, .	6.0	37
18	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2019, 18, 4098-4107.	3.7	41

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19	Matrix metalloproteinases inactivate the proinflammatory functions of secreted moonlighting tryptophanyl-tRNA synthetase. Journal of Biological Chemistry, 2019, 294, 12866-12879.	3.4	20
20	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. Journal of Proteome Research, 2019, 18, 3419-3428.	3.7	15
21	Novel Human Aminopeptidase N Inhibitors: Discovery and Optimization of Subsite Binding Interactions. Journal of Medicinal Chemistry, 2019, 62, 7185-7209.	6.4	17
22	Proteomic and N-Terminomic TAILS Analyses of Human Alveolar Bone Proteins: Improved Protein Extraction Methodology and LysargiNase Digestion Strategies Increase Proteome Coverage and Missing Protein Identification. Journal of Proteome Research, 2019, 18, 4167-4179.	3.7	21
23	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116.	3.7	82
24	Simplified high yield TAILS terminomics using a new HPG-ALD 800K-2000 polymer with precipitation. Methods in Enzymology, 2019, 626, 429-446.	1.0	4
25	An allosteric MALT1 inhibitor is a molecular corrector rescuing function in an immunodeficient patient. Nature Chemical Biology, 2019, 15, 304-313.	8.0	50
26	Matrix metalloproteinases in the CNS: interferons get nervous. Cellular and Molecular Life Sciences, 2019, 76, 3083-3095.	5.4	36
27	Persistent Salmonella enterica Serovar Typhimurium Infection Induces Protease Expression During Intestinal Fibrosis. Inflammatory Bowel Diseases, 2019, 25, 1629-1643.	1.9	14
28	Proteases and their inhibitors as prognostic factors for high-grade serous ovarian cancer. Pathology Research and Practice, 2019, 215, 152369.	2.3	2
29	Intracellular Localization in Zebrafish Muscle and Conserved Sequence Features Suggest Roles for Gelatinase A Moonlighting in Sarcomere Maintenance. Biomedicines, 2019, 7, 93.	3.2	14
30	Advances in Identifying and Characterizing the Human Proteome. Journal of Proteome Research, 2019, 18, 4079-4084.	3.7	4
31	Precision De Novo Peptide Sequencing Using Mirror Proteases of Ac-LysargiNase and Trypsin for Large-scale Proteomics. Molecular and Cellular Proteomics, 2019, 18, 773-785.	3.8	36
32	Hydroxamic Acid Inhibitors Provide Cross-Species Inhibition of Plasmodium M1 and M17 Aminopeptidases. Journal of Medicinal Chemistry, 2019, 62, 622-640.	6.4	30
33	Neutrophil elastase-cleaved corticosteroid-binding globulin is absent in human plasma. Journal of Endocrinology, 2019, 240, 27-39.	2.6	4
34	Hydrolases (version 2019.4) in the IUPHAR/BPS Guide to Pharmacology Database. IUPHAR/BPS Guide To Pharmacology CITE, 2019, 2019, .	0.2	0
35	Hydrolases (version 2019.5) in the IUPHAR/BPS Guide to Pharmacology Database. IUPHAR/BPS Guide To Pharmacology CITE, 2019, 2019, .	0.2	1
36	N-Terminomics TAILS Identifies Host Cell Substrates of Poliovirus and Coxsackievirus B3 3C Proteinases That Modulate Virus Infection. Journal of Virology, 2018, 92, .	3.4	61

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37	Proteolytic Cleavageâ€"Mechanisms, Function, and â€œOmicâ€•Approaches for a Near-Ubiquitous Posttranslational Modification. Chemical Reviews, 2018, 118, 1137-1168.	47.7	145
38	Identification of Protease Cleavage Sites and Substrates in Cancer by Carboxy-TAILS (C-TAILS). Methods in Molecular Biology, 2018, 1731, 15-28.	0.9	3
39	TAILS N-terminomics and proteomics reveal complex regulation of proteolytic cleavage by O-glycosylation. Journal of Biological Chemistry, 2018, 293, 7629-7644.	3.4	25
40	Aging-associated modifications of collagen affect its degradation by matrix metalloproteinases. Matrix Biology, 2018, 65, 30-44.	3.6	109
41	The Human Odontoblast Cell Layer and Dental Pulp Proteomes and N-Terminomes. Journal of Dental Research, 2018, 97, 338-346.	5.2	11
42	Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini. Genome Research, 2018, 28, 25-36.	5.5	75
43	Toward Completion of the Human Proteome Parts List: Progress Uncovering Proteins That Are Missing or Have Unknown Function and Developing Analytical Methods. Journal of Proteome Research, 2018, 17, 4023-4030.	3.7	22
44	Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. Journal of Proteome Research, 2018, 17, 4042-4050.	3.7	41
45	TAILS proteomics reveals dynamic changes in airway proteolysis controlling protease activity and innate immunity during COPD exacerbations. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2018, 315, L1003-L1014.	2.9	20
46	Highlight: Frontiers in Proteolysis. Biological Chemistry, 2018, 399, 1351-1351.	2.5	2
47	Global Profiling of Proteolysis from the Mitochondrial Amino Terminome during Early Intrinsic Apoptosis Prior to Caspase-3 Activation. Journal of Proteome Research, 2018, 17, 4279-4296.	3.7	33
48	Melanocyte development in the mouse tail epidermis requires the Adamts9 metalloproteinase. Pigment Cell and Melanoma Research, 2018, 31, 693-707.	3.3	17
49	Granzyme B is elevated in autoimmune blistering diseases and cleaves key anchoring proteins of the dermal-epidermal junction. Scientific Reports, 2018, 8, 9690.	3.3	54
50	Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2018, 17, 4031-4041.	3.7	59
51	C-terminal truncation of IFN-Î³ inhibits proinflammatory macrophage responses and is deficient in autoimmune disease. Nature Communications, 2018, 9, 2416.	12.8	50
52	Interactome disassembly during apoptosis occurs independent of caspase cleavage. Molecular Systems Biology, 2017, 13, 906.	7.2	49
53	Highly sensitive and adaptable fluorescence-quenched pair discloses the substrate specificity profiles in diverse protease families. Scientific Reports, 2017, 7, 43135.	3.3	51
54	Sharpening Host Defenses during Infection: Proteases Cut to the Chase. Molecular and Cellular Proteomics, 2017, 16, S161-S171.	3.8	49

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55	Protean proteases: at the cutting edgeÂofÂlung diseases. European Respiratory Journal, 2017, 49, 1501200.	6.7	49
56	Site-specific O-Glycosylation by Polypeptide N-Acetylgalactosaminyltransferase 2 (GalNAc-transferase) Tj ETQq0 0 0 rgBT /Overlock 10 T 4714-4726.	3.4	35
57	Protease-Inhibitor Interaction Predictions: Lessons on the Complexity of Proteinâ€“Protein Interactions. Molecular and Cellular Proteomics, 2017, 16, 1038-1051.	3.8	16
58	New intracellular activities of matrix metalloproteinases shine in the moonlight. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 2043-2055.	4.1	122
59	Advances in the Chromosome-Centric Human Proteome Project: looking to the future. Expert Review of Proteomics, 2017, 14, 1059-1071.	3.0	25
60	Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. Journal of Proteome Research, 2017, 16, 4281-4287.	3.7	55
61	Discovery of a proteolytic flagellin family in diverse bacterial phyla that assembles enzymatically active flagella. Nature Communications, 2017, 8, 521.	12.8	35
62	The Human Plasma Proteome Draft of 2017: Building on the Human Plasma PeptideAtlas from Mass Spectrometry and Complementary Assays. Journal of Proteome Research, 2017, 16, 4299-4310.	3.7	185
63	Overview of transcriptomic analysis of all human proteases, non-proteolytic homologs and inhibitors: Organ, tissue and ovarian cancer cell line expression profiling of the human protease degradome by the CLIP-CHIPâ„¢ DNA microarray. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 2210-2219.	4.1	34
64	Progress and Future Direction of Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2017, 16, 4253-4258.	3.7	14
65	Traumatic brain injury induced matrix metalloproteinase2 cleaves CXCL12Î± (stromal cell derived factor) Tj ETQq1 1 0.784314 rgBT /O	4.1	30
66	Degradomic and yeast 2-hybrid inactive catalytic domain substrate trapping identifies new membrane-type 1 matrix metalloproteinase (MMP14) substrates: CCN3 (Nov) and CCN5 (WISP2). Matrix Biology, 2017, 59, 23-38.	3.6	29
67	Opposite Electron-Transfer Dissociation and Higher-Energy Collisional Dissociation Fragmentation Characteristics of Proteolytic K/R(X)_n and (X)_nK/R Peptides Provide Benefits for Peptide Sequencing in Proteomics and Phosphoproteomics. Journal of Proteome Research, 2017, 16, 852-861.	3.7	21
68	Can we predict protein from mRNA levels?. Nature, 2017, 547, E19-E20.	27.8	170
69	Novel grooved substrata stimulate macrophage fusion, CCL2 and MMPâ€9 secretion. Journal of Biomedical Materials Research - Part A, 2016, 104, 2243-2254.	4.0	11
70	Uncovering a Dual Regulatory Role for Caspases During Endoplasmic Reticulum Stress-induced Cell Death. Molecular and Cellular Proteomics, 2016, 15, 2293-2307.	3.8	7
71	Quantitative proteomics and terminomics to elucidate the role of ubiquitination and proteolysis in adaptive immunity. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2016, 374, 20150372.	3.4	8
72	Positional proteomics in the era of the human proteome project on the doorstep of precision medicine. Biochimie, 2016, 122, 110-118.	2.6	42

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73	TAILS N-Terminomics and Proteomics Show Protein Degradation Dominates over Proteolytic Processing by Cathepsins in Pancreatic Tumors. Cell Reports, 2016, 16, 1762-1773.	6.4	66
74	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970.	3.7	158
75	Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. Journal of Proteome Research, 2016, 15, 3951-3960.	3.7	72
76	iRhom2 regulates CSF1R cell surface expression and nonâ€steady state myelopoiesis in mice. European Journal of Immunology, 2016, 46, 2737-2748.	2.9	14
77	Progress in the Chromosome-Centric Human Proteome Project as Highlighted in the Annual Special Issue IV. Journal of Proteome Research, 2016, 15, 3945-3950.	3.7	17
78	Active site specificity profiling datasets of matrix metalloproteinases (MMPs) 1, 2, 3, 7, 8, 9, 12, 13 and 14. Data in Brief, 2016, 7, 299-310.	1.0	21
79	Novel N-terminal and Lysine Methyltransferases That Target Translation Elongation Factor 1A in Yeast and Human. Molecular and Cellular Proteomics, 2016, 15, 164-176.	3.8	57
80	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. Matrix Biology, 2016, 49, 37-60.	3.6	177
81	TAILS N-terminomic and proteomic datasets of healthy human dental pulp. Data in Brief, 2015, 5, 542-548.	1.0	9
82	The path of no returnâ€"Truncated protein Nâ€termini and current ignorance of their genesis. Proteomics, 2015, 15, 2547-2552.	2.2	39
83	The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen lymphocyte NF-Î²B signalling. Nature Communications, 2015, 6, 8777.	12.8	139
84	Protein Termini and Their Modifications Revealed by Positional Proteomics. ACS Chemical Biology, 2015, 10, 1754-1764.	3.4	90
85	Proteome TopFIND 3.0 with TopFINDer and PathFINDer: database and analysis tools for the association of protein termini to pre- and post-translational events. Nucleic Acids Research, 2015, 43, D290-D297.	14.5	124
86	Cysteine Cathepsins Activate ELR Chemokines and Inactivate Non-ELR Chemokines. Journal of Biological Chemistry, 2015, 290, 13800-13811.	3.4	66
87	Proteolytic control of TGF-Î² co-receptor activity by BMP-1/tolloid-like proteases revealed by quantitative iTRAQ proteomics. Cellular and Molecular Life Sciences, 2015, 72, 1009-1027.	5.4	27
88	Heterogeneous Nuclear Ribonucleoprotein M Facilitates Enterovirus Infection. Journal of Virology, 2015, 89, 7064-7078.	3.4	45
89	The Human Dental Pulp Proteome and N-Terminome: Levering the Unexplored Potential of Semitryptic Peptides Enriched by TAILS to Identify Missing Proteins in the Human Proteome Project in Underexplored Tissues. Journal of Proteome Research, 2015, 14, 3568-3582.	3.7	41
90	Recent Advances in the Chromosome-Centric Human Proteome Project: Missing Proteins in the Spot Light. Journal of Proteome Research, 2015, 14, 3409-3414.	3.7	16

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91	LysargiNase mirrors trypsin for protein C-terminal and methylation-site identification. Nature Methods, 2015, 12, 55-58.	19.0	128
92	Snake venom serine proteinases specificity mapping by proteomic identification of cleavage sites. Journal of Proteomics, 2015, 113, 260-267.	2.4	23
93	Network Analyses Reveal Pervasive Functional Regulation Between Proteases in the Human Protease Web. PLoS Biology, 2014, 12, e1001869.	5.6	137
94	RC1339/APRc from Rickettsia conorii Is a Novel Aspartic Protease with Properties of Retropepsin-Like Enzymes. PLoS Pathogens, 2014, 10, e1004324.	4.7	17
95	Family-wide characterization of matrix metalloproteinases from Arabidopsis thaliana reveals their distinct proteolytic activity and cleavage site specificity. Biochemical Journal, 2014, 457, 335-346.	3.7	33
96	Macrophage Matrix Metalloproteinase-12 Dampens Inflammation and Neutrophil Influx in Arthritis. Cell Reports, 2014, 9, 618-632.	6.4	93
97	Ensembles of protein termini and specific proteolytic signatures as candidate biomarkers of disease. Proteomics - Clinical Applications, 2014, 8, 338-350.	1.6	28
98	Absolute proteomic quantification of the activity state of proteases and proteolytic cleavages using proteolytic signature peptides and isobaric tags. Journal of Proteomics, 2014, 100, 79-91.	2.4	26
99	Can proteomics fill the gap between genomics and phenotypes?. Journal of Proteomics, 2014, 100, 1-2.	2.4	6
100	A new transcriptional role for matrix metalloproteinase-12 in antiviral immunity. Nature Medicine, 2014, 20, 493-502.	30.7	218
101	The Human Proteome Organization Chromosome 6 Consortium: Integrating chromosome-centric and biology/disease driven strategies. Journal of Proteomics, 2014, 100, 60-67.	2.4	8
102	Proteomic protease specificity profiling of clostridial collagenases reveals their intrinsic nature as dedicated degraders of collagen. Journal of Proteomics, 2014, 100, 102-114.	2.4	60
103	Annotating N Termini for the Human Proteome Project: N Termini and NÎ±-Acetylation Status Differentiate Stable Cleaved Protein Species from Degradation Remnants in the Human Erythrocyte Proteome. Journal of Proteome Research, 2014, 13, 2028-2044.	3.7	95
104	TAILS N-terminomics of human platelets reveals pervasive metalloproteinase-dependent proteolytic processing in storage. Blood, 2014, 124, e49-e60.	1.4	53
105	Cleavage Specificity Analysis of Six Type II Transmembrane Serine Proteases (TTSPs) Using PICS with Proteome-Derived Peptide Libraries. PLoS ONE, 2014, 9, e105984.	2.5	46
106	Matrix metalloproteinase processing of signaling molecules to regulate inflammation. Periodontology 2000, 2013, 63, 123-148.	13.4	42
107	Structure of the Mycosin-1 Protease from the Mycobacterial ESX-1 Protein Type VII Secretion System. Journal of Biological Chemistry, 2013, 288, 17782-17790.	3.4	48
108	Missing the target: matrix metalloproteinase antitargets in inflammation and cancer. Trends in Pharmacological Sciences, 2013, 34, 233-242.	8.7	282

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109	The Peri-islet Basement Membrane, a Barrier to Infiltrating Leukocytes in Type 1 Diabetes in Mouse and Human. Diabetes, 2013, 62, 531-542.	0.6	130
110	Protein TAILS: when termini tell tales of proteolysis and function. Current Opinion in Chemical Biology, 2013, 17, 73-82.	6.1	80
111	The substrate degradome of meprin metalloproteases reveals an unexpected proteolytic link between meprinÂÎ² and ADAM10. Cellular and Molecular Life Sciences, 2013, 70, 309-333.	5.4	112
112	Proteolytic Post-translational Modification of Proteins: Proteomic Tools and Methodology. Molecular and Cellular Proteomics, 2013, 12, 3532-3542.	3.8	127
113	Metalloproteases meprin Î± and meprin Î² are C- and N-procollagen proteinases important for collagen assembly and tensile strength. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14219-14224.	7.1	115
114	Identifying Natural Substrates for Dipeptidyl Peptidases 8 and 9 Using Terminal Amine Isotopic Labeling of Substrates (TAILS) Reveals in Vivo Roles in Cellular Homeostasis and Energy Metabolism. Journal of Biological Chemistry, 2013, 288, 13936-13949.	3.4	73
115	Systems-Level Analysis of Proteolytic Events in Increased Vascular Permeability and Complement Activation in Skin Inflammation. Science Signaling, 2013, 6, rs2.	3.6	99
116	Proteomic Amino-Termini Profiling Reveals Targeting Information for Protein Import into Complex Plastids. PLoS ONE, 2013, 8, e74483.	2.5	41
117	Biochemical Analysis of Matrix Metalloproteinase Activation of Chemokines CCL15 and CCL23 and Increased Glycosaminoglycan Binding of CCL16. Journal of Biological Chemistry, 2012, 287, 5848-5860.	3.4	58
118	Biochemical Characterization and N-terminomics Analysis of Leukolysin, the Membrane-type 6 Matrix Metalloprotease (MMP25). Journal of Biological Chemistry, 2012, 287, 13382-13395.	3.4	90
119	Proteolysis of cystatin C by cathepsin D in the breast cancer microenvironment. FASEB Journal, 2012, 26, 5172-5181.	0.5	58
120	TopFIND 2.0--linking protein termini with proteolytic processing and modifications altering protein function. Nucleic Acids Research, 2012, 40, D351-D361.	14.5	54
121	CLIPPER: an add-on to the Trans-Proteomic Pipeline for the automated analysis of TAILS N-terminomics data. Biological Chemistry, 2012, 393, 1477-1483.	2.5	33
122	4.7 Rock, paper, and molecular scissors: regulating the game of extracellular matrix homeostasis, remodeling, and inflammation. , 2012, , 377-400.		0
123	Nâ€and Câ€terminal degradomics: new approaches to reveal biological roles for plant proteases from substrate identification. Physiologia Plantarum, 2012, 145, 5-17.	5.2	45
124	Site Specific Cleavage Mediated by MMPs Regulates Function of Agrin. PLoS ONE, 2012, 7, e43669.	2.5	22
125	Towards kit-like 18F-labeling of marimastat, a noncovalent inhibitor drug for in vivo PET imaging cancer associated matrix metalloproteases. MedChemComm, 2011, 2, 942.	3.4	44
126	Protease Specificity Profiling by Tandem Mass Spectrometry Using Proteome-Derived Peptide Libraries. Methods in Molecular Biology, 2011, 753, 257-272.	0.9	24

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127	Development of Soluble Ester-Linked Aldehyde Polymers for Proteomics. Analytical Chemistry, 2011, 83, 6500-6510.	6.5	9
128	Identifying and quantifying proteolytic events and the natural N terminome by terminal amine isotopic labeling of substrates. Nature Protocols, 2011, 6, 1578-1611.	12.0	291
129	Targeting Tumor Hypoxia: Suppression of Breast Tumor Growth and Metastasis by Novel Carbonic Anhydrase IX Inhibitors. Cancer Research, 2011, 71, 3364-3376.	0.9	662
130	Identification of Proteolytic Products and Natural Protein N-Termini by Terminal Amine Isotopic Labeling of Substrates (TAILS). Methods in Molecular Biology, 2011, 753, 273-287.	0.9	40
131	Amino-Terminal Oriented Mass Spectrometry of Substrates (ATOMS). Methods in Enzymology, 2011, 501, 275-293.	1.0	16
132	Characterization of the prime and non-prime active site specificities of proteases by proteome-derived peptide libraries and tandem mass spectrometry. Nature Protocols, 2011, 6, 111-120.	12.0	97
133	Microarray and Proteomic Analysis of Breast Cancer Cell and Osteoblast Co-cultures. Journal of Biological Chemistry, 2011, 286, 34271-34285.	3.4	56
134	Factor Xa subsite mapping by proteome-derived peptide libraries improved using WebPICS, a resource for proteomic identification of cleavage sites. Biological Chemistry, 2011, 392, 1031-1037.	2.5	54
135	Proteomic Analyses Reveal an Acidic Prime Side Specificity for the Astacin Metalloprotease Family Reflected by Physiological Substrates. Molecular and Cellular Proteomics, 2011, 10, M111.009233.	3.8	113
136	Broad Coverage Identification of Multiple Proteolytic Cleavage Site Sequences in Complex High Molecular Weight Proteins Using Quantitative Proteomics as a Complement to Edman Sequencing. Molecular and Cellular Proteomics, 2011, 10, M110.003533.	3.8	47
137	Membrane-type Matrix Metalloproteinase-3 Regulates Neuronal Responsiveness to Myelin through Nogo-66 Receptor 1 Cleavage. Journal of Biological Chemistry, 2011, 286, 31418-31424.	3.4	30
138	Metalloprotease Meprin Î² Generates Nontoxic N-terminal Amyloid Precursor Protein Fragments in Vivo. Journal of Biological Chemistry, 2011, 286, 27741-27750.	3.4	87
139	TopFIND, a knowledgebase linking protein termini with function. Nature Methods, 2011, 8, 703-704.	19.0	91
140	Identification and Relative Quantification of Native and Proteolytically Generated Protein C-Termini from Complex Proteomes: C-Terminome Analysis. Methods in Molecular Biology, 2011, 781, 59-69.	0.9	23
141	Matrix metalloproteinases: What do they not do? New substrates and biological roles identified by murine models and proteomics. Biochimica Et Biophysica Acta - Molecular Cell Research, 2010, 1803, 39-54.	4.1	449
142	Matrix metalloproteinase 8 deficiency in mice exacerbates inflammatory arthritis through delayed neutrophil apoptosis and reduced caspase 11 expression. Arthritis and Rheumatism, 2010, 62, 3645-3655.	6.7	64
143	Cleaved high molecular weight kininogen inhibits tube formation of endothelial progenitor cells via suppression of matrix metalloproteinase 2. Journal of Thrombosis and Haemostasis, 2010, 8, 185-193.	3.8	25
144	Monocyte chemotactic proteinâ€3: possible involvement in apical periodontitis chemotaxis. International Endodontic Journal, 2010, 43, 902-908.	5.0	11

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145	Isotopic labeling of terminal amines in complex samples identifies protein N-termini and protease cleavage products. Nature Biotechnology, 2010, 28, 281-288.	17.5	510
146	Proteome-wide analysis of protein carboxy termini: C terminomics. Nature Methods, 2010, 7, 508-511.	19.0	144
147	Stromal regulation of vessel stability by MMP14 and TGFÎ². DMM Disease Models and Mechanisms, 2010, 3, 317-332.	2.4	82
148	A Statistics-based Platform for Quantitative N-terminome Analysis and Identification of Protease Cleavage Products. Molecular and Cellular Proteomics, 2010, 9, 912-927.	3.8	68
149	Multiplex N-terminome Analysis of MMP-2 and MMP-9 Substrate Degradomes by iTRAQ-TAILS Quantitative Proteomics. Molecular and Cellular Proteomics, 2010, 9, 894-911.	3.8	240
150	Novel Matrix Metalloproteinase Inhibitor [18F]Marimastat-Aryltrifluoroborate as a Probe for In vivo Positron Emission Tomography Imaging in Cancer. Cancer Research, 2010, 70, 7562-7569.	0.9	79
151	Chemokine Monocyte Chemoattractant Protein-3 in Progressive Periodontal Lesions in Patients With Chronic Periodontitis. Journal of Periodontology, 2010, 81, 267-276.	3.4	19
152	Chemokine Proteolytic Processing in HIV Infection: Neurotoxic and Neuroimmune Consequences. , 2010, , 149-172.		1
153	Analysis of the Degradome with the CLIP-CHIPâ„¢ Microarray. Methods in Molecular Biology, 2010, 622, 175-193.	0.9	12
154	Src Stimulates Fibroblast Growth Factor Receptor-2 Shedding by an ADAM15 Splice Variant Linked to Breast Cancer. Cancer Research, 2009, 69, 4573-4576.	0.9	30
155	Bone sialoprotein does not interact with pro-gelatinase A (MMP-2) or mediate MMP-2 activation. BMC Cancer, 2009, 9, 121.	2.6	8
156	Matrix metalloproteinase proteomics: substrates, targets, and therapy. Current Opinion in Cell Biology, 2009, 21, 645-653.	5.4	239
157	Proteomic identification of multitasking proteins in unexpected locations complicates drug targeting. Nature Reviews Drug Discovery, 2009, 8, 935-948.	46.4	127
158	CXCR3 activation by lentivirus infection suppresses neuronal autophagy: neuroprotective effects of antiretroviral therapy. FASEB Journal, 2009, 23, 2928-2941.	0.5	39
159	Deciphering complex mechanisms in neurodegenerative diseases: the advent of systems biology. Trends in Neurosciences, 2009, 32, 88-100.	8.6	92
160	The Collagen Binding Domain of Gelatinase A Modulates Degradation of Collagen IV by Gelatinase B. Journal of Molecular Biology, 2009, 386, 419-434.	4.2	44
161	Updated Biological Roles for Matrix Metalloproteinases and New â€œIntracellularâ€•Substrates Revealed by Degradomics. Biochemistry, 2009, 48, 10830-10845.	2.5	195
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