Christopher M Overall

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

266 84 24,559 149 h-index g-index citations papers 26,926 8.3 283 7.07 L-index avg, IF ext. citations ext. papers

| # | Paper | IF | Citations |
|-----|---|-----------------|-----------|
| 266 | MALT1-Dependent Cleavage of HOIL1 Modulates Canonical NF-B Signaling and Inflammatory Responsiveness. <i>Frontiers in Immunology</i> , 2021 , 12, 749794 | 8.4 | 1 |
| 265 | Mechanistic insights into COVID-19 by global analysis of the SARS-CoV-2 3CL substrate degradome. <i>Cell Reports</i> , 2021 , 37, 109892 | 10.6 | 11 |
| 264 | Progress Identifying and Analyzing the Human Proteome: 2021[Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2021 , 20, 5227-5240 | 5.6 | 7 |
| 263 | Mechanistic understanding of the combined immunodeficiency in complete human CARD11 deficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 148, 1559-1574.e13 | 11.5 | 9 |
| 262 | MMP8 increases tongue carcinoma cell-cell adhesion and diminishes migration via cleavage of anti-adhesive FXYD5. <i>Oncogenesis</i> , 2021 , 10, 44 | 6.6 | 2 |
| 261 | 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 | 12.1 | 8 |
| 260 | Enzymatically releasable polyethylene glycol - host defense peptide conjugates with improved activity and biocompatibility. <i>Journal of Controlled Release</i> , 2021 , 339, 220-231 | 11.7 | 1 |
| 259 | Classification and Nomenclature of Metacaspases and Paracaspases: No More Confusion with Caspases. <i>Molecular Cell</i> , 2020 , 77, 927-929 | 17.6 | 35 |
| 258 | Kallikrein-Related Peptidase 14 Activates Zymogens of Membrane Type Matrix Metalloproteinases (MT-MMPs)-A CleavEx Based Analysis. <i>International Journal of Molecular Sciences</i> , 2020 , 21, | 6.3 | 2 |
| 257 | Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020 , 5, | 7.6 | 3 |
| 256 | DIPPER, a spatiotemporal proteomics atlas of human intervertebral discs for exploring ageing and degeneration dynamics. <i>ELife</i> , 2020 , 9, | 8.9 | 11 |
| 255 | Moonlighting matrix metalloproteinase substrates: Enhancement of proinflammatory functions of extracellular tyrosyl-tRNA synthetase upon cleavage. <i>Journal of Biological Chemistry</i> , 2020 , 295, 2186-2 | 25 2 | 7 |
| 254 | A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301 | 17.4 | 59 |
| 253 | Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020 , 19, 4735-4746 | 5.6 | 25 |
| 252 | An allosteric MALT1 inhibitor is a molecular corrector rescuing function in an immunodeficient patient. <i>Nature Chemical Biology</i> , 2019 , 15, 304-313 | 11.7 | 30 |
| 251 | Matrix metalloproteinases in the CNS: interferons get nervous. <i>Cellular and Molecular Life Sciences</i> , 2019 , 76, 3083-3095 | 10.3 | 22 |
| 250 | Persistent Salmonella enterica Serovar Typhimurium Infection Induces Protease Expression During Intestinal Fibrosis. <i>Inflammatory Bowel Diseases</i> , 2019 , 25, 1629-1643 | 4.5 | 7 |

(2018-2019)

| 249 | Proteases and their inhibitors as prognostic factors for high-grade serous ovarian cancer. <i>Pathology Research and Practice</i> , 2019 , 215, 152369 | 3.4 | 1 |
|-----|---|------|----|
| 248 | Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2019 , 18, 4098-4107 | 5.6 | 32 |
| 247 | Matrix metalloproteinases inactivate the proinflammatory functions of secreted moonlighting tryptophanyl-tRNA synthetase. <i>Journal of Biological Chemistry</i> , 2019 , 294, 12866-12879 | 5.4 | 12 |
| 246 | 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</i> | 5.6 | 8 |
| 245 | Novel Human Aminopeptidase N Inhibitors: Discovery and Optimization of Subsite Binding Interactions. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 7185-7209 | 8.3 | 11 |
| 244 | 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. <i>Journal of Proteome Research</i> , 2019 , 18, 4167-4179 | 5.6 | 13 |
| 243 | Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. <i>Journal of Proteome Research</i> , 2019 , 18, 4108-4116 | 5.6 | 37 |
| 242 | Simplified high yield TAILS terminomics using a new HPG-ALD 800K-2000 polymer with precipitation. <i>Methods in Enzymology</i> , 2019 , 626, 429-446 | 1.7 | 4 |
| 241 | Neutrophil elastase-cleaved corticosteroid-binding globulin is absent in human plasma. <i>Journal of Endocrinology</i> , 2019 , 240, 27-39 | 4.7 | 3 |
| 240 | Intracellular Localization in Zebrafish Muscle and Conserved Sequence Features Suggest Roles for Gelatinase A Moonlighting in Sarcomere Maintenance. <i>Biomedicines</i> , 2019 , 7, | 4.8 | 7 |
| 239 | Precision Peptide Sequencing Using Mirror Proteases of Ac-LysargiNase and Trypsin for Large-scale Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 773-785 | 7.6 | 19 |
| 238 | Hydroxamic Acid Inhibitors Provide Cross-Species Inhibition of Plasmodium M1 and M17 Aminopeptidases. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 622-640 | 8.3 | 16 |
| 237 | N-Terminomics TAILS Identifies Host Cell Substrates of Poliovirus and Coxsackievirus B3 3C Proteinases That Modulate Virus Infection. <i>Journal of Virology</i> , 2018 , 92, | 6.6 | 39 |
| 236 | Proteolytic Cleavage-Mechanisms, Function, and "Omic" Approaches for a Near-Ubiquitous Posttranslational Modification. <i>Chemical Reviews</i> , 2018 , 118, 1137-1168 | 68.1 | 99 |
| 235 | Identification of Protease Cleavage Sites and Substrates in Cancer by Carboxy-TAILS (C-TAILS). <i>Methods in Molecular Biology</i> , 2018 , 1731, 15-28 | 1.4 | 3 |
| 234 | TAILS N-terminomics and proteomics reveal complex regulation of proteolytic cleavage by -glycosylation. <i>Journal of Biological Chemistry</i> , 2018 , 293, 7629-7644 | 5.4 | 17 |
| 233 | Aging-associated modifications of collagen affect its degradation by matrix metalloproteinases. <i>Matrix Biology</i> , 2018 , 65, 30-44 | 11.4 | 67 |
| 232 | The Human Odontoblast Cell Layer and Dental Pulp Proteomes and N-Terminomes. <i>Journal of Dental Research</i> , 2018 , 97, 338-346 | 8.1 | 8 |

| 231 | Granzyme B is elevated in autoimmune blistering diseases and cleaves key anchoring proteins of the dermal-epidermal junction. <i>Scientific Reports</i> , 2018 , 8, 9690 | 4.9 | 25 |
|-----|---|------|----|
| 230 | Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2018 , 17, 4031-4041 | 5.6 | 46 |
| 229 | C-terminal truncation of IFN-IInhibits proinflammatory macrophage responses and is deficient in autoimmune disease. <i>Nature Communications</i> , 2018 , 9, 2416 | 17.4 | 33 |
| 228 | Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini. <i>Genome Research</i> , 2018 , 28, 25-36 | 9.7 | 41 |
| 227 | Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. <i>Journal of Proteome Research</i> , 2018 , 17, 4042-4050 | 5.6 | 31 |
| 226 | TAILS proteomics reveals dynamic changes in airway proteolysis controlling protease activity and innate immunity during COPD exacerbations. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018 , 315, L1003-L1014 | 5.8 | 14 |
| 225 | Global Profiling of Proteolysis from the Mitochondrial Amino Terminome during Early Intrinsic Apoptosis Prior to Caspase-3 Activation. <i>Journal of Proteome Research</i> , 2018 , 17, 4279-4296 | 5.6 | 14 |
| 224 | Melanocyte development in the mouse tail epidermis requires the Adamts9 metalloproteinase. <i>Pigment Cell and Melanoma Research</i> , 2018 , 31, 693-707 | 4.5 | 8 |
| 223 | Interactome disassembly during apoptosis occurs independent of caspase cleavage. <i>Molecular Systems Biology</i> , 2017 , 13, 906 | 12.2 | 37 |
| 222 | Highly sensitive and adaptable fluorescence-quenched pair discloses the substrate specificity profiles in diverse protease families. <i>Scientific Reports</i> , 2017 , 7, 43135 | 4.9 | 36 |
| 221 | Sharpening Host Defenses during Infection: Proteases Cut to the Chase. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, S161-S171 | 7.6 | 28 |
| 220 | Protean proteases: at the cutting edge[bf]]ung diseases. <i>European Respiratory Journal</i> , 2017 , 49, | 13.6 | 38 |
| 219 | Site-specific -Glycosylation by Polypeptide -Acetylgalactosaminyltransferase 2 (GalNAc-transferase T2) Co-regulates EAdrenergic Receptor N-terminal Cleavage. <i>Journal of Biological Chemistry</i> , 2017 , 292, 4714-4726 | 5.4 | 23 |
| 218 | Protease-Inhibitor Interaction Predictions: Lessons on the Complexity of Protein-Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1038-1051 | 7.6 | 12 |
| 217 | New intracellular activities of matrix metalloproteinases shine in the moonlight. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017 , 1864, 2043-2055 | 4.9 | 78 |
| 216 | Advances in the Chromosome-Centric Human Proteome Project: looking to the future. <i>Expert Review of Proteomics</i> , 2017 , 14, 1059-1071 | 4.2 | 21 |
| 215 | Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. Journal of Proteome Research, 2017, 16, 4281-4287 | 5.6 | 46 |
| 214 | Discovery of a proteolytic flagellin family in diverse bacterial phyla that assembles enzymatically active flagella. <i>Nature Communications</i> , 2017 , 8, 521 | 17.4 | 27 |

| 213 | The Human Plasma Proteome Draft of 2017: Building on the Human Plasma PeptideAtlas from Mass Spectrometry and Complementary Assays. <i>Journal of Proteome Research</i> , 2017 , 16, 4299-4310 | 5.6 | 119 |
|-----|---|------|-----|
| 212 | Characterizing the Termini of Recombinant Proteins 2017 , 43-71 | | |
| 211 | 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-CHIPIDNA microarray. <i>Biochimica Et Biophysica Acta - Molecular Cell</i> | 4.9 | 25 |
| 210 | Research, 2017, 1864, 2210-2219 Traumatic brain injury induced matrix metalloproteinase2 cleaves CXCL12\(\frac{1}{4}\)stromal cell derived factor 1\(\frac{1}{4}\)and causes neurodegeneration. Brain, Behavior, and Immunity, 2017, 59, 190-199 | 16.6 | 27 |
| 209 | Degradomic and yeast 2-hybrid inactive catalytic domain substrate trapping identifies new membrane-type 1 matrix metalloproteinase (MMP14) substrates: CCN3 (Nov) and CCN5 (WISP2). <i>Matrix Biology</i> , 2017 , 59, 23-38 | 11.4 | 20 |
| 208 | Opposite Electron-Transfer Dissociation and Higher-Energy Collisional Dissociation Fragmentation Characteristics of Proteolytic K/R(X) and (X)K/R Peptides Provide Benefits for Peptide Sequencing in Proteomics and Phosphoproteomics. <i>Journal of Proteome Research</i> , 2017 , 16, 852-861 | 5.6 | 15 |
| 207 | Can we predict protein from mRNA levels?. <i>Nature</i> , 2017 , 547, E19-E20 | 50.4 | 95 |
| 206 | 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 | 11.4 | 113 |
| 205 | iRhom2 regulates CSF1R cell surface expression and non-steady state myelopoiesis in mice. <i>European Journal of Immunology</i> , 2016 , 46, 2737-2748 | 6.1 | 11 |
| 204 | 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 | 1.2 | 13 |
| 203 | Novel N-terminal and Lysine Methyltransferases That Target Translation Elongation Factor 1A in Yeast and Human. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 164-76 | 7.6 | 41 |
| 202 | Novel grooved substrata stimulate macrophage fusion, CCL2 and MMP-9 secretion. <i>Journal of Biomedical Materials Research - Part A</i> , 2016 , 104, 2243-54 | 5.4 | 8 |
| 201 | Uncovering a Dual Regulatory Role for Caspases During Endoplasmic Reticulum Stress-induced Cell Death. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2293-307 | 7.6 | 6 |
| 200 | Quantitative proteomics and terminomics to elucidate the role of ubiquitination and proteolysis in adaptive immunity. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016 , 374, | 3 | 7 |
| 199 | Positional proteomics in the era of the human proteome project on the doorstep of precision medicine. <i>Biochimie</i> , 2016 , 122, 110-8 | 4.6 | 35 |
| 198 | TAILS N-Terminomics and Proteomics Show Protein Degradation Dominates over Proteolytic Processing by Cathepsins in Pancreatic Tumors. <i>Cell Reports</i> , 2016 , 16, 1762-1773 | 10.6 | 51 |
| 197 | Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016 , 15, 3961-3970 | 5.6 | 130 |
| 196 | Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. <i>Journal of Proteome Research</i> , 2016 , 15, 3951-3960 | 5.6 | 60 |

| 195 | Proteome TopFIND 3.0 with TopFINDer and PathFINDer: database and analysis tools for the association of protein termini to pre- and post-translational events. <i>Nucleic Acids Research</i> , 2015 , 43, D290-7 | 20.1 | 82 |
|--------------------------|---|---------------------------|---|
| 194 | Cysteine Cathepsins Activate ELR Chemokines and Inactivate Non-ELR Chemokines. <i>Journal of Biological Chemistry</i> , 2015 , 290, 13800-11 | 5.4 | 47 |
| 193 | Proteolytic control of TGF-Izo-receptor activity by BMP-1/tolloid-like proteases revealed by quantitative iTRAQ proteomics. <i>Cellular and Molecular Life Sciences</i> , 2015 , 72, 1009-27 | 10.3 | 20 |
| 192 | Heterogeneous Nuclear Ribonucleoprotein M Facilitates Enterovirus Infection. <i>Journal of Virology</i> , 2015 , 89, 7064-78 | 6.6 | 35 |
| 191 | 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. <i>Journal of Proteome Research</i> , 2015 , 14, 3568-82 | 5.6 | 36 |
| 190 | LysargiNase mirrors trypsin for protein C-terminal and methylation-site identification. <i>Nature Methods</i> , 2015 , 12, 55-8 | 21.6 | 103 |
| 189 | Snake venom serine proteinases specificity mapping by proteomic identification of cleavage sites. Journal of Proteomics, 2015 , 113, 260-7 | 3.9 | 20 |
| 188 | TAILS N-terminomic and proteomic datasets of healthy human dental pulp. <i>Data in Brief</i> , 2015 , 5, 542-8 | 1.2 | 7 |
| 187 | The path of no returnTruncated protein N-termini and current ignorance of their genesis. <i>Proteomics</i> , 2015 , 15, 2547-52 | 4.8 | 28 |
| | | | |
| 186 | Subtracting Matrix Out of the Equation: New Key Roles of Matrix Metalloproteinases in Innate Immunity and Disease 2015 , 131-152 | | 3 |
| 186 185 | | 17.4 | 3 |
| | Immunity and Disease 2015, 131-152 The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen | 17.4 4.9 | |
| 185 | Immunity and Disease 2015, 131-152 The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen lymphocyte NF-B signalling. <i>Nature Communications</i> , 2015, 6, 8777 Protein Termini and Their Modifications Revealed by Positional Proteomics. <i>ACS Chemical Biology</i> , | , , | 108 |
| 185 184 | Immunity and Disease 2015, 131-152 The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen lymphocyte NF-B signalling. <i>Nature Communications</i> , 2015, 6, 8777 Protein Termini and Their Modifications Revealed by Positional Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 1754-64 A new transcriptional role for matrix metalloproteinase-12 in antiviral immunity. <i>Nature Medicine</i> , | 4.9 | 108 73 |
| 185 184 183 | Immunity and Disease 2015, 131-152 The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen lymphocyte NF-B signalling. <i>Nature Communications</i> , 2015, 6, 8777 Protein Termini and Their Modifications Revealed by Positional Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 1754-64 A new transcriptional role for matrix metalloproteinase-12 in antiviral immunity. <i>Nature Medicine</i> , 2014, 20, 493-502 The Human Proteome Organization Chromosome 6 Consortium: integrating chromosome-centric | 4.9 | 10873182 |
| 185 184 183 | Immunity and Disease 2015, 131-152 The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen lymphocyte NF-B signalling. <i>Nature Communications</i> , 2015, 6, 8777 Protein Termini and Their Modifications Revealed by Positional Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 1754-64 A new transcriptional role for matrix metalloproteinase-12 in antiviral immunity. <i>Nature Medicine</i> , 2014, 20, 493-502 The Human Proteome Organization Chromosome 6 Consortium: integrating chromosome-centric and biology/disease driven strategies. <i>Journal of Proteomics</i> , 2014, 100, 60-7 Proteomic protease specificity profiling of clostridial collagenases reveals their intrinsic nature as | 4.9 50.5 3.9 | 108731825 |
| 185 184 183 182 | Immunity and Disease 2015, 131-152 The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen lymphocyte NF-B signalling. Nature Communications, 2015, 6, 8777 Protein Termini and Their Modifications Revealed by Positional Proteomics. ACS Chemical Biology, 2015, 10, 1754-64 A new transcriptional role for matrix metalloproteinase-12 in antiviral immunity. Nature Medicine, 2014, 20, 493-502 The Human Proteome Organization Chromosome 6 Consortium: integrating chromosome-centric and biology/disease driven strategies. Journal of Proteomics, 2014, 100, 60-7 Proteomic protease specificity profiling of clostridial collagenases reveals their intrinsic nature as dedicated degraders of collagen. Journal of Proteomics, 2014, 100, 102-14 Annotating N termini for the human proteome project: N termini and Nacetylation status differentiate stable cleaved protein species from degradation remnants in the human erythrocyte | 4.9 50.5 3.9 3.9 | 10873182549 |

(2012-2014)

| 177 | RC1339/APRc from Rickettsia conorii is a novel aspartic protease with properties of retropepsin-like enzymes. <i>PLoS Pathogens</i> , 2014 , 10, e1004324 | 7.6 | 15 |
|-----|--|------|-----|
| 176 | Family-wide characterization of matrix metalloproteinases from Arabidopsis thaliana reveals their distinct proteolytic activity and cleavage site specificity. <i>Biochemical Journal</i> , 2014 , 457, 335-46 | 3.8 | 30 |
| 175 | Macrophage matrix metalloproteinase-12 dampens inflammation and neutrophil influx in arthritis. <i>Cell Reports</i> , 2014 , 9, 618-32 | 10.6 | 70 |
| 174 | Ensembles of protein termini and specific proteolytic signatures as candidate biomarkers of disease. <i>Proteomics - Clinical Applications</i> , 2014 , 8, 338-50 | 3.1 | 23 |
| 173 | Absolute proteomic quantification of the activity state of proteases and proteolytic cleavages using proteolytic signature peptides and isobaric tags. <i>Journal of Proteomics</i> , 2014 , 100, 79-91 | 3.9 | 24 |
| 172 | Cleavage specificity analysis of six type II transmembrane serine proteases (TTSPs) using PICS with proteome-derived peptide libraries. <i>PLoS ONE</i> , 2014 , 9, e105984 | 3.7 | 40 |
| 171 | Matrix metalloproteinase processing of signaling molecules to regulate inflammation. <i>Periodontology 2000</i> , 2013 , 63, 123-48 | 12.9 | 35 |
| 170 | Structure of the mycosin-1 protease from the mycobacterial ESX-1 protein type VII secretion system. <i>Journal of Biological Chemistry</i> , 2013 , 288, 17782-90 | 5.4 | 43 |
| 169 | Missing the target: matrix metalloproteinase antitargets in inflammation and cancer. <i>Trends in Pharmacological Sciences</i> , 2013 , 34, 233-42 | 13.2 | 241 |
| 168 | The peri-islet basement membrane, a barrier to infiltrating leukocytes in type 1 diabetes in mouse and human. <i>Diabetes</i> , 2013 , 62, 531-42 | 0.9 | 97 |
| 167 | Protein TAILS: when termini tell tales of proteolysis and function. <i>Current Opinion in Chemical Biology</i> , 2013 , 17, 73-82 | 9.7 | 73 |
| 166 | The substrate degradome of meprin metalloproteases reveals an unexpected proteolytic link between meprin and ADAM10. <i>Cellular and Molecular Life Sciences</i> , 2013 , 70, 309-33 | 10.3 | 100 |
| 165 | Proteolytic post-translational modification of proteins: proteomic tools and methodology. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3532-42 | 7.6 | 98 |
| 164 | Metalloproteases meprin hand meprin hare C- and N-procollagen proteinases important for collagen assembly and tensile strength. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 14219-24 | 11.5 | 97 |
| 163 | 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. <i>Journal of Biological Chemistry</i> , 2013 , 288, 13936-13949 | 5.4 | 52 |
| 162 | Systems-level analysis of proteolytic events in increased vascular permeability and complement activation in skin inflammation. <i>Science Signaling</i> , 2013 , 6, rs2 | 8.8 | 89 |
| 161 | Proteomic amino-termini profiling reveals targeting information for protein import into complex plastids. <i>PLoS ONE</i> , 2013 , 8, e74483 | 3.7 | 28 |
| 160 | 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 | 4.6 | 40 |

| 159 | Biochemical analysis of matrix metalloproteinase activation of chemokines CCL15 and CCL23 and increased glycosaminoglycan binding of CCL16. <i>Journal of Biological Chemistry</i> , 2012 , 287, 5848-60 | 5.4 | 48 |
|-----|---|------|-----|
| 158 | Biochemical characterization and N-terminomics analysis of leukolysin, the membrane-type 6 matrix metalloprotease (MMP25): chemokine and vimentin cleavages enhance cell migration and macrophage phagocytic activities. <i>Journal of Biological Chemistry</i> , 2012 , 287, 13382-95 | 5.4 | 72 |
| 157 | Proteolysis of cystatin C by cathepsin D in the breast cancer microenvironment. <i>FASEB Journal</i> , 2012 , 26, 5172-81 | 0.9 | 48 |
| 156 | TopFIND 2.0linking protein termini with proteolytic processing and modifications altering protein function. <i>Nucleic Acids Research</i> , 2012 , 40, D351-61 | 20.1 | 50 |
| 155 | CLIPPER: an add-on to the Trans-Proteomic Pipeline for the automated analysis of TAILS N-terminomics data. <i>Biological Chemistry</i> , 2012 , 393, 1477-83 | 4.5 | 32 |
| 154 | Site specific cleavage mediated by MMPs regulates function of agrin. <i>PLoS ONE</i> , 2012 , 7, e43669 | 3.7 | 17 |
| 153 | Identifying and quantifying proteolytic events and the natural N terminome by terminal amine isotopic labeling of substrates. <i>Nature Protocols</i> , 2011 , 6, 1578-611 | 18.8 | 221 |
| 152 | Targeting tumor hypoxia: suppression of breast tumor growth and metastasis by novel carbonic anhydrase IX inhibitors. <i>Cancer Research</i> , 2011 , 71, 3364-76 | 10.1 | 563 |
| 151 | Identification of proteolytic products and natural protein N-termini by Terminal Amine Isotopic Labeling of Substrates (TAILS). <i>Methods in Molecular Biology</i> , 2011 , 753, 273-87 | 1.4 | 22 |
| 150 | Amino-Terminal Oriented Mass Spectrometry of Substrates (ATOMS) N-terminal sequencing of proteins and proteolytic cleavage sites by quantitative mass spectrometry. <i>Methods in Enzymology</i> , 2011 , 501, 275-93 | 1.7 | 11 |
| 149 | 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, 111-20 | 18.8 | 84 |
| 148 | Towards kit-like 18F-labeling of marimastat, a noncovalent inhibitor drug for in vivo PET imaging cancer associated matrix metalloproteases. <i>MedChemComm</i> , 2011 , 2, 942 | 5 | 42 |
| 147 | Protease specificity profiling by tandem mass spectrometry using proteome-derived peptide libraries. <i>Methods in Molecular Biology</i> , 2011 , 753, 257-72 | 1.4 | 18 |
| 146 | Development of soluble ester-linked aldehyde polymers for proteomics. <i>Analytical Chemistry</i> , 2011 , 83, 6500-10 | 7.8 | 9 |
| 145 | Microarray and proteomic analysis of breast cancer cell and osteoblast co-cultures: role of osteoblast matrix metalloproteinase (MMP)-13 in bone metastasis. <i>Journal of Biological Chemistry</i> , 2011 , 286, 34271-85 | 5.4 | 48 |
| 144 | Factor Xa subsite mapping by proteome-derived peptide libraries improved using WebPICS, a resource for proteomic identification of cleavage sites. <i>Biological Chemistry</i> , 2011 , 392, 1031-7 | 4.5 | 50 |
| 143 | Proteomic analyses reveal an acidic prime side specificity for the astacin metalloprotease family reflected by physiological substrates. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.009233 | 7.6 | 100 |
| 142 | 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 | 7.6 | 36 |

(2009-2011)

| 141 | Membrane-type matrix metalloproteinase-3 regulates neuronal responsiveness to myelin through Nogo-66 receptor 1 cleavage. <i>Journal of Biological Chemistry</i> , 2011 , 286, 31418-24 | 5.4 | 27 |
|-----|---|---------------|-----|
| 140 | Metalloprotease meprin beta generates nontoxic N-terminal amyloid precursor protein fragments in vivo. <i>Journal of Biological Chemistry</i> , 2011 , 286, 27741-50 | 5.4 | 76 |
| 139 | TopFIND, a knowledgebase linking protein termini with function. <i>Nature Methods</i> , 2011 , 8, 703-4 | 21.6 | 76 |
| 138 | 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 | 1.4 | 21 |
| 137 | Monocyte chemotactic protein-3: possible involvement in apical periodontitis chemotaxis. <i>International Endodontic Journal</i> , 2010 , 43, 902-8 | 5.4 | 10 |
| 136 | Isotopic labeling of terminal amines in complex samples identifies protein N-termini and protease cleavage products. <i>Nature Biotechnology</i> , 2010 , 28, 281-8 | 44.5 | 403 |
| 135 | Proteome-wide analysis of protein carboxy termini: C terminomics. <i>Nature Methods</i> , 2010 , 7, 508-11 | 21.6 | 126 |
| 134 | Stromal regulation of vessel stability by MMP14 and TGFbeta. <i>DMM Disease Models and Mechanisms</i> , 2010 , 3, 317-32 | 4.1 | 67 |
| 133 | A statistics-based platform for quantitative N-terminome analysis and identification of protease cleavage products. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 912-27 | 7.6 | 63 |
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