

Mark Hochstrasser

List of Publications by Year in descending order

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22,538
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docs citations

191
times ranked

16272
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | UBIQUITIN-DEPENDENT PROTEIN DEGRADATION. Annual Review of Genetics, 1996, 30, 405-439. | 3.2 | 1,566 |
| 2 | Modification of Proteins by Ubiquitin and Ubiquitin-Like Proteins. Annual Review of Cell and Developmental Biology, 2006, 22, 159-180. | 4.0 | 1,352 |
| 3 | Quantitative Proteomics Reveals the Function of Unconventional Ubiquitin Chains in Proteasomal Degradation. Cell, 2009, 137, 133-145. | 13.5 | 948 |
| 4 | Ubiquitin, proteasomes, and the regulation of intracellular protein degradation. Current Opinion in Cell Biology, 1995, 7, 215-223. | 2.6 | 859 |
| 5 | Mechanism and function of deubiquitinating enzymes. Biochimica Et Biophysica Acta - Molecular Cell Research, 2004, 1695, 189-207. | 1.9 | 799 |
| 6 | Diversity of degradation signals in the ubiquitin-proteasome system. Nature Reviews Molecular Cell Biology, 2008, 9, 679-689. | 16.1 | 701 |
| 7 | A new protease required for cell-cycle progression in yeast. Nature, 1999, 398, 246-251. | 13.7 | 672 |
| 8 | Origin and function of ubiquitin-like proteins. Nature, 2009, 458, 422-429. | 13.7 | 670 |
| 9 | Function and regulation of SUMO proteases. Nature Reviews Molecular Cell Biology, 2012, 13, 755-766. | 16.1 | 523 |
| 10 | A conserved ubiquitin ligase of the nuclear envelope/endoplasmic reticulum that functions in both ER-associated and Matalpha 2 repressor degradation. Genes and Development, 2001, 15, 2660-2674. | 2.7 | 421 |
| 11 | Substrate Targeting in the Ubiquitin System. Cell, 1999, 97, 427-430. | 13.5 | 417 |
| 12 | Multiple ubiquitin-conjugating enzymes participate in the in vivo degradation of the yeast MAT1±2 repressor. Cell, 1993, 74, 357-369. | 13.5 | 415 |
| 13 | The yeast DOA4 gene encodes a deubiquitinating enzyme related to a product of the human tre-2 oncogene. Nature, 1993, 366, 313-319. | 13.7 | 394 |
| 14 | Autocatalytic Subunit Processing Couples Active Site Formation in the 20S Proteasome to Completion of Assembly. Cell, 1996, 86, 961-972. | 13.5 | 376 |
| 15 | Evolution and function of ubiquitin-like protein-conjugation systems. Nature Cell Biology, 2000, 2, E153-E157. | 4.6 | 364 |
| 16 | A superfamily of protein tags: ubiquitin, SUMO and related modifiers. Trends in Biochemical Sciences, 2003, 28, 321-328. | 3.7 | 359 |
| 17 | Defining the SUMO-modified Proteome by Multiple Approaches in Saccharomyces cerevisiae*. Journal of Biological Chemistry, 2005, 280, 4102-4110. | 1.6 | 354 |
| 18 | The Yeast ULP2 (SMT4) Gene Encodes a Novel Protease Specific for the Ubiquitin-Like Smt3 Protein. Molecular and Cellular Biology, 2000, 20, 2367-2377. | 1.1 | 337 |

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|----|---|------|-----------|
| 19 | Molecular Architecture and Assembly of the Eukaryotic Proteasome. Annual Review of Biochemistry, 2013, 82, 415-445. | 5.0 | 330 |
| 20 | A Wolbachia deubiquitylating enzyme induces cytoplasmic incompatibility. Nature Microbiology, 2017, 2, 17007. | 5.9 | 307 |
| 21 | The Doa4 Deubiquitinating Enzyme Is Functionally Linked to the Vacuolar Protein-sorting and Endocytic Pathways. Molecular Biology of the Cell, 2000, 11, 3365-3380. | 0.9 | 282 |
| 22 | Identification of the yeast 20S proteasome catalytic centers and subunit interactions required for active-site formation. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 7156-7161. | 3.3 | 275 |
| 23 | Proteasome Structure and Assembly. Journal of Molecular Biology, 2017, 429, 3500-3524. | 2.0 | 275 |
| 24 | Protein Degradation or Regulation: Ub the Judge. Cell, 1996, 84, 813-815. | 13.5 | 273 |
| 25 | The Doa4 Deubiquitinating Enzyme Is Required for Ubiquitin Homeostasis in Yeast. Molecular Biology of the Cell, 1999, 10, 2583-2594. | 0.9 | 264 |
| 26 | SP-RING for SUMO. Cell, 2001, 107, 5-8. | 13.5 | 257 |
| 27 | Spatial organization of chromosomes in the salivary gland nuclei of Drosophila melanogaster.. Journal of Cell Biology, 1986, 102, 112-123. | 2.3 | 256 |
| 28 | The short-lived MAT alpha 2 transcriptional regulator is ubiquitinated in vivo.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 4606-4610. | 3.3 | 255 |
| 29 | In vivo degradation of a transcriptional regulator: The yeast $\hat{I}\pm 2$ repressor. Cell, 1990, 61, 697-708. | 13.5 | 251 |
| 30 | Membrane and soluble substrates of the Doa10 ubiquitin ligase are degraded by distinct pathways. EMBO Journal, 2006, 25, 533-543. | 3.5 | 249 |
| 31 | Distinct Machinery Is Required in Saccharomyces cerevisiae for the Endoplasmic Reticulum-associated Degradation of a Multispanning Membrane Protein and a Soluble Luminal Protein. Journal of Biological Chemistry, 2004, 279, 38369-38378. | 1.6 | 232 |
| 32 | Lingering Mysteries of Ubiquitin-Chain Assembly. Cell, 2006, 124, 27-34. | 13.5 | 230 |
| 33 | In vivo disassembly of free polyubiquitin chains by yeast Ubp14 modulates rates of protein degradation by the proteasome. EMBO Journal, 1997, 16, 4826-4838. | 3.5 | 211 |
| 34 | The Yeast Hex3 \hat{A} -Slx8 Heterodimer Is a Ubiquitin Ligase Stimulated by Substrate Sumoylation. Journal of Biological Chemistry, 2007, 282, 34176-34184. | 1.6 | 200 |
| 35 | Degradation Signal Masking by Heterodimerization of MAT $\hat{I}\pm 2$ and MATa1 Blocks Their Mutual Destruction by the Ubiquitin-Proteasome Pathway. Cell, 1998, 94, 217-227. | 13.5 | 189 |
| 36 | Characteristic folding pattern of polytene chromosomes in Drosophila salivary gland nuclei. Nature, 1984, 308, 414-421. | 13.7 | 188 |

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|----|--|------|-----------|
| 37 | The Ulp1 SUMO isopeptidase. <i>Journal of Cell Biology</i> , 2003, 160, 1069-1082. | 2.3 | 186 |
| 38 | DUB-1, a deubiquitinating enzyme with growth-suppressing activity.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 3275-3279. | 3.3 | 166 |
| 39 | Analysis of the Deubiquitinating Enzymes of the Yeast <i>Saccharomyces cerevisiae</i> . <i>Biological Chemistry</i> , 2000, 381, 981-92. | 1.2 | 162 |
| 40 | Spatially regulated ubiquitin ligation by an ER/nuclear membrane ligase. <i>Nature</i> , 2006, 443, 827-831. | 13.7 | 155 |
| 41 | Multiple Assembly Chaperones Govern Biogenesis of the Proteasome Regulatory Particle Base. <i>Cell</i> , 2009, 137, 887-899. | 13.5 | 153 |
| 42 | A multimeric assembly factor controls the formation of alternative 20S proteasomes. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 237-244. | 3.6 | 144 |
| 43 | Autoregulation of an E2 enzyme by ubiquitin-chain assembly on its catalytic residue. <i>Nature Cell Biology</i> , 2007, 9, 422-427. | 4.6 | 142 |
| 44 | Eukaryotic 20S proteasome catalytic subunit propeptides prevent active site inactivation by N-terminal acetylation and promote particle assembly. <i>EMBO Journal</i> , 1999, 18, 3575-3585. | 3.5 | 134 |
| 45 | Î²-Subunit appendages promote 20S proteasome assembly by overcoming an Ump1-dependent checkpoint. <i>EMBO Journal</i> , 2007, 26, 2339-2349. | 3.5 | 132 |
| 46 | Heterohexameric Ring Arrangement of the Eukaryotic Proteasomal ATPases: Implications for Proteasome Structure and Assembly. <i>Molecular Cell</i> , 2010, 38, 393-403. | 4.5 | 130 |
| 47 | Unified nomenclature for subunits of the <i>Saccharomyces cerevisiae</i> proteasome regulatory particle. <i>Trends in Biochemical Sciences</i> , 1998, 23, 244-245. | 3.7 | 127 |
| 48 | Membrane Topology of the Yeast Endoplasmic Reticulum-localized Ubiquitin Ligase Doa10 and Comparison with Its Human Ortholog TEB4 (MARCH-VI). <i>Journal of Biological Chemistry</i> , 2006, 281, 4646-4653. | 1.6 | 126 |
| 49 | Properties of the T4 bacteriophage DNA replication apparatus: The T4 dda DNA helicase is required to pass a bound RNA polymerase molecule. <i>Cell</i> , 1983, 34, 115-123. | 13.5 | 120 |
| 50 | Three-dimensional organization of <i>Drosophila melanogaster</i> interphase nuclei. I. Tissue-specific aspects of polytene nuclear architecture.. <i>Journal of Cell Biology</i> , 1987, 104, 1455-1470. | 2.3 | 119 |
| 51 | There's the Rub: a novel ubiquitin-like modification linked to cell cycle regulation. <i>Genes and Development</i> , 1998, 12, 901-907. | 2.7 | 119 |
| 52 | Interaction of the Doa4 Deubiquitinating Enzyme with the Yeast 26S Proteasome. <i>Molecular Biology of the Cell</i> , 1999, 10, 741-756. | 0.9 | 118 |
| 53 | The Toxin "Antidote Model of Cytoplasmic Incompatibility: Genetics and Evolutionary Implications. <i>Trends in Genetics</i> , 2019, 35, 175-185. | 2.9 | 111 |
| 54 | Rtt106p is a histone chaperone involved in heterochromatin-mediated silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13410-13415. | 3.3 | 110 |

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|----|--|-----|-----------|
| 55 | Three-dimensional organization of <i>Drosophila melanogaster</i> interphase nuclei. II. Chromosome spatial organization and gene regulation.. <i>Journal of Cell Biology</i> , 1987, 104, 1471-1483. | 2.3 | 108 |
| 56 | BIOCHEMISTRY: All in the Ubiquitin Family. <i>Science</i> , 2000, 289, 563-564. | 6.0 | 106 |
| 57 | Molecular Organization of the 20S Proteasome Gene Family from <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 1998, 149, 677-692. | 1.2 | 103 |
| 58 | A nuclear envelope protein linking nuclear pore basket assembly, SUMO protease regulation, and mRNA surveillance. <i>Journal of Cell Biology</i> , 2007, 178, 813-827. | 2.3 | 99 |
| 59 | Ubiquitin-dependent protein degradation at the endoplasmic reticulum and nuclear envelope. <i>Seminars in Cell and Developmental Biology</i> , 2019, 93, 111-124. | 2.3 | 98 |
| 60 | Sem1, the yeast ortholog of a human BRCA2-binding protein, is a component of the proteasome regulatory particle that enhances proteasome stability. <i>Journal of Cell Science</i> , 2004, 117, 6447-6454. | 1.2 | 94 |
| 61 | Substrate specificity of the ubiquitin and Ubl proteases. <i>Cell Research</i> , 2016, 26, 441-456. | 5.7 | 92 |
| 62 | Small epitope-linker modules for PCR-based C-terminal tagging in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2009, 26, 185-192. | 0.8 | 89 |
| 63 | A unified mechanism for proteolysis and autocatalytic activation in the 20S proteasome. <i>Nature Communications</i> , 2016, 7, 10900. | 5.8 | 88 |
| 64 | Plasticity in eucaryotic 20S proteasome ring assembly revealed by a subunit deletion in yeast. <i>EMBO Journal</i> , 2004, 23, 500-510. | 3.5 | 85 |
| 65 | A Tetrahedral Transition State at the Active Sites of the 20S Proteasome Is Coupled to Opening of the Ω -Ring Channel. <i>Structure</i> , 2009, 17, 1137-1147. | 1.6 | 84 |
| 66 | A <i>Wolbachia</i> nuclease and its binding partner provide a distinct mechanism for cytoplasmic incompatibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22314-22321. | 3.3 | 82 |
| 67 | SUMO-independent in vivo activity of a SUMO-targeted ubiquitin ligase toward a short-lived transcription factor. <i>Genes and Development</i> , 2010, 24, 893-903. | 2.7 | 80 |
| 68 | Assembly of the 20S proteasome. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 2-12. | 1.9 | 80 |
| 69 | SUMO-1: Ubiquitin gains weight. <i>Trends in Cell Biology</i> , 1997, 7, 408-413. | 3.6 | 79 |
| 70 | An amphipathic helix targets serum and glucocorticoid-induced kinase 1 to the endoplasmic reticulum-associated ubiquitin-conjugation machinery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11178-11183. | 3.3 | 79 |
| 71 | Ubiquitin and intracellular protein degradation. <i>Current Opinion in Cell Biology</i> , 1992, 4, 1024-1031. | 2.6 | 76 |
| 72 | The yeast SEN3 gene encodes a regulatory subunit of the 26S proteasome complex required for ubiquitin-dependent protein degradation in vivo. <i>Molecular and Cellular Biology</i> , 1995, 15, 6311-6321. | 1.1 | 75 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 73 | A Single α Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly. <i>Cell</i> , 2015, 163, 432-444. | 13.5 | 73 |
| 74 | Ubiquitin-dependent protein degradation at the yeast endoplasmic reticulum and nuclear envelope. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2015, 50, 1-17. | 2.3 | 72 |
| 75 | Degradation of the bile salt export pump at endoplasmic reticulum in progressive familial intrahepatic cholestasis type II. <i>Hepatology</i> , 2008, 48, 1558-1569. | 3.6 | 70 |
| 76 | A conserved 20S proteasome assembly factor requires a C-terminal HbYX motif for proteasomal precursor binding. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 622-629. | 3.6 | 70 |
| 77 | Histone sumoylation and chromatin dynamics. <i>Nucleic Acids Research</i> , 2021, 49, 6043-6052. | 6.5 | 70 |
| 78 | The Intrinsically Disordered Sem1 Protein Functions as a Molecular Tether during Proteasome Lid Biogenesis. <i>Molecular Cell</i> , 2014, 53, 433-443. | 4.5 | 64 |
| 79 | Incorporation of the Rpn12 Subunit Couples Completion of Proteasome Regulatory Particle Lid Assembly to Lid-Base Joining. <i>Molecular Cell</i> , 2011, 44, 907-917. | 4.5 | 63 |
| 80 | The Wolbachia cytoplasmic incompatibility enzyme CidB targets nuclear import and protamine-histone exchange factors. <i>ELife</i> , 2019, 8, . | 2.8 | 61 |
| 81 | Aberrant substrate engagement of the ER translocon triggers degradation by the Hrd1 ubiquitin ligase. <i>Journal of Cell Biology</i> , 2012, 197, 761-773. | 2.3 | 59 |
| 82 | Degradation of the yeast MAT α 2 transcriptional regulator is mediated by the proteasome. <i>FEBS Letters</i> , 1994, 354, 50-52. | 1.3 | 56 |
| 83 | Order of the Proteasomal ATPases and Eukaryotic Proteasome Assembly. <i>Cell Biochemistry and Biophysics</i> , 2011, 60, 13-20. | 0.9 | 51 |
| 84 | Structure and functional analysis of the 26S proteasome subunits from plants. <i>Molecular Biology Reports</i> , 1999, 26, 137-146. | 1.0 | 48 |
| 85 | Ubiquitin-dependent degradation of the yeast Mat α 2 repressor enables a switch in developmental state. <i>Genes and Development</i> , 2003, 17, 2259-2270. | 2.7 | 48 |
| 86 | Designed Proteins To Modulate Cellular Networks. <i>ACS Chemical Biology</i> , 2010, 5, 545-552. | 1.6 | 46 |
| 87 | The Deubiquitinating Enzymes. , 1998, , 99-125. | | 46 |
| 88 | Site-specific cation release drives actin filament severing by vertebrate cofilin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17821-17826. | 3.3 | 45 |
| 89 | A Deubiquitinating Enzyme That Disassembles Free Polyubiquitin Chains Is Required for Development but Not Growth in Dictyostelium. <i>Journal of Biological Chemistry</i> , 1998, 273, 29178-29187. | 1.6 | 44 |
| 90 | N-terminal acetylation of the yeast Derlin Der1 is essential for Hrd1 ubiquitin-ligase activity toward luminal ER substrates. <i>Molecular Biology of the Cell</i> , 2013, 24, 890-900. | 0.9 | 43 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 91 | A conserved late endosome targeting signal required for Doa4 deubiquitylating enzyme function. <i>Journal of Cell Biology</i> , 2006, 175, 825-835. | 2.3 | 41 |
| 92 | The Ulp2 SUMO Protease Is Required for Cell Division following Termination of the DNA Damage Checkpoint. <i>Molecular and Cellular Biology</i> , 2007, 27, 6948-6961. | 1.1 | 40 |
| 93 | The SUMO-targeted ubiquitin ligase subunit Slx5 resides in nuclear foci and at sites of DNA breaks. <i>Cell Cycle</i> , 2009, 8, 1080-1089. | 1.3 | 40 |
| 94 | Assembly of an Evolutionarily Conserved Alternative Proteasome Isoform in Human Cells. <i>Cell Reports</i> , 2016, 14, 2962-2974. | 2.9 | 39 |
| 95 | Some assembly required: dedicated chaperones in eukaryotic proteasome biogenesis. <i>Biological Chemistry</i> , 2008, 389, 1143-1151. | 1.2 | 38 |
| 96 | Loss of the SUMO protease Ulp2 triggers a specific multichromosome aneuploidy. <i>Genes and Development</i> , 2016, 30, 1881-1894. | 2.7 | 37 |
| 97 | A Conserved C-terminal Element in the Yeast Doa10 and Human MARCH6 Ubiquitin Ligases Required for Selective Substrate Degradation. <i>Journal of Biological Chemistry</i> , 2016, 291, 12105-12118. | 1.6 | 36 |
| 98 | An Unusual Transmembrane Helix in the Endoplasmic Reticulum Ubiquitin Ligase Doa10 Modulates Degradation of Its Cognate E2 Enzyme. <i>Journal of Biological Chemistry</i> , 2011, 286, 20163-20174. | 1.6 | 35 |
| 99 | Cholesterol increases protein levels of the E3 ligase MARCH6 and thereby stimulates protein degradation. <i>Journal of Biological Chemistry</i> , 2019, 294, 2436-2448. | 1.6 | 33 |
| 100 | The Biochemistry of Cytoplasmic Incompatibility Caused by Endosymbiotic Bacteria. <i>Genes</i> , 2020, 11, 852. | 1.0 | 33 |
| 101 | Structural and mechanistic insights into the complexes formed by <i>Wolbachia</i> cytoplasmic incompatibility factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 33 |
| 102 | Essential Role of Nuclear Localization for Yeast Ulp2 SUMO Protease Function. <i>Molecular Biology of the Cell</i> , 2009, 20, 2196-2206. | 0.9 | 31 |
| 103 | Analysis of Protein Ubiquitination. <i>Current Protocols in Protein Science</i> , 2011, 66, Unit14.5. | 2.8 | 29 |
| 104 | Proteasomes: Isolation and Activity Assays. <i>Current Protocols in Cell Biology</i> , 2015, 67, 3.43.1-3.43.20. | 2.3 | 29 |
| 105 | Identification of SUMO-Interacting Proteins by Yeast Two-Hybrid Analysis. <i>Methods in Molecular Biology</i> , 2009, 497, 107-120. | 0.4 | 29 |
| 106 | Chromosome structure in four wild-type polytene tissues of <i>Drosophila melanogaster</i> . <i>Chromosoma</i> , 1987, 95, 197-208. | 1.0 | 28 |
| 107 | Ubiquitin signalling: what's in a chain?. <i>Nature Cell Biology</i> , 2004, 6, 571-572. | 4.6 | 28 |
| 108 | The Ulp2 SUMO protease promotes transcription elongation through regulation of histone sumoylation. <i>EMBO Journal</i> , 2019, 38, e102003. | 3.5 | 28 |

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|-----|--|-----|-----------|
| 109 | Histone sumoylation promotes Set3 histone-deacetylase complex-mediated transcriptional regulation. <i>Nucleic Acids Research</i> , 2020, 48, 12151-12168. | 6.5 | 28 |
| 110 | A viable ubiquitin-activating enzyme mutant for evaluating ubiquitin system function in <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2000, 477, 193-198. | 1.3 | 27 |
| 111 | MOLECULAR BIOLOGY: New Proteases in a Ubiquitin Stew. <i>Science</i> , 2002, 298, 549-552. | 6.0 | 26 |
| 112 | NF- κ B signaling: Flipping the Switch with Polyubiquitin Chains. <i>Current Biology</i> , 2004, 14, R898-R900. | 1.8 | 25 |
| 113 | Desumoylation of the Endoplasmic Reticulum Membrane VAP Family Protein Scs2 by Ulp1 and SUMO Regulation of the Inositol Synthesis Pathway. <i>Molecular and Cellular Biology</i> , 2012, 32, 64-75. | 1.1 | 24 |
| 114 | Microautophagy regulates proteasome homeostasis. <i>Current Genetics</i> , 2020, 66, 683-687. | 0.8 | 24 |
| 115 | Light microscope based analysis of three-dimensional structure: Applications to the study of <i>Drosophila</i> salivary gland nuclei. I. Data collection and analysis. <i>Journal of Microscopy</i> , 1985, 137, 241-252. | 0.8 | 23 |
| 116 | A Conserved Protein with AN1 Zinc Finger and Ubiquitin-like Domains Modulates Cdc48 (p97) Function in the Ubiquitin-Proteasome Pathway. <i>Journal of Biological Chemistry</i> , 2013, 288, 33682-33696. | 1.6 | 23 |
| 117 | SUMO Pathway Modulation of Regulatory Protein Binding at the Ribosomal DNA Locus in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 202, 1377-1394. | 1.2 | 22 |
| 118 | A deubiquitylase with an unusually high-affinity ubiquitin-binding domain from the scrub typhus pathogen <i>Orientia tsutsugamushi</i> . <i>Nature Communications</i> , 2020, 11, 2343. | 5.8 | 22 |
| 119 | SUMO and cellular adaptive mechanisms. <i>Experimental and Molecular Medicine</i> , 2020, 52, 931-939. | 3.2 | 22 |
| 120 | Ubiquitin Ligase Redundancy and Nuclear-Cytoplasmic Localization in Yeast Protein Quality Control. <i>Biomolecules</i> , 2021, 11, 1821. | 1.8 | 22 |
| 121 | Distinct adaptive mechanisms drive recovery from aneuploidy caused by loss of the Ulp2 SUMO protease. <i>Nature Communications</i> , 2018, 9, 5417. | 5.8 | 21 |
| 122 | Caution Does Not Preclude Predictive and Testable Models of Cytoplasmic Incompatibility: A Reply to Shropshire et al.. <i>Trends in Genetics</i> , 2019, 35, 399-400. | 2.9 | 21 |
| 123 | AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation. <i>PLoS Genetics</i> , 2019, 15, e1008387. | 1.5 | 21 |
| 124 | The CinB Nuclease from <i>Wolbachia</i> Is Sufficient for Induction of Cytoplasmic Incompatibility in <i>Drosophila</i> . <i>MBio</i> , 2022, 13, e0317721. | 1.8 | 21 |
| 125 | STuBL-mediated degradation of the transcription factor MAT α 2 requires degradation elements that coincide with corepressor binding sites. <i>Molecular Biology of the Cell</i> , 2015, 26, 3401-3412. | 0.9 | 20 |
| 126 | The DOA Pathway: Studies on the Functions and Mechanisms of Ubiquitin-dependent Protein Degradation in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1995, 60, 503-513. | 2.0 | 20 |

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|-----|--|-----|-----------|
| 127 | Unraveling the means to the end in ATP-dependent proteases. , 2001, 8, 294-296. | | 19 |
| 128 | An Evolutionarily Conserved Gene on Human Chromosome 5q33â€“q34,UBH1,Encodes a Novel Deubiquitinating Enzyme. Genomics, 1998, 49, 411-418. | 1.3 | 18 |
| 129 | Redundancy and variation in the ubiquitin-mediated proteolytic targeting of a transcription factor. Cell Cycle, 2010, 9, 4282-4285. | 1.3 | 18 |
| 130 | The Short-Lived MatÎ±2 Transcriptional Repressor Is Protected from Degradation In Vivo by Interactions with Its Corepressors Tup1 and Ssn6. Molecular and Cellular Biology, 2006, 26, 371-380. | 1.1 | 17 |
| 131 | Endoplasmic reticulum stress differentially inhibits endoplasmic reticulum and inner nuclear membrane protein quality control degradation pathways. Journal of Biological Chemistry, 2019, 294, 19814-19830. | 1.6 | 17 |
| 132 | Recent progress in ubiquitin and ubiquitin-like protein (Ubl) signaling. Cell Research, 2016, 26, 389-390. | 5.7 | 16 |
| 133 | Assaying protein ubiquitination in Saccharomyces cerevisiae. Methods in Enzymology, 2002, 351, 248-257. | 0.4 | 15 |
| 134 | Distinct Elements in the Proteasomal Î±5 Subunit Propeptide Required for Autocatalytic Processing and Proteasome Assembly. Journal of Biological Chemistry, 2016, 291, 1991-2003. | 1.6 | 15 |
| 135 | Crystal Structures of Wolbachia CidA and CidB Reveal Determinants of Bacteria-induced Cytoplasmic Incompatibility and Rescue. Nature Communications, 2022, 13, 1608. | 5.8 | 15 |
| 136 | New Structural Clues to Substrate Specificity in the â€œUbiquitin Systemâ€œ. Molecular Cell, 2002, 9, 453-454. | 4.5 | 14 |
| 137 | Protein quality control degron-containing substrates are differentially targeted in the cytoplasm and nucleus by ubiquitin ligases. Genetics, 2021, 217, 1-19. | 1.2 | 14 |
| 138 | Ulp2 and the DNA damage response: Desumoylation enables safe passage through mitosis. Cell Cycle, 2008, 7, 52-56. | 1.3 | 13 |
| 139 | Ubiquitin-Dependent Degradation of Transcription Regulators. , 1998, , 279-302. | | 13 |
| 140 | DNA binding by the MATÎ±2 transcription factor controls its access to alternative ubiquitin-modification pathways. Molecular Biology of the Cell, 2018, 29, 542-556. | 0.9 | 12 |
| 141 | Varshavsky's Contributions. Science, 2004, 306, 1290-1292. | 6.0 | 11 |
| 142 | Rapid degradation of progressive ankylosis protein (ANKH) in craniometaphyseal dysplasia. Scientific Reports, 2018, 8, 15710. | 1.6 | 11 |
| 143 | The Sts1 nuclear import adaptor uses a noncanonical bipartite NLS and is directly degraded by the proteasome. Journal of Cell Science, 2020, 133, . | 1.2 | 11 |
| 144 | Selective microautophagy of proteasomes is initiated by ESCRT-0 and is promoted by proteasome ubiquitylation. Journal of Cell Science, 2022, 135, . | 1.2 | 11 |

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|-----|---|------|-----------|
| 145 | A new class of SUMO proteases. <i>EMBO Reports</i> , 2012, 13, 284-285. | 2.0 | 10 |
| 146 | Epigenetic Mechanisms Contribute to Evolutionary Adaptation of Gene Network Activity under Environmental Selection. <i>Cell Reports</i> , 2020, 33, 108306. | 2.9 | 10 |
| 147 | Ubiquitin Ligation without a Ligase. <i>Developmental Cell</i> , 2007, 13, 4-6. | 3.1 | 9 |
| 148 | Introduction to Intracellular Protein Degradation. <i>Chemical Reviews</i> , 2009, 109, 1479-1480. | 23.0 | 9 |
| 149 | Analysis of Protein Ubiquitination. <i>Current Protocols in Protein Science</i> , 2002, 29, Unit 14.5. | 2.8 | 8 |
| 150 | Ubiquitin-dependent control of development in <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Microbiology</i> , 2004, 7, 647-654. | 2.3 | 7 |
| 151 | The Regulation of Chromatin by Dynamic SUMO Modifications. <i>Methods in Molecular Biology</i> , 2016, 1475, 23-38. | 0.4 | 7 |
| 152 | Crystal structure of a guanine nucleotide exchange factor encoded by the scrub typhus pathogen <i>Orientia tsutsugamushi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30380-30390. | 3.3 | 7 |
| 153 | A WLM Protein with SUMO-Directed Protease Activity. <i>Molecular and Cellular Biology</i> , 2010, 30, 3734-3736. | 1.1 | 6 |
| 154 | Split-Doa10: A Naturally Split Polytopic Eukaryotic Membrane Protein Generated by Fission of a Nuclear Gene. <i>PLoS ONE</i> , 2012, 7, e45194. | 1.1 | 6 |
| 155 | OtDUB from the Human Pathogen <i>Orientia tsutsugamushi</i> Modulates Host Membrane Trafficking by Multiple Mechanisms. <i>Molecular and Cellular Biology</i> , 0, , . | 1.1 | 6 |
| 156 | Disulfide Engineering to Map Subunit Interactions in the Proteasome and Other Macromolecular Complexes. <i>Methods in Molecular Biology</i> , 2012, 832, 349-362. | 0.4 | 5 |
| 157 | Adaptive aneuploidy counters a dysregulated SUMO system. <i>Cell Cycle</i> , 2017, 16, 383-385. | 1.3 | 4 |
| 158 | Preparation and Characterization of Yeast and Human Desumoylating Enzymes. <i>Methods in Enzymology</i> , 2005, 398, 457-467. | 0.4 | 3 |
| 159 | Cyre and gimble in the proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12896-12898. | 3.3 | 3 |
| 160 | The DUB blade goes snicker-snack: Novel ubiquitin cleavage by a <i>Legionella</i> effector protein. <i>Cell Research</i> , 2017, 27, 845-846. | 5.7 | 3 |
| 161 | Conserved proline residues in the coiled coil OB domain linkers of Rpt proteins facilitate eukaryotic proteasome base assembly. <i>Journal of Biological Chemistry</i> , 2021, 296, 100660. | 1.6 | 3 |
| 162 | Cytoplasmic incompatibility: A <i>Wolbachia</i> toxin antidote mechanism comes into view. <i>Current Biology</i> , 2022, 32, R287-R289. | 1.8 | 3 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 163 | Protein Modification: Bacterial Effectors Rewrite the Rules of Ubiquitylation. <i>Current Biology</i> , 2016, 26, R539-R542. | 1.8 | 2 |
| 164 | Yeast Nst1 is a novel component of P-bodies and is a specific suppressor of proteasome base assembly defects. <i>Molecular Biology of the Cell</i> , 2021, 32, ar6. | 0.9 | 2 |
| 165 | Functions of Intracellular Protein Degradation in Yeast. , 1991, 13, 307-329. | | 2 |
| 166 | A versatile new tool derived from a bacterial deubiquitylase to detect and purify ubiquitylated substrates and their interacting proteins. <i>PLoS Biology</i> , 2022, 20, e3001501. | 2.6 | 2 |
| 167 | The Ubiquitin-Proteasome System. , 2003, , 347-350. | | 0 |
| 168 | Cecile M. Pickart 1954â€“2006. <i>Nature Cell Biology</i> , 2006, 8, 542-543. | 4.6 | 0 |
| 169 | The Ubiquitinâ€“Proteasome System. , 2010, , 1293-1296. | | 0 |
| 170 | Preface. <i>Methods in Enzymology</i> , 2019, 619, xv-xvii. | 0.4 | 0 |
| 171 | Preface. <i>Methods in Enzymology</i> , 2019, 618, xvii-xix. | 0.4 | 0 |
| 172 | An emerging role for thioesterâ€linked polyubiquitin chains in protein degradation. <i>FASEB Journal</i> , 2008, 22, 605.7. | 0.2 | 0 |
| 173 | Ulp2 SUMO Protease. , 2013, , 2362-2365. | | 0 |
| 174 | The Doa4 Deubiquitylating Enzyme (<i>Saccharomyces cerevisiae</i>). , 2013, , 2049-2052. | | 0 |
| 175 | Title is missing!. , 2019, 15, e1008387. | | 0 |
| 176 | Title is missing!. , 2019, 15, e1008387. | | 0 |
| 177 | Title is missing!. , 2019, 15, e1008387. | | 0 |
| 178 | Title is missing!. , 2019, 15, e1008387. | | 0 |