Rasmus Hartmann-Petersen

List of Publications by Year
in descending order

77 papers	3,469 citations	126907 33 h-index	161849 54 g-index
94 all docs	94 docs citations	94 times ranked	3993 citing authors

#	Article	IF	Citations
1	Proteins containing the UBA domain are able to bind to multi-ubiquitin chains. Nature Cell Biology, 2001, 3, 939-943.	10.3	375
2	Transferring substrates to the 26S proteasome. Trends in Biochemical Sciences, 2003, 28, 26-31.	7.5	160
3	DVC1 (C1orf124) is a DNA damageâ€“targeting p97 adaptor that promotes ubiquitin-dependent responses to replication blocks. Nature Structural and Molecular Biology, 2012, 19, 1084-1092.	8.2	153
4	Biophysical and Mechanistic Models for Disease-Causing Protein Variants. Trends in Biochemical Sciences, 2019, 44, 575-588.	7.5	143
5	Molecular chaperones in targeting misfolded proteins for ubiquitinâ€dependent degradation. FEBS Journal, 2012, 279, 532-542.	4.7	117
6	NCAM regulates cell motility. Journal of Cell Science, 2002, 115, 283-292.	2.0	98
7	The Ubx2 and Ubx3 Cofactors Direct Cdc48 Activity to Proteolytic and Nonproteolytic Ubiquitin-Dependent Processes. Current Biology, 2004, 14, 824-828.	3.9	94
8	Predicting the impact of Lynch syndrome-causing missense mutations from structural calculations. PLoS Genetics, 2017, 13, e1006739.	3.5	90
9	Uch2/Uch37 is the Major Deubiquitinating Enzyme Associated with the 26S Proteasome in Fission Yeast. Journal of Molecular Biology, 2004, 344, 697-706.	4.2	83
10	Dss1 Is a 26S Proteasome Ubiquitin Receptor. Molecular Cell, 2014, 56, 453-461.	9.7	81
11	Integral UBL domain proteins: a family of proteasome interacting proteins. Seminars in Cell and Developmental Biology, 2004, 15, 247-259.	5.0	79
12	Quaternary Structure of the ATPase Complex of Human 26S Proteasomes Determined by Chemical Cross-Linking. Archives of Biochemistry and Biophysics, 2001, 386, 89-94.	3.0	71
13	Thioredoxin Txnl1/TRP32 Is a Redox-active Cofactor of the 26 S Proteasome. Journal of Biological Chemistry, 2009, 284, 15246-15254.	3.4	68
14	New ATPase regulatorsâ€”p97 goes to the PUB. International Journal of Biochemistry and Cell Biology, 2009, 41, 2380-2388.	2.8	67
15	A Chaperone-Assisted Degradation Pathway Targets Kinetochore Proteins to Ensure Genome Stability. PLoS Genetics, 2014, 10, e1004140.	3.5	66
16	Understanding the Origins of Loss of Protein Function by Analyzing the Effects of Thousands of Variants on Activity and Abundance. Molecular Biology and Evolution, 2021, 38, 3235-3246.	8.9	65
17	Redox Control of the Ubiquitin-Proteasome System: From Molecular Mechanisms to Functional Significance. Antioxidants and Redox Signaling, 2011, 15, 2265-2299.	5.4	62
18	Regulation of NF-Î¹B activity and inducible nitric oxide synthase by regulatory particle non-ATPase subunit 13 (Rpn13). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13854-13859.	7.1	61

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19	26 S proteasomes function as stable entities 1 1Edited by R. Huber. Journal of Molecular Biology, 2002, 315, 627-636.	4.2	60
20	Interaction of the Anaphase-promoting Complex/Cyclosome and Proteasome Protein Complexes with Multiubiquitin Chain-binding Proteins. Journal of Biological Chemistry, 2003, 278, 16791-16796.	3.4	60
21	Adrm1, a Putative Cell Adhesion Regulating Protein, is a Novel Proteasome-associated Factor. Journal of Molecular Biology, 2006, 360, 1043-1052.	4.2	58
22	Herp Regulates Hrd1-mediated Ubiquitylation in a Ubiquitin-like Domain-dependent Manner. Journal of Biological Chemistry, 2011, 286, 5151-5156.	3.4	58
23	Toward mechanistic models for genotypeâ€“phenotype correlations in phenylketonuria using protein stability calculations. Human Mutation, 2019, 40, 444-457.	2.5	56
24	A luminal flavoprotein in endoplasmic reticulum-associated degradation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14831-14836.	7.1	52
25	The 20S Proteasome as an Assembly Platform for the 19S Regulatory Complex. Journal of Molecular Biology, 2009, 394, 320-328.	4.2	50
26	Computational and cellular studies reveal structural destabilization and degradation of MLH1 variants in Lynch syndrome. ELife, 2019, 8, .	6.0	49
27	Ubiquitin binding proteins protect ubiquitin conjugates from disassembly. FEBS Letters, 2003, 535, 77-81.	2.8	43
28	Ubxd1 is a novel co-factor of the human p97 ATPase. International Journal of Biochemistry and Cell Biology, 2008, 40, 2927-2942.	2.8	42
29	DSS1/Sem1, a Multifunctional and Intrinsically Disordered Protein. Trends in Biochemical Sciences, 2016, 41, 446-459.	7.5	42
30	Protein Quality Control in the Nucleus. Biomolecules, 2014, 4, 646-661.	4.0	39
31	Ciprofloxacin intercalated in fluorohectorite clay: identical pure drug activity and toxicity with higher adsorption and controlled release rate. RSC Advances, 2017, 7, 26537-26545.	3.6	38
32	Protein Degradation: Recognition of Ubiquitinylated Substrates. Current Biology, 2004, 14, R754-R756.	3.9	37
33	Ubiquitin-proteasome system. Cellular and Molecular Life Sciences, 2004, 61, 1589-95.	5.4	37
34	Mammalian 26S Proteasomes Remain Intact during Protein Degradation. Cell, 2008, 135, 355-365.	28.9	36
35	Individual cell motility studied by time-lapse video recording: Influence of experimental conditions. Cytometry, 2000, 40, 260-270.	1.8	34
36	Proteasomes: A Complex Story. Current Protein and Peptide Science, 2004, 5, 135-151.	1.4	32

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37	The Ku70 80 ring in Non-Homologous End-Joining easy to slip on hard to remove. Frontiers in Bioscience - Landmark, 2016, 21, 514-527.	3.0	32
38	HUWE1 and TRIP12 Collaborate in Degradation of Ubiquitin-Fusion Proteins and Misframed Ubiquitin. PLoS ONE, 2012, 7, e50548.	2.5	32
39	Protein stability and degradation in health and disease. Advances in Protein Chemistry and Structural Biology, 2019, 114, 61-83.	2.3	31
40	UBA domain containing proteins in fission yeast. International Journal of Biochemistry and Cell Biology, 2003, 35, 629-636.	2.8	30
41	Ubiquitin domain proteins in disease. BMC Biochemistry, 2007, 8, S1.	4.4	30
42	Co-Chaperones in Targeting and Delivery of Misfolded Proteins to the 26S Proteasome. Biomolecules, 2020, 10, 1141.	4.0	29
43	Bioinformatics analysis identifies several intrinsically disordered human E3 ubiquitin-protein ligases. PeerJ, 2016, 4, e1725.	2.0	24
44	Cell-cycle-dependent regulation of cell motility and determination of the role of Rac1. Experimental Cell Research, 2004, 295, 407-420.	2.6	23
45	Blocking protein quality control to counter hereditary cancers. Genes Chromosomes and Cancer, 2017, 56, 823-831.	2.8	23
46	Water dynamics in MCF-7 breast cancer cells: a neutron scattering descriptive study. Scientific Reports, 2019, 9, 8704.	3.3	23
47	A Two-step Protein Quality Control Pathway for a Misfolded DJ-1 Variant in Fission Yeast. Journal of Biological Chemistry, 2015, 290, 21141-21153.	3.4	22
48	Mass spectrometry analyses of normal and polyglutamine expanded ataxin-3 reveal novel interaction partners involved in mitochondrial function. Neurochemistry International, 2018, 112, 5-17.	3.8	22
49	The exocyst subunit Sec3 is regulated by a protein quality control pathway. Journal of Biological Chemistry, 2017, 292, 15240-15253.	3.4	21
50	Classifying disease-associated variants using measures of protein activity and stability. , 2020, , 91-107.		21
51	Proteasome Nuclear Import Mediated by Arc3 Can Influence Efficient DNA Damage Repair and Mitosis in Schizosaccharomyces Pombe. Molecular Biology of the Cell, 2010, 21, 3125-3136.	2.1	18
52	Txl1 and Txc1 Are Co-Factors of the 26S Proteasome in Fission Yeast. Antioxidants and Redox Signaling, 2011, 14, 1601-1608.	5.4	18
53	UBL/BAG-domain co-chaperones cause cellular stress upon overexpression through constitutive activation of Hsf1. Cell Stress and Chaperones, 2017, 22, 143-154.	2.9	18
54	Ubiquitin-binding proteins: similar, but different. Essays in Biochemistry, 2005, 41, 49.	4.7	17

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55	Characterisation of the nascent polypeptide-associated complex in fission yeast. Molecular Biology Reports, 2007, 34, 275-281.	2.3	16
56	Folliculin variants linked to Birt-Hogg-DubÃ© syndrome are targeted for proteasomal degradation. PLoS Genetics, 2020, 16, e1009187.	3.5	16
57	The proteasome cap RPT5/Rpt5p subunit prevents aggregation of unfolded ricin A chain. Biochemical Journal, 2013, 453, 435-445.	3.7	14
58	Expanded Interactome of the Intrinsically Disordered Protein Dss1. Cell Reports, 2018, 25, 862-870.	6.4	14
59	Mutations in a Single Signaling Pathway Allow Cell Growth in Heavy Water. ACS Synthetic Biology, 2020, 9, 733-748.	3.8	14
60	Ubiquitin-binding proteins: similar, but different. Essays in Biochemistry, 2005, 41, 49-67.	4.7	14
61	Disease-linked mutations cause exposure of a protein quality control degron. Structure, 2022, 30, 1245-1253.e5.	3.3	14
62	Multiplexed assays reveal effects of missense variants in MSH2 and cancer predisposition. PLoS Genetics, 2021, 17, e1009496.	3.5	13
63	The Tissue-Specific Rep8/UBXD6 Tethers p97 to the Endoplasmic Reticulum Membrane for Degradation of Misfolded Proteins. PLoS ONE, 2011, 6, e25061.	2.5	12
64	Mapping the degradation pathway of a disease-linked aspartoacylase variant. PLoS Genetics, 2021, 17, e1009539.	3.5	12
65	Fission Yeast 26S Proteasome Mutants Are Multi-Drug Resistant Due to Stabilization of the Pap1 Transcription Factor. PLoS ONE, 2012, 7, e50796.	2.5	12
66	Quantifying Proteinâ€“Protein Interactions in the Ubiquitin Pathway by Surface Plasmon Resonance. Methods in Enzymology, 2005, 399, 164-177.	1.0	11
67	Random Mutagenesis Analysis of the Influenza A M2 Proton Channel Reveals Novel Resistance Mutants. Biochemistry, 2018, 57, 5957-5968.	2.5	11
68	Human ASPL/TUG interacts with p97 and complements the proteasome mislocalization of a yeast ubx4 mutant, but not the ER-associated degradation defect. BMC Cell Biology, 2014, 15, 31.	3.0	10
69	Polyglutamine expansion of ataxin-3 alters its degree of ubiquitination and phosphorylation at specific sites. Neurochemistry International, 2017, 105, 42-50.	3.8	10
70	Effects of taurine depletion on cell migration and NCAM expression in cultures of dissociated mouse cerebellum and N2A cells. Amino Acids, 1998, 15, 77-88.	2.7	9
71	Novel HARS2 missense variants identified in individuals with sensorineural hearing impairment and Perrault syndrome. European Journal of Medical Genetics, 2020, 63, 103733.	1.3	9
72	The disordered PCI â€binding human proteins CSNAP and DSS1 have diverged in structure and function. Protein Science, 2021, 30, 2069-2082.	7.6	8

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73	Single Site Suppressors of a Fission Yeast Temperature-Sensitive Mutant in cdc48 Identified by Whole Genome Sequencing. PLoS ONE, 2015, 10, e0117779.	2.5	8
74	Nedd8 processing enzymes in Schizosaccharomyces pombe. BMC Biochemistry, 2013, 14, 8.	4.4	6
75	Protein destabilization and degradation as a mechanism for hereditary disease. , 2020, , 111-125.		5
76	High-Throughput siRNA Screening Applied to the Ubiquitinâ€“Proteasome System. Methods in Molecular Biology, 2016, 1449, 421-439.	0.9	2
77	Cdc48 connects with eIF3. Cell Cycle, 2010, 9, 22-27.	2.6	0