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	Disease-linked mutations cause exposure of a protein quality control degron. Structure, 2022, 30, 1245-1253.e5.	3.3	14
2	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
3	Multiplexed assays reveal effects of missense variants in MSH2 and cancer predisposition. PLoS Genetics, 2021, 17, e1009496.	3.5	13
4	Mapping the degradation pathway of a disease-linked aspartoacylase variant. PLoS Genetics, 2021, 17, e1009539.	3.5	12
5	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
6	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
7	Classifying disease-associated variants using measures of protein activity and stability. , 2020, , 91-107.		21
8	Co-Chaperones in Targeting and Delivery of Misfolded Proteins to the 26S Proteasome. Biomolecules, 2020, 10, 1141.	4.0	29
9	Mutations in a Single Signaling Pathway Allow Cell Growth in Heavy Water. ACS Synthetic Biology, 2020, 9, 733-748.	3.8	14
10	Protein destabilization and degradation as a mechanism for hereditary disease. , 2020, , 111-125.		5
11	Folliculin variants linked to Birt-Hogg-DubÃ© syndrome are targeted for proteasomal degradation. PLoS Genetics, 2020, 16, e1009187.	3.5	16
12	Biophysical and Mechanistic Models for Disease-Causing Protein Variants. Trends in Biochemical Sciences, 2019, 44, 575-588.	7.5	143
13	Water dynamics in MCF-7 breast cancer cells: a neutron scattering descriptive study. Scientific Reports, 2019, 9, 8704.	3.3	23
14	Toward mechanistic models for genotypeâ€“phenotype correlations in phenylketonuria using protein stability calculations. Human Mutation, 2019, 40, 444-457.	2.5	56
15	Protein stability and degradation in health and disease. Advances in Protein Chemistry and Structural Biology, 2019, 114, 61-83.	2.3	31
16	Computational and cellular studies reveal structural destabilization and degradation of MLH1 variants in Lynch syndrome. ELife, 2019, 8, .	6.0	49
17	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
18	Random Mutagenesis Analysis of the Influenza A M2 Proton Channel Reveals Novel Resistance Mutants. Biochemistry, 2018, 57, 5957-5968.	2.5	11

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19	Expanded Interactome of the Intrinsically Disordered Protein Dss1. Cell Reports, 2018, 25, 862-870.	6.4	14
20	Polyglutamine expansion of ataxin-3 alters its degree of ubiquitination and phosphorylation at specific sites. Neurochemistry International, 2017, 105, 42-50.	3.8	10
21	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
22	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
23	The exocyst subunit Sec3 is regulated by a protein quality control pathway. Journal of Biological Chemistry, 2017, 292, 15240-15253.	3.4	21
24	Blocking protein quality control to counter hereditary cancers. Genes Chromosomes and Cancer, 2017, 56, 823-831.	2.8	23
25	Predicting the impact of Lynch syndrome-causing missense mutations from structural calculations. PLoS Genetics, 2017, 13, e1006739.	3.5	90
26	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
27	DSS1/Sem1, a Multifunctional and Intrinsically Disordered Protein. Trends in Biochemical Sciences, 2016, 41, 446-459.	7.5	42
28	High-Throughput siRNA Screening Applied to the Ubiquitinâ€“Proteasome System. Methods in Molecular Biology, 2016, 1449, 421-439.	0.9	2
29	Bioinformatics analysis identifies several intrinsically disordered human E3 ubiquitin-protein ligases. PeerJ, 2016, 4, e1725.	2.0	24
30	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
31	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
32	Dss1 Is a 26S Proteasome Ubiquitin Receptor. Molecular Cell, 2014, 56, 453-461.	9.7	81
33	A Chaperone-Assisted Degradation Pathway Targets Kinetochore Proteins to Ensure Genome Stability. PLoS Genetics, 2014, 10, e1004140.	3.5	66
34	Protein Quality Control in the Nucleus. Biomolecules, 2014, 4, 646-661.	4.0	39
35	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
36	Nedd8 processing enzymes in Schizosaccharomyces pombe. BMC Biochemistry, 2013, 14, 8.	4.4	6

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37	The proteasome cap RPT5/Rpt5p subunit prevents aggregation of unfolded ricin A chain. Biochemical Journal, 2013, 453, 435-445.	3.7	14
38	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
39	Molecular chaperones in targeting misfolded proteins for ubiquitinâ€dependent degradation. FEBS Journal, 2012, 279, 532-542.	4.7	117
40	HUWE1 and TRIP12 Collaborate in Degradation of Ubiquitin-Fusion Proteins and Misframed Ubiquitin. PLoS ONE, 2012, 7, e50548.	2.5	32
41	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
42	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
43	Txl1 and Txc1 Are Co-Factors of the 26S Proteasome in Fission Yeast. Antioxidants and Redox Signaling, 2011, 14, 1601-1608.	5.4	18
44	Redox Control of the Ubiquitin-Proteasome System: From Molecular Mechanisms to Functional Significance. Antioxidants and Redox Signaling, 2011, 15, 2265-2299.	5.4	62
45	Herp Regulates Hrd1-mediated Ubiquitylation in a Ubiquitin-like Domain-dependent Manner. Journal of Biological Chemistry, 2011, 286, 5151-5156.	3.4	58
46	Regulation of NF-Î¤B 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
47	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
48	Cdc48 connects with eIF3. Cell Cycle, 2010, 9, 22-27.	2.6	0
49	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
50	Thioredoxin Txnl1/TRP32 Is a Redox-active Cofactor of the 26 S Proteasome. Journal of Biological Chemistry, 2009, 284, 15246-15254.	3.4	68
51	New ATPase regulatorsâ€”p97 goes to the PUB. International Journal of Biochemistry and Cell Biology, 2009, 41, 2380-2388.	2.8	67
52	The 20S Proteasome as an Assembly Platform for the 19S Regulatory Complex. Journal of Molecular Biology, 2009, 394, 320-328.	4.2	50
53	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
54	Mammalian 26S Proteasomes Remain Intact during Protein Degradation. Cell, 2008, 135, 355-365.	28.9	36

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55	Ubiquitin domain proteins in disease. BMC Biochemistry, 2007, 8, S1.	4.4	30
56	Characterisation of the nascent polypeptide-associated complex in fission yeast. Molecular Biology Reports, 2007, 34, 275-281.	2.3	16
57	Adrm1, a Putative Cell Adhesion Regulating Protein, is a Novel Proteasome-associated Factor. Journal of Molecular Biology, 2006, 360, 1043-1052.	4.2	58
58	Quantifying Proteinâ€"Protein Interactions in the Ubiquitin Pathway by Surface Plasmon Resonance. Methods in Enzymology, 2005, 399, 164-177.	1.0	11
59	Ubiquitin-binding proteins: similar, but different. Essays in Biochemistry, 2005, 41, 49-67.	4.7	14
60	Ubiquitin-binding proteins: similar, but different. Essays in Biochemistry, 2005, 41, 49.	4.7	17
61	The Ubx2 and Ubx3 Cofactors Direct Cdc48 Activity to Proteolytic and Nonproteolytic Ubiquitin-Dependent Processes. Current Biology, 2004, 14, 824-828.	3.9	94
62	Protein Degradation: Recognition of Ubiquitinylated Substrates. Current Biology, 2004, 14, R754-R756.	3.9	37
63	Ubiquitin-proteasome system. Cellular and Molecular Life Sciences, 2004, 61, 1589-95.	5.4	37
64	Cell-cycle-dependent regulation of cell motility and determination of the role of Rac1. Experimental Cell Research, 2004, 295, 407-420.	2.6	23
65	Integral UBL domain proteins: a family of proteasome interacting proteins. Seminars in Cell and Developmental Biology, 2004, 15, 247-259.	5.0	79
66	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
67	Proteasomes: A Complex Story. Current Protein and Peptide Science, 2004, 5, 135-151.	1.4	32
68	Transferring substrates to the 26S proteasome. Trends in Biochemical Sciences, 2003, 28, 26-31.	7.5	160
69	Ubiquitin binding proteins protect ubiquitin conjugates from disassembly. FEBS Letters, 2003, 535, 77-81.	2.8	43
70	UBA domain containing proteins in fission yeast. International Journal of Biochemistry and Cell Biology, 2003, 35, 629-636.	2.8	30
71	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
72	26 S proteasomes function as stable entities 1 1Edited by R. Huber. Journal of Molecular Biology, 2002, 315, 627-636.	4.2	60

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73	NCAM regulates cell motility. Journal of Cell Science, 2002, 115, 283-292.	2.0	98
74	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
75	Proteins containing the UBA domain are able to bind to multi-ubiquitin chains. Nature Cell Biology, 2001, 3, 939-943.	10.3	375
76	Individual cell motility studied by time-lapse video recording: Influence of experimental conditions. Cytometry, 2000, 40, 260-270.	1.8	34
77	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