

Roman Kärrner

List of Publications by Year in descending order

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37
papers

6,228
citations

218677

26
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377865

34
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all docs

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docs citations

37
times ranked

7537
citing authors

#	ARTICLE	IF	CITATIONS
1	An inventory of interactors of the human HSP60/HSP10 chaperonin in the mitochondrial matrix space. <i>Cell Stress and Chaperones</i> , 2020, 25, 407-416.	2.9	18
2	The Hsp70 Chaperone System Stabilizes a Thermo-sensitive Subproteome in E.Âcoli. <i>Cell Reports</i> , 2019, 28, 1335-1345.e6.	6.4	37
3	Chaperone Function of Hgh1 in the Biogenesis of Eukaryotic Elongation Factor 2. <i>Molecular Cell</i> , 2019, 74, 88-100.e9.	9.7	18
4	Absolute Quantitation of Proteins by Acid Hydrolysis Combined with Amino Acid Detection by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 2030, 11-16.	0.9	0
5	High capacity of the endoplasmic reticulum to prevent secretion and aggregation of amyloidogenic proteins. <i>EMBO Journal</i> , 2018, 37, 337-350.	7.8	29
6	Exosomes mediate cell contactâ€independent ephrin-Eph signaling during axon guidance. <i>Journal of Cell Biology</i> , 2016, 214, 35-44.	5.2	105
7	Failure of RQC machinery causes protein aggregation and proteotoxic stress. <i>Nature</i> , 2016, 531, 191-195.	27.8	185
8	Interplay of Acetyltransferase EP300 and the Proteasome System in Regulating Heat Shock Transcription Factor 1. <i>Cell</i> , 2014, 156, 975-985.	28.9	130
9	Uncovering the Molecular Machinery of the Human Spindleâ€An Integration of Wet and Dry Systems Biology. <i>PLoS ONE</i> , 2012, 7, e31813.	2.5	14
10	Absolute Quantitation of Proteins by Acid Hydrolysis Combined with Amino Acid Detection by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2012, 828, 115-120.	0.9	7
11	The Plk1-dependent Phosphoproteome of the Early Mitotic Spindle. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.004457.	3.8	201
12	Quantitative Mass Spectrometry Analysis Reveals Similar Substrate Consensus Motif for Human Mps1 Kinase and Plk1. <i>PLoS ONE</i> , 2011, 6, e18793.	2.5	65
13	Quantitative Site-specific Phosphorylation Dynamics of Human Protein Kinases during Mitotic Progression. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1167-1181.	3.8	46
14	Quantitative Analysis of the Human Spindle Phosphoproteome at Distinct Mitotic Stages. <i>Journal of Proteome Research</i> , 2009, 8, 4553-4563.	3.7	110
15	Kinase-Selective Enrichment Enables Quantitative Phosphoproteomics of the Kinome across the Cell Cycle. <i>Molecular Cell</i> , 2008, 31, 438-448.	9.7	548
16	Evaluation of the Low-Specificity Protease Elastase for Large-Scale Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2008, 80, 9526-9533.	6.5	71
17	Phosphorylation-dependent Binding of Cyclin B1 to a Cdc6-like Domain of Human Separase. <i>Journal of Biological Chemistry</i> , 2008, 283, 816-823.	3.4	32
18	Comparative conservation analysis of the human mitotic phosphoproteome. <i>Bioinformatics</i> , 2008, 24, 1426-1432.	4.1	48

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19	PICH, a Centromere-Associated SNF2 Family ATPase, Is Regulated by Plk1 and Required for the Spindle Checkpoint. <i>Cell</i> , 2007, 128, 101-114.	28.9	297
20	Phosphoproteome analysis of the human mitotic spindle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5391-5396.	7.1	301
21	HURP Is a Ran-Importin β -Regulated Protein that Stabilizes Kinetochores Microtubules in the Vicinity of Chromosomes. <i>Current Biology</i> , 2006, 16, 731-742.	3.9	242
22	Proteome Analysis of the Human Mitotic Spindle. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 35-43.	3.8	225
23	Absolute Quantitation of Proteins by a Combination of Acid Hydrolysis and Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2004, 76, 3569-3575.	6.5	23
24	Exploring the Functional Interactions between Aurora B, INCENP, and Survivin in Mitosis. <i>Molecular Biology of the Cell</i> , 2003, 14, 3325-3341.	2.1	466
25	Human TPX2 is required for targeting Aurora-A kinase to the spindle. <i>Journal of Cell Biology</i> , 2002, 158, 617-623.	5.2	516
26	Negative and positive ion matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and positive ion nano-electrospray ionization quadrupole ion trap mass spectrometry of peptidoglycan fragments isolated from various <i>Bacillus</i> species. <i>Journal of Mass Spectrometry</i> , 2001, 36, 124-139.	1.6	24
27	Quantitation of peptides and proteins by matrix-assisted laser desorption/ionization mass spectrometry using ^{18}O -labeled internal standards. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 1226-1232.	1.5	365
28	Analysis of different de-esterification mechanisms for pectin by enzymatic fingerprinting using endopectin lyase and endopolygalacturonase II from <i>A. Niger</i> . <i>Carbohydrate Research</i> , 2000, 327, 293-307.	2.3	192
29	The Intestinal T Cell Response to α -Gliadin in Adult Celiac Disease Is Focused on a Single Deamidated Glutamine Targeted by Tissue Transglutaminase. <i>Journal of Experimental Medicine</i> , 2000, 191, 603-612.	8.5	609
30	Quantitation of peptides and proteins by matrix-assisted laser desorption/ionization mass spectrometry using ^{18}O -labeled internal standards. , 2000, 14, 1226.		1
31	Quantitation of peptides and proteins by matrix-assisted laser desorption/ionization mass spectrometry using ^{18}O -labeled internal standards. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 1226-1232.	1.5	2
32	Sequencing of Partially Methyl-Esterified Oligogalacturonates by Tandem Mass Spectrometry and Its Use To Determine Pectinase Specificities. <i>Analytical Chemistry</i> , 1999, 71, 1421-1427.	6.5	88
33	Structural analysis of <i>Bacillus megaterium</i> KM spore peptidoglycan and its dynamics during germination. <i>Microbiology (United Kingdom)</i> , 1999, 145, 1033-1041.	1.8	34
34	Tissue transglutaminase selectively modifies gliadin peptides that are recognized by gut-derived T cells in celiac disease. <i>Nature Medicine</i> , 1998, 4, 713-717.	30.7	1,041
35	Electrophoresis-related protein modification: Alkylation of carboxy residues revealed by mass spectrometry. <i>Electrophoresis</i> , 1998, 19, 679-686.	2.4	45
36	Characterization of enzymatic pectin digests by matrix-assisted laser desorption/ionization mass spectrometry. , 1998, 33, 836-842.		62

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37	Nanospray-ESI low-energy CID and MALDI post-source decay for determination of O-glycosylation sites in MUC4 peptides. Journal of Mass Spectrometry, 1998, 33, 1124-1133.	1.6	31