

# Roman KÄrner

## List of Publications by Year in descending order

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37  
papers

6,228  
citations

218677

26  
h-index

377865

34  
g-index

37  
all docs

37  
docs citations

37  
times ranked

7537  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The Intestinal T Cell Response to Î±-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
3	Kinase-Selective Enrichment Enables Quantitative Phosphoproteomics of the Kinome across the Cell Cycle. <i>Molecular Cell</i> , 2008, 31, 438-448.	9.7	548
4	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
5	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
6	Quantitation of peptides and proteins by matrix-assisted laser desorption/ionization mass spectrometry using <sup>18</sup> O-labeled internal standards. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 1226-1232.	1.5	365
7	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
8	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
9	HURP Is a Ran-Importin Î²-Regulated Protein that Stabilizes Kinetochores Microtubules in the Vicinity of Chromosomes. <i>Current Biology</i> , 2006, 16, 731-742.	3.9	242
10	Proteome Analysis of the Human Mitotic Spindle. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 35-43.	3.8	225
11	The Plk1-dependent Phosphoproteome of the Early Mitotic Spindle. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.004457.	3.8	201
12	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
13	Failure of RQC machinery causes protein aggregation and proteotoxic stress. <i>Nature</i> , 2016, 531, 191-195.	27.8	185
14	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
15	Quantitative Analysis of the Human Spindle Phosphoproteome at Distinct Mitotic Stages. <i>Journal of Proteome Research</i> , 2009, 8, 4553-4563.	3.7	110
16	Exosomes mediate cell contact-independent ephrin-Eph signaling during axon guidance. <i>Journal of Cell Biology</i> , 2016, 214, 35-44.	5.2	105
17	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
18	Evaluation of the Low-Specificity Protease Elastase for Large-Scale Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2008, 80, 9526-9533.	6.5	71

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19	Quantitative Mass Spectrometry Analysis Reveals Similar Substrate Consensus Motif for Human Mps1 Kinase and Plk1. PLoS ONE, 2011, 6, e18793.	2.5	65
20	Characterization of enzymatic pectin digests by matrix-assisted laser desorption/ionization mass spectrometry. , 1998, 33, 836-842.		62
21	Comparative conservation analysis of the human mitotic phosphoproteome. Bioinformatics, 2008, 24, 1426-1432.	4.1	48
22	Quantitative Site-specific Phosphorylation Dynamics of Human Protein Kinases during Mitotic Progression. Molecular and Cellular Proteomics, 2010, 9, 1167-1181.	3.8	46
23	Electrophoresis-related protein modification: Alkylation of carboxy residues revealed by mass spectrometry. Electrophoresis, 1998, 19, 679-686.	2.4	45
24	The Hsp70 Chaperone System Stabilizes a Thermo-sensitive Subproteome in E.Âcoli. Cell Reports, 2019, 28, 1335-1345.e6.	6.4	37
25	Structural analysis of Bacillus megaterium KM spore peptidoglycan and its dynamics during germination. Microbiology (United Kingdom), 1999, 145, 1033-1041.	1.8	34
26	Phosphorylation-dependent Binding of Cyclin B1 to a Cdc6-like Domain of Human Separase. Journal of Biological Chemistry, 2008, 283, 816-823.	3.4	32
27	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
28	High capacity of the endoplasmic reticulum to prevent secretion and aggregation of amyloidogenic proteins. EMBO Journal, 2018, 37, 337-350.	7.8	29
29	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 Bacillus species. Journal of Mass Spectrometry, 2001, 36, 124-139.	1.6	24
30	Absolute Quantitation of Proteins by a Combination of Acid Hydrolysis and Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. Analytical Chemistry, 2004, 76, 3569-3575.	6.5	23
31	Chaperone Function of Hgh1 in the Biogenesis of Eukaryotic Elongation Factor 2. Molecular Cell, 2019, 74, 88-100.e9.	9.7	18
32	An inventory of interactors of the human HSP60/HSP10 chaperonin in the mitochondrial matrix space. Cell Stress and Chaperones, 2020, 25, 407-416.	2.9	18
33	Uncovering the Molecular Machinery of the Human Spindleâ€”An Integration of Wet and Dry Systems Biology. PLoS ONE, 2012, 7, e31813.	2.5	14
34	Absolute Quantitation of Proteins by Acid Hydrolysis Combined with Amino Acid Detection by Mass Spectrometry. Methods in Molecular Biology, 2012, 828, 115-120.	0.9	7
35	Quantitation of peptides and proteins by matrix-assisted laser desorption/ionization mass spectrometry using <sup>18</sup> O-labeled internal standards. Rapid Communications in Mass Spectrometry, 2000, 14, 1226-1232.	1.5	2
36	Quantitation of peptides and proteins by matrix-assisted laser desorption/ionization mass spectrometry using <sup>18</sup> O-labeled internal standards. , 2000, 14, 1226.		1

#	ARTICLE	IF	CITATIONS
37	Absolute Quantitation of Proteins by Acid Hydrolysis Combined with Amino Acid Detection by Mass Spectrometry. Methods in Molecular Biology, 2019, 2030, 11-16.	0.9	0