

Markus M Rinschen

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

3,259
citations

185998

28
h-index

174990

52
g-index

83
all docs

83
docs citations

83
times ranked

4641
citing authors

#	ARTICLE	IF	CITATIONS
1	MAGED2 controls vasopressin-induced aquaporin-2 expression in collecting duct cells. <i>Journal of Proteomics</i> , 2022, 252, 104424.	1.2	1
2	Super-Resolution Imaging of the Filtration Barrier Suggests a Role for Podocin R229Q in Genetic Predisposition to Glomerular Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 138-154.	3.0	7
3	The calcium-sensing receptor stabilizes podocyte function in proteinuric humans and mice. <i>Kidney International</i> , 2022, 101, 1186-1199.	2.6	6
4	Consensus draft of the native mouse podocyte-ome. <i>American Journal of Physiology - Renal Physiology</i> , 2022, 323, F182-F197.	1.3	6
5	Accelerated lysine metabolism conveys kidney protection in salt-sensitive hypertension. <i>Nature Communications</i> , 2022, 13, .	5.8	18
6	The tissue proteome in the multi-omic landscape of kidney disease. <i>Nature Reviews Nephrology</i> , 2021, 17, 205-219.	4.1	31
7	MANTI: Automated Annotation of Protein N-Termini for Rapid Interpretation of N-Terminome Data Sets. <i>Analytical Chemistry</i> , 2021, 93, 5596-5605.	3.2	9
8	Proteolysis and inflammation of the kidney glomerulus. <i>Cell and Tissue Research</i> , 2021, 385, 489-500.	1.5	4
9	A stressed barrier left behind: stochastic podocyte ablation triggers secondary injury. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 320, F866-F869.	1.3	2
10	Tripartite Separation of Glomerular Cell Types and Proteomes from Reporter-Free Mice. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2175-2193.	3.0	16
11	Maintaining proteostasis under mechanical stress. <i>EMBO Reports</i> , 2021, 22, e52507.	2.0	28
12	Specific disruption of calcineurin-signaling in the distal convoluted tubule impacts the transcriptome and proteome, and causes hypomagnesemia and metabolic acidosis. <i>Kidney International</i> , 2021, 100, 850-869.	2.6	16
13	Cognitive analysis of metabolomics data for systems biology. <i>Nature Protocols</i> , 2021, 16, 1376-1418.	5.5	13
14	Viewing Cortical Collecting Duct Function Through Phenotype-guided Single-Tubule Proteomics. <i>Function</i> , 2020, 1, zqaa007.	1.1	2
15	The proteomic landscape of small urinary extracellular vesicles during kidney transplantation. <i>Journal of Extracellular Vesicles</i> , 2020, 10, e12026.	5.5	30
16	A molecular mechanism explaining albuminuria in kidney disease. <i>Nature Metabolism</i> , 2020, 2, 461-474.	5.1	99
17	The ubiquitin-conjugating enzyme UBE2K determines neurogenic potential through histone H3 in human embryonic stem cells. <i>Communications Biology</i> , 2020, 3, 262.	2.0	18
18	Cloud-based archived metabolomics data: A resource for in-source fragmentation/annotation, meta-analysis and systems biology. <i>Analytical Science Advances</i> , 2020, 1, 70-80.	1.2	3

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19	Injured Podocytes Are Sensitized to Angiotensin II-Induced Calcium Signaling. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 532-542.	3.0	23
20	Enhanced in-Source Fragmentation Annotation Enables Novel Data Independent Acquisition and Autonomous METLIN Molecular Identification. <i>Analytical Chemistry</i> , 2020, 92, 6051-6059.	3.2	42
21	PKA-Independent vasopressin signaling in renal collecting duct. <i>FASEB Journal</i> , 2020, 34, 6129-6146.	0.2	24
22	Proteome Analysis of Isolated Podocytes Reveals Stress Responses in Glomerular Sclerosis. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 544-559.	3.0	23
23	An integrative approach to cisplatin chronic toxicities in mice reveals importance of organic cation-transporter-dependent protein networks for renoprotection. <i>Archives of Toxicology</i> , 2019, 93, 2835-2848.	1.9	16
24	Single glomerular proteomics: A novel tool for translational glomerular cell biology. <i>Methods in Cell Biology</i> , 2019, 154, 1-14.	0.5	6
25	A knowledge-guided kidney cell census-reconciling bulk omics with cellular heterogeneity?. <i>Kidney International</i> , 2019, 95, 733-735.	2.6	1
26	Big science and big data in nephrology. <i>Kidney International</i> , 2019, 95, 1326-1337.	2.6	56
27	Ubiquitin C-terminal hydrolase L1 (UCH-L1) loss causes neurodegeneration by altering protein turnover in the first postnatal weeks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7963-7972.	3.3	36
28	The RNA-Protein Interactome of Differentiated Kidney Tubular Epithelial Cells. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 564-576.	3.0	16
29	Identification of bioactive metabolites using activity metabolomics. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 353-367.	16.1	602
30	The authors reply. <i>Kidney International</i> , 2019, 96, 1422-1423.	2.6	0
31	Metabolic rewiring of the hypertensive kidney. <i>Science Signaling</i> , 2019, 12, .	1.6	40
32	Bevacizumab-associated glomerular microangiopathy. <i>Modern Pathology</i> , 2019, 32, 684-700.	2.9	37
33	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. <i>Kidney International</i> , 2019, 95, 333-349.	2.6	55
34	Quantification of molecular heterogeneity in kidney tissue by targeted proteomics. <i>Journal of Proteomics</i> , 2019, 193, 85-92.	1.2	15
35	Autosomal Tubulointerstitial Kidney Disease-MUC1 Type: Differential Proteomics Suggests that Mutated MUC1 (insC) Affects Vesicular Transport in Renal Epithelial Cells. <i>Proteomics</i> , 2018, 18, e1700456.	1.3	13
36	Single-nephron proteomes connect morphology and function in proteinuric kidney disease. <i>Kidney International</i> , 2018, 93, 1308-1319.	2.6	49

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37	Proline-dependent and basophilic kinases phosphorylate human TRPC6 at serine 14 to control channel activity through increased membrane expression. <i>FASEB Journal</i> , 2018, 32, 208-219.	0.2	6
38	From Molecules to Mechanisms: Functional Proteomics and Its Application to Renal Tubule Physiology. <i>Physiological Reviews</i> , 2018, 98, 2571-2606.	13.1	27
39	The podocyte protease web: uncovering the gatekeepers of glomerular disease. <i>American Journal of Physiology - Renal Physiology</i> , 2018, 315, F1812-F1816.	1.3	17
40	A Multi-layered Quantitative In Vivo Expression Atlas of the Podocyte Unravels Kidney Disease Candidate Genes. <i>Cell Reports</i> , 2018, 23, 2495-2508.	2.9	81
41	A Single-Cell Transcriptome Atlas of the Mouse Glomerulus. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 2060-2068.	3.0	137
42	Targeted deletion of the AAA-ATPase Ruvbl1 in mice disrupts ciliary integrity and causes renal disease and hydrocephalus. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-17.	3.2	22
43	Urine-derived cells: a promising diagnostic tool in Fabry disease patients. <i>Scientific Reports</i> , 2018, 8, 11042.	1.6	22
44	Protein half-life determines expression of proteostatic networks in podocyte differentiation. <i>FASEB Journal</i> , 2018, 32, 4696-4713.	0.2	15
45	Mechanism suppressing H3K9 trimethylation in pluripotent stem cells and its demise by polyQ-expanded huntingtin mutations. <i>Human Molecular Genetics</i> , 2018, 27, 4117-4134.	1.4	21
46	mTOR Regulates Endocytosis and Nutrient Transport in Proximal Tubular Cells. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 230-241.	3.0	79
47	Construction of a viral T2A-peptide based knock-in mouse model for enhanced Cre recombinase activity and fluorescent labeling of podocytes. <i>Kidney International</i> , 2017, 91, 1510-1517.	2.6	9
48	YAP-mediated mechanotransduction determines the podocyte's response to damage. <i>Science Signaling</i> , 2017, 10, .	1.6	61
49	N-Degradomic Analysis Reveals a Proteolytic Network Processing the Podocyte Cytoskeleton. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 2867-2878.	3.0	41
50	The ciliary membrane-associated proteome reveals actin-binding proteins as key components of cilia. <i>EMBO Reports</i> , 2017, 18, 1521-1535.	2.0	119
51	Quantitative deep mapping of the cultured podocyte proteome uncovers shifts in proteostatic mechanisms during differentiation. <i>American Journal of Physiology - Cell Physiology</i> , 2016, 311, C404-C417.	2.1	31
52	Cysteine S-Glutathionylation Promotes Stability and Activation of the Hippo Downstream Effector Transcriptional Co-activator with PDZ-binding Motif (TAZ). <i>Journal of Biological Chemistry</i> , 2016, 291, 11596-11607.	1.6	28
53	Polyhydramnios, Transient Antenatal Bartter's Syndrome, and <i>MAGED2</i> Mutations. <i>New England Journal of Medicine</i> , 2016, 374, 1853-1863.	13.9	148
54	The ubiquitin ligase Ubr4 controls stability of podocin/MEC-2 supercomplexes. <i>Human Molecular Genetics</i> , 2016, 25, 1328-1344.	1.4	45

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55	Jade-1S phosphorylation induced by CK1 β contributes to cell cycle progression. <i>Cell Cycle</i> , 2016, 15, 1034-1045.	1.3	9
56	Three-layered proteomic characterization of a novel <i>ACTN4</i> mutation unravels its pathogenic potential in FSGS. <i>Human Molecular Genetics</i> , 2016, 25, 1152-1164.	1.4	36
57	A flexible, multilayered protein scaffold maintains the slit in between glomerular podocytes. <i>JCI Insight</i> , 2016, 1, .	2.3	69
58	Altered lipid metabolism in the aging kidney identified by three layered omic analysis. <i>Aging</i> , 2016, 8, 441-454.	1.4	46
59	Proteomic analysis of the kidney filtration barrier—Problems and perspectives. <i>Proteomics - Clinical Applications</i> , 2015, 9, 1053-1068.	0.8	19
60	(Sugar-) Sweet Biomarkers? Clinical Proteomics Enters Sepsis Research*. <i>Critical Care Medicine</i> , 2015, 43, 2245-2246.	0.4	1
61	Water transport running deep. Focus on “Deep proteomic profiling of vasopressin-sensitive collecting duct cells”. <i>American Journal of Physiology - Cell Physiology</i> , 2015, 309, C783-C784.	2.1	2
62	WT1 targets <i>Gas1</i> to maintain nephron progenitor cells by modulating FGF signals. <i>Development (Cambridge)</i> , 2015, 142, 1254-1266.	1.2	42
63	Comparative phosphoproteomic analysis of mammalian glomeruli reveals conserved podocin C-terminal phosphorylation as a determinant of slit diaphragm complex architecture. <i>Proteomics</i> , 2015, 15, 1326-1331.	1.3	21
64	Casein Kinase 1 β Phosphorylates the Wnt Regulator Jade-1 and Modulates Its Activity. <i>Journal of Biological Chemistry</i> , 2014, 289, 26344-26356.	1.6	19
65	The Cleaved Cytoplasmic Tail of Polycystin-1 Regulates Src-Dependent STAT3 Activation. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 1737-1748.	3.0	61
66	Phosphoproteomic Analysis Reveals Regulatory Mechanisms at the Kidney Filtration Barrier. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 1509-1522.	3.0	40
67	Label-free quantitative proteomic analysis of the YAP/TAZ interactome. <i>American Journal of Physiology - Cell Physiology</i> , 2014, 306, C805-C818.	2.1	59
68	Vasopressin-2 Receptor Signaling and Autosomal Dominant Polycystic Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 1140-1147.	3.0	33
69	A Disease-causing Mutation Illuminates the Protein Membrane Topology of the Kidney-expressed Prohibitin Homology (PHB) Domain Protein Podocin. <i>Journal of Biological Chemistry</i> , 2014, 289, 11262-11271.	1.6	16
70	Characterization of a short isoform of the kidney protein podocin in human kidney. <i>BMC Nephrology</i> , 2013, 14, 102.	0.8	18
71	Loss of the <i>Birc6</i> gene product folliculin induces longevity in a hypoxia-inducible factor-dependent manner. <i>Aging Cell</i> , 2013, 12, 593-603.	3.0	12
72	Quantitative Proteomics Identifies Vasopressin-Responsive Nuclear Proteins in Collecting Duct Cells. <i>Journal of the American Society of Nephrology: JASN</i> , 2012, 23, 1008-1018.	3.0	50

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73	Different effects of CsA and FK506 on aquaporin-2 abundance in rat primary cultured collecting duct cells. <i>Pflügers Archiv European Journal of Physiology</i> , 2011, 462, 611-622.	1.3	13
74	Cyclosporin-A Induced Toxicity in Rat Renal Collecting Duct Cells: Interference with Enhanced Hypertonicity Induced Apoptosis. <i>Cellular Physiology and Biochemistry</i> , 2010, 26, 887-900.	1.1	11
75	Quantitative phosphoproteomic analysis reveals cAMP/vasopressin-dependent signaling pathways in native renal thick ascending limb cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15653-15658.	3.3	107
76	Quantitative phosphoproteomic analysis reveals vasopressin V2-receptor-dependent signaling pathways in renal collecting duct cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3882-3887.	3.3	155
77	Vasopressin increases phosphorylation of Ser84 and Ser486 in Slc14a2 collecting duct urea transporters. <i>American Journal of Physiology - Renal Physiology</i> , 2010, 299, F559-F567.	1.3	28
78	Systems-level analysis of cell-specific <i>AQP2</i> gene expression in renal collecting duct. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2441-2446.	3.3	117