Mark A Knepper

List of Publications by Year
in descending order

221 papers	17,901 citations	12330 69 h-index	15266 126 g-index
228 all docs	228 docs citations	228 times ranked	14407 citing authors

#	Article	IF	Citations
1	Systems Biology of the Vasopressin V2 Receptor: New Tools for Discovery of Molecular Actions of a GPCR. Annual Review of Pharmacology and Toxicology, 2022, 62, 595-616.	9.4	5
2	â€œADPKD-omicsâ€ determinants of cyclic AMP levels in renal epithelial cells. Kidney International, 2022, 101, 47-62.	5.2	5
3	Fortyâ€five Vasopressinâ€Regulated Phosphoproteins Involved in Control of Collecting Duct Water Transport. FASEB Journal, 2022, 36, .	0.5	0
4	Bayesian analysis of dynamic phosphoproteomic data identifies protein kinases mediating GPCR responses. Cell Communication and Signaling, 2022, 20, .	6.5	7
5	Maurice B. Burg (1931â€"2022), discoverer of kidney transport mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	0
6	Phosphoproteomic Identification of Vasopressin/cAMP/Protein Kinase Aâ€"Dependent Signaling in Kidney. Molecular Pharmacology, 2021, 99, 358-369.	2.3	15
7	Transcriptomes of Major Proximal Tubule Cell Culture Models. Journal of the American Society of Nephrology: JASN, 2021, 32, 86-97.	6.1	35
8	Phosphoproteomic identification of vasopressinâ€regulated protein kinases in collecting duct cells. British Journal of Pharmacology, 2021, 178, 1426-1444.	5.4	15
9	A Comprehensive Map of mRNAs and Their Isoforms across All 14 Renal Tubule Segments of Mouse. Journal of the American Society of Nephrology: JASN, 2021, 32, 897-912.	6.1	110
10	Targeted Single-Cell RNA-seq Identifies Minority Cell Types of Kidney Distal Nephron. Journal of the American Society of Nephrology: JASN, 2021, 32, 886-896.	6.1	67
11	Urinary extracellular vesicles: A position paper by the Urine Task Force of the International Society for Extracellular Vesicles. Journal of Extracellular Vesicles, 2021, 10, e12093.	12.2	182
12	GPCRâ€omics of the Nephron: Mapping Receptors Along the Renal Tubule. FASEB Journal, 2021, 35, .	0.5	0
13	Landscape of GPCR expression along the mouse nephron. American Journal of Physiology - Renal Physiology, 2021, 321, F50-F68.	2.7	11
14	â€œSLC-omicsâ€• of the kidney: solute transporters along the nephron. American Journal of Physiology - Cell Physiology, 2021, 321, C507-C518.	4.6	22
15	Bayesian identification of candidate transcription factors for the regulation of <i>Aqp2</i> gene expression. American Journal of Physiology - Renal Physiology, 2021, 321, F389-F401.	2.7	12
16	CRISPR-Cas9/phosphoproteomics identifies multiple noncanonical targets of myosin light chain kinase. American Journal of Physiology - Renal Physiology, 2020, 318, F600-F616.	2.7	21
17	Does SARS-CoV-2 Infect the Kidney?. Journal of the American Society of Nephrology: JASN, 2020, 31, 2746-2748.	6.1	43
18	Protein kinase A catalytic-Î± and catalytic-Î² proteins have nonredundant regulatory functions. American Journal of Physiology - Renal Physiology, 2020, 319, F848-F862.	2.7	12

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19	NGS-Integrator: An efficient tool for combining multiple NGS data tracks using minimum Bayesâ€™ factors. BMC Genomics, 2020, 21, 806.	2.8	3
20	An integrative proteogenomics approach reveals peptides encoded by annotated lincRNA in the mouse kidney inner medulla. Physiological Genomics, 2020, 52, 485-491.	2.3	6
21	Quantitative Proteomics of All 14 Renal Tubule Segments in Rat. Journal of the American Society of Nephrology: JASN, 2020, 31, 1255-1266.	6.1	99
22	PKAâ€independent vasopressin signaling in renal collecting duct. FASEB Journal, 2020, 34, 6129-6146.	0.5	24
23	PTM-Logo: a program for generation of sequence logos based on position-specific background amino-acid probabilities. Bioinformatics, 2019, 35, 5313-5314.	4.1	11
24	Phosphoproteomic identification of vasopressin V2 receptor-dependent signaling in the renal collecting duct. American Journal of Physiology - Renal Physiology, 2019, 317, F789-F804.	2.7	22
25	Renal-Tubule Epithelial Cell Nomenclature for Single-Cell RNA-Sequencing Studies. Journal of the American Society of Nephrology: JASN, 2019, 30, 1358-1364.	6.1	79
26	Sickle cell disease upâ€regulates vasopressin, aquaporin 2, urea transporter A1, Naâ€Kâ€Cl cotransporter 2, and epithelial Na channels in the mouse kidney medulla despite compromising urinary concentration ability. Physiological Reports, 2019, 7, e14066.	1.7	6
27	RNA-Seq and protein mass spectrometry in microdissected kidney tubules reveal signaling processes initiating lithium-induced nephrogenic diabetes insipidus. Kidney International, 2019, 96, 363-377.	5.2	27
28	Representation and relative abundance of cell-type selective markers in whole-kidney RNA-Seq data. Kidney International, 2019, 95, 787-796.	5.2	89
29	Phosphorylation Changes in Response to Kinase Inhibitor H89 in PKA-Null Cells. Scientific Reports, 2019, 9, 2814.	3.3	24
30	Prioritizing Functional Goals as We Rebuild the Kidney. Journal of the American Society of Nephrology: JASN, 2019, 30, 2287-2288.	6.1	5
31	AbDesigner3D: a structure-guided tool for peptide-based antibody production. Bioinformatics, 2018, 34, 2158-2160.	4.1	3
32	Single-tubule RNA-Seq uncovers signaling mechanisms that defend against hyponatremia in SIADH. Kidney International, 2018, 93, 128-146.	5.2	23
33	Reply to Edemir: Physiological regulation and single-cell RNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E351-E352.	7.1	1
34	Genome-Wide Mapping of DNA Accessibility and Binding Sites for CREB and C/EBPÎ² in Vasopressin-Sensitive Collecting Duct Cells. Journal of the American Society of Nephrology: JASN, 2018, 29, 1490-1500.	6.1	29
35	Identification of UT-A1- and AQP2-interacting proteins in rat inner medullary collecting duct. American Journal of Physiology - Cell Physiology, 2018, 314, C99-C117.	4.6	15
36	Sequence-based searching of custom proteome and transcriptome databases. Physiological Reports, 2018, 6, e13846.	1.7	0

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37	Modulation of Cl ^{â^’} signaling and ion transport by recruitment of kinases and phosphatases mediated by the regulatory protein IRBIT. Science Signaling, 2018, 11, .	3.6	16
38	From Molecules to Mechanisms: Functional Proteomics and Its Application to Renal Tubule Physiology. Physiological Reviews, 2018, 98, 2571-2606.	28.8	27
39	Proteomic determination of the lysine acetylome and phosphoproteome in the rat native inner medullary collecting duct. Physiological Genomics, 2018, 50, 669-679.	2.3	8
40	Protein Mass Spectrometry Made Simple. Journal of the American Society of Nephrology: JASN, 2018, 29, 1585-1587.	6.1	2
41	Flow resistance along the rat renal tubule. American Journal of Physiology - Renal Physiology, 2018, 315, F1398-F1405.	2.7	18
42	Proteomic Determination of the Rat Native Inner Medullary Collecting Duct Lysine Acetylome and Phosphoproteome. FASEB Journal, 2018, 32, 850.3.	0.5	0
43	Roflumilast and aquaporinâ€2 regulation in rat renal inner medullary collecting duct. Physiological Reports, 2017, 5, e13121.	1.7	3
44	Serine/threonine phosphatases and aquaporin-2 regulation in renal collecting duct. American Journal of Physiology - Renal Physiology, 2017, 312, F84-F95.	2.7	9
45	From 20th century metabolic wall charts to 21st century systems biology: database of mammalian metabolic enzymes. American Journal of Physiology - Renal Physiology, 2017, 312, F533-F542.	2.7	21
46	Vasopressin-induced serine 269 phosphorylation reduces Sipa1l1 (signal-induced) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 Td (prolifera 2017, 292, 7984-7993.	3.4	23
47	Data integration in physiology using Bayesâ€™ rule and minimum Bayesâ€™ factors: deubiquitylating enzymes in the renal collecting duct. Physiological Genomics, 2017, 49, 151-159.	2.3	9
48	Identification of Î²-catenin-interacting proteins in nuclear fractions of native rat collecting duct cells. American Journal of Physiology - Renal Physiology, 2017, 313, F30-F46.	2.7	13
49	Transcriptomes of major renal collecting duct cell types in mouse identified by single-cell RNA-seq. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9989-E9998.	7.1	198
50	Systems-level identification of PKA-dependent signaling in epithelial cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8875-E8884.	7.1	100
51	Dynamic regulation of lysine acetylation: the balance between acetyltransferase and deacetylase activities. American Journal of Physiology - Renal Physiology, 2017, 313, F842-F846.	2.7	34
52	Expression and functional implications of the renal apelinergic system in rodents. PLoS ONE, 2017, 12, e0183094.	2.5	17
53	Comprehensive database of human E3 ubiquitin ligases: application to aquaporin-2 regulation. Physiological Genomics, 2016, 48, 502-512.	2.3	75
54	Proteomic profiling of nuclear fractions from native renal inner medullary collecting duct cells. Physiological Genomics, 2016, 48, 154-166.	2.3	13

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55	Systems-level analysis reveals selective regulation of Aqp2 gene expression by vasopressin. Scientific Reports, 2016, 6, 34863.	3.3	35
56	BIG: a large-scale data integration tool for renal physiology. American Journal of Physiology - Renal Physiology, 2016, 311, F787-F792.	2.7	20
57	Deubiquitylation of Protein Cargo Is Not an Essential Step in Exosome Formation. Molecular and Cellular Proteomics, 2016, 15, 1556-1571.	3.8	49
58	Peptide Labeling Using Isobaric Tagging Reagents for Quantitative Phosphoproteomics. Methods in Molecular Biology, 2016, 1355, 53-70.	0.9	10
59	Deep proteomic profiling of vasopressin-sensitive collecting duct cells. I. Virtual Western blots and molecular weight distributions. American Journal of Physiology - Cell Physiology, 2015, 309, C785-C798.	4.6	27
60	Deep Sequencing in Microdissected Renal Tubules Identifies Nephron Segmentâ€“Specific Transcriptomes. Journal of the American Society of Nephrology: JASN, 2015, 26, 2669-2677.	6.1	455
61	Deep proteomic profiling of vasopressin-sensitive collecting duct cells. II. Bioinformatic analysis of vasopressin signaling. American Journal of Physiology - Cell Physiology, 2015, 309, C799-C812.	4.6	32
62	Systems biology of diuretic resistance. Journal of Clinical Investigation, 2015, 125, 1793-1795.	8.2	13
63	Molecular Physiology of Water Balance. New England Journal of Medicine, 2015, 372, 1349-1358.	27.0	210
64	Activation of EP3 receptors suppresses COXâ€2 in thick ascending limb (TAL) and inhibits water excretion. FASEB Journal, 2015, 29, 809.21.	0.5	0
65	Integrated Design of Antibodies for Systems Biology Using Ab Designer. Journal of Proteomics and Bioinformatics, 2014, 07, 088-94.	0.4	2
66	Early targets of lithium in rat kidney inner medullary collecting duct include p38 and ERK1/2. Kidney International, 2014, 86, 757-767.	5.2	44
67	Use of LC-MS/MS and Bayes' theorem to identify protein kinases that phosphorylate aquaporin-2 at Ser²⁵⁶. American Journal of Physiology - Cell Physiology, 2014, 307, C123-C139.	4.6	40
68	Letter to the editor: â€œSystems biology versus reductionism in cell physiologyâ€. American Journal of Physiology - Cell Physiology, 2014, 307, C308-C309.	4.6	1
69	Tolvaptan as a tool in renal physiology. American Journal of Physiology - Renal Physiology, 2014, 306, F359-F366.	2.7	24
70	Global analysis of the effects of the V2 receptor antagonist satavaptan on protein phosphorylation in collecting duct. American Journal of Physiology - Renal Physiology, 2014, 306, 410-421.	2.7	13
71	Proteomic pearl diving versus systems biology in cell physiology. Focus on â€œProteomic mapping of proteins released during necrosis and apoptosis from cultured neonatal cardiac myocytesâ€. American Journal of Physiology - Cell Physiology, 2014, 306, C634-C635.	4.6	3
72	Four-dimensional MRI of renal function in the developing mouse. NMR in Biomedicine, 2014, 27, 1094-1102.	2.8	5

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73	A knowledge base of vasopressin actions in the kidney. American Journal of Physiology - Renal Physiology, 2014, 307, F747-F755.	2.7	10
74	Exploiting thread-level and instruction-level parallelism to cluster mass spectrometry data using multicore architectures. Network Modeling Analysis in Health Informatics and Bioinformatics, 2014, 3, 54.	2.1	1
75	Database of osmoregulated proteins in mammalian cells. Physiological Reports, 2014, 2, e12180.	1.7	12
76	Quantitative apical membrane proteomics reveals vasopressin-induced actin dynamics in collecting duct cells. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17119-17124.	7.1	58
77	Vasopressin and the regulation of aquaporin-2. Clinical and Experimental Nephrology, 2013, 17, 751-764.	1.6	102
78	Vasopressin inhibits apoptosis in renal collecting duct cells. American Journal of Physiology - Renal Physiology, 2013, 304, F177-F188.	2.7	29
79	Urea channel inhibitors: a new functional class of aquaretics. Kidney International, 2013, 83, 991-993.	5.2	21
80	Proteome-Wide Measurement of Protein Half-Lives and Translation Rates in Vasopressin-Sensitive Collecting Duct Cells. Journal of the American Society of Nephrology: JASN, 2013, 24, 1793-1805.	6.1	93
81	Endogenous Carbamylation of Renal Medullary Proteins. PLoS ONE, 2013, 8, e82655.	2.5	13
82	Identifying protein kinase target preferences using mass spectrometry. American Journal of Physiology - Cell Physiology, 2012, 303, C715-C727.	4.6	58
83	An online tool for calculation of free-energy balance for the renal inner medulla. American Journal of Physiology - Renal Physiology, 2012, 303, F366-F372.	2.7	3
84	Quantitative phosphoproteomics in nuclei of vasopressin-sensitive renal collecting duct cells. American Journal of Physiology - Cell Physiology, 2012, 303, C1006-C1020.	4.6	26
85	Large-scale phosphotyrosine proteomic profiling of rat renal collecting duct epithelium reveals predominance of proteins involved in cell polarity determination. American Journal of Physiology - Cell Physiology, 2012, 302, C27-C45.	4.6	11
86	Gene expression databases for kidney epithelial cells. American Journal of Physiology - Renal Physiology, 2012, 302, F401-F407.	2.7	27
87	NHLBI-<i>AbDesigner</i>: an online tool for design of peptide-directed antibodies. American Journal of Physiology - Cell Physiology, 2012, 302, C154-C164.	4.6	33
88	An efficient dynamic programming algorithm for phosphorylation site assignment of large-scale mass spectrometry data. , 2012, , 618-625.		13
89	Dynamics of the G Protein-coupled Vasopressin V2 Receptor Signaling Network Revealed by Quantitative Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, M111.014613.	3.8	70
90	Systems biology in physiology: the vasopressin signaling network in kidney. American Journal of Physiology - Cell Physiology, 2012, 303, C1115-C1124.	4.6	26

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91	Aquaporinâ€2 regulation in health and disease. Veterinary Clinical Pathology, 2012, 41, 455-470.	0.7	51
92	Quantitative Proteomics Identifies Vasopressin-Responsive Nuclear Proteins in Collecting Duct Cells. Journal of the American Society of Nephrology: JASN, 2012, 23, 1008-1018.	6.1	50
93	Application of systems biology principles to protein biomarker discovery: Urinary exosomal proteome in renal transplantation. Proteomics - Clinical Applications, 2012, 6, 268-278.	1.6	52
94	Identification of proteins regulated by 24â€hour aldosterone treatment in late distal convoluted tubules, connecting tubules and initial cortical collecting ducts. FASEB Journal, 2012, 26, 885.9.	0.5	0
95	Exosomes and the kidney: prospects for diagnosis and therapy of renal diseases. Kidney International, 2011, 80, 1138-1145.	5.2	182
96	Quantitative Protein and mRNA Profiling Shows Selective Post-Transcriptional Control of Protein Expression by Vasopressin in Kidney Cells. Molecular and Cellular Proteomics, 2011, 10, M110.004036.	3.8	51
97	Phosphoproteomics of vasopressin signaling in the kidney. Expert Review of Proteomics, 2011, 8, 157-163.	3.0	18
98	Large-scale phosphoproteomic analysis of membrane proteins in renal proximal and distal tubule. American Journal of Physiology - Cell Physiology, 2011, 300, C755-C770.	4.6	37
99	Mappingâ€based temporal pattern mining algorithm (MTPMA) identifies unique clusters of phosphopeptides regulated by vasopressin in collecting duct. FASEB Journal, 2011, 25, 921.4.	0.5	0
100	Proteomic profiling of nuclei from native renal inner medullary collecting duct cells using LC-MS/MS. Physiological Genomics, 2010, 40, 167-183.	2.3	43
101	Phosphoproteomic Profiling Reveals Vasopressin-Regulated Phosphorylation Sites in Collecting Duct. Journal of the American Society of Nephrology: JASN, 2010, 21, 303-315.	6.1	54
102	Quantitative analysis of aquaporin-2 phosphorylation. American Journal of Physiology - Renal Physiology, 2010, 298, F1018-F1023.	2.7	51
103	Quantitative phosphoproteomic analysis reveals cAMP/vasopressin-dependent signaling pathways in native renal thick ascending limb cells. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15653-15658.	7.1	107
104	Quantitative phosphoproteomic analysis reveals vasopressin V2-receptorâ€"dependent signaling pathways in renal collecting duct cells. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3882-3887.	7.1	155
105	Vasopressin increases phosphorylation of Ser84 and Ser486 in Slc14a2 collecting duct urea transporters. American Journal of Physiology - Renal Physiology, 2010, 299, F559-F567.	2.7	28
106	Serine 269 phosphorylated aquaporin-2 is targeted to the apical membrane of collecting duct principal cells. Kidney International, 2009, 75, 295-303.	5.2	124
107	Role of multiple phosphorylation sites in the COOH-terminal tail of aquaporin-2 for water transport: evidence against channel gating. American Journal of Physiology - Renal Physiology, 2009, 296, F649-F657.	2.7	66
108	Common Sense Approaches to Urinary Biomarker Study Design. Journal of the American Society of Nephrology: JASN, 2009, 20, 1175-1178.	6.1	41

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109	Molecular coin slots for urea. Nature, 2009, 462, 733-734.	27.8	16
110	Systems-level analysis of cell-specific <i>AQP2</i> gene expression in renal collecting duct. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2441-2446.	7.1	117
111	Large-Scale Proteomics and Phosphoproteomics of Urinary Exosomes. Journal of the American Society of Nephrology: JASN, 2009, 20, 363-379.	6.1	634
112	A selective EP4 PGE2 receptor agonist alleviates disease in a new mouse model of X-linked nephrogenic diabetes insipidus. Journal of Clinical Investigation, 2009, 119, 3115-3126.	8.2	99
113	Taking aim at shotgun phosphoproteomics. Analytical Biochemistry, 2008, 375, 1-10.	2.4	42
114	Courier service for ammonia. Nature, 2008, 456, 336-337.	27.8	4
115	Vasopressin: friend or foe?. Nature Medicine, 2008, 14, 14-16.	30.7	16
116	Proteomic Approaches for the Study of Cell Signaling in the Renal Collecting Duct. , 2008, 160, 172-185.		8
117	Vasopressin-stimulated Increase in Phosphorylation at Ser269 Potentiates Plasma Membrane Retention of Aquaporin-2. Journal of Biological Chemistry, 2008, 283, 24617-24627.	3.4	222
118	Akt and ERK1/2 pathways are components of the vasopressin signaling network in rat native IMCD. American Journal of Physiology - Renal Physiology, 2008, 295, F1030-F1043.	2.7	71
119	Transcriptional profiling of native inner medullary collecting duct cells from rat kidney. Physiological Genomics, 2008, 32, 229-253.	2.3	93
120	Roles of basolateral solute uptake via NKCC1 and of myosin II in vasopressin-induced cell swelling in inner medullary collecting duct. American Journal of Physiology - Renal Physiology, 2008, 295, F192-F201.	2.7	29
121	Treating lithium-induced nephrogenic diabetes insipidus with a COX-2 inhibitor improves polyuria via upregulation of AQP2 and NKCC2. American Journal of Physiology - Renal Physiology, 2008, 294, F702-F709.	2.7	48
122	LC-MS/MS analysis of differential centrifugation fractions from native inner medullary collecting duct of rat. American Journal of Physiology - Renal Physiology, 2008, 295, F1799-F1806.	2.7	33
123	Acute regulation of aquaporin-2 phosphorylation at Ser-264 by vasopressin. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3134-3139.	7.1	135
124	Proteomic analysis of lithium-induced nephrogenic diabetes insipidus: Mechanisms for aquaporin 2 down-regulation and cellular proliferation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3634-3639.	7.1	110
125	Urinary exosomes: is there a future?. Nephrology Dialysis Transplantation, 2008, 23, 1799-1801.	0.7	58
126	COX-2 activity transiently contributes to increased water and NaCl excretion in the polyuric phase after release of ureteral obstruction. American Journal of Physiology - Renal Physiology, 2007, 292, F1322-F1333.	2.7	34

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127	Dynamics of aquaporin-2 serine-261 phosphorylation in response to short-term vasopressin treatment in collecting duct. American Journal of Physiology - Renal Physiology, 2007, 292, F691-F700.	2.7	141
128	Tandem Mass Spectrometry in Physiology. Physiology, 2007, 22, 390-400.	3.1	23
129	Urea and Renal Function in the 21st Century. Journal of the American Society of Nephrology: JASN, 2007, 18, 679-688.	6.1	94
130	An Automated Platform for Analysis of Phosphoproteomic Datasets:Â Application to Kidney Collecting Duct Phosphoproteins. Journal of Proteome Research, 2007, 6, 3501-3508.	3.7	58
131	Mouse Models and the Urinary Concentrating Mechanism in the New Millennium. Physiological Reviews, 2007, 87, 1083-1112.	28.8	171
132	Automated Quantification Tool for High-Throughput Proteomics Using Stable Isotope Labeling and LCâ[^]MSn. Analytical Chemistry, 2006, 78, 5752-5761.	6.5	35
133	Discovery of Urinary Biomarkers. Molecular and Cellular Proteomics, 2006, 5, 1760-1771.	3.8	351
134	High-throughput identification of IMCD proteins using LC-MS/MS. Physiological Genomics, 2006, 25, 263-276.	2.3	74
135	In vacuo isotope coded alkylation technique (IVICAT); an N-terminal stable isotopic label for quantitative liquid chromatography/mass spectrometry proteomics. Rapid Communications in Mass Spectrometry, 2006, 20, 2463-2477.	1.5	28
136	Angiotensin II mediates downregulation of aquaporin water channels and key renal sodium transporters in response to urinary tract obstruction. American Journal of Physiology - Renal Physiology, 2006, 291, F1021-F1032.	2.7	65
137	LC-MS/MS Analysis of Apical and Basolateral Plasma Membranes of Rat Renal Collecting Duct Cells. Molecular and Cellular Proteomics, 2006, 5, 2131-2145.	3.8	67
138	Effect of peristaltic contractions of the renal pelvic wall on solute concentrations of the renal inner medulla in the hamster. American Journal of Physiology - Renal Physiology, 2006, 290, F892-F896.	2.7	17
139	Gamble's â€œeconomy of waterâ€•revisited: studies in urea transporter knockout mice. American Journal of Physiology - Renal Physiology, 2006, 291, F148-F154.	2.7	40
140	The Application of DIGE-Based Proteomics to Renal Physiology. Nephron Physiology, 2006, 104, p61-p72.	1.2	26
141	Quantitative phosphoproteomics of vasopressin-sensitive renal cells: Regulation of aquaporin-2 phosphorylation at two sites. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7159-7164.	7.1	331
142	Sodium retention in cirrhotic rats is associated with increased renal abundance of sodium transporter proteins. Kidney International, 2005, 67, 622-630.	5.2	29
143	Prospects for urinary proteomics: Exosomes as a source of urinary biomarkers (Review Article). Nephrology, 2005, 10, 283-290.	1.6	168
144	COX-2 inhibition prevents downregulation of key renal water and sodium transport proteins in response to bilateral ureteral obstruction. American Journal of Physiology - Renal Physiology, 2005, 289, F322-F333.	2.7	95

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145	Increased expression of ENaC subunits and increased apical targeting of AQP2 in the kidneys of spontaneously hypertensive rats. American Journal of Physiology - Renal Physiology, 2005, 289, F957-F968.	2.7	39
146	Combined Proteomics and Pathways Analysis of Collecting Duct Reveals a Protein Regulatory Network Activated in Vasopressin Escape. Journal of the American Society of Nephrology: JASN, 2005, 16, 2852-2863.	6.1	45
147	Large Scale Protein Identification in Intracellular Aquaporin-2 Vesicles from Renal Inner Medullary Collecting Duct. Molecular and Cellular Proteomics, 2005, 4, 1095-1106.	3.8	154
148	Molecular Physiology of Renal Aquaporins and Sodium Transporters: Exciting Approaches to Understand Regulation of Renal Water Handling. Journal of the American Society of Nephrology: JASN, 2005, 16, 2827-2829.	6.1	10
149	Calmodulin Is Required for Vasopressin-stimulated Increase in Cyclic AMP Production in Inner Medullary Collecting Duct. Journal of Biological Chemistry, 2005, 280, 13624-13630.	3.4	67
150	Renal Phenotype of UT-A Urea Transporter Knockout Mice. Journal of the American Society of Nephrology: JASN, 2005, 16, 1583-1592.	6.1	112
151	Diuretics: Mechanisms of Action. , 2005, , 638-652.		1
152	Proteomic analysis of long-term vasopressin action in the inner medullary collecting duct of the Brattleboro rat. American Journal of Physiology - Renal Physiology, 2004, 286, F216-F224.	2.7	51
153	Urinary concentrating defect in mice with selective deletion of phloretin-sensitive urea transporters in the renal collecting duct. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7469-7474.	7.1	230
154	Peter Agre, 2003 Nobel Prize Winner in Chemistry. Journal of the American Society of Nephrology: JASN, 2004, 15, 1093-1095.	6.1	21
155	Rosiglitazone Activates Renal Sodium- and Water-Reabsorptive Pathways and Lowers Blood Pressure in Normal Rats. Journal of Pharmacology and Experimental Therapeutics, 2004, 308, 426-433.	2.5	128
156	Non-muscle Myosin II and Myosin Light Chain Kinase Are Downstream Targets for Vasopressin Signaling in the Renal Collecting Duct. Journal of Biological Chemistry, 2004, 279, 49026-49035.	3.4	97
157	STRUCTURAL BIOLOGY: The Atomic Architecture of a Gas Channel. Science, 2004, 305, 1573-1574.	12.6	31
158	Effects of dietary fat, NaCl, and fructose on renal sodium and water transporter abundances and systemic blood pressure. American Journal of Physiology - Renal Physiology, 2004, 287, F1204-F1212.	2.7	55
159	Acute endotoxemia in rats induces down-regulation of V2 vasopressin receptors and aquaporin-2 content in the kidney medulla. Kidney International, 2004, 65, 54-62.	5.2	86
160	Identification and proteomic profiling of exosomes in human urine. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13368-13373.	7.1	1,875
161	Application of difference gel electrophoresis to the identification of inner medullary collecting duct proteins. American Journal of Physiology - Renal Physiology, 2004, 286, F170-F179.	2.7	37
162	Renal Tubule Sodium Transporter Abundance Profiling in Rat Kidney. Annals of the New York Academy of Sciences, 2003, 986, 562-569.	3.8	33

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163	Downregulation of renal aquaporins in response to unilateral ureteral obstruction. American Journal of Physiology - Renal Physiology, 2003, 284, F1066-F1079.	2.7	85
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