Chin-Rang Yang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	An NQO1- and PARP-1-mediated cell death pathway induced in non-small-cell lung cancer cells by β-lapachone. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11832-11837.	7.1	318
2	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
3	Isolation of Ku70-binding proteins (KUBs). Nucleic Acids Research, 1999, 27, 2165-2174.	14.5	97
4	miR-337-3p and Its Targets STAT3 and RAP1A Modulate Taxane Sensitivity in Non-Small Cell Lung Cancers. PLoS ONE, 2012, 7, e39167.	2.5	96
5	Linking Splicing to Pol II Transcription Stabilizes Pre-mRNAs and Influences Splicing Patterns. PLoS Biology, 2006, 4, e147.	5.6	76
6	Coordinate modulation of Sp1, NFâ€kappa B, and p53 in confluent human malignant melanoma cells after ionizing radiation. FASEB Journal, 2000, 14, 379-390.	0.5	73
7	When X-ray-inducible proteins meet DNA double strand break repair. Seminars in Radiation Oncology, 2001, 11, 352-372.	2.2	63
8	An enzyme mechanism language for the mathematical modeling of metabolic pathways. Bioinformatics, 2005, 21, 774-780.	4.1	44
9	Does SARS-CoV-2 Infect the Kidney?. Journal of the American Society of Nephrology: JASN, 2020, 31, 2746-2748.	6.1	43
10	Alterations in Transcription Factor Binding in Radioresistant Human Melanoma Cells after Ionizing Radiation. Radiation Research, 1994, 138, S47.	1.5	42
11	Genetic Mutation of p53 and Suppression of the miR-17â^¼92 Cluster Are Synthetic Lethal in Non–Small Cell Lung Cancer due to Upregulation of Vitamin D Signaling. Cancer Research, 2015, 75, 666-675.	0.9	39
12	Tumor-Selective, Futile Redox Cycle-Induced Bystander Effects Elicited by NQO1 Bioactivatable Radiosensitizing Drugs in Triple-Negative Breast Cancers. Antioxidants and Redox Signaling, 2014, 21, 237-250.	5.4	37
13	A Mathematical Model for the Branched Chain Amino Acid Biosynthetic Pathways of Escherichia coli K12. Journal of Biological Chemistry, 2005, 280, 11224-11232.	3.4	36
14	Transcriptomes of Major Proximal Tubule Cell Culture Models. Journal of the American Society of Nephrology: JASN, 2021, 32, 86-97.	6.1	35
15	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
16	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
17	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
18	Phosphorylation Changes in Response to Kinase Inhibitor H89 in PKA-Null Cells. Scientific Reports, 2019 9, 2814	3.3	24

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19	PKAâ€independent vasopressin signaling in renal collecting duct. FASEB Journal, 2020, 34, 6129-6146.	0.5	24
20	APPLICATION OF A GENERALIZED MWC MODEL FOR THE MATHEMATICAL SIMULATION OF METABOLIC PATHWAYS REGULATED BY ALLOSTERIC ENZYMES. Journal of Bioinformatics and Computational Biology, 2006, 04, 335-355.	0.8	23
21	Learning biological network using mutual information and conditional independence. BMC Bioinformatics, 2010, 11, S9.	2.6	23
22	"SLC-omics―of the kidney: solute transporters along the nephron. American Journal of Physiology - Cell Physiology, 2021, 321, C507-C518.	4.6	22
23	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
24	Mornings with art, lessons learned: Feedback regulation, restriction threshold biology, and redundancy govern molecular stress responses. Journal of Cellular Physiology, 2006, 209, 604-610.	4.1	20
25	BIG: a large-scale data integration tool for renal physiology. American Journal of Physiology - Renal Physiology, 2016, 311, F787-F792.	2.7	20
26	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
27	Phosphoproteomic Identification of Vasopressin/cAMP/Protein Kinase A–Dependent Signaling in Kidney. Molecular Pharmacology, 2021, 99, 358-369.	2.3	15
28	Phosphoproteomic identification of vasopressinâ€regulated protein kinases in collecting duct cells. British Journal of Pharmacology, 2021, 178, 1426-1444.	5.4	15
29	Biosynthesis and Regulation of the Branched-Chain Amino Acidsâ€. EcoSal Plus, 2006, 2, .	5.4	14
30	Proteomic profiling of nuclear fractions from native renal inner medullary collecting duct cells. Physiological Genomics, 2016, 48, 154-166.	2.3	13
31	Damage-Sensing mechanisms in human cells after ionizing radiation. Stem Cells, 1997, 15, 27-42.	3.2	12
32	Protein kinase A catalytic-α and catalytic-β proteins have nonredundant regulatory functions. American Journal of Physiology - Renal Physiology, 2020, 319, F848-F862.	2.7	12
33	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
34	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
35	A framework for personalized medicine: prediction of drug sensitivity in cancer by proteomic profiling. Proteome Science, 2012, 10, S13.	1.7	9
36	Improved protein arrays for quantitative systems analysis of the dynamics of signaling pathway interactions. Proteome Science, 2011, 9, 53.	1.7	8

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37	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
38	Bayesian analysis of dynamic phosphoproteomic data identifies protein kinases mediating GPCR responses. Cell Communication and Signaling, 2022, 20, .	6.5	7
39	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
40	An enzyme-centric approach for modelling non-linear biological complexity. BMC Systems Biology, 2008, 2, 70.	3.0	5
41	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
42	"ADPKD-omics― determinants of cyclic AMP levels in renal epithelial cells. Kidney International, 2022, 101, 47-62.	5.2	5
43	Functional proteomic pattern identification under low dose ionizing radiation. Artificial Intelligence in Medicine, 2010, 49, 177-185.	6.5	4
44	Effects of low dose ionizing radiation on DNA damage-caused pathways by reverse-phase protein array and Bayesian networks. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750006.	0.8	4
45	A Framework for Personalized Medicine with Reverse Phase Protein Array and Drug Sensitivity. , 2011, ,		0
46	Proteomic Determination of the Rat Native Inner Medullary Collecting Duct Lysine Acetylome and Phosphoproteome. FASEB Journal, 2018, 32, 850.3.	0.5	0
47	Fortyâ€five Vasopressinâ€Regulated Phosphoproteins Involved in Control of Collecting Duct Water Transport. FASEB Journal. 2022. 36	0.5	0