

Chin-Rang Yang

List of Publications by Year in descending order

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47
papers

1,543
citations

361296

20
h-index

315616

38
g-index

50
all docs

50
docs citations

50
times ranked

2207
citing authors

#	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.	3.3	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.	3.3	100
3	Isolation of Ku70-binding proteins (KUBs). Nucleic Acids Research, 1999, 27, 2165-2174.	6.5	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.	1.1	96
5	Linking Splicing to Pol II Transcription Stabilizes Pre-mRNAs and Influences Splicing Patterns. PLoS Biology, 2006, 4, e147.	2.6	76
6	Coordinate modulation of Sp1, NF κ B, and p53 in confluent human malignant melanoma cells after ionizing radiation. FASEB Journal, 2000, 14, 379-390.	0.2	73
7	When X-ray-inducible proteins meet DNA double strand break repair. Seminars in Radiation Oncology, 2001, 11, 352-372.	1.0	63
8	An enzyme mechanism language for the mathematical modeling of metabolic pathways. Bioinformatics, 2005, 21, 774-780.	1.8	44
9	Does SARS-CoV-2 Infect the Kidney?. Journal of the American Society of Nephrology: JASN, 2020, 31, 2746-2748.	3.0	43
10	Alterations in Transcription Factor Binding in Radioresistant Human Melanoma Cells after Ionizing Radiation. Radiation Research, 1994, 138, S47.	0.7	42
11	Genetic Mutation of p53 and Suppression of the miR-17 ^{~1} /492 Cluster Are Synthetic Lethal in Non ^{~1} Small Cell Lung Cancer due to Upregulation of Vitamin D Signaling. Cancer Research, 2015, 75, 666-675.	0.4	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.	2.5	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.	1.6	36
14	Transcriptomes of Major Proximal Tubule Cell Culture Models. Journal of the American Society of Nephrology: JASN, 2021, 32, 86-97.	3.0	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.	2.1	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.	2.1	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.	2.6	27
18	Phosphorylation Changes in Response to Kinase Inhibitor H89 in PKA-Null Cells. Scientific Reports, 2019, 9, 2814.	1.6	24

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19	PKA-independent vasopressin signaling in renal collecting duct. <i>FASEB Journal</i> , 2020, 34, 6129-6146.	0.2	24
20	APPLICATION OF A GENERALIZED MWC MODEL FOR THE MATHEMATICAL SIMULATION OF METABOLIC PATHWAYS REGULATED BY ALLOSTERIC ENZYMES. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 335-355.	0.3	23
21	Learning biological network using mutual information and conditional independence. <i>BMC Bioinformatics</i> , 2010, 11, S9.	1.2	23
22	“SLC-omics” of the kidney: solute transporters along the nephron. <i>American Journal of Physiology - Cell Physiology</i> , 2021, 321, C507-C518.	2.1	22
23	CRISPR-Cas9/phosphoproteomics identifies multiple noncanonical targets of myosin light chain kinase. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 318, F600-F616.	1.3	21
24	Mornings with art, lessons learned: Feedback regulation, restriction threshold biology, and redundancy govern molecular stress responses. <i>Journal of Cellular Physiology</i> , 2006, 209, 604-610.	2.0	20
25	BIG: a large-scale data integration tool for renal physiology. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 311, F787-F792.	1.3	20
26	Modulation of Cl ⁻ signaling and ion transport by recruitment of kinases and phosphatases mediated by the regulatory protein IRBIT. <i>Science Signaling</i> , 2018, 11, .	1.6	16
27	Phosphoproteomic Identification of Vasopressin/cAMP/Protein Kinase A-Dependent Signaling in Kidney. <i>Molecular Pharmacology</i> , 2021, 99, 358-369.	1.0	15
28	Phosphoproteomic identification of vasopressin-regulated protein kinases in collecting duct cells. <i>British Journal of Pharmacology</i> , 2021, 178, 1426-1444.	2.7	15
29	Biosynthesis and Regulation of the Branched-Chain Amino Acids. <i>EcoSal Plus</i> , 2006, 2, .	2.1	14
30	Proteomic profiling of nuclear fractions from native renal inner medullary collecting duct cells. <i>Physiological Genomics</i> , 2016, 48, 154-166.	1.0	13
31	Damage-Sensing mechanisms in human cells after ionizing radiation. <i>Stem Cells</i> , 1997, 15, 27-42.	1.4	12
32	Protein kinase A catalytic- α and catalytic- β proteins have nonredundant regulatory functions. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 319, F848-F862.	1.3	12
33	Bayesian identification of candidate transcription factors for the regulation of <i>Aqp2</i> gene expression. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 321, F389-F401.	1.3	12
34	PTM-Logo: a program for generation of sequence logos based on position-specific background amino-acid probabilities. <i>Bioinformatics</i> , 2019, 35, 5313-5314.	1.8	11
35	A framework for personalized medicine: prediction of drug sensitivity in cancer by proteomic profiling. <i>Proteome Science</i> , 2012, 10, S13.	0.7	9
36	Improved protein arrays for quantitative systems analysis of the dynamics of signaling pathway interactions. <i>Proteome Science</i> , 2011, 9, 53.	0.7	8

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37	Proteomic determination of the lysine acetylome and phosphoproteome in the rat native inner medullary collecting duct. <i>Physiological Genomics</i> , 2018, 50, 669-679.	1.0	8
38	Bayesian analysis of dynamic phosphoproteomic data identifies protein kinases mediating GPCR responses. <i>Cell Communication and Signaling</i> , 2022, 20, .	2.7	7
39	An integrative proteogenomics approach reveals peptides encoded by annotated lincRNA in the mouse kidney inner medulla. <i>Physiological Genomics</i> , 2020, 52, 485-491.	1.0	6
40	An enzyme-centric approach for modelling non-linear biological complexity. <i>BMC Systems Biology</i> , 2008, 2, 70.	3.0	5
41	Systems Biology of the Vasopressin V2 Receptor: New Tools for Discovery of Molecular Actions of a GPCR. <i>Annual Review of Pharmacology and Toxicology</i> , 2022, 62, 595-616.	4.2	5
42	â€œADPKD-omicsâ€• determinants of cyclic AMP levels in renal epithelial cells. <i>Kidney International</i> , 2022, 101, 47-62.	2.6	5
43	Functional proteomic pattern identification under low dose ionizing radiation. <i>Artificial Intelligence in Medicine</i> , 2010, 49, 177-185.	3.8	4
44	Effects of low dose ionizing radiation on DNA damage-caused pathways by reverse-phase protein array and Bayesian networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750006.	0.3	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. <i>FASEB Journal</i> , 2018, 32, 850.3.	0.2	0
47	Fortyâ€•five Vasopressinâ€•Regulated Phosphoproteins Involved in Control of Collecting Duct Water Transport. <i>FASEB Journal</i> , 2022, 36, .	0.2	0