

Wan Kyu Kim

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

45
papers

1,742
citations

19
h-index

41
g-index

47
ext. papers

2,068
ext. citations

10.1
avg, IF

4.38
L-index

#	Paper	IF	Citations
45	Crosstalk between YAP and TGF β regulates SERPINE1 expression in mesenchymal lung cancer cells. <i>International Journal of Oncology</i> , 2021 , 58, 111-121	4.4	4
44	Circulating Small Extracellular Vesicles Activate TYRO3 to Drive Cancer Metastasis and Chemoresistance. <i>Cancer Research</i> , 2021 , 81, 3539-3553	10.1	3
43	Enhanced Sensitivity of Nonsmall Cell Lung Cancer with Acquired Resistance to Epidermal Growth Factor Receptor-Tyrosine Kinase Inhibitors to Phenformin: The Roles of a Metabolic Shift to Oxidative Phosphorylation and Redox Balance. <i>Oxidative Medicine and Cellular Longevity</i> , 2021 , 2021, 5428814	6.7	1
42	Comprehensive Survey of Recent Drug Discovery Using Deep Learning. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	11
41	Connectivity map-based drug repositioning of bortezomib to reverse the metastatic effect of GALNT14 in lung cancer. <i>Oncogene</i> , 2020 , 39, 4567-4580	9.2	11
40	MiR-4435 is an UQCRB-related circulating miRNA in human colorectal cancer. <i>Scientific Reports</i> , 2020 , 10, 2833	4.9	4
39	Systematic identification of a nuclear receptor-enriched predictive signature for erastin-induced ferroptosis. <i>Redox Biology</i> , 2020 , 37, 101719	11.3	12
38	Safe scarless cassette-free selection of genome-edited human pluripotent stem cells using temporary drug resistance. <i>Biomaterials</i> , 2020 , 262, 120295	15.6	5
37	Naa20, the catalytic subunit of NatB complex, contributes to hepatocellular carcinoma by regulating the LKB1-AMPK-mTOR axis. <i>Experimental and Molecular Medicine</i> , 2020 , 52, 1831-1844	12.8	1
36	Identification of MYC as an antineoplastic protein that stifles RIPK1-RIPK3 complex formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 19982-19993	11.5	4
35	Osteoclast-associated receptor blockade prevents articular cartilage destruction via chondrocyte apoptosis regulation. <i>Nature Communications</i> , 2020 , 11, 4343	17.4	19
34	In silico drug repositioning: from large-scale transcriptome data to therapeutics. <i>Archives of Pharmacal Research</i> , 2019 , 42, 879-889	6.1	10
33	CSgator: an integrated web platform for compound set analysis. <i>Journal of Cheminformatics</i> , 2019 , 11, 17	8.6	4
32	Comparison of Target Features for Predicting Drug-Target Interactions by Deep Neural Network Based on Large-Scale Drug-Induced Transcriptome Data. <i>Pharmaceutics</i> , 2019 , 11,	6.4	11
31	CDRgator: An Integrative Navigator of Cancer Drug Resistance Gene Signatures. <i>Molecules and Cells</i> , 2019 , 42, 237-244	3.5	1
30	Hsa-miR-10a-5p downregulation in mutant UQCRB-expressing cells promotes the cholesterol biosynthesis pathway. <i>Scientific Reports</i> , 2018 , 8, 12407	4.9	5
29	Large-scale pharmacogenomics based drug discovery for ITGB3 dependent chemoresistance in mesenchymal lung cancer. <i>Molecular Cancer</i> , 2018 , 17, 175	42.1	25

28	Selective Elimination of Culture-Adapted Human Embryonic Stem Cells with BH3 Mimetics. <i>Stem Cell Reports</i> , 2018 , 11, 1244-1256	8	4
27	Drug Repositioning for Cancer Therapy Based on Large-Scale Drug-Induced Transcriptional Signatures. <i>PLoS ONE</i> , 2016 , 11, e0150460	3.7	51
26	Modulation of mRNA and lncRNA expression dynamics by the Set2-Rpd3S pathway. <i>Nature Communications</i> , 2016 , 7, 13534	17.4	64
25	miRseqViewer: multi-panel visualization of sequence, structure and expression for analysis of microRNA sequencing data. <i>Bioinformatics</i> , 2015 , 31, 596-8	7.2	3
24	A Novel Human scFv Library with Non-Combinatorial Synthetic CDR Diversity. <i>PLoS ONE</i> , 2015 , 10, e0141045	10.5	9
23	gsGator: an integrated web platform for cross-species gene set analysis. <i>BMC Bioinformatics</i> , 2014 , 15, 13	3.6	5
22	lncRNATOR: a comprehensive resource for functional investigation of long non-coding RNAs. <i>Bioinformatics</i> , 2014 , 30, 2480-5	7.2	105
21	A recurrent inactivating mutation in RHOA GTPase in angioimmunoblastic T cell lymphoma. <i>Nature Genetics</i> , 2014 , 46, 371-5	36.3	264
20	GEPdb: a database for investigating the ternary association of genotype, gene expression and phenotype. <i>Bioinformatics</i> , 2014 , 30, 2540-2	7.2	1
19	Identification of upstream regulators for prognostic expression signature genes in colorectal cancer. <i>BMC Systems Biology</i> , 2013 , 7, 86	3.5	9
18	The atypical mechanosensitive microRNA-712 derived from pre-ribosomal RNA induces endothelial inflammation and atherosclerosis. <i>Nature Communications</i> , 2013 , 4, 3000	17.4	162
17	A high-dimensional, deep-sequencing study of lung adenocarcinoma in female never-smokers. <i>PLoS ONE</i> , 2013 , 8, e55596	3.7	56
16	MiRGator v3.0: a microRNA portal for deep sequencing, expression profiling and mRNA targeting. <i>Nucleic Acids Research</i> , 2013 , 41, D252-7	20.1	118
15	Transcriptomic analysis of insulin-sensitive tissues from anti-diabetic drug treated ZDF rats, a T2DM animal model. <i>PLoS ONE</i> , 2013 , 8, e69624	3.7	2
14	Dissection of the dimerization modes in the DJ-1 superfamily. <i>Molecules and Cells</i> , 2012 , 33, 163-71	3.5	9
13	hiPathDB: a human-integrated pathway database with facile visualization. <i>Nucleic Acids Research</i> , 2012 , 40, D797-802	20.1	30
12	GARNET--gene set analysis with exploration of annotation relations. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 1, S25	3.6	7
11	Clinical validation of colorectal cancer biomarkers identified from bioinformatics analysis of public expression data. <i>Clinical Cancer Research</i> , 2011 , 17, 700-9	12.9	65

10	miRGator v2.0: an integrated system for functional investigation of microRNAs. <i>Nucleic Acids Research</i> , 2011 , 39, D158-62	20.1	44
9	Inferring mouse gene functions from genomic-scale data using a combined functional network/classification strategy. <i>Genome Biology</i> , 2008 , 9 Suppl 1, S5	18.3	60
8	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. <i>Genome Biology</i> , 2008 , 9 Suppl 1, S2	18.3	194
7	Age-dependent evolution of the yeast protein interaction network suggests a limited role of gene duplication and divergence. <i>PLoS Computational Biology</i> , 2008 , 4, e1000232	5	61
6	Using structural motif descriptors for sequence-based binding site prediction. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 4, S5	3.6	15
5	Equivalent binding sites reveal convergently evolved interaction motifs. <i>Bioinformatics</i> , 2006 , 22, 550-5	7.2	24
4	The many faces of protein-protein interactions: A compendium of interface geometry. <i>PLoS Computational Biology</i> , 2006 , 2, e124	5	92
3	SCOPPI: a structural classification of protein-protein interfaces. <i>Nucleic Acids Research</i> , 2006 , 34, D310-4	20.1	130
2	Survey of the geometric association of domain-domain interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 1075-88	4.2	25
1	Computational drug repositioning of bortezomib to reverse metastatic effect of GALNT14 in lung cancer		1