Wan Kyu Kim

List of Publications by Year
in descending order

45	2,330	304368	223531
papers	citations	22	46
		h-index	g-index

47	47	47	4214
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A recurrent inactivating mutation in RHOA GTPase in angioimmunoblastic T cell lymphoma. Nature Genetics, 2014, 46, 371-375.	9.4	326
2	A critical assessment of Mus musculus gene function prediction using integrated genomic evidence. Genome Biology, 2008, 9, S2.	13.9	214
3	The atypical mechanosensitive microRNA-712 derived from pre-ribosomal RNA induces endothelial inflammation and atherosclerosis. Nature Communications, 2013, 4, 3000.	5.8	198
4	SCOPPI: a structural classification of protein-protein interfaces. Nucleic Acids Research, 2006, 34, D310-D314.	6.5	142
5	miRGator v3.0: a microRNA portal for deep sequencing, expression profiling and mRNA targeting. Nucleic Acids Research, 2012, 41, D252-D257.	6.5	140
6	lncRNAtor: a comprehensive resource for functional investigation of long non-coding RNAs. Bioinformatics, 2014, 30, 2480-2485.	1.8	135
7	The Many Faces of Protein–Protein Interactions: A Compendium of Interface Geometry. PLoS Computational Biology, 2006, 2, e124.	1.5	103
8	Modulation of mRNA and lncRNA expression dynamics by the Set2–Rpd3S pathway. Nature Communications, 2016, 7, 13534.	5.8	93
9	Clinical Validation of Colorectal Cancer Biomarkers Identified from Bioinformatics Analysis of Public Expression Data. Clinical Cancer Research, 2011, 17, 700-709.	3.2	80
10	Age-Dependent Evolution of the Yeast Protein Interaction Network Suggests a Limited Role of Gene Duplication and Divergence. PLoS Computational Biology, 2008, 4, e1000232.	1.5	71
11	Drug Repositioning for Cancer Therapy Based on Large-Scale Drug-Induced Transcriptional Signatures. PLoS ONE, 2016, 11, e0150460.	1.1	71
12	A High-Dimensional, Deep-Sequencing Study of Lung Adenocarcinoma in Female Never-Smokers. PLoS ONE, 2013, 8, e55596.	1.1	70
13	Inferring mouse gene functions from genomic-scale data using a combined functional network/classification strategy. Genome Biology, 2008, 9, S5.	13.9	66
14	Osteoclast-associated receptor blockade prevents articular cartilage destruction via chondrocyte apoptosis regulation. Nature Communications, 2020, 11, 4343.	5.8	60
15	Comprehensive Survey of Recent Drug Discovery Using Deep Learning. International Journal of Molecular Sciences, 2021, 22, 9983.	1.8	55
16	miRGator v2.0 : an integrated system for functional investigation of microRNAs. Nucleic Acids Research, 2011, 39, D158-D162.	6.5	50
17	hiPathDB: a human-integrated pathway database with facile visualization. Nucleic Acids Research, 2012, 40, D797-D802.	6.5	35
18	Large-scale pharmacogenomics based drug discovery for ITGB3 dependent chemoresistance in mesenchymal lung cancer. Molecular Cancer, 2018, 17, 175.	7.9	34

#	Article	IF	Citations
19	In silico drug repositioning: from large-scale transcriptome data to therapeutics. Archives of Pharmacal Research, 2019, 42, 879-889.	2.7	30
20	Equivalent binding sites reveal convergently evolved interaction motifs. Bioinformatics, 2006, 22, 550-555.	1.8	28
21	Survey of the geometric association of domain-domain interfaces. Proteins: Structure, Function and Bioinformatics, 2005, 61, 1075-1088.	1.5	26
22	Comparison of Target Features for Predicting Drug-Target Interactions by Deep Neural Network Based on Large-Scale Drug-Induced Transcriptome Data. Pharmaceutics, 2019, 11, 377.	2.0	26
23	Systematic identification of a nuclear receptor-enriched predictive signature for erastin-induced ferroptosis. Redox Biology, 2020, 37, 101719.	3.9	23
24	Using structural motif descriptors for sequence-based binding site prediction. BMC Bioinformatics, 2007, 8, S5.	1.2	22
25	Connectivity map-based drug repositioning of bortezomib to reverse the metastatic effect of GALNT14 in lung cancer. Oncogene, 2020, 39, 4567-4580.	2.6	22
26	A Novel Human scFv Library with Non-Combinatorial Synthetic CDR Diversity. PLoS ONE, 2015, 10, e0141045.	1.1	18
27	Crosstalk between YAP and TGFÎ² regulates SERPINE1 expression in mesenchymal lung cancer cells. International Journal of Oncology, 2020, 58, 111-121.	1.4	18
28	Hsa-miR-10a-5p downregulation in mutant UQCRB-expressing cells promotes the cholesterol biosynthesis pathway. Scientific Reports, 2018, 8, 12407.	1.6	17
29	Safe scarless cassette-free selection of genome-edited human pluripotent stem cells using temporary drug resistance. Biomaterials, 2020, 262, 120295.	5.7	17
30	Identification of MYC as an antinecroptotic protein that stifles RIPK1â€"RIPK3 complex formation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19982-19993.	3.3	17
31	Dissection of the Dimerization Modes in the DJ-1 Superfamily. Molecules and Cells, 2012, 33, 163-172.	1.0	13
32	Selective Elimination of Culture-Adapted Human Embryonic Stem Cells with BH3 Mimetics. Stem Cell Reports, 2018, 11, 1244-1256.	2.3	12
33	Naa20, the catalytic subunit of NatB complex, contributes to hepatocellular carcinoma by regulating the LKB1â€"AMPKâ€"mTOR axis. Experimental and Molecular Medicine, 2020, 52, 1831-1844.	3.2	12
34	Circulating Small Extracellular Vesicles Activate TYRO3 to Drive Cancer Metastasis and Chemoresistance. Cancer Research, 2021, 81, 3539-3553.	0.4	12
35	GARNET â€" gene set analysis with exploration of annotation relations. BMC Bioinformatics, 2011, 12, S25.	1.2	11
36	Identification of upstream regulators for prognostic expression signature genes in colorectal cancer. BMC Systems Biology, 2013, 7, 86.	3.0	11

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37	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. Oxidative Medicine and Cellular Longevity, 2021, 2021, 1-17.	1.9	11
38	MiR-4435 is an UQCRB-related circulating miRNA in human colorectal cancer. Scientific Reports, 2020, 10, 2833.	1.6	10
39	gsGator: an integrated web platform for cross-species gene set analysis. BMC Bioinformatics, 2014, 15, 13.	1.2	7
40	CSgator: an integrated web platform for compound set analysis. Journal of Cheminformatics, 2019, 11, 17.	2.8	7
41	Discovery of dipeptidyl peptidase-4 inhibitor specific biomarker in non-alcoholic fatty liver disease mouse models using modified basket trial. Clinical and Molecular Hepatology, 2022, 28, 497-509.	4.5	5
42	Transcriptomic Analysis of Insulin-Sensitive Tissues from Anti-Diabetic Drug Treated ZDF Rats, a T2DM Animal Model. PLoS ONE, 2013, 8, e69624.	1.1	4
43	miRseqViewer: multi-panel visualization of sequence, structure and expression for analysis of microRNA sequencing data. Bioinformatics, 2015, 31, 596-598.	1.8	3
44	CDRgator: An Integrative Navigator of Cancer Drug Resistance Gene Signatures. Molecules and Cells, 2019, 42, 237-244.	1.0	2
45	GEPdb: a database for investigating the ternary association of genotype, gene expression and phenotype. Bioinformatics, 2014, 30, 2540-2542.	1.8	1