Keunsoo Kang

List of Publications by Year
in descending order

116 papers	3,403 citations	186265 28 h-index	175258 52 g-index
122 all docs	122 docs citations	122 times ranked	6549 citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Differentially-Methylated Genes and Pathways in Patients with Delayed Cerebral Ischemia Following Subarachnoid Hemorrhage. Journal of Korean Neurosurgical Society, 2022, 65, 4-12.	1.2	2
2	A Brief Review of Machine Learning-Based Bioactive Compound Research. Applied Sciences (Switzerland), 2022, 12, 2906.	2.5	3
3	ZEB1-regulated lnc-Nr2f1 promotes the migration and invasion of lung adenocarcinoma cells. Cancer Letters, 2022, 533, 215601.	7.2	2
4	Characterization of transcriptome diversity and in vitro behavior of primary human high-risk breast cells. Scientific Reports, 2022, 12, 6159.	3.3	4
5	Enhancer RNAs stimulate Pol II pause release by harnessing multivalent interactions to NELF. Nature Communications, 2022, 13, 2429.	12.8	19
6	MarkerCount: A stable, count-based cell type identifier for single-cell RNA-seq experiments. Computational and Structural Biotechnology Journal, 2022, 20, 3120-3132.	4.1	10
7	Alu RNA induces NLRP3 expression through TLR7 activation in α-1-antitrypsin–deficient macrophages. JCI Insight, 2022, 7, .	5.0	4
8	Abstract LB043: Identification and characterization of cancer-associated fibroblast subpopulations in lung adenocarcinoma. Cancer Research, 2022, 82, LB043-LB043.	0.9	0
9	Nucleoporin 210 Serves a Key Scaffold for SMARCB1 in Liver Cancer. Cancer Research, 2021, 81, 356-370.	0.9	16
10	Arsenic hexoxide has differential effects on cell proliferation and genome-wide gene expression in human primary mammary epithelial and MCF7 cells. Scientific Reports, 2021, 11, 3761.	3.3	10
11	Machine learning based anti-cancer drug response prediction and search for predictor genes using cancer cell line gene expression. Genomics and Informatics, 2021, 19, e10.	0.8	5
12	A study of transposable element-associated structural variations (TASVs) using a de novo-assembled Korean genome. Experimental and Molecular Medicine, 2021, 53, 615-630.	7.7	9
13	Tetraarsenic oxide affects non-coding RNA transcriptome through deregulating polycomb complexes in MCF7 cells. Advances in Biological Regulation, 2021, 80, 100809.	2.3	4
14	Functional coordination of BET family proteins underlies altered transcription associated with memory impairment in fragile X syndrome. Science Advances, 2021, 7, .	10.3	7
15	Epigenomic Analysis of RAD51 ChIP-seq Data Reveals cis-regulatory Elements Associated with Autophagy in Cancer Cell Lines. Cancers, 2021, 13, 2547.	3.7	4
16	SMARCA4 oncogenic potential via IRAK1 enhancer to activate Gankyrin and AKR1B10 in liver cancer. Oncogene, 2021, 40, 4652-4662.	5.9	13
17	Cancer-associated fibroblasts activated by miR-196a promote the migration and invasion of lung cancer cells. Cancer Letters, 2021, 508, 92-103.	7.2	26
18	Molecular laterality encodes stress susceptibility in the medial prefrontal cortex. Molecular Brain, 2021, 14, 92.	2.6	4

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19	Epigenetic Upregulation of MAGE-A Isoforms Promotes Breast Cancer Cell Aggressiveness. Cancers, 2021, 13, 3176.	3.7	7
20	Inhibition of STAT3 enhances sensitivity to tamoxifen in tamoxifen-resistant breast cancer cells. BMC Cancer, 2021, 21, 931.	2.6	14
21	Integrative Transcriptome Profiling Reveals SKA3 as a Novel Prognostic Marker in Non-Muscle Invasive Bladder Cancer. Cancers, 2021, 13, 4673.	3.7	5
22	Modulation of Human Mesenchymal Stem Cells by Electrical Stimulation Using an Enzymatic Biofuel Cell. Catalysts, 2021, 11, 62.	3.5	1
23	BRCA1-BARD1 regulates transcription through modulating topoisomerase IIβ. Open Biology, 2021, 11, 210221.	3.6	9
24	Differentially Expressed Genes in Matched Normal, Cancer, and Lymph Node Metastases Predict Clinical Outcomes in Patients With Breast Cancer. Applied Immunohistochemistry and Molecular Morphology, 2020, 28, 111-122.	1.2	22
25	Genome-wide blood DNA methylation analysis in patients with delayed cerebral ischemia after subarachnoid hemorrhage. Scientific Reports, 2020, 10, 11419.	3.3	16
26	Identification of Novel microRNA Prognostic Markers Using Cascaded Wx, a Neural Network-Based Framework, in Lung Adenocarcinoma Patients. Cancers, 2020, 12, 1890.	3.7	8
27	Target-Centered Drug Repurposing Predictions of Human Angiotensin-Converting Enzyme 2 (ACE2) and Transmembrane Protease Serine Subtype 2 (TMPRSS2) Interacting Approved Drugs for Coronavirus Disease 2019 (COVID-19) Treatment through a Drug-Target Interaction Deep Learning Model. Viruses, 2020, 12, 1325.	3.3	24
28	Tiotropium Is Predicted to Be a Promising Drug for COVID-19 Through Transcriptome-Based Comprehensive Molecular Pathway Analysis. Viruses, 2020, 12, 776.	3.3	17
29	Predicting FOXM1-Mediated Gene Regulation through the Analysis of Genome-Wide FOXM1 Binding Sites in MCF-7, K562, SK-N-SH, GM12878 and ECC-1 Cell Lines. International Journal of Molecular Sciences, 2020, 21, 6141.	4.1	12
30	Hormone Receptor-Status Prediction in Breast Cancer Using Gene Expression Profiles and Their Macroscopic Landscape. Cancers, 2020, 12, 1165.	3.7	4
31	Genome-Wide Analysis of the DNA Methylation Profile Identifies the Fragile Histidine Triad (FHIT) Gene as a New Promising Biomarker of Crohn's Disease. Journal of Clinical Medicine, 2020, 9, 1338.	2.4	9
32	ETS1 Suppresses Tumorigenesis of Human Breast Cancer via Trans-Activation of Canonical Tumor Suppressor Genes. Frontiers in Oncology, 2020, 10, 642.	2.8	15
33	Integration of transcriptomics, proteomics and metabolomics identifies biomarkers for pulmonary injury by polyhexamethylene guanidine phosphate (PHMG-p), a humidifier disinfectant, in rats. Archives of Toxicology, 2020, 94, 887-909.	4.2	20
34	Predicting commercially available antiviral drugs that may act on the novel coronavirus (SARS-CoV-2) through a drug-target interaction deep learning model. Computational and Structural Biotechnology Journal, 2020, 18, 784-790.	4.1	568
35	Cascaded Wx: A Novel Prognosis-Related Feature Selection Framework in Human Lung Adenocarcinoma Transcriptomes. Frontiers in Genetics, 2019, 10, 662.	2.3	9
36	Transposable element-mediated structural variation analysis in dog breeds using whole-genome sequencing. Mammalian Genome, 2019, 30, 289-300.	2.2	9

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37	Aberrantly hypermethylated tumor suppressor genes were identified in oral squamous cell carcinoma (OSCC). Clinical Epigenetics, 2019, 11, 116.	4.1	41
38	Whole Transcriptome Analysis Identifies TNS4 as a Key Effector of Cetuximab and a Regulator of the Oncogenic Activity of KRAS Mutant Colorectal Cancer Cell Lines. Cells, 2019, 8, 878.	4.1	17
39	Wx: a neural network-based feature selection algorithm for transcriptomic data. Scientific Reports, 2019, 9, 10500.	3.3	12
40	IFN-λ selectively suppresses a subset of TLR4-activated genes and enhancers to potentiate macrophage activation. Nature Communications, 2019, 10, 3320.	12.8	71
41	Expression of EEF1A1 Is Associated with Prognosis of Patients with Colon Adenocarcinoma. Journal of Clinical Medicine, 2019, 8, 1903.	2.4	15
42	Bcl11b prevents catastrophic autoimmunity by controlling multiple aspects of a regulatory T cell gene expression program. Science Advances, 2019, 5, eaaw0706.	10.3	15
43	Genome-wide analysis of DNA methylation identifies novel differentially methylated regions associated with lipid accumulation improved by ethanol extracts of Allium tubersosum and Capsella bursa-pastoris in a cell model. PLoS ONE, 2019, 14, e0217877.	2.5	6
44	P-TEFb Regulates Transcriptional Activation in Non-coding RNA Genes. Frontiers in Genetics, 2019, 10, 342.	2.3	12
45	QKI, a miR‐200 target gene, suppresses epithelial‐to‐mesenchymal transition and tumor growth. International Journal of Cancer, 2019, 145, 1585-1595.	5.1	59
46	MiR-34a and miR-34b/c have distinct effects on the suppression of lung adenocarcinomas. Experimental and Molecular Medicine, 2019, 51, 1-10.	7.7	39
47	Gramella fulva sp. nov., isolated from a dry surface of tidal flat. Journal of Microbiology, 2019, 57, 23-29.	2.8	13
48	Ets1 suppresses atopic dermatitis by suppressing pathogenic T cell responses. JCI Insight, 2019, 4, .	5.0	10
49	Octopus-toolkit: a workflow to automate mining of public epigenomic and transcriptomic next-generation sequencing data. Nucleic Acids Research, 2018, 46, e53-e53.	14.5	61
50	Barrier to autointegration factor 1, procollagen‐lysine, 2‐oxoglutarate 5‐dioxygenase 3, and splicing factor 3b subunit 4 as early‐stage cancer decision markers and drivers of hepatocellular carcinoma. Hepatology, 2018, 67, 1360-1377.	7.3	90
51	TAp73 inhibits cell invasion and migration by directly activating KAI1 expression in colorectal carcinoma. Cancer Letters, 2018, 415, 106-116.	7.2	18
52	A Simple Guideline to Assess the Characteristics of RNA-Seq Data. BioMed Research International, 2018, 2018, 1-9.	1.9	32
53	Upregulation of Ets1 expression by NFATc2 and NFKB1/RELA promotes breast cancer cell invasiveness. Oncogenesis, 2018, 7, 91.	4.9	41
54	TraRECo: a greedy approach based de novo transcriptome assembler with read error correction using consensus matrix. BMC Genomics, 2018, 19, 653.	2.8	3

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55	The transcription factor Foxp1 preserves integrity of an active Foxp3 locus in extrathymic Treg cells. Nature Communications, 2018, 9, 4473.	12.8	29
56	Genetic variations using whole-exome sequencing might predict response for neoadjuvant chemoradiotherapy in locally advanced rectal cancer. Medical Oncology, 2018, 35, 145.	2.5	17
57	RNA-seq data of invasive ductal carcinoma and adjacent normal tissues from a Korean patient with breast cancer. Data in Brief, 2018, 18, 736-739.	1.0	4
58	Flavobacterium parvum sp. nov., isolated from soil polluted by sewer water. Journal of Microbiology, 2018, 56, 542-548.	2.8	2
59	RNA variant identification discrepancy among splice-aware alignment algorithms. PLoS ONE, 2018, 13, e0201822.	2.5	7
60	Integrative Bioinformatics and Functional Analyses of GEO, ENCODE, and TCGA Reveal FADD as a Direct Target of the Tumor Suppressor BRCA1. International Journal of Molecular Sciences, 2018, 19, 1458.	4.1	7
61	A case of interdigitating dendritic cell sarcoma studied by whole-exome sequencing. Genes and Genomics, 2018, 40, 1279-1285.	1.4	4
62	Roseomonas fluminis sp. nov. isolated from sediment of a shallow stream. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 782-787.	1.7	8
63	Uliginosibacterium sediminicola sp. nov., isolated from freshwater sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 924-929.	1.7	7
64	Ahniella affigens gen. nov., sp. nov., a gammaproteobacterium isolated from sandy soil near a stream. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2478-2484.	1.7	11
65	Paludirhabdus telluriireducens gen. nov., sp. nov. and Paludirhabdus pumila sp. nov., isolated from soil of a mountain wetland and emended description of Gorillibacterium massiliense. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3040-3046.	1.7	11
66	Chromatin remodeller Fun30Fft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. Nature Communications, 2017, 8, 14527.	12.8	41
67	The T47D cell line is an ideal experimental model to elucidate the progesterone-specific effects of a luminal A subtype of breast cancer. Biochemical and Biophysical Research Communications, 2017, 486, 752-758.	2.1	62
68	Type I interferons and the cytokine TNF cooperatively reprogram the macrophage epigenome to promote inflammatory activation. Nature Immunology, 2017, 18, 1104-1116.	14.5	204
69	The Ino80 complex mediates epigenetic centromere propagation via active removal of histone H3. Nature Communications, 2017, 8, 529.	12.8	14
70	Interferon-γ Represses M2 Gene Expression in Human Macrophages by Disassembling Enhancers Bound by the Transcription Factor MAF. Immunity, 2017, 47, 235-250.e4.	14.3	153
71	The 19S proteasome is directly involved in the regulation of heterochromatin spreading in fission yeast. Journal of Biological Chemistry, 2017, 292, 17144-17155.	3.4	22
72	Transcriptome analysis of non-small cell lung cancer and genetically matched adjacent normal tissues identifies novel prognostic marker genes. Genes and Genomics, 2017, 39, 277-284.	1.4	6

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73	Flavobacterium eburneum sp. nov., isolated from reclaimed saline land soil. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 55-59.	1.7	11
74	Chthonobacter albigriseus gen. nov., sp. nov., isolated from grass-field soil. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 883-888.	1.7	20
75	Sphingomonas silvisoli sp. nov., isolated from forest soil. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2704-2710.	1.7	15
76	Epigenetically altered miR-1247 functions as a tumor suppressor in pancreatic cancer. Oncotarget, 2017, 8, 26600-26612.	1.8	24
77	Combinatorial effects of an epigenetic inhibitor and ionizing radiation contribute to targeted elimination of pancreatic cancer stem cell. Oncotarget, 2017, 8, 89005-89020.	1.8	26
78	Dormant tumor cells expressing LOXL2 acquire a stem-like phenotype mediating their transition to proliferative growth. Oncotarget, 2016, 7, 71362-71377.	1.8	51
79	A Genome-Wide Methylation Approach Identifies a New Hypermethylated Gene Panel in Ulcerative Colitis. International Journal of Molecular Sciences, 2016, 17, 1291.	4.1	29
80	Janus Kinase 1 Is Essential for Inflammatory Cytokine Signaling and Mammary Gland Remodeling. Molecular and Cellular Biology, 2016, 36, 1673-1690.	2.3	24
81	Dankookia rubra gen. nov., sp. nov., an alphaproteobacterium isolated from sediment of a shallow stream. Journal of Microbiology, 2016, 54, 420-425.	2.8	15
82	Primary cancer cell culture: mammary-optimized vs conditional reprogramming. Endocrine-Related Cancer, 2016, 23, 535-554.	3.1	16
83	Histone Demethylase KDM6A Controls the Mammary Luminal Lineage through Enzyme-Independent Mechanisms. Molecular and Cellular Biology, 2016, 36, 2108-2120.	2.3	25
84	ETS family protein GABP is a novel co-factor strongly associated with genomic YY1 binding sites in various cell lines. Genes and Genomics, 2016, 38, 119-125.	1.4	3
85	An autoregulatory enhancer controls mammary-specific STAT5 functions. Nucleic Acids Research, 2016, 44, 1052-1063.	14.5	44
86	Sediminibacterium aquarii sp. nov., isolated from sediment in a fishbowl. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4501-4505.	1.7	14
87	Comparison of tamoxifen and letrozole response in mammary preneoplasia of ER and aromatase overexpressing mice defines an immune-associated gene signature linked to tamoxifen resistance. Carcinogenesis, 2015, 36, 122-132.	2.8	16
88	The methyltransferases enhancer of zeste homolog (EZH) 1 and EZH2 control hepatocyte homeostasis and regeneration. FASEB Journal, 2015, 29, 1653-1662.	0.5	45
89	An automated analysis pipeline for a large set of ChIP-seq data: AutoChIP. Genes and Genomics, 2015, 37, 305-311.	1.4	2
90	Genome-wide target site triplication of Alu elements in the human genome. Gene, 2015, 561, 283-291.	2.2	5

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91	Loss of EZH2 results in precocious mammary gland development and activation of STAT5-dependent genes. Nucleic Acids Research, 2015, 43, 8774-8789.	14.5	38
92	BLAT-Based Comparative Analysis for Transposable Elements: BLATCAT. BioMed Research International, 2014, 2014, 1-7.	1.9	0
93	Trp63 is regulated by STAT5 in mammary tissue and subject to differentiation in cancer. Endocrine-Related Cancer, 2014, 21, 443-457.	3.1	11
94	Coregulation of Genetic Programs by the Transcription Factors NFIB and STAT5. Molecular Endocrinology, 2014, 28, 758-767.	3.7	16
95	Mammary-Specific Gene Activation Is Defined by Progressive Recruitment of STAT5 during Pregnancy and the Establishment of H3K4me3 Marks. Molecular and Cellular Biology, 2014, 34, 464-473.	2.3	30
96	The STAT5-regulated miR-193b locus restrains mammary stem and progenitor cell activity and alveolar differentiation. Developmental Biology, 2014, 395, 245-254.	2.0	18
97	MiR-21 Is under Control of STAT5 but Is Dispensable for Mammary Development and Lactation. PLoS ONE, 2014, 9, e85123.	2.5	18
98	Comprehensive meta-analysis of Signal Transducers and Activators of Transcription (STAT) genomic binding patterns discerns cell-specific cis-regulatory modules. BMC Genomics, 2013, 14, 4.	2.8	67
99	Sequential activation of genetic programs in mouse mammary epithelium during pregnancy depends on STAT5A/B concentration. Nucleic Acids Research, 2013, 41, 1622-1636.	14.5	72
100	*MiR-193b* and *miR-365-1* are not required for the development and function of brown fat in the mouse. RNA Biology, 2013, 10, 1807-1814.	3.1	32
101	Hrp3 controls nucleosome positioning to suppress non-coding transcription in eu- and heterochromatin. EMBO Journal, 2012, 31, 4375-4387.	7.8	55
102	Genome-wide analyses reveal the extent of opportunistic STAT5 binding that does not yield transcriptional activation of neighboring genes. Nucleic Acids Research, 2012, 40, 4461-4472.	14.5	38
103	Retrotransposons as a major source of epigenetic variations in the mammalian genome. Epigenetics, 2012, 7, 370-382.	2.7	26
104	Genomic and bioinformatics tools to understand the biology of signal transducers and activators of transcription. Hormone Molecular Biology and Clinical Investigation, 2012, 10, 207-10.	0.7	0
105	Human Histone H3K79 Methyltransferase DOT1L Methyltransferase Binds Actively Transcribing RNA Polymerase II to Regulate Gene Expression. Journal of Biological Chemistry, 2012, 287, 39698-39709.	3.4	96
106	The liver-specific tumor suppressor STAT5 controls expression of the reactive oxygen species-generating enzyme NOX4 and the proapoptotic proteins PUMA and BIM in mice. Hepatology, 2012, 56, 2375-2386.	7.3	44
107	The *miR‑17/92* cluster is targeted by STAT5 but dispensable for mammary development. Genesis, 2012, 50, 665-671.	1.6	25
108	α1‑3/4 fucosylation at Asn 241 of β‑haptoglobin is a novel marker for colon cancer: A combinatorial approach for development of glycan biomarkers. International Journal of Cancer, 2012, 130, 2366-2376.	5.1	52

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109	Transcriptional changes of secreted Wnt antagonists in hindlimb skeletal muscle during the lifetime of the C57BL/6J mouse. Mechanisms of Ageing and Development, 2011, 132, 511-514.	4.6	0
110	Transcriptional repression of repeat-derived transcripts correlates with histone hypoacetylation at repetitive DNA elements in aged mice brain. Experimental Gerontology, 2011, 46, 811-818.	2.8	23
111	Decoding the genome with an integrative analysis tool: Combinatorial CRM Decoder. Nucleic Acids Research, 2011, 39, e116-e116.	14.5	6
112	Aebp2 as an Epigenetic Regulator for Neural Crest Cells. PLoS ONE, 2011, 6, e25174.	2.5	45
113	Evolutionary Conserved Motif Finder (ECMFinder) for genome-wide identification of clustered YY1- and CTCF-binding sites. Nucleic Acids Research, 2009, 37, 2003-2013.	14.5	18
114	YY1's role in DNA methylation of Peg3 and Xist. Nucleic Acids Research, 2009, 37, 5656-5664.	14.5	30
115	AEBP2 as a potential targeting protein for Polycomb Repression Complex PRC2. Nucleic Acids Research, 2009, 37, 2940-2950.	14.5	165
116	RhoB is epigenetically regulated in an age- and tissue-specific manner. Biochemical and Biophysical Research Communications, 2007, 362, 164-169.	2.1	15