

Keunsoo Kang

List of Publications by Year in descending order

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Version: 2024-02-01

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	Predicting commercially available antiviral drugs that may act on the novel coronavirus (SARS-CoV-2) through a drug-target interaction deep learning model. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 784-790.	4.1	568
2	Type I interferons and the cytokine TNF cooperatively reprogram the macrophage epigenome to promote inflammatory activation. <i>Nature Immunology</i> , 2017, 18, 1104-1116.	14.5	204
3	AEBP2 as a potential targeting protein for Polycomb Repression Complex PRC2. <i>Nucleic Acids Research</i> , 2009, 37, 2940-2950.	14.5	165
4	Interferon- β Represses M2 Gene Expression in Human Macrophages by Disassembling Enhancers Bound by the Transcription Factor MAF. <i>Immunity</i> , 2017, 47, 235-250.e4.	14.3	153
5	Human Histone H3K79 Methyltransferase DOT1L Methyltransferase Binds Actively Transcribing RNA Polymerase II to Regulate Gene Expression. <i>Journal of Biological Chemistry</i> , 2012, 287, 39698-39709.	3.4	96
6	Barrier to autointegration factor 1, procollagen α 1(I) lysine, 2-oxoglutarate 5- α -dioxygenase 3, and splicing factor 3b subunit 4 as early-stage cancer decision markers and drivers of hepatocellular carcinoma. <i>Hepatology</i> , 2018, 67, 1360-1377.	7.3	90
7	Sequential activation of genetic programs in mouse mammary epithelium during pregnancy depends on STAT5A/B concentration. <i>Nucleic Acids Research</i> , 2013, 41, 1622-1636.	14.5	72
8	IFN- β selectively suppresses a subset of TLR4-activated genes and enhancers to potentiate macrophage activation. <i>Nature Communications</i> , 2019, 10, 3320.	12.8	71
9	Comprehensive meta-analysis of Signal Transducers and Activators of Transcription (STAT) genomic binding patterns discerns cell-specific cis-regulatory modules. <i>BMC Genomics</i> , 2013, 14, 4.	2.8	67
10	The T47D cell line is an ideal experimental model to elucidate the progesterone-specific effects of a luminal A subtype of breast cancer. <i>Biochemical and Biophysical Research Communications</i> , 2017, 486, 752-758.	2.1	62
11	Octopus-toolkit: a workflow to automate mining of public epigenomic and transcriptomic next-generation sequencing data. <i>Nucleic Acids Research</i> , 2018, 46, e53-e53.	14.5	61
12	QKI, a miR-200 target gene, suppresses epithelial-to-mesenchymal transition and tumor growth. <i>International Journal of Cancer</i> , 2019, 145, 1585-1595.	5.1	59
13	Hrp3 controls nucleosome positioning to suppress non-coding transcription in eu- and heterochromatin. <i>EMBO Journal</i> , 2012, 31, 4375-4387.	7.8	55
14	β 1-4 fucosylation at Asn 241 of α 1-haptoglobin is a novel marker for colon cancer: A combinatorial approach for development of glycan biomarkers. <i>International Journal of Cancer</i> , 2012, 130, 2366-2376.	5.1	52
15	Dormant tumor cells expressing LOXL2 acquire a stem-like phenotype mediating their transition to proliferative growth. <i>Oncotarget</i> , 2016, 7, 71362-71377.	1.8	51
16	The methyltransferases enhancer of zeste homolog (EZH) 1 and EZH2 control hepatocyte homeostasis and regeneration. <i>FASEB Journal</i> , 2015, 29, 1653-1662.	0.5	45
17	Aebp2 as an Epigenetic Regulator for Neural Crest Cells. <i>PLoS ONE</i> , 2011, 6, e25174.	2.5	45
18	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. <i>Hepatology</i> , 2012, 56, 2375-2386.	7.3	44

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19	An autoregulatory enhancer controls mammary-specific STAT5 functions. <i>Nucleic Acids Research</i> , 2016, 44, 1052-1063.	14.5	44
20	Chromatin remodeller Fun30ft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. <i>Nature Communications</i> , 2017, 8, 14527.	12.8	41
21	Upregulation of Ets1 expression by NFATc2 and NFkB1/RELA promotes breast cancer cell invasiveness. <i>Oncogenesis</i> , 2018, 7, 91.	4.9	41
22	Aberrantly hypermethylated tumor suppressor genes were identified in oral squamous cell carcinoma (OSCC). <i>Clinical Epigenetics</i> , 2019, 11, 116.	4.1	41
23	MiR-34a and miR-34b/c have distinct effects on the suppression of lung adenocarcinomas. <i>Experimental and Molecular Medicine</i> , 2019, 51, 1-10.	7.7	39
24	Genome-wide analyses reveal the extent of opportunistic STAT5 binding that does not yield transcriptional activation of neighboring genes. <i>Nucleic Acids Research</i> , 2012, 40, 4461-4472.	14.5	38
25	Loss of EZH2 results in precocious mammary gland development and activation of STAT5-dependent genes. <i>Nucleic Acids Research</i> , 2015, 43, 8774-8789.	14.5	38
26	<i>miR-193b</i> and <i>miR-365-1</i> are not required for the development and function of brown fat in the mouse. <i>RNA Biology</i> , 2013, 10, 1807-1814.	3.1	32
27	A Simple Guideline to Assess the Characteristics of RNA-Seq Data. <i>BioMed Research International</i> , 2018, 2018, 1-9.	1.9	32
28	YY1's role in DNA methylation of Peg3 and Xist. <i>Nucleic Acids Research</i> , 2009, 37, 5656-5664.	14.5	30
29	Mammary-Specific Gene Activation Is Defined by Progressive Recruitment of STAT5 during Pregnancy and the Establishment of H3K4me3 Marks. <i>Molecular and Cellular Biology</i> , 2014, 34, 464-473.	2.3	30
30	A Genome-Wide Methylation Approach Identifies a New Hypermethylated Gene Panel in Ulcerative Colitis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1291.	4.1	29
31	The transcription factor Foxp1 preserves integrity of an active Foxp3 locus in extrathymic Treg cells. <i>Nature Communications</i> , 2018, 9, 4473.	12.8	29
32	Retrotransposons as a major source of epigenetic variations in the mammalian genome. <i>Epigenetics</i> , 2012, 7, 370-382.	2.7	26
33	Cancer-associated fibroblasts activated by miR-196a promote the migration and invasion of lung cancer cells. <i>Cancer Letters</i> , 2021, 508, 92-103.	7.2	26
34	Combinatorial effects of an epigenetic inhibitor and ionizing radiation contribute to targeted elimination of pancreatic cancer stem cell. <i>Oncotarget</i> , 2017, 8, 89005-89020.	1.8	26
35	The <i>miR-17/92</i> cluster is targeted by STAT5 but dispensable for mammary development. <i>Genesis</i> , 2012, 50, 665-671.	1.6	25
36	Histone Demethylase KDM6A Controls the Mammary Luminal Lineage through Enzyme-Independent Mechanisms. <i>Molecular and Cellular Biology</i> , 2016, 36, 2108-2120.	2.3	25

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37	Janus Kinase 1 Is Essential for Inflammatory Cytokine Signaling and Mammary Gland Remodeling. <i>Molecular and Cellular Biology</i> , 2016, 36, 1673-1690.	2.3	24
38	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. <i>Viruses</i> , 2020, 12, 1325.	3.3	24
39	Epigenetically altered miR-1247 functions as a tumor suppressor in pancreatic cancer. <i>Oncotarget</i> , 2017, 8, 26600-26612.	1.8	24
40	Transcriptional repression of repeat-derived transcripts correlates with histone hypoacetylation at repetitive DNA elements in aged mice brain. <i>Experimental Gerontology</i> , 2011, 46, 811-818.	2.8	23
41	The 19S proteasome is directly involved in the regulation of heterochromatin spreading in fission yeast. <i>Journal of Biological Chemistry</i> , 2017, 292, 17144-17155.	3.4	22
42	Differentially Expressed Genes in Matched Normal, Cancer, and Lymph Node Metastases Predict Clinical Outcomes in Patients With Breast Cancer. <i>Applied Immunohistochemistry and Molecular Morphology</i> , 2020, 28, 111-122.	1.2	22
43	Integration of transcriptomics, proteomics and metabolomics identifies biomarkers for pulmonary injury by polyhexamethylene guanidine phosphate (PHMG-p), a humidifier disinfectant, in rats. <i>Archives of Toxicology</i> , 2020, 94, 887-909.	4.2	20
44	<i>Chthonobacter albigriseus</i> gen. nov., sp. nov., isolated from grass-field soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 883-888.	1.7	20
45	Enhancer RNAs stimulate Pol II pause release by harnessing multivalent interactions to NELF. <i>Nature Communications</i> , 2022, 13, 2429.	12.8	19
46	Evolutionary Conserved Motif Finder (ECMFinder) for genome-wide identification of clustered YY1- and CTCF-binding sites. <i>Nucleic Acids Research</i> , 2009, 37, 2003-2013.	14.5	18
47	The STAT5-regulated miR-193b locus restrains mammary stem and progenitor cell activity and alveolar differentiation. <i>Developmental Biology</i> , 2014, 395, 245-254.	2.0	18
48	MiR-21 Is under Control of STAT5 but Is Dispensable for Mammary Development and Lactation. <i>PLoS ONE</i> , 2014, 9, e85123.	2.5	18
49	TAp73 inhibits cell invasion and migration by directly activating KAI1 expression in colorectal carcinoma. <i>Cancer Letters</i> , 2018, 415, 106-116.	7.2	18
50	Genetic variations using whole-exome sequencing might predict response for neoadjuvant chemoradiotherapy in locally advanced rectal cancer. <i>Medical Oncology</i> , 2018, 35, 145.	2.5	17
51	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. <i>Cells</i> , 2019, 8, 878.	4.1	17
52	Tiotropium Is Predicted to Be a Promising Drug for COVID-19 Through Transcriptome-Based Comprehensive Molecular Pathway Analysis. <i>Viruses</i> , 2020, 12, 776.	3.3	17
53	Coregulation of Genetic Programs by the Transcription Factors NFIB and STAT5. <i>Molecular Endocrinology</i> , 2014, 28, 758-767.	3.7	16
54	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. <i>Carcinogenesis</i> , 2015, 36, 122-132.	2.8	16

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55	Primary cancer cell culture: mammary-optimized vs conditional reprogramming. <i>Endocrine-Related Cancer</i> , 2016, 23, 535-554.	3.1	16
56	Genome-wide blood DNA methylation analysis in patients with delayed cerebral ischemia after subarachnoid hemorrhage. <i>Scientific Reports</i> , 2020, 10, 11419.	3.3	16
57	Nucleoporin 210 Serves a Key Scaffold for SMARCB1 in Liver Cancer. <i>Cancer Research</i> , 2021, 81, 356-370.	0.9	16
58	RhoB is epigenetically regulated in an age- and tissue-specific manner. <i>Biochemical and Biophysical Research Communications</i> , 2007, 362, 164-169.	2.1	15
59	<i>Dankookia rubra</i> gen. nov., sp. nov., an alphaproteobacterium isolated from sediment of a shallow stream. <i>Journal of Microbiology</i> , 2016, 54, 420-425.	2.8	15
60	Expression of EEF1A1 Is Associated with Prognosis of Patients with Colon Adenocarcinoma. <i>Journal of Clinical Medicine</i> , 2019, 8, 1903.	2.4	15
61	Bcl11b prevents catastrophic autoimmunity by controlling multiple aspects of a regulatory T cell gene expression program. <i>Science Advances</i> , 2019, 5, eaaw0706.	10.3	15
62	ETS1 Suppresses Tumorigenesis of Human Breast Cancer via Trans-Activation of Canonical Tumor Suppressor Genes. <i>Frontiers in Oncology</i> , 2020, 10, 642.	2.8	15
63	<i>Sphingomonas silvisoli</i> sp. nov., isolated from forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2704-2710.	1.7	15
64	The Ino80 complex mediates epigenetic centromere propagation via active removal of histone H3. <i>Nature Communications</i> , 2017, 8, 529.	12.8	14
65	Inhibition of STAT3 enhances sensitivity to tamoxifen in tamoxifen-resistant breast cancer cells. <i>BMC Cancer</i> , 2021, 21, 931.	2.6	14
66	<i>Sediminibacterium aquarii</i> sp. nov., isolated from sediment in a fishbowl. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4501-4505.	1.7	14
67	<i>Gramella fulva</i> sp. nov., isolated from a dry surface of tidal flat. <i>Journal of Microbiology</i> , 2019, 57, 23-29.	2.8	13
68	SMARCA4 oncogenic potential via IRAK1 enhancer to activate Gankyrin and AKR1B10 in liver cancer. <i>Oncogene</i> , 2021, 40, 4652-4662.	5.9	13
69	Wx: a neural network-based feature selection algorithm for transcriptomic data. <i>Scientific Reports</i> , 2019, 9, 10500.	3.3	12
70	P-TEFb Regulates Transcriptional Activation in Non-coding RNA Genes. <i>Frontiers in Genetics</i> , 2019, 10, 342.	2.3	12
71	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. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6141.	4.1	12
72	Trp63 is regulated by STAT5 in mammary tissue and subject to differentiation in cancer. <i>Endocrine-Related Cancer</i> , 2014, 21, 443-457.	3.1	11

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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	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
75	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
76	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
77	Ets1 suppresses atopic dermatitis by suppressing pathogenic T cell responses. JCI Insight, 2019, 4, .	5.0	10
78	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
79	Cascaded Wx: A Novel Prognosis-Related Feature Selection Framework in Human Lung Adenocarcinoma Transcriptomes. Frontiers in Genetics, 2019, 10, 662.	2.3	9
80	Transposable element-mediated structural variation analysis in dog breeds using whole-genome sequencing. Mammalian Genome, 2019, 30, 289-300.	2.2	9
81	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
82	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
83	BRCA1-BARD1 regulates transcription through modulating topoisomerase II β . Open Biology, 2021, 11, 210221.	3.6	9
84	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
85	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
86	RNA variant identification discrepancy among splice-aware alignment algorithms. PLoS ONE, 2018, 13, e0201822.	2.5	7
87	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
88	Functional coordination of BET family proteins underlies altered transcription associated with memory impairment in fragile X syndrome. Science Advances, 2021, 7, .	10.3	7
89	Epigenetic Upregulation of MAGE-A Isoforms Promotes Breast Cancer Cell Aggressiveness. Cancers, 2021, 13, 3176.	3.7	7
90	Uliginosibacterium sediminicola sp. nov., isolated from freshwater sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 924-929.	1.7	7

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91	Decoding the genome with an integrative analysis tool: Combinatorial CRM Decoder. <i>Nucleic Acids Research</i> , 2011, 39, e116-e116.	14.5	6
92	Transcriptome analysis of non-small cell lung cancer and genetically matched adjacent normal tissues identifies novel prognostic marker genes. <i>Genes and Genomics</i> , 2017, 39, 277-284.	1.4	6
93	Genome-wide analysis of DNA methylation identifies novel differentially methylated regions associated with lipid accumulation improved by ethanol extracts of <i>Allium tuberosum</i> and <i>Capsella bursa-pastoris</i> in a cell model. <i>PLoS ONE</i> , 2019, 14, e0217877.	2.5	6
94	Genome-wide target site triplication of Alu elements in the human genome. <i>Gene</i> , 2015, 561, 283-291.	2.2	5
95	Machine learning based anti-cancer drug response prediction and search for predictor genes using cancer cell line gene expression. <i>Genomics and Informatics</i> , 2021, 19, e10.	0.8	5
96	Integrative Transcriptome Profiling Reveals SKA3 as a Novel Prognostic Marker in Non-Muscle Invasive Bladder Cancer. <i>Cancers</i> , 2021, 13, 4673.	3.7	5
97	RNA-seq data of invasive ductal carcinoma and adjacent normal tissues from a Korean patient with breast cancer. <i>Data in Brief</i> , 2018, 18, 736-739.	1.0	4
98	A case of interdigitating dendritic cell sarcoma studied by whole-exome sequencing. <i>Genes and Genomics</i> , 2018, 40, 1279-1285.	1.4	4
99	Hormone Receptor-Status Prediction in Breast Cancer Using Gene Expression Profiles and Their Macroscopic Landscape. <i>Cancers</i> , 2020, 12, 1165.	3.7	4
100	Tetraarsenic oxide affects non-coding RNA transcriptome through deregulating polycomb complexes in MCF7 cells. <i>Advances in Biological Regulation</i> , 2021, 80, 100809.	2.3	4
101	Epigenomic Analysis of RAD51 ChIP-seq Data Reveals cis-regulatory Elements Associated with Autophagy in Cancer Cell Lines. <i>Cancers</i> , 2021, 13, 2547.	3.7	4
102	Molecular laterality encodes stress susceptibility in the medial prefrontal cortex. <i>Molecular Brain</i> , 2021, 14, 92.	2.6	4
103	Characterization of transcriptome diversity and in vitro behavior of primary human high-risk breast cells. <i>Scientific Reports</i> , 2022, 12, 6159.	3.3	4
104	Alu RNA induces NLRP3 expression through TLR7 activation in α -1-antitrypsin-deficient macrophages. <i>JCI Insight</i> , 2022, 7, .	5.0	4
105	ETS family protein GABP is a novel co-factor strongly associated with genomic YY1 binding sites in various cell lines. <i>Genes and Genomics</i> , 2016, 38, 119-125.	1.4	3
106	TraRECO: a greedy approach based de novo transcriptome assembler with read error correction using consensus matrix. <i>BMC Genomics</i> , 2018, 19, 653.	2.8	3
107	A Brief Review of Machine Learning-Based Bioactive Compound Research. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 2906.	2.5	3
108	An automated analysis pipeline for a large set of ChIP-seq data: AutoChIP. <i>Genes and Genomics</i> , 2015, 37, 305-311.	1.4	2

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109	Flavobacterium parvum sp. nov., isolated from soil polluted by sewer water. Journal of Microbiology, 2018, 56, 542-548.	2.8	2
110	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
111	ZEB1-regulated Inc-Nr2f1 promotes the migration and invasion of lung adenocarcinoma cells. Cancer Letters, 2022, 533, 215601.	7.2	2
112	Modulation of Human Mesenchymal Stem Cells by Electrical Stimulation Using an Enzymatic Biofuel Cell. Catalysts, 2021, 11, 62.	3.5	1
113	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
114	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
115	BLAT-Based Comparative Analysis for Transposable Elements: BLATCAT. BioMed Research International, 2014, 2014, 1-7.	1.9	0
116	Abstract LB043: Identification and characterization of cancer-associated fibroblast subpopulations in lung adenocarcinoma. Cancer Research, 2022, 82, LB043-LB043.	0.9	0