Sung-Min Ahn

List of Publications by Year
in descending order

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62 papers	4,385 citations	236925 25 h-index	138484 58 g-index
63 all docs	63 docs citations	63 times ranked	11690 citing authors

#	Article	IF	Citations
1	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
2	Genomic portrait of resectable hepatocellular carcinomas: Implications of <i>RB1</i> and <i>FGF19</i> aberrations for patient stratification. Hepatology, 2014, 60, 1972-1982.	7.3	345
3	The first Korean genome sequence and analysis: Full genome sequencing for a socio-ethnic group. Genome Research, 2009, 19, 1622-1629.	5.5	282
4	Proteomic Analysis of Exosomes from Human Neural Stem Cells by Flow Field-Flow Fractionation and Nanoflow Liquid Chromatographyâˆ’Tandem Mass Spectrometry. Journal of Proteome Research, 2008, 7, 3475-3480.	3.7	161
5	Monogenic and polygenic determinants of sarcoma risk: an international genetic study. Lancet Oncology, The, 2016, 17, 1261-1271.	10.7	161
6	Population Specific Biomarkers of Human Aging: A Big Data Study Using South Korean, Canadian, and Eastern European Patient Populations. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2018, 73, 1482-1490.	3.6	133
7	Integrated Expression Profiling and Genome-Wide Analysis of ChREBP Targets Reveals the Dual Role for ChREBP in Glucose-Regulated Gene Expression. PLoS ONE, 2011, 6, e22544.	2.5	130
8	FGF19â€“FGFR4 Signaling in Hepatocellular Carcinoma. Cells, 2019, 8, 536.	4.1	101
9	Comparative Genomic Analysis of Primary and Synchronous Metastatic Colorectal Cancers. PLoS ONE, 2014, 9, e90459.	2.5	98
10	Body fluid proteomics: Prospects for biomarker discovery. Proteomics - Clinical Applications, 2007, 1, 1004-1015.	1.6	91
11	Smad3 regulates E-cadherin via miRNA-200 pathway. Oncogene, 2012, 31, 3051-3059.	5.9	91
12	Alterations in peripheral blood levels of TIMP-1, MMP-2, and MMP-9 in patients with type-2 diabetes. Diabetes Research and Clinical Practice, 2005, 69, 175-179.	2.8	84
13	Human Microglial Cells Synthesize Albumin in Brain. PLoS ONE, 2008, 3, e2829.	2.5	76
14	Antiâ€“miR-21 Suppresses Hepatocellular Carcinoma Growth via Broad Transcriptional Network Deregulation. Molecular Cancer Research, 2015, 13, 1009-1021.	3.4	69
15	Genome-wide copy number variation in Hanwoo, Black Angus, and Holstein cattle. Mammalian Genome, 2013, 24, 151-163.	2.2	66
16	The somatic <i>POLE</i> P286R mutation defines a unique subclass of colorectal cancer featuring hypermutation, representing a potential genomic biomarker for immunotherapy. Oncotarget, 2016, 7, 68638-68649.	1.8	59
17	Whole-genome resequencing of Hanwoo (Korean cattle) and insight into regions of homozygosity. BMC Genomics, 2013, 14, 519.	2.8	55
18	Cell cycle-regulated expression and subcellular localization of a kinesin-8 member human KIF18B. Gene, 2010, 466, 16-25.	2.2	51

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19	Dualâ€Specificity Phosphatase 5 Attenuates Autoimmune Arthritis in Mice via Reciprocal Regulation of the Th17/Treg Cell Balance and Inhibition of Osteoclastogenesis. Arthritis and Rheumatology, 2014, 66, 3083-3095.	5.6	40
20	Cold-inducible RNA-binding protein, CIRP, inhibits DNA damage-induced apoptosis by regulating p53. Biochemical and Biophysical Research Communications, 2015, 464, 916-921.	2.1	39
21	Miniaturized asymmetrical flow field-flow fractionation: Application to biological vesicles. Journal of Separation Science, 2007, 30, 1082-1087.	2.5	38
22	Olig2-Induced Neural Stem Cell Differentiation Involves Downregulation of Wnt Signaling and Induction of Dickkopf-1 Expression. PLoS ONE, 2008, 3, e3917.	2.5	36
23	The Fos-Related Antigen 1â€"JUNB/Activator Protein 1 Transcription Complex, a Downstream Target of Signal Transducer and Activator of Transcription 3, Induces T Helper 17 Differentiation and Promotes Experimental Autoimmune Arthritis. Frontiers in Immunology, 2017, 8, 1793.	4.8	31
24	RNA-binding properties and RNA chaperone activity of human peroxiredoxin 1. Biochemical and Biophysical Research Communications, 2012, 425, 730-734.	2.1	29
25	Characterization of Hepatocellular Carcinoma Patients with FGF19 Amplification Assessed by Fluorescence in situ Hybridization: A Large Cohort Study. Liver Cancer, 2019, 8, 12-23.	7.7	27
26	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
27	Stem cell markers: Insights from membrane proteomics?. Proteomics, 2008, 8, 4946-4957.	2.2	25
28	Secretome Analysis of Human Oligodendrocytes Derived from Neural Stem Cells. PLoS ONE, 2014, 9, e84292.	2.5	24
29	Role of Interleukin 28B-related Gene Polymorphisms in Chronic Hepatitis C and the Response to Antiviral Therapy in Koreans. Journal of Clinical Gastroenterology, 2013, 47, 644-650.	2.2	21
30	Targeted exon sequencing fails to identify rare coding variants with large effect in rheumatoid arthritis. Arthritis Research and Therapy, 2014, 16, 447.	3.5	20
31	Large-scale production of soluble recombinant amyloid-Î² peptide 1â€"42 using cold-inducible expression system. Protein Expression and Purification, 2012, 86, 53-57.	1.3	19
32	Paired Primary and Metastatic Tumor Analysis of Somatic Mutations in Synchronous and Metachronous Colorectal Cancer. Cancer Research and Treatment, 2017, 49, 161-167.	3.0	19
33	FGFR1 expression defines clinically distinct subtypes in pancreatic cancer. Journal of Translational Medicine, 2018, 16, 374.	4.4	18
34	A Nine-Gene Signature for Predicting the Response to Preoperative Chemoradiotherapy in Patients with Locally Advanced Rectal Cancer. Cancers, 2020, 12, 800.	3.7	18
35	Genomic Alterations in the RB Pathway Indicate Prognostic Outcomes of Early-Stage Lung Adenocarcinoma. Clinical Cancer Research, 2015, 21, 2613-2623.	7.0	16
36	Cold-inducible RNA-binding protein promotes epithelial-mesenchymal transition by activating ERK and p38 pathways. Biochemical and Biophysical Research Communications, 2016, 477, 1038-1044.	2.1	13

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37	Genomics and proteomics in stem cell research: the road ahead. Anatomy and Cell Biology, 2010, 43, 1.	1.0	12
38	The Impact of Inosine Triphosphatase Variants on Hemoglobin Level and Sustained Virologic Response of Chronic Hepatitis C in Korean. Journal of Korean Medical Science, 2013, 28, 1213.	2.5	10
39	Distribution pattern of tumor infiltrating lymphocytes and tumor microenvironment composition as prognostic indicators in anorectal malignant melanoma. Modern Pathology, 2021, 34, 141-160.	5.5	9
40	KF-1607, a Novel Pan Src Kinase Inhibitor, Attenuates Obstruction-Induced Tubulointerstitial Fibrosis in Mice. Biomolecules and Therapeutics, 2021, 29, 41-51.	2.4	9
41	The clinical implications of G1-G6 transcriptomic signature and 5-gene score in Korean patients with hepatocellular carcinoma. BMC Cancer, 2018, 18, 571.	2.6	8
42	Peroxiredoxin 1 post-transcriptionally regulates snoRNA expression. Free Radical Biology and Medicine, 2019, 141, 1-9.	2.9	8
43	SOLiDzipper: A High Speed Encoding Method for the Next-Generation Sequencing Data. Evolutionary Bioinformatics, 2011, 7, EBO.S6618.	1.2	7
44	Characterization of human SMARCE1r high-mobility-group protein. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1574, 269-276.	2.4	6
45	Increased genomic damage and vitamin B status in inflammatory bowel disease patients: A case-control, prospective, pilot study. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2019, 837, 42-47.	1.7	6
46	Revising a Personal Genome by Comparing and Combining Data from Two Different Sequencing Platforms. PLoS ONE, 2013, 8, e60585.	2.5	5
47	Establishment and characterization of patient-derived xenograft models of gastrointestinal stromal tumor resistant to standard tyrosine kinase inhibitors. Oncotarget, 2017, 8, 76712-76721.	1.8	5
48	Src is essential for the endosomal delivery of the FGFR4 signaling complex in hepatocellular carcinoma. Journal of Translational Medicine, 2021, 19, 138.	4.4	4
49	cMapper: gene-centric connectivity mapper for EBI-RDF platform. Bioinformatics, 2017, 33, 266-271.	4.1	3
50	Genomics of drug sensitivity in bladder cancer: an integrated resource for pharmacogenomic analysis in bladder cancer. BMC Medical Genomics, 2018, 11, 88.	1.5	3
51	IPCT: Integrated Pharmacogenomic Platform of Human Cancer Cell Lines and Tissues. Genes, 2019, 10, 171.	2.4	3
52	Validation for Accuracy of Cancer Diagnosis in Electronic Medical Records Using a Text Mining Method. Studies in Health Technology and Informatics, 2015, 216, 882.	0.3	3
53	Gevab: a prototype genome variation analysis browsing server. BMC Bioinformatics, 2009, 10, S3.	2.6	2
54	Phenotype-Genotype Association Study: From GWAS to NGS. Endocrinology and Metabolism, 2011, 26, 187.	3.0	2

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55	Proteomic Strategies for Analyzing Body Fluids. , 2007, , 3-30.		2
56	Human microglial cells synthesize albumin in brain. Nature Precedings, 2008, , .	0.1	1
57	Influence of DNA Concentration on the Interfacial Electrode Impedance. Journal of Nanoscience and Nanotechnology, 2013, 13, 7291-7294.	0.9	1
58	Characterization of HLAâ€A33:03 epitopes via immunoprecipitation and LCâ€MS/MS. Proteomics, 2021, , 2100171.	2.2	1
59	Genetic characterization of Northeast Asian cattle based on sequence polymorphisms in the complete mitochondrial genome. Open Journal of Animal Sciences, 2012, 02, 217-223.	0.6	1
60	Genotoxicity in Patients on Long-term Proton Pump Inhibitor Therapy in Korea: A Nested Case-control, Prospective, Pilot Study. The Korean Journal of Helicobacter and Upper Gastrointestinal Research, 2020, 20, 47-53.	0.4	1
61	Reply. Hepatology, 2015, 62, 1324-1325.	7.3	0
62	Data on the stability of Prx1-associated snRNAs and mRNAs. Data in Brief, 2019, 25, 104309.	1.0	0