

Sung-Min Ahn

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

4,385
citations

236925

25
h-index

138484

58
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63
all docs

63
docs citations

63
times ranked

11690
citing authors

#	ARTICLE	IF	CITATIONS
1	Distribution pattern of tumor infiltrating lymphocytes and tumor microenvironment composition as prognostic indicators in anorectal malignant melanoma. <i>Modern Pathology</i> , 2021, 34, 141-160.	5.5	9
2	KF-1607, a Novel Pan Src Kinase Inhibitor, Attenuates Obstruction-Induced Tubulointerstitial Fibrosis in Mice. <i>Biomolecules and Therapeutics</i> , 2021, 29, 41-51.	2.4	9
3	Src is essential for the endosomal delivery of the FGFR4 signaling complex in hepatocellular carcinoma. <i>Journal of Translational Medicine</i> , 2021, 19, 138.	4.4	4
4	Characterization of HLA-A*33:03 epitopes via immunoprecipitation and LC-MS/MS. <i>Proteomics</i> , 2021, , 2100171.	2.2	1
5	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	12.8	27
6	A Nine-Gene Signature for Predicting the Response to Preoperative Chemoradiotherapy in Patients with Locally Advanced Rectal Cancer. <i>Cancers</i> , 2020, 12, 800.	3.7	18
7	Genotoxicity in Patients on Long-term Proton Pump Inhibitor Therapy in Korea: A Nested Case-control, Prospective, Pilot Study. <i>The Korean Journal of Helicobacter and Upper Gastrointestinal Research</i> , 2020, 20, 47-53.	0.4	1
8	Data on the stability of Prx1-associated snRNAs and mRNAs. <i>Data in Brief</i> , 2019, 25, 104309.	1.0	0
9	Characterization of Hepatocellular Carcinoma Patients with FGF19 Amplification Assessed by Fluorescence in situ Hybridization: A Large Cohort Study. <i>Liver Cancer</i> , 2019, 8, 12-23.	7.7	27
10	FGF19-FGFR4 Signaling in Hepatocellular Carcinoma. <i>Cells</i> , 2019, 8, 536.	4.1	101
11	Peroxiredoxin 1 post-transcriptionally regulates snoRNA expression. <i>Free Radical Biology and Medicine</i> , 2019, 141, 1-9.	2.9	8
12	IPCT: Integrated Pharmacogenomic Platform of Human Cancer Cell Lines and Tissues. <i>Genes</i> , 2019, 10, 171.	2.4	3
13	Increased genomic damage and vitamin B status in inflammatory bowel disease patients: A case-control, prospective, pilot study. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2019, 837, 42-47.	1.7	6
14	Population Specific Biomarkers of Human Aging: A Big Data Study Using South Korean, Canadian, and Eastern European Patient Populations. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 1482-1490.	3.6	133
15	FGFR1 expression defines clinically distinct subtypes in pancreatic cancer. <i>Journal of Translational Medicine</i> , 2018, 16, 374.	4.4	18
16	Genomics of drug sensitivity in bladder cancer: an integrated resource for pharmacogenomic analysis in bladder cancer. <i>BMC Medical Genomics</i> , 2018, 11, 88.	1.5	3
17	The clinical implications of G1-G6 transcriptomic signature and 5-gene score in Korean patients with hepatocellular carcinoma. <i>BMC Cancer</i> , 2018, 18, 571.	2.6	8
18	cMapper: gene-centric connectivity mapper for EBI-RDF platform. <i>Bioinformatics</i> , 2017, 33, 266-271.	4.1	3

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19	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. <i>Frontiers in Immunology</i> , 2017, 8, 1793.	4.8	31
20	Establishment and characterization of patient-derived xenograft models of gastrointestinal stromal tumor resistant to standard tyrosine kinase inhibitors. <i>Oncotarget</i> , 2017, 8, 76712-76721.	1.8	5
21	Paired Primary and Metastatic Tumor Analysis of Somatic Mutations in Synchronous and Metachronous Colorectal Cancer. <i>Cancer Research and Treatment</i> , 2017, 49, 161-167.	3.0	19
22	The somatic <i>POLE</i> P286R mutation defines a unique subclass of colorectal cancer featuring hypermutation, representing a potential genomic biomarker for immunotherapy. <i>Oncotarget</i> , 2016, 7, 68638-68649.	1.8	59
23	Cold-inducible RNA-binding protein promotes epithelial-mesenchymal transition by activating ERK and p38 pathways. <i>Biochemical and Biophysical Research Communications</i> , 2016, 477, 1038-1044.	2.1	13
24	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
25	Monogenic and polygenic determinants of sarcoma risk: an international genetic study. <i>Lancet Oncology</i> , The, 2016, 17, 1261-1271.	10.7	161
26	Reply. <i>Hepatology</i> , 2015, 62, 1324-1325.	7.3	0
27	Antiâ€“miR-21 Suppresses Hepatocellular Carcinoma Growth via Broad Transcriptional Network Dereglulation. <i>Molecular Cancer Research</i> , 2015, 13, 1009-1021.	3.4	69
28	Genomic Alterations in the RB Pathway Indicate Prognostic Outcomes of Early-Stage Lung Adenocarcinoma. <i>Clinical Cancer Research</i> , 2015, 21, 2613-2623.	7.0	16
29	Cold-inducible RNA-binding protein, CIRP, inhibits DNA damage-induced apoptosis by regulating p53. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 916-921.	2.1	39
30	Validation for Accuracy of Cancer Diagnosis in Electronic Medical Records Using a Text Mining Method. <i>Studies in Health Technology and Informatics</i> , 2015, 216, 882.	0.3	3
31	Targeted exon sequencing fails to identify rare coding variants with large effect in rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2014, 16, 447.	3.5	20
32	Dualâ€“Specificity Phosphatase 5 Attenuates Autoimmune Arthritis in Mice via Reciprocal Regulation of the Th17/Treg Cell Balance and Inhibition of Osteoclastogenesis. <i>Arthritis and Rheumatology</i> , 2014, 66, 3083-3095.	5.6	40
33	Genomic portrait of resectable hepatocellular carcinomas: Implications of <i>RB1</i> and <i>FGF19</i> aberrations for patient stratification. <i>Hepatology</i> , 2014, 60, 1972-1982.	7.3	345
34	Secretome Analysis of Human Oligodendrocytes Derived from Neural Stem Cells. <i>PLoS ONE</i> , 2014, 9, e84292.	2.5	24
35	Comparative Genomic Analysis of Primary and Synchronous Metastatic Colorectal Cancers. <i>PLoS ONE</i> , 2014, 9, e90459.	2.5	98
36	Genome-wide copy number variation in Hanwoo, Black Angus, and Holstein cattle. <i>Mammalian Genome</i> , 2013, 24, 151-163.	2.2	66

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37	Whole-genome resequencing of Hanwoo (Korean cattle) and insight into regions of homozygosity. <i>BMC Genomics</i> , 2013, 14, 519.	2.8	55
38	Influence of DNA Concentration on the Interfacial Electrode Impedance. <i>Journal of Nanoscience and Nanotechnology</i> , 2013, 13, 7291-7294.	0.9	1
39	Role of Interleukin 28B-related Gene Polymorphisms in Chronic Hepatitis C and the Response to Antiviral Therapy in Koreans. <i>Journal of Clinical Gastroenterology</i> , 2013, 47, 644-650.	2.2	21
40	The Impact of Inosine Triphosphatase Variants on Hemoglobin Level and Sustained Virologic Response of Chronic Hepatitis C in Korean. <i>Journal of Korean Medical Science</i> , 2013, 28, 1213.	2.5	10
41	Revising a Personal Genome by Comparing and Combining Data from Two Different Sequencing Platforms. <i>PLoS ONE</i> , 2013, 8, e60585.	2.5	5
42	RNA-binding properties and RNA chaperone activity of human peroxiredoxin 1. <i>Biochemical and Biophysical Research Communications</i> , 2012, 425, 730-734.	2.1	29
43	Smad3 regulates E-cadherin via miRNA-200 pathway. <i>Oncogene</i> , 2012, 31, 3051-3059.	5.9	91
44	Large-scale production of soluble recombinant amyloid- β peptide 1-42 using cold-inducible expression system. <i>Protein Expression and Purification</i> , 2012, 86, 53-57.	1.3	19
45	Genetic characterization of Northeast Asian cattle based on sequence polymorphisms in the complete mitochondrial genome. <i>Open Journal of Animal Sciences</i> , 2012, 02, 217-223.	0.6	1
46	Phenotype-Genotype Association Study: From GWAS to NGS. <i>Endocrinology and Metabolism</i> , 2011, 26, 187.	3.0	2
47	SOLiDzipper: A High Speed Encoding Method for the Next-Generation Sequencing Data. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S6618.	1.2	7
48	Integrated Expression Profiling and Genome-Wide Analysis of ChREBP Targets Reveals the Dual Role for ChREBP in Glucose-Regulated Gene Expression. <i>PLoS ONE</i> , 2011, 6, e22544.	2.5	130
49	Genomics and proteomics in stem cell research: the road ahead. <i>Anatomy and Cell Biology</i> , 2010, 43, 1.	1.0	12
50	Cell cycle-regulated expression and subcellular localization of a kinesin-8 member human KIF18B. <i>Gene</i> , 2010, 466, 16-25.	2.2	51
51	Gevab: a prototype genome variation analysis browsing server. <i>BMC Bioinformatics</i> , 2009, 10, S3.	2.6	2
52	The first Korean genome sequence and analysis: Full genome sequencing for a socio-ethnic group. <i>Genome Research</i> , 2009, 19, 1622-1629.	5.5	282
53	Stem cell markers: Insights from membrane proteomics?. <i>Proteomics</i> , 2008, 8, 4946-4957.	2.2	25
54	Proteomic Analysis of Exosomes from Human Neural Stem Cells by Flow Field-Flow Fractionation and Nanoflow Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 3475-3480.	3.7	161

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55	Human Microglial Cells Synthesize Albumin in Brain. PLoS ONE, 2008, 3, e2829.	2.5	76
56	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
57	Human microglial cells synthesize albumin in brain. Nature Precedings, 2008, , .	0.1	1
58	Miniaturized asymmetrical flow field-flow fractionation: Application to biological vesicles. Journal of Separation Science, 2007, 30, 1082-1087.	2.5	38
59	Body fluid proteomics: Prospects for biomarker discovery. Proteomics - Clinical Applications, 2007, 1, 1004-1015.	1.6	91
60	Proteomic Strategies for Analyzing Body Fluids. , 2007, , 3-30.		2
61	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
62	Characterization of human SMARCE1r high-mobility-group protein. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1574, 269-276.	2.4	6