Young Seok Ju

List of Publications by Year
in descending order

77 papers	10,164 citations	109137 35 h-index	66788 78 g-index
94 all docs	94 docs citations	94 times ranked	20203 citing authors

#	Article	IF	Citations
1	Patientâ€derived organoids as a preclinical platform for precision medicine in colorectal cancer. Molecular Oncology, 2022, 16, 2396-2412.	2.1	17
2	Asymmetric Contribution of Blastomere Lineages of First Division of the Zygote to Entire Human Body Using Post-Zygotic Variants. Tissue Engineering and Regenerative Medicine, 2022, , 1.	1.6	0
3	Weight-bearing activity impairs nuclear membrane and genome integrity via YAP activation in plantar melanoma. Nature Communications, 2022, 13, 2214.	5.8	11
4	p57Kip2 imposes the reserve stem cell state of gastric chief cells. Cell Stem Cell, 2022, 29, 826-839.e9.	5.2	17
5	Heterogeneous genetic landscape of congenital neutropenia in Korean patients revealed by whole exome sequencing: genetic, phenotypic and histologic correlations. Scientific Reports, 2022, 12, 7515.	1.6	2
6	Adenosine Deaminase 2 Deficiency Caused by Biallele Variants Including Splicing Variant: The First Case in Korea. Journal of Rheumatic Diseases, 2022, , .	0.4	0
7	A fusion of CD63â€"BCAR4 identified in lung adenocarcinoma promotes tumorigenicity and metastasis. British Journal of Cancer, 2021, 124, 290-298.	2.9	5
8	Tumor hypoxia represses Î³Î´ T cell-mediated antitumor immunity against brain tumors. Nature Immunology, 2021, 22, 336-346.	7.0	70
9	Implication of CD69⁺CD103⁺ tissueâ€residentâ€like CD8⁺ T cells as a potential immunotherapeutic target for cholangiocarcinoma. Liver International, 2021, 41, 764-776.	1.9	18
10	Cerebral Cavernous Malformation 1 Determines YAP/TAZ Signaling-Dependent Metastatic Hallmarks of Prostate Cancer Cells. Cancers, 2021, 13, 1125.	1.7	3
11	A large-scale snapshot of intratumor heterogeneity in human cancer. Cancer Cell, 2021, 39, 463-465.	7.7	5
12	Experimental Models for SARS-CoV-2 Infection. Molecules and Cells, 2021, 44, 377-383.	1.0	6
13	Nasal ciliated cells are primary targets for SARS-CoV-2 replication in the early stage of COVID-19. Journal of Clinical Investigation, 2021, 131, .	3.9	169
14	Single-cell transcriptome of bronchoalveolar lavage fluid reveals sequential change of macrophages during SARS-CoV-2 infection in ferrets. Nature Communications, 2021, 12, 4567.	5.8	43
15	Acquired Resistance to Third-Generation EGFR Tyrosine Kinase Inhibitors in Patients With De Novo EGFRT790M-Mutant NSCLC. Journal of Thoracic Oncology, 2021, 16, 1859-1871.	0.5	16
16	Mutational spectrum of SARS-CoV-2 during the global pandemic. Experimental and Molecular Medicine, 2021, 53, 1229-1237.	3.2	30
17	Clonal dynamics in early human embryogenesis inferred from somatic mutation. Nature, 2021, 597, 393-397.	13.7	70
18	Dissecting single-cell genomes through the clonal organoid technique. Experimental and Molecular Medicine, 2021, 53, 1503-1511.	3.2	9

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19	4â€1BB Delineates Distinct Activation Status of Exhausted Tumorâ€Infiltrating CD8+ T Cells in Hepatocellular Carcinoma. Hepatology, 2020, 71, 955-971.	3.6	70
20	PRMT1 Is Required for the Maintenance of Mature Î²-Cell Identity. Diabetes, 2020, 69, 355-368.	0.3	22
21	Germline gain-of-function mutation of STAT1 rescued by somatic mosaicism in immune dysregulation-polyendocrinopathy-enteropathy-X-linked-like disorder. Journal of Allergy and Clinical Immunology, 2020, 145, 1017-1021.	1.5	9
22	Three-Dimensional Human Alveolar Stem Cell Culture Models Reveal Infection Response to SARS-CoV-2. Cell Stem Cell, 2020, 27, 905-919.e10.	5.2	195
23	Dll4 Suppresses Transcytosis for Arterial Blood-Retinal Barrier Homeostasis. Circulation Research, 2020, 126, 767-783.	2.0	35
24	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
25	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
26	The genome-wide landscape of C:G > T:A polymorphism at the CpG contexts in the human population. BMC Genomics, 2020, 21, 270.	1.2	20
27	Comprehensive molecular characterization of mitochondrial genomes in human cancers. Nature Genetics, 2020, 52, 342-352.	9.4	256
28	Effects of Cryopreservation and Thawing on Single-Cell Transcriptomes of Human T Cells. Immune Network, 2020, 20, e34.	1.6	14
29	4-1BB co-stimulation further enhances anti-PD-1-mediated reinvigoration of exhausted CD39 CD8 T cells from primary and metastatic sites of epithelial ovarian cancers. , 2020, 8, .		7
30	Tracing Oncogene Rearrangements in the Mutational History of Lung Adenocarcinoma. Cell, 2019, 177, 1842-1857.e21.	13.5	153
31	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	13.5	298
32	Identification of a quadruple mutation that confers tenofovir resistance in chronic hepatitis B patients. Journal of Hepatology, 2019, 70, 1093-1102.	1.8	107
33	FIREVAT: finding reliable variants without artifacts in human cancer samples using etiologically relevant mutational signatures. Genome Medicine, 2019, 11, 81.	3.6	8
34	Alterations in the Rho pathway contribute to Epstein-Barr virusâ€"induced lymphomagenesis in immunosuppressed environments. Blood, 2018, 131, 1931-1941.	0.6	7
35	Sox7 promotes high-grade glioma by increasing VEGFR2-mediated vascular abnormality. Journal of Experimental Medicine, 2018, 215, 963-983.	4.2	36
36	Serotonin signals through a gut-liver axis to regulate hepatic steatosis. Nature Communications, 2018, 9, 4824.	5.8	98

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37	Association Between Expression Level of PD1 by Tumor-Infiltrating CD8+ T Cells and Features of HepatocellularÂCarcinoma. Gastroenterology, 2018, 155, 1936-1950.e17.	0.6	211
38	Mutalisk: a web-based somatic MUTation AnaLyIS toolKit for genomic, transcriptional and epigenomic signatures. Nucleic Acids Research, 2018, 46, W102-W108.	6.5	77
39	Human glioblastoma arises from subventricular zone cells with low-level driver mutations. Nature, 2018, 560, 243-247.	13.7	460
40	Patterns and mechanisms of structural variations in human cancer. Experimental and Molecular Medicine, 2018, 50, 1-11.	3.2	73
41	Genomic and Immune Profiles of Multiple Myeloma Revealed By Whole Genome and Transcriptome Sequencing. Blood, 2018, 132, 4493-4493.	0.6	2
42	Complex chromosomal rearrangements by single catastrophic pathogenesis in NUT midline carcinoma. Annals of Oncology, 2017, 28, 890-897.	0.6	54
43	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	13.7	229
44	Clonal History and Genetic Predictors of Transformation Into Small-Cell Carcinomas From Lung Adenocarcinomas. Journal of Clinical Oncology, 2017, 35, 3065-3074.	0.8	349
45	The mutational signatures and molecular alterations of bladder cancer. Translational Cancer Research, 2017, 6, S689-S701.	0.4	6
46	BRAF V600E Kinase Domain Duplication Identified in Therapy-Refractory Melanoma Patient-Derived Xenografts. Cell Reports, 2016, 16, 263-277.	2.9	61
47	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
48	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	2.9	36
49	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	6.0	842
50	Intracellular mitochondrial DNA transfers to the nucleus in human cancer cells. Current Opinion in Genetics and Development, 2016, 38, 23-30.	1.5	5
51	Recurrent fusion transcripts detected by wholeâ€transcriptome sequencing of 120 primary breast cancer samples. Genes Chromosomes and Cancer, 2015, 54, 681-691.	1.5	38
52	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	15.2	711
53	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	2.4	69
54	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	2.8	318

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55	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348
56	Abstract 4322: The landscape of mitochondrial DNA mutations in human cancer. Cancer Research, 2014, 74, 4322-4322.	0.4	3
57	Fine-scale mapping of meiotic recombination in Asians. BMC Genetics, 2013, 14, 19.	2.7	16
58	Combined linkage and association analyses identify a novel locus for obesity near PROX1 in Asians. Obesity, 2013, 21, 2405-2412.	1.5	21
59	Diagnostic method for the detection of KIF5B-RET transformation in lung adenocarcinoma. Lung Cancer, 2013, 82, 44-50.	0.9	43
60	TIARA genome database: update 2013. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat003-bat003.	1.4	6
61	A family-based association study after genome-wide linkage analysis identified two genetic loci for renal function in a Mongolian population. Kidney International, 2013, 83, 285-292.	2.6	13
62	Gene mapping study for constitutive skin color in an isolated Mongolian population. Experimental and Molecular Medicine, 2012, 44, 241.	3.2	8
63	Comprehensive genomic analyses associateUGT8variants with musical ability in a Mongolian population. Journal of Medical Genetics, 2012, 49, 747-752.	1.5	48
64	FX: an RNA-Seq analysis tool on the cloud. Bioinformatics, 2012, 28, 721-723.	1.8	66
65	The transcriptional landscape and mutational profile of lung adenocarcinoma. Genome Research, 2012, 22, 2109-2119.	2.4	524
66	A transforming KIF5B and RET gene fusion in lung adenocarcinoma revealed from whole-genome and transcriptome sequencing. Genome Research, 2012, 22, 436-445.	2.4	433
67	Abstract LB-402: New fusion genes in lung adenocarcinoma revealed from next generation RNA-seq. , 2012, , .		0
68	Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals. Nature Genetics, 2011, 43, 745-752.	9.4	121
69	TIARA: a database for accurate analysis of multiple personal genomes based on cross-technology. Nucleic Acids Research, 2011, 39, D883-D888.	6.5	15
70	Linkage and association scan for tanning ability in an isolated Mongolian population. BMB Reports, 2011, 44, 741-746.	1.1	8
71	Discovery of common Asian copy number variants using integrated high-resolution array CGH and massively parallel DNA sequencing. Nature Genetics, 2010, 42, 400-405.	9.4	179
72	Reference-unbiased copy number variant analysis using CGH microarrays. Nucleic Acids Research, 2010, 38, e190-e190.	6.5	22

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73	The first Irish genome and ways of improving sequence accuracy. Genome Biology, 2010, 11, 132.	13.9	4
74	Higher mitochondrial DNA copy number is associated with lower prevalence of microalbuminuria. Experimental and Molecular Medicine, 2009, 41, 253.	3.2	33
75	A highly annotated whole-genome sequence of a Korean individual. Nature, 2009, 460, 1011-1015.	13.7	295
76	A genome-wide Asian genetic map and ethnic comparison: The GENDISCAN study. BMC Genomics, 2008, 9, 554.	1.2	25
77	Heritability and linkage study on heart rates in a Mongolian population. Experimental and Molecular Medicine, 2008, 40, 558.	3.2	7