Young Seok Ju

List of Publications by Citations

80 papers	6,540 citations	31 h-index	80 g-index
94 ext. papers	8,674 ext. citations	15.8 avg, IF	5.08 L-index

#	Paper	IF	Citations
80	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	50.4	1193
79	Mutational signatures associated with tobacco smoking in human cancer. *Science*, **2016**, 354, 618-622	33.3	562
78	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. *Nature Medicine*, **2015**, 21, 751-9	50.5	521
77	The transcriptional landscape and mutational profile of lung adenocarcinoma. *Genome Research*, **2012**, 22, 2109-19	9.7	435
76	A transforming KIF5B and RET gene fusion in lung adenocarcinoma revealed from whole-genome and transcriptome sequencing. *Genome Research*, **2012**, 22, 436-45	9.7	367
75	A highly annotated whole-genome sequence of a Korean individual. *Nature*, **2009**, 460, 1011-5	50.4	265
74	Human glioblastoma arises from subventricular zone cells with low-level driver mutations. *Nature*, **2018**, 560, 243-247	50.4	257
73	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. *Science*, **2014**, 345, 1251343	33.3	250
72	Clonal History and Genetic Predictors of Transformation Into Small-Cell Carcinomas From Lung Adenocarcinomas. *Journal of Clinical Oncology*, **2017**, 35, 3065-3074	2.2	229
71	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. *ELife*, **2014**, 3,	8.9	229
70	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
69	Discovery of common Asian copy number variants using integrated high-resolution array CGH and massively parallel DNA sequencing. *Nature Genetics*, **2010**, 42, 400-5	36.3	167
68	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. *Cell*, **2019**, 176, 1282-1294.e20	56.2	165
67	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. *Nature*, **2017**, 543, 714-718	50.4	157
66	Association Between Expression Level of PD1 by Tumor-Infiltrating CD8 T Cells and Features of Hepatocellular Carcinoma. *Gastroenterology*, **2018**, 155, 1936-1950.e17	13.3	141
65	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
64	Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals. *Nature Genetics*, **2011**, 43, 745-52	36.3	110

63	Comprehensive molecular characterization of mitochondrial genomes in human cancers. *Nature Genetics*, **2020**, 52, 342-352	36.3	105
62	Three-Dimensional Human Alveolar Stem Cell Culture Models Reveal Infection Response to SARS-CoV-2. *Cell Stem Cell*, **2020**, 27, 905-919.e10	18	92
61	Tracing Oncogene Rearrangements in the Mutational History of Lung Adenocarcinoma. *Cell*, **2019**, 177, 1842-1857.e21	56.2	84
60	Identification of a quadruple mutation that confers tenofovir resistance in chronic hepatitis B patients. *Journal of Hepatology*, **2019**, 70, 1093-1102	13.4	78
59	Serotonin signals through a gut-liver axis to regulate hepatic steatosis. *Nature Communications*, **2018**, 9, 4824	17.4	58
58	FX: an RNA-Seq analysis tool on the cloud. *Bioinformatics*, **2012**, 28, 721-3	7.2	57
57	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. *Genome Research*, **2015**, 25, 814-24	9.7	52
56	BRAF(V600E) Kinase Domain Duplication Identified in Therapy-Refractory Melanoma Patient-Derived Xenografts. *Cell Reports*, **2016**, 16, 263-277	10.6	40
55	Comprehensive genomic analyses associate UGT8 variants with musical ability in a Mongolian population. *Journal of Medical Genetics*, **2012**, 49, 747-52	5.8	38
54	Patterns and mechanisms of structural variations in human cancer. *Experimental and Molecular Medicine*, **2018**, 50, 1-11	12.8	36
53	Nasal ciliated cells are primary targets for SARS-CoV-2 replication in the early stage of COVID-19. *Journal of Clinical Investigation*, **2021**, 131,	15.9	35
52	Complex chromosomal rearrangements by single catastrophic pathogenesis in NUT midline carcinoma. *Annals of Oncology*, **2017**, 28, 890-897	10.3	33
51	Diagnostic method for the detection of KIF5B-RET transformation in lung adenocarcinoma. *Lung Cancer*, **2013**, 82, 44-50	5.9	32
50	4-1BB Delineates Distinct Activation Status of Exhausted Tumor-Infiltrating CD8 T Cells in Hepatocellular Carcinoma. *Hepatology*, **2020**, 71, 955-971	11.2	31
49	Recurrent fusion transcripts detected by whole-transcriptome sequencing of 120 primary breast cancer samples. *Genes Chromosomes and Cancer*, **2015**, 54, 681-91	5	30
48	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. *Cell Reports*, **2016**, 16, 2032-**46**.6		30
47	Mutalisk: a web-based somatic MUTation AnaLyIS toolKit for genomic, transcriptional and epigenomic signatures. *Nucleic Acids Research*, **2018**, 46, W102-W108	20.1	29
46	Higher mitochondrial DNA copy number is associated with lower prevalence of microalbuminuria. *Experimental and Molecular Medicine*, **2009**, 41, 253-8	12.8	27

45	Sox7 promotes high-grade glioma by increasing VEGFR2-mediated vascular abnormality. *Journal of Experimental Medicine*, **2018**, 215, 963-983	16.6	25
44	Reference-unbiased copy number variant analysis using CGH microarrays. *Nucleic Acids Research*, **2010**, 38, e190	20.1	20
43	Selective and mechanistic sources of recurrent rearrangements across the cancer genome		20
42	Clonal dynamics in early human embryogenesis inferred from somatic mutation. *Nature*, **2021**, 597, 393-397	50.4	17
41	Dll4 Suppresses Transcytosis for Arterial Blood-Retinal Barrier Homeostasis. *Circulation Research*, **2020**, 126, 767-783	15.7	16
40	A genome-wide Asian genetic map and ethnic comparison: the GENDISCAN study. *BMC Genomics*, **2008**, 9, 554	4.5	16
39	Combined linkage and association analyses identify a novel locus for obesity near PROX1 in Asians. *Obesity*, **2013**, 21, 2405-12	8	15
38	TIARA: a database for accurate analysis of multiple personal genomes based on cross-technology. *Nucleic Acids Research*, **2011**, 39, D883-8	20.1	15
37	Tumor hypoxia represses T cell-mediated antitumor immunity against brain tumors. *Nature Immunology*, **2021**, 22, 336-346	19.1	14
36	Fine-scale mapping of meiotic recombination in Asians. *BMC Genetics*, **2013**, 14, 19	2.6	12
35	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, 285-92	9.9	12
34	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
33	PRMT1 Is Required for the Maintenance of Mature Cell Identity. *Diabetes*, **2020**, 69, 355-368	0.9	9
32	Gene mapping study for constitutive skin color in an isolated Mongolian population. *Experimental and Molecular Medicine*, **2012**, 44, 241-9	12.8	8
31	Linkage and association scan for tanning ability in an isolated Mongolian population. *BMB Reports*, **2011**, 44, 741-6	5.5	7
30	Single-cell transcriptome of bronchoalveolar lavage fluid reveals sequential change of macrophages during SARS-CoV-2 infection in ferrets. *Nature Communications*, **2021**, 12, 4567	17.4	7
29	Mutational spectrum of SARS-CoV-2 during the global pandemic. *Experimental and Molecular Medicine*, **2021**, 53, 1229-1237	12.8	7
28	Comprehensive Molecular Characterization of Mitochondrial Genomes in Human Cancers		6

27	TIARA genome database: update 2013. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat003	5	5
26	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,		5
25	Effects of Cryopreservation and Thawing on Single-Cell Transcriptomes of Human T Cells. *Immune Network*, **2020**, 20, e34	6.1	5
24	Spatial genomics maps the structure, character and evolution of cancer clones		5
23	FIREVAT: finding reliable variants without artifacts in human cancer samples using etiologically relevant mutational signatures. *Genome Medicine*, **2019**, 11, 81	14.4	5
22	The genome-wide landscape of C:G > T:A polymorphism at the CpG contexts in the human population. *BMC Genomics*, **2020**, 21, 270	4.5	4
21	Alterations in the Rho pathway contribute to Epstein-Barr virus-induced lymphomagenesis in immunosuppressed environments. *Blood*, **2018**, 131, 1931-1941	2.2	4
20	Intracellular mitochondrial DNA transfers to the nucleus in human cancer cells. *Current Opinion in Genetics and Development*, **2016**, 38, 23-30	4.9	4
19	The first Irish genome and ways of improving sequence accuracy. *Genome Biology*, **2010**, 11, 132	18.3	4
18	Heritability and linkage study on heart rates in a Mongolian population. *Experimental and Molecular Medicine*, **2008**, 40, 558-64	12.8	4
17	The mutational signatures and molecular alterations of bladder cancer. *Translational Cancer Research*, **2017**, 6, S689-S701	0.3	4
16	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	11.5	4
15	Experimental Models for SARS-CoV-2 Infection. *Molecules and Cells*, **2021**, 44, 377-383	3.5	4
14	Patient-derived organoids as a preclinical platform for precision medicine in colorectal cancer. *Molecular Oncology*, **2021**,	7.9	3
13	Implication of CD69 CD103 tissue-resident-like CD8 T cells as a potential immunotherapeutic target for cholangiocarcinoma. *Liver International*, **2021**, 41, 764-776	7.9	3
12	Abstract 4322: The landscape of mitochondrial DNA mutations in human cancer **2014**,		2
11	Genomic and Immune Profiles of Multiple Myeloma Revealed By Whole Genome and Transcriptome Sequencing. *Blood*, **2018**, 132, 4493-4493	2.2	2
10	Acquired Resistance to Third-Generation EGFR Tyrosine Kinase Inhibitors in Patients With De Novo EGFR-Mutant NSCLC. *Journal of Thoracic Oncology*, **2021**, 16, 1859-1871	8.9	2

9	Dissecting single-cell genomes through the clonal organoid technique. *Experimental and Molecular Medicine*, **2021**, 53, 1503-1511	12.8	1
8	Single-cell Transcriptome of Bronchoalveolar Lavage Fluid Reveals Dynamic Change of Macrophages During SARS-CoV-2 Infection in Ferrets		1
7	A large-scale snapshot of intratumor heterogeneity in human cancer. *Cancer Cell*, **2021**, 39, 463-465	24.3	1
6	Weight-bearing activity impairs nuclear membrane and genome integrity via YAP activation in plantar melanoma.. *Nature Communications*, **2022**, 13, 2214	17.4	1
5	p57 imposes the reserve stem cell state of gastric chief cells.. *Cell Stem Cell*, **2022**, 29, 826-839.e9	18	1
4	A fusion of CD63-BCAR4 identified in lung adenocarcinoma promotes tumorigenicity and metastasis. *British Journal of Cancer*, **2021**, 124, 290-298	8.7	0
3	Heterogeneous genetic landscape of congenital neutropenia in Korean patients revealed by whole exome sequencing: genetic, phenotypic and histologic correlations.. *Scientific Reports*, **2022**, 12, 7515	4.9	0
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	4.5	
1	Identifying Somatic Mitochondrial DNA Mutations. *Methods in Molecular Biology*, **2022**, 153-165	1.4	