Semin Lee

List of Publications by Year
in descending order

56 papers	19,271 citations	172457 29 h-index	155660 55 g-index
58 all docs	58 docs citations	58 times ranked	32355 citing authors

#	Article	IF	Citations
1	Sex-specific difference of in-hospital mortality from COVID-19 in South Korea. PLoS ONE, 2022, 17, e0262861.	2.5	8
2	Somatic mosaicism reveals clonal distributions of neocortical development. Nature, 2022, 604, 689-696.	27.8	26
3	A functional genomic approach to actionable gene fusions for precision oncology. Science Advances, 2022, 8, eabm2382.	10.3	9
4	PWWP2B promotes DNA end resection and homologous recombination. EMBO Reports, 2022, , e53492.	4.5	4
5	A Clinical Risk Score to Predict In-hospital Mortality from COVID-19 in South Korea. Journal of Korean Medical Science, 2021, 36, e108.	2.5	5
6	Welfare Genome Project: A Participatory Korean Personal Genome Project With Free Health Check-Up and Genetic Report Followed by Counseling. Frontiers in Genetics, 2021, 12, 633731.	2.3	6
7	Polygenic risk score validation using Korean genomes of 265 early-onset acute myocardial infarction patients and 636 healthy controls. PLoS ONE, 2021, 16, e0246538.	2.5	7
8	An integrated mRNAâ€"microRNA regulatory network identified INHBA and has-miR-135a-5p as predictors of gastric cancer recurrence. Molecular and Cellular Toxicology, 2021, 17, 213-220.	1.7	3
9	Loss of BubR1 acetylation provokes replication stress and leads to complex chromosomal rearrangements. FEBS Journal, 2021, 288, 5925-5942.	4.7	0
10	Microbiome of Saliva and Plaque in Children According to Age and Dental Caries Experience. Diagnostics, 2021, 11, 1324.	2.6	22
11	Single-cell RNA sequencing reveals distinct cellular factors for response to immunotherapy targeting CD73 and PD-1 in colorectal cancer. , 2021, 9, e002503.		36
12	Circulating Tumor Cell Clusters Are Cloaked with Platelets and Correlate with Poor Prognosis in Unresectable Pancreatic Cancer. Cancers, 2021, 13, 5272.	3.7	17
13	Androgen-induced expression of DRP1 regulates mitochondrial metabolic reprogramming in prostate cancer. Cancer Letters, 2020, 471, 72-87.	7.2	45
14	Defining the mutation signatures of DNA polymerase Î¸ in cancer genomes. NAR Cancer, 2020, 2, zcaa017.	3.1	33
15	The whale shark genome reveals how genomic and physiological properties scale with body size. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20662-20671.	7.1	32
16	Prediction of Chronic Periodontitis Severity Using Machine Learning Models Based On Salivary Bacterial Copy Number. Frontiers in Cellular and Infection Microbiology, 2020, 10, 571515.	3.9	23
17	A lab-on-a-disc platform enables serial monitoring of individual CTCs associated with tumor progression during EGFR-targeted therapy for patients with NSCLC. Theranostics, 2020, 10, 5181-5194.	10.0	17
18	Korean Genome Project: 1094 Korean personal genomes with clinical information. Science Advances, 2020, 6, eaaz7835.	10.3	75

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19	ATAD5 restricts R-loop formation through PCNA unloading and RNA helicase maintenance at the replication fork. Nucleic Acids Research, 2020, 48, 7218-7238.	14.5	30
20	Delineation of the genetic and clinical spectrum, including candidate genes, of monogenic diabetes: a multicenter study in South Korea. Journal of Pediatric Endocrinology and Metabolism, 2020, 33, 1539-1550.	0.9	5
21	An enhanced genetic model of colorectal cancer progression history. Genome Biology, 2019, 20, 168.	8.8	34
22	Depression and suicide risk prediction models using blood-derived multi-omics data. Translational Psychiatry, 2019, 9, 262.	4.8	38
23	Global impact of somatic structural variation on the DNA methylome of human cancers. Genome Biology, 2019, 20, 209.	8.8	40
24	CPEM: Accurate cancer type classification based on somatic alterations using an ensemble of aÂrandom forest and a deep neural network. Scientific Reports, 2019, 9, 16927.	3.3	21
25	Chromosome-scale assembly comparison of the Korean Reference Genome KOREF from PromethION and PacBio with Hi-C mapping information. GigaScience, 2019, 8, .	6.4	18
26	KoVariome: Korean National Standard Reference Variome database of whole genomes with comprehensive SNV, indel, CNV, and SV analyses. Scientific Reports, 2018, 8, 5677.	3.3	39
27	Genomic analysis reveals secondary glioblastoma after radiotherapy in a subset of recurrent medulloblastomas. Acta Neuropathologica, 2018, 135, 939-953.	7.7	32
28	Potential involvement of *Drosophila* flightless-1 in carbohydrate metabolism. BMB Reports, 2018, 51, 462-467.	2.4	4
29	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. Cell Reports, 2018, 24, 515-527.	6.4	70
30	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. Genome Research, 2018, 28, 1217-1227.	5.5	172
31	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. Cancer Cell, 2017, 31, 820-832.e3.	16.8	433
32	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. Nature Communications, 2016, 7, 13637.	12.8	58
33	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. Genome Biology, 2016, 17, 211.	8.8	101
34	Copy number analysis of whole-genome data using BIC-seq2 and its application to detection of cancer susceptibility variants. Nucleic Acids Research, 2016, 44, 6274-6286.	14.5	117
35	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
36	Evaluation of somatic copy number estimation tools for whole-exome sequencing data. Briefings in Bioinformatics, 2016, 17, 185-192.	6.5	44

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37	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
38	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
39	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
40	BubR1 kinase: protection against aneuploidy and premature aging. Trends in Molecular Medicine, 2015, 21, 364-372.	6.7	48
41	Somatic mutation in single human neurons tracks developmental and transcriptional history. Science, 2015, 350, 94-98.	12.6	486
42	Failure to replicate the STAP cell phenomenon. Nature, 2015, 525, E6-E9.	27.8	41
43	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
44	The dynamics of signal amplification by macromolecular assemblies for the control of chromosome segregation. Frontiers in Physiology, 2014, 5, 368.	2.8	4
45	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
46	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
47	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
48	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
49	Characterization of Spindle Checkpoint Kinase Mps1 Reveals Domain with Functional and Structural Similarities to Tetratricopeptide Repeat Motifs of Bub1 and BubR1 Checkpoint Kinases. Journal of Biological Chemistry, 2012, 287, 5988-6001.	3.4	32
50	QTL analysis of fruit length using rRAMP, WRKY, and AFLP markers in chili pepper. Horticulture Environment and Biotechnology, 2011, 52, 602-613.	2.1	14
51	BIPA: a database for protein–nucleic acid interaction in 3D structures. Bioinformatics, 2009, 25, 1559-1560.	4.1	50
52	Ulla: a program for calculating environment-specific amino acid substitution tables. Bioinformatics, 2009, 25, 1976-1977.	4.1	13
53	Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics. Molecular BioSystems, 2009, 5, 1456.	2.9	8
54	Structural and functional restraints in the evolution of protein families and superfamilies. Biochemical Society Transactions, 2009, 37, 727-733.	3.4	40

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55	A STRUCTURAL BIOINFORMATICS APPROACH TO THE ANALYSIS OF NONSYNONYMOUS SINGLE NUCLEOTIDE POLYMORPHISMS (nsSNPs) AND THEIR RELATION TO DISEASE. Journal of Bioinformatics and Computational Biology, 2007, 05, 1297-1318.	0.8	56
56	Comparative interactomics analysis of protein family interaction networks using PSIMAP (protein) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	4.1	33