

# Semin Lee

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

19,271  
citations

172207

29  
h-index

155451

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. <i>PLoS ONE</i> , 2022, 17, e0262861.	1.1	8
2	Somatic mosaicism reveals clonal distributions of neocortical development. <i>Nature</i> , 2022, 604, 689-696.	13.7	26
3	A functional genomic approach to actionable gene fusions for precision oncology. <i>Science Advances</i> , 2022, 8, eabm2382.	4.7	9
4	PWWP2B promotes DNA end resection and homologous recombination. <i>EMBO Reports</i> , 2022, , e53492.	2.0	4
5	A Clinical Risk Score to Predict In-hospital Mortality from COVID-19 in South Korea. <i>Journal of Korean Medical Science</i> , 2021, 36, e108.	1.1	5
6	Welfare Genome Project: A Participatory Korean Personal Genome Project With Free Health Check-Up and Genetic Report Followed by Counseling. <i>Frontiers in Genetics</i> , 2021, 12, 633731.	1.1	6
7	Polygenic risk score validation using Korean genomes of 265 early-onset acute myocardial infarction patients and 636 healthy controls. <i>PLoS ONE</i> , 2021, 16, e0246538.	1.1	7
8	An integrated mRNA-microRNA regulatory network identified INHBA and has-miR-135a-5p as predictors of gastric cancer recurrence. <i>Molecular and Cellular Toxicology</i> , 2021, 17, 213-220.	0.8	3
9	Loss of BubR1 acetylation provokes replication stress and leads to complex chromosomal rearrangements. <i>FEBS Journal</i> , 2021, 288, 5925-5942.	2.2	0
10	Microbiome of Saliva and Plaque in Children According to Age and Dental Caries Experience. <i>Diagnostics</i> , 2021, 11, 1324.	1.3	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. <i>Cancers</i> , 2021, 13, 5272.	1.7	17
13	Androgen-induced expression of DRP1 regulates mitochondrial metabolic reprogramming in prostate cancer. <i>Cancer Letters</i> , 2020, 471, 72-87.	3.2	45
14	Defining the mutation signatures of DNA polymerase $\delta$ in cancer genomes. <i>NAR Cancer</i> , 2020, 2, zcaa017.	1.6	33
15	The whale shark genome reveals how genomic and physiological properties scale with body size. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20662-20671.	3.3	32
16	Prediction of Chronic Periodontitis Severity Using Machine Learning Models Based On Salivary Bacterial Copy Number. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 571515.	1.8	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. <i>Theranostics</i> , 2020, 10, 5181-5194.	4.6	17
18	Korean Genome Project: 1094 Korean personal genomes with clinical information. <i>Science Advances</i> , 2020, 6, eaaz7835.	4.7	75

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19	ATAD5 restricts R-loop formation through PCNA unloading and RNA helicase maintenance at the replication fork. <i>Nucleic Acids Research</i> , 2020, 48, 7218-7238.	6.5	30
20	Delineation of the genetic and clinical spectrum, including candidate genes, of monogenic diabetes: a multicenter study in South Korea. <i>Journal of Pediatric Endocrinology and Metabolism</i> , 2020, 33, 1539-1550.	0.4	5
21	An enhanced genetic model of colorectal cancer progression history. <i>Genome Biology</i> , 2019, 20, 168.	3.8	34
22	Depression and suicide risk prediction models using blood-derived multi-omics data. <i>Translational Psychiatry</i> , 2019, 9, 262.	2.4	38
23	Global impact of somatic structural variation on the DNA methylome of human cancers. <i>Genome Biology</i> , 2019, 20, 209.	3.8	40
24	CPEM: Accurate cancer type classification based on somatic alterations using an ensemble of a Random forest and a deep neural network. <i>Scientific Reports</i> , 2019, 9, 16927.	1.6	21
25	Chromosome-scale assembly comparison of the Korean Reference Genome KOREF from PromethION and PacBio with Hi-C mapping information. <i>GigaScience</i> , 2019, 8, .	3.3	18
26	KoVariome: Korean National Standard Reference Variome database of whole genomes with comprehensive SNV, indel, CNV, and SV analyses. <i>Scientific Reports</i> , 2018, 8, 5677.	1.6	39
27	Genomic analysis reveals secondary glioblastoma after radiotherapy in a subset of recurrent medulloblastomas. <i>Acta Neuropathologica</i> , 2018, 135, 939-953.	3.9	32
28	Potential involvement of <i>Drosophila</i> flightless-1 in carbohydrate metabolism. <i>BMB Reports</i> , 2018, 51, 462-467.	1.1	4
29	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. <i>Cell Reports</i> , 2018, 24, 515-527.	2.9	70
30	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. <i>Genome Research</i> , 2018, 28, 1217-1227.	2.4	172
31	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017, 31, 820-832.e3.	7.7	433
32	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. <i>Nature Communications</i> , 2016, 7, 13637.	5.8	58
33	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016, 17, 211.	3.8	101
34	Copy number analysis of whole-genome data using BIC-seq2 and its application to detection of cancer susceptibility variants. <i>Nucleic Acids Research</i> , 2016, 44, 6274-6286.	6.5	117
35	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	13.5	1,695
36	Evaluation of somatic copy number estimation tools for whole-exome sequencing data. <i>Briefings in Bioinformatics</i> , 2016, 17, 185-192.	3.2	44

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37	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	5.8	266
38	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
39	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
40	BubR1 kinase: protection against aneuploidy and premature aging. <i>Trends in Molecular Medicine</i> , 2015, 21, 364-372.	3.5	48
41	Somatic mutation in single human neurons tracks developmental and transcriptional history. <i>Science</i> , 2015, 350, 94-98.	6.0	486
42	Failure to replicate the STAP cell phenomenon. <i>Nature</i> , 2015, 525, E6-E9.	13.7	41
43	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
44	The dynamics of signal amplification by macromolecular assemblies for the control of chromosome segregation. <i>Frontiers in Physiology</i> , 2014, 5, 368.	1.3	4
45	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
46	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15544-15549.	3.3	317
47	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
48	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	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. <i>Journal of Biological Chemistry</i> , 2012, 287, 5988-6001.	1.6	32
50	QTL analysis of fruit length using rRAMP, WRKY, and AFLP markers in chili pepper. <i>Horticulture Environment and Biotechnology</i> , 2011, 52, 602-613.	0.7	14
51	BIPA: a database for protein-nucleic acid interaction in 3D structures. <i>Bioinformatics</i> , 2009, 25, 1559-1560.	1.8	50
52	Ulla: a program for calculating environment-specific amino acid substitution tables. <i>Bioinformatics</i> , 2009, 25, 1976-1977.	1.8	13
53	Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics. <i>Molecular BioSystems</i> , 2009, 5, 1456.	2.9	8
54	Structural and functional restraints in the evolution of protein families and superfamilies. <i>Biochemical Society Transactions</i> , 2009, 37, 727-733.	1.6	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.	0.3	56
56	Comparative interactomics analysis of protein family interaction networks using PSIMAP (protein) Tj ETQq0 0 0 rgBT/Overlock, 10 Tf 50	1.8	33