# Semin Lee

List of Publications by Year
in descending order

| 56 | 19,271 | 172386 | 155592 |
|---|---|---|---|
| papers | citations | 29 | 55 |
| | | h-index | g-index |

| 58 | 58 | 58 | 32355 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477. | 13.5 | 3,979 |
| 2 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498. | 13.9 | 2,582 |
| 3 | Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696. | 13.5 | 2,562 |
| 4 | The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025. | 13.5 | 2,435 |
| 5 | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690. | 13.5 | 2,318 |
| 6 | Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563. | 13.5 | 1,695 |
| 7 | The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330. | 7.7 | 665 |
| 8 | Somatic mutation in single human neurons tracks developmental and transcriptional history. Science, 2015, 350, 94-98. | 6.0 | 486 |
| 9 | A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. Cancer Cell, 2017, 31, 820-832.e3. | 7.7 | 433 |
| 10 | 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. | 3.3 | 317 |
| 11 | A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001. | 5.8 | 266 |
| 12 | Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. Genome Research, 2018, 28, 1217-1227. | 2.4 | 172 |
| 13 | 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. | 6.5 | 117 |
| 14 | Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. Genome Biology, 2016, 17, 211. | 3.8 | 101 |
| 15 | Korean Genome Project: 1094 Korean personal genomes with clinical information. Science Advances, 2020, 6, eaaz7835. | 4.7 | 75 |
| 16 | A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. Cell Reports, 2018, 24, 515-527. | 2.9 | 70 |
| 17 | An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. Nature Communications, 2016, 7, 13637. | 5.8 | 58 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 19 | BIPA: a database for protein–nucleic acid interaction in 3D structures. Bioinformatics, 2009, 25, 1559-1560. | 1.8 | 50 |
| 20 | BubR1 kinase: protection against aneuploidy and premature aging. Trends in Molecular Medicine, 2015, 21, 364-372. | 3.5 | 48 |
| 21 | Androgen-induced expression of DRP1 regulates mitochondrial metabolic reprogramming in prostate cancer. Cancer Letters, 2020, 471, 72-87. | 3.2 | 45 |
| 22 | Evaluation of somatic copy number estimation tools for whole-exome sequencing data. Briefings in Bioinformatics, 2016, 17, 185-192. | 3.2 | 44 |
| 23 | Failure to replicate the STAP cell phenomenon. Nature, 2015, 525, E6-E9. | 13.7 | 41 |
| 24 | Structural and functional restraints in the evolution of protein families and superfamilies. Biochemical Society Transactions, 2009, 37, 727-733. | 1.6 | 40 |
| 25 | Global impact of somatic structural variation on the DNA methylome of human cancers. Genome Biology, 2019, 20, 209. | 3.8 | 40 |
| 26 | KoVariome: Korean National Standard Reference Variome database of whole genomes with comprehensive SNV, indel, CNV, and SV analyses. Scientific Reports, 2018, 8, 5677. | 1.6 | 39 |
| 27 | Depression and suicide risk prediction models using blood-derived multi-omics data. Translational Psychiatry, 2019, 9, 262. | 2.4 | 38 |
| 28 | Single-cell RNA sequencing reveals distinct cellular factors for response to immunotherapy targeting CD73 and PD-1 in colorectal cancer. , 2021, 9, e002503. |  | 36 |
| 29 | An enhanced genetic model of colorectal cancer progression history. Genome Biology, 2019, 20, 168. | 3.8 | 34 |
| 30 | Comparative interactomics analysis of protein family interaction networks using PSIMAP (protein) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 1.8 | 33 |
| 31 | Defining the mutation signatures of DNA polymerase η in cancer genomes. NAR Cancer, 2020, 2, zcaa017. | 1.6 | 33 |
| 32 | 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. | 1.6 | 32 |
| 33 | Genomic analysis reveals secondary glioblastoma after radiotherapy in a subset of recurrent medulloblastomas. Acta Neuropathologica, 2018, 135, 939-953. | 3.9 | 32 |
| 34 | 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. | 3.3 | 32 |
| 35 | ATAD5 restricts R-loop formation through PCNA unloading and RNA helicase maintenance at the replication fork. Nucleic Acids Research, 2020, 48, 7218-7238. | 6.5 | 30 |
| 36 | Somatic mosaicism reveals clonal distributions of neocortical development. Nature, 2022, 604, 689-696. | 13.7 | 26 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 37 | Prediction of Chronic Periodontitis Severity Using Machine Learning Models Based On Salivary Bacterial Copy Number. Frontiers in Cellular and Infection Microbiology, 2020, 10, 571515. | 1.8 | 23 |
| 38 | Microbiome of Saliva and Plaque in Children According to Age and Dental Caries Experience. Diagnostics, 2021, 11, 1324. | 1.3 | 22 |
| 39 | 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. | 1.6 | 21 |
| 40 | Chromosome-scale assembly comparison of the Korean Reference Genome KOREF from PromethION and PacBio with Hi-C mapping information. GigaScience, 2019, 8, . | 3.3 | 18 |
| 41 | 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. | 4.6 | 17 |
| 42 | Circulating Tumor Cell Clusters Are Cloaked with Platelets and Correlate with Poor Prognosis in Unresectable Pancreatic Cancer. Cancers, 2021, 13, 5272. | 1.7 | 17 |
| 43 | QTL analysis of fruit length using rRAMP, WRKY, and AFLP markers in chili pepper. Horticulture Environment and Biotechnology, 2011, 52, 602-613. | 0.7 | 14 |
| 44 | Ulla: a program for calculating environment-specific amino acid substitution tables. Bioinformatics, 2009, 25, 1976-1977. | 1.8 | 13 |
| 45 | A functional genomic approach to actionable gene fusions for precision oncology. Science Advances, 2022, 8, eabm2382. | 4.7 | 9 |
| 46 | 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 |
| 47 | Sex-specific difference of in-hospital mortality from COVID-19 in South Korea. PLoS ONE, 2022, 17, e0262861. | 1.1 | 8 |
| 48 | Polygenic risk score validation using Korean genomes of 265 early-onset acute myocardial infarction patients and 636 healthy controls. PLoS ONE, 2021, 16, e0246538. | 1.1 | 7 |
| 49 | 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. | 1.1 | 6 |
| 50 | A Clinical Risk Score to Predict In-hospital Mortality from COVID-19 in South Korea. Journal of Korean Medical Science, 2021, 36, e108. | 1.1 | 5 |
| 51 | 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. | 0.4 | 5 |
| 52 | The dynamics of signal amplification by macromolecular assemblies for the control of chromosome segregation. Frontiers in Physiology, 2014, 5, 368. | 1.3 | 4 |
| 53 | Potential involvement of *Drosophila* flightless-1 in carbohydrate metabolism. BMB Reports, 2018, 51, 462-467. | 1.1 | 4 |
| 54 | PWWP2B promotes DNA end resection and homologous recombination. EMBO Reports, 2022, , e53492. | 2.0 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------|
| 55 | 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. | 0.8 | 3 |
| 56 | Loss of BubR1 acetylation provokes replication stress and leads to complex chromosomal rearrangements. FEBS Journal, 2021, 288, 5925-5942. | 2.2 | 0 |