

Semin Lee

List of Publications by Year in descending order

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Version: 2024-02-01

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 | The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477. | 28.9 | 3,979 |
| 2 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498. | 27.0 | 2,582 |
| 3 | Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696. | 28.9 | 2,562 |
| 4 | The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025. | 28.9 | 2,435 |
| 5 | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690. | 28.9 | 2,318 |
| 6 | Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563. | 28.9 | 1,695 |
| 7 | The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330. | 16.8 | 665 |
| 8 | Somatic mutation in single human neurons tracks developmental and transcriptional history. <i>Science</i> , 2015, 350, 94-98. | 12.6 | 486 |
| 9 | A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017, 31, 820-832.e3. | 16.8 | 433 |
| 10 | 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. | 7.1 | 317 |
| 11 | A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001. | 12.8 | 266 |
| 12 | Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. <i>Genome Research</i> , 2018, 28, 1217-1227. | 5.5 | 172 |
| 13 | 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. | 14.5 | 117 |
| 14 | Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016, 17, 211. | 8.8 | 101 |
| 15 | Korean Genome Project: 1094 Korean personal genomes with clinical information. <i>Science Advances</i> , 2020, 6, eaaz7835. | 10.3 | 75 |
| 16 | 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. | 6.4 | 70 |
| 17 | An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. <i>Nature Communications</i> , 2016, 7, 13637. | 12.8 | 58 |
| 18 | A STRUCTURAL BIOINFORMATICS APPROACH TO THE ANALYSIS OF NONSYNONYMOUS SINGLE NUCLEOTIDE POLYMORPHISMS (nsSNPs) AND THEIR RELATION TO DISEASE. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 1297-1318. | 0.8 | 56 |

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|----|---|------|-----------|
| 19 | BIPA: a database for protein-nucleic acid interaction in 3D structures. <i>Bioinformatics</i> , 2009, 25, 1559-1560. | 4.1 | 50 |
| 20 | BubR1 kinase: protection against aneuploidy and premature aging. <i>Trends in Molecular Medicine</i> , 2015, 21, 364-372. | 6.7 | 48 |
| 21 | Androgen-induced expression of DRP1 regulates mitochondrial metabolic reprogramming in prostate cancer. <i>Cancer Letters</i> , 2020, 471, 72-87. | 7.2 | 45 |
| 22 | Evaluation of somatic copy number estimation tools for whole-exome sequencing data. <i>Briefings in Bioinformatics</i> , 2016, 17, 185-192. | 6.5 | 44 |
| 23 | Failure to replicate the STAP cell phenomenon. <i>Nature</i> , 2015, 525, E6-E9. | 27.8 | 41 |
| 24 | Structural and functional restraints in the evolution of protein families and superfamilies. <i>Biochemical Society Transactions</i> , 2009, 37, 727-733. | 3.4 | 40 |
| 25 | Global impact of somatic structural variation on the DNA methylome of human cancers. <i>Genome Biology</i> , 2019, 20, 209. | 8.8 | 40 |
| 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. | 3.3 | 39 |
| 27 | Depression and suicide risk prediction models using blood-derived multi-omics data. <i>Translational Psychiatry</i> , 2019, 9, 262. | 4.8 | 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. <i>Genome Biology</i> , 2019, 20, 168. | 8.8 | 34 |
| 30 | Comparative interactomics analysis of protein family interaction networks using PSIMAP (protein) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 4.1 | 33 |
| 31 | Defining the mutation signatures of DNA polymerase δ in cancer genomes. <i>NAR Cancer</i> , 2020, 2, zcaa017. | 3.1 | 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. <i>Journal of Biological Chemistry</i> , 2012, 287, 5988-6001. | 3.4 | 32 |
| 33 | Genomic analysis reveals secondary glioblastoma after radiotherapy in a subset of recurrent medulloblastomas. <i>Acta Neuropathologica</i> , 2018, 135, 939-953. | 7.7 | 32 |
| 34 | 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. | 7.1 | 32 |
| 35 | 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. | 14.5 | 30 |
| 36 | Somatic mosaicism reveals clonal distributions of neocortical development. <i>Nature</i> , 2022, 604, 689-696. | 27.8 | 26 |

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|----|---|------|-----------|
| 37 | 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. | 3.9 | 23 |
| 38 | Microbiome of Saliva and Plaque in Children According to Age and Dental Caries Experience. <i>Diagnostics</i> , 2021, 11, 1324. | 2.6 | 22 |
| 39 | CPEM: Accurate cancer type classification based on somatic alterations using an ensemble of aRandom forest and a deep neural network. <i>Scientific Reports</i> , 2019, 9, 16927. | 3.3 | 21 |
| 40 | Chromosome-scale assembly comparison of the Korean Reference Genome KOREF from PromethION and PacBio with Hi-C mapping information. <i>GigaScience</i> , 2019, 8, . | 6.4 | 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. <i>Theranostics</i> , 2020, 10, 5181-5194. | 10.0 | 17 |
| 42 | Circulating Tumor Cell Clusters Are Cloaked with Platelets and Correlate with Poor Prognosis in Unresectable Pancreatic Cancer. <i>Cancers</i> , 2021, 13, 5272. | 3.7 | 17 |
| 43 | QTL analysis of fruit length using rRAMP, WRKY, and AFLP markers in chili pepper. <i>Horticulture Environment and Biotechnology</i> , 2011, 52, 602-613. | 2.1 | 14 |
| 44 | Ulla: a program for calculating environment-specific amino acid substitution tables. <i>Bioinformatics</i> , 2009, 25, 1976-1977. | 4.1 | 13 |
| 45 | A functional genomic approach to actionable gene fusions for precision oncology. <i>Science Advances</i> , 2022, 8, eabm2382. | 10.3 | 9 |
| 46 | 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 |
| 47 | Sex-specific difference of in-hospital mortality from COVID-19 in South Korea. <i>PLoS ONE</i> , 2022, 17, e0262861. | 2.5 | 8 |
| 48 | 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. | 2.5 | 7 |
| 49 | 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. | 2.3 | 6 |
| 50 | 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. | 2.5 | 5 |
| 51 | 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. | 0.9 | 5 |
| 52 | The dynamics of signal amplification by macromolecular assemblies for the control of chromosome segregation. <i>Frontiers in Physiology</i> , 2014, 5, 368. | 2.8 | 4 |
| 53 | Potential involvement of <i>Drosophila</i> flightless-1 in carbohydrate metabolism. <i>BMB Reports</i> , 2018, 51, 462-467. | 2.4 | 4 |
| 54 | PWWP2B promotes DNA end resection and homologous recombination. <i>EMBO Reports</i> , 2022, , e53492. | 4.5 | 4 |

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|----|---|-----|-----------|
| 55 | 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. | 1.7 | 3 |
| 56 | Loss of BubR1 acetylation provokes replication stress and leads to complex chromosomal rearrangements. <i>FEBS Journal</i> , 2021, 288, 5925-5942. | 4.7 | 0 |