# Peter J. Park

## Personal Data


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| Date prepared: | October 20, 2023 |
| Place and Date of Birth: | Seoul Korea \| October 12, 1971 |
| Office: | Department of Biomedical Informatics<br>Harvard Medical School<br>10 Shattuck St, Boston, MA, USA |
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## Education

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|---|---|
| 1990-1994 | AB/SM in Applied Mathematics, Harvard University |
| 1994-1999 | PhD in Applied Mathematics, California Institute of Technology<br>Thesis: *Multiscale numerical methods for the singularly perturbed convection-diffusion equation*, Advisor: Thomas Y. Hou |
| 1999-2000 | SM Biostatistics, Harvard School of Public Health |
| 2000-2001 | Postdoctoral Fellowship, Harvard School of Public Health |

## Academic Appointments

| | | |
|---|---|---|
| 2001-2006 | Instructor | Harvard Medical School |
| 2006-2010 | Assistant Professor | Harvard Medical School |
| 2010-2016 | Associate Professor | Harvard Medical School |
| 2016- | Professor of Biomedical Informatics | Harvard Medical School |

## Other Appointments

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|---|---|
| 2001-2015 | Scientific Staff, Informatics Program, Boston Children's Hospital |
| 2003-2008 | Assoc Dir of Bioinformatics, Harvard-Partners Ctr for Genetics and Genomics |
| 2003- | Associate Research Staff, Dept of Medicine, Brigham and Women's Hospital |
| 2005- | Affiliate Faculty, Harvard-MIT Health Sciences and Technology |
| 2007- | Member, Dana-Farber Harvard Cancer Center |
| 2010 | Visiting Fellow, Isaac Newton Institute for Mathematical Sciences<br>University of Cambridge, UK |
| 2011- | Affiliate Faculty, Harvard Stem Cell Institute, Harvard University |
| 2013- | Director, PhD Program in Bioinformatics & Integrative Genomics (BIG)<br>Chair, Admissions Committee |
| 2015-2022 | Co-Leader, Cancer Data Sciences Program, Data-Farber Harvard Cancer Center |
| 2015- | Standing Committee on Higher Degrees in Medical Sciences<br>Faculty of Arts and Sciences, Harvard University |
| 2015- | Member, Harvard Ludwig Center |
| 2011- | Faculty Search Committees, Depts of Biomedical Informatics (2011-; Chair, 2019-)<br>Cell Biology (2012), Systems Biology (2014); Harvard-affiliated hospitals (2016-) |

## Honors

| | |
|---|---|
| 1990 | National Merit Scholar |
| 1992 | Harvard College Scholar |
| 1993 | John Harvard Scholar |
| 2010 | Sloan Research Fellowship |
| 2012 | Young Mentor Award, Harvard Medical School |
| 2013 | Emily Frederick DiMaggio Lecture, Dana-Farber Cancer Institute |
| 2022 | Waun Ki Hong Lecture, American Assoc. for Cancer Research-Korean Cancer Assoc. |

## Committee Service

**Promotion Committees (non-Harvard)**

2013: Johns Hopkins
2014: University of California, San Diego
2015: University of Conneticut Health Center
2016: Univ of Massachusetts Medical School, Scripps Research Institute
2017: Stanford, Johns Hopkins, KAIST
2018: Washington University in St. Louis, Brown
2019: IST Austria, University of Virginia
2020: Stanford, Baylor College of Medicine
2022: Ichan School of Medicine at Mount Sinai, Univ of Arkansas
2023: Stanford, Univ of Pennsylvania, University of Conneticut

**Consortia Steering Committees**

The Cancer Genome Atlas (2007-2011)
Model Organism Encyclopedia of DNA Elements (2007-2012)
4D Nucleome (2015-2025)
Brain Somatic Mosiacism Consortium (2016-2022)
Somatic Mosaicism Across Human Tissues (SMaHT) Network (2023-)

**Advisory: Boards**

External Advisory Committee (Chair) (2016-), Center of Excellence on Computational Biology of Human Disease, Brown University
Statistics Editor, Cell Press journals (2019-)
National Advisory Council for Human Genome Research (NIH) (2021)

**Grant Reviews**

AIRC (The Italian Foundation for Cancer Research) (2017-9,2023)
American Association for the Advancement of Science (2014)
BioNexus KC Patton Trust Grant (2019)
Breakthrough Breast Cancer Research Centre (UK) (2009)
European Research Council (2016)
Excellence Initiative for Université Bourgogne Franche-Comté (2017)
Florida Department of Health (2010-2)
FNP Prize, Foundation for Polish Science (2019)
Fondazione Telethon (meeting in Milan) (2019)
French National Research Agency (2010)
Genome Canada/Alberta/Quebec (2013,2016,2017,2018,2019,2000)
Research grants, Saudi Arabia (2011,2016,2021)
Hood Foundation (2015-6)
Medical Research Council (UK) (2013)
National Cancer Institute (2009-12)
National Research Foundation of Korea (2020, 2023)
Netherlands Genomics Initiative (2010)
NIH Study Sections (Common Fund/NIAID/NCI/NHGRI/NICHD/NIDDK/SBIR/Special Emphasis) (2009-; section chairs, 2021-)
Samsung Research Funding & Incubation Center (2019, 2021)
Schmidt Science Fellowship (2020-2023)
Science Foundation Ireland (2007)
Suh Kyungbae Foundation (2019)
Swiss National Science Foundation (2009,2019)
The Wellcome Trust (UK) (2010,2016)
United Arab Emirates (2023)
United States-Israel Binational Science Foundation (2009)
University of Nebraska, Biomedical Research Excellence (2020)

## Software & Databases

2005 SigPathway - statistical analysis for pathway enrichment analysis
2005 CrossChip - comparative analysis of different microarrays
2008 SPP (Solexa Processing Pipeline) - package for ChIP-seq analysis
2008 CGHweb - copy number analysis using multiple segmentation algorithms
2008 nuScore - likelihood estimation for positioned nucleosomes
2010 Quantized correlation coefficient - correlation analysis for ChIP-chip analysis
2010 Repeat Enrichment Estimator - copy number for repetitive elements
2011 Tea (Transposable element analyzer) - identification of transposable elements in WGS
2011 BIC-seq (Bayesian information criterion-seq) - copy number analysis for WGS
2011 Antibody Validation Database - experimental validation data for histone modifications
2011 Chromatin browser - exploring profiles of histone marks and chromosomal proteins
2013 MSIProfiler - detection of microsatellite mutations in exomes/WGS
2013 Meerkat - detection of structual alterations in WGS
2013 MetaCGH - copy number profiles from >8000 Array CGH experiments
2014 Nozzle - report generation toolkit for data analysis
2014 StratomeX - interactive visualization for heterogeneous datasets
2015 Emsar - transcript quantification for RNA-seq data
2016 BIC-seq2 - improved copy number analysis for WGS
2017 NGSCheckmate - validation of matched sequencing samples
2017 LiRA (Linked-Read Analysis) - mutation detection in single cells using read-phasing
2018 PaSDqc (Power Spectral Density-qc) - quality control for single cell WGS
2019 SigMA (Signature Multivariate Analysis) - mutational signature analysis
2019 SCAN-SNV - single cell genotyper for WGS
2019 Tibanna - software for scalable execution of portable pipelines on the cloud
2020 MosaicForecast - mosaic mutation detection in bulk samples
2020 CGAP (Clinical Genome Analysis Platform) - genome analysis for clinicians
2020 HiNT (Hi-C for copy Number variation and Translocation detection)
2021 xTea (x-Transposable element analyzer) - TE detection for multiple platforms
2021 HiTea - Identification of trasposable element insertions using Hi-C data
2021 BAMsnap - lightweight read-level viewer for sequencing data
2022 Shatterseek - identification of chromothripsis in WGS
2022 SCAN2 (Single Cell ANalysis 2) - SNV/indel detection in single cells genomewide
2023 SVA Catalog - database of germline SINE-VNTR-Alu (SVA) retrotransposons
2023 MuSiCal (Mutational Signature Calculator) - package for robust signature analysis

## Role in Companies

Co-founder: Claritas Genomics, RegUp
Scientific Advisory Board: Bioskryb Genomics
Consultant: Black Diamond Therapeutics, Claritas Genomics, CJ, FutuRx, KEW, Palleon Pharmaceuticals, Pfizer, RaNA Therapeutics, Third Rock Ventures, Vor Bio

## Patent

2019 Systems and methods for classifying tumors (WO2020068506A1)
2020 Compositions and methods for identifying a single-nucleotide variant (US20210062265A1)
2021 Antisense oligonucleotide-based progranulin augmentation therapy in neurodegenerative diseases (US11359199B2)
2022 Antisense oligonucleotide drug targets (WO2023107531A2)

## Current Grants

(direct cost to the lab over the grant period)

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|---|---|
| 2015-25 | The Function of Snf5, an Epigenetic Tumor Suppressor (with C. Roberts; 150K) |
| 2019-24 | Reverse Transcriptase Inhibitor Effects on the Cancer Mobilome (with D. Ting; 270K) |
| 2019-23 | SPECIFICANCER: Dissecting the Tissue Specificity of Cancer Drivers, Cancer Research UK Grand Challenge (team led by S. Elledge; 1.5M) |
| 2020-25 | Cell Identity Determination in Human Brain (with C. Walsh; 490K) |
| 2020-23 | Antisense Oligonucleotide-Based Progranulin Augmentation Therapy in Neurodegenerative Diseases (870K) |
| 2020-25 | 4D Nucleome Network Data Coordination and Integration Center (7.8M) |
| 2021-23 | Interoperability and Collaboration with the Common Fund Data Ecosystem (570K) |
| 2022-26 | Development and Appl of Computational Methods for Single Cell DNA-seq Data (1.6M) |
| 2022-27 | Mutational Signature Analysis: Methods and Applications to the Clinic (1.4M) |
| 2023-28 | Data Analysis Center for Somatic Mosaicism Across Human Tissues Network (12M) |

## Presentations

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|---|---|
| 2023 | Advances in Genome Biology and Technology (AGBT) Conference, Hollywood, FL<br>Emerging Approaches for Tumor Analyses, National Cancer Institute<br>St Jude Children's Research Hospital, Memphis |
| 2022 | European Society of Human Genetics, Vienna, Austria<br>Computing+Mathematical Sciences, California Institute of Technology<br>Center for Human Genetics and Genomics, New York University<br>Suhkyungbae Foundation Symposium (keynote), Seoul, Korea<br>AACR-KCR (Award lecture), Seoul, Korea<br>KAIST (Korea Advanced Institute of Science and Technology), Seoul, Korea<br>Korean Society of Molecular Oncology International Conference, Seoul, Korea |
| 2021 | NCI Symposium on Mutational Signature and Cancer, online<br>KOGO (Korean Genome Organization) Conference, Seoul, Korea |
| 2020 | Cancer Working Group, Harvard School of Public Health<br>Broad Cell Circuits and Epigenomics, Broad Institute |
| 2019 | MIT Bioinformatics seminar, Cambridge, MA<br>Genomics of MPNST Conference, Boston<br>Symposium on 3D Architecture of the Genome Cancer, Boston<br>Pfizer Integrative Biology Meeting (keynote), Cambridge MA<br>Cancer Genetics Retreat, Dana-Farber Harvard Cancer Center, Boston<br>Bridge-to-Industry Seminar, Harvard Medical School<br>Center of Mathematical Sciences and Applications, Harvard University<br>Systems Biology Seminars, Boston University<br>Genome Sciences Seminar Series, University of Virginia<br>The New Mexico Bioinformatics, Science, & Technology Symposium, Santa Fe<br>US-Korea Conference, Chicago<br>Cancer Center Symposium (keynote), Seoul National Univ Bundang Hospital, Korea |
| 2018 | IFOM (Institute of Molecular Oncology), Milan, Italy<br>CONTRA (Computational ONcology TRaining Alliance) Workshop, Warsaw, Poland<br>Winter Quantitative Biology Conference, Hawaii<br>Yonsei Medical School, Seoul, Korea<br>geXc (Genomic Exchange Community) symposium, Broad Institute, Cambridge, MA |

Dana-Farber Center for Functional Cancer Epigenetics, Boston

2017
The Norwegian Cancer Symposium (Keynote), Oslo, Norway
Program in Quantitative Genomics, Harvard School of Public Health, Boston
Broad Institute, Cambridge, MA
Genetics and Molecular Biology program, University of North Carolina, Chapel Hill
Abcam Conf in Genome Rearrangements and Mutation Signature, Boston
MidAtlantic Bioinformatics Conference (keynote), Children's Hospital, Philadelphia
AstraZeneca, Waltham, MA
International Conference in Medical Big Data (keynote), Chongqing, China
Peking University, Beijing, China
Abcam Conference in Epigenetic Regulatory Pathways, Seoul, Korea
Int'l Symposium on Genomic Medicine, Samsung Medical Center, Seoul, Korea
Department of Biological Sciences, Seoul National University, Seoul, Korea
RIKEN, Yokohama, Japan

2016
Department of Genetics, Yale School of Medicine
Center for Computational Molecular Biology, Brown University
Computational Analysis of Biological Information, Microsoft Research, Cambridge, MA
Boston Computational Biology Meet-up, Microsoft Research, Cambridge, MA
Advances in Genome Biology and Technology Meeting, Orlando
American Association for Cancer Research (AACR) Annual Meeting, New Orleans
Research Center for Cellular Homeostasis Int'l Symposium, Ewha University, Seoul, Korea
Int'l Symposium on Genomic Medicine, Samsung Medical Center, Seoul, Korea
Armenise-Harvard Foundation Symposium, Gubio, Italy
IFOM (Institute of Molecular Oncology), Milan, Italy
SEMM European School of Molecular Medicine, Milan, Italy

2015
Harvard Medical School Board of Fellows, Cambridge, MA
Harvard University Committee on University Resources Symposium, Boston
Big Data Seminar, Harvard School of Public Health, Boston
Renal Division Research Seminar Series, Brigham and Women's Hospital, Boston
Adult Hydrocephalus Symposium, Brigham and Women's Hospital, Boston
University of Texas Southwestern Medical Center, Dallas
Workshop on The Role of Mobilome in Cancer National Cancer Institute, Bethesda
Department of Human Genetics, University of Michigan, Ann Arbor, MI
The Hospital for Sick Children, University of Toronto, Toronto, Canada

2014
Clarity Conference, Harvard Medical School, Boston
HMS Center for Biomedical Informatics Executive Education course, Boston
Center for Computational and Molecular Biology, Brown University
The Cancer Genome Atlas (TCGA) Network Meeting, Bethesda
American Associate for Cancer Research (AACR) Annual Meeting, San Diego
International Collaboration for Clinical Genomics conference, Washington DC
Conf on Chromothripsis/Clustered Mutation/Complex Rearrangement, Cambridge, MA
Keynote speaker, Bioinformatics and Genomics retreat, Pennsylvania State University
Beyond the Genome: Cancer Genomics, Boston
Genentech, San Francisco, CA
University of Texas Southwestern Medical Center, Dallas, TX
Asian Institute in Statistical Genetics and Genomics, Seoul, Korea
School of Biological Sciences, Seoul National University, Seoul, Korea
Korean Society for Molecular and Cellular Biology Annual Meeting (keynote), Seoul, Korea
King Saud University Liver Disease Research Center, Riyadh, Saudi Arabia
Int'l Symposium on Genomic Medicine, Samsung Medical Center, Seoul, Korea

2013 Department of Pediatric Oncology, Dana-Farber Cancer Institute, Boston
Seminars in Oncology, Dana Farber Cancer Institute, Boston
Adult Hydrocephalus Program Symposium, Brigham and Women's Hospital, Boston
4th Annual Pfizer Omics Workshop (keynote), Cambridge, MA
National Institute of Diabetes and Digestive and Kidney Diseases, Bethesda
Fourth Annual X-Gen Congress and Expo, San Diego
Genome Research conference, Boston
The Cancer Genome Atlas (TCGA) Network Meeting, Bethesda
Meeting of Italian Genetics Association, Cortona, Italy
Asian Institute in Statistical Genetics and Genomics, Seoul, Korea
The 4th Institute for Refractory Cancer Research Int'l Symposium, Seoul, Korea
School of Biological Sciences, Seoul National University, Seoul, Korea
Yonsei University College of Medicine, Seoul, Korea

2012 Massachusetts General Hospital Cancer Center, Boston
Center for Functional Cancer Epigenetics, Dana-Farber Cancer Institute, Boston
Department of Biology, Brandeis University, Waltham, MA
The Cancer Genome Atlas steering committee, Houston
Beyond the Genome conference, Harvard Medical School, Boston
Select Biosciences Genome Research conference, Boston
School of Biological Sciences, Seoul National University, Seoul, Korea
Seoul National University Bioinformatics Institute, Seoul, Korea
Seoul National University Medical School, Seoul, Korea
Korea Bioinformatics Center (KOBIC), Daejeon, Korea
The Catholic University Medical College, Seoul, Korea
Samsung Advanced Institute of Technology, Seoul, Korea

2011 Harvard Stem Cell Institute Blood Symposium, Boston
Genome Science Institute Seminar Series, Boston University Medical Campus
Biochemistry Seminar, Univ of Massachusetts Medical Center, Worcester, MA
The Cancer Genome Atlas Steering Committee, Gaithersburg, VA
Bioconductor conference, Fred Hutchinson Cancer Research Center, Seattle
Institute for Genome Sciences and Policy, Computational Biology, Duke University
BioPharma Research Council, Innovations in Epigenetics and Cancer, Bridgewater, NJ
Bio-IT World Conference and Expo, World Trade Center, Boston
INSERM workshop, Bordeaux, France
The 8th Int'l Conf on Bioinformatics: From Genomics to Synthetic Biology, Atlanta

2010 Department of Biostatistics, Harvard School of Public Health
Sanofi-Aventis Cambridge Cancer Center, Cambridge, MA
Next-generation Sequencing Data Analysis Symposium, Brown University
Conf on Next-Generation Sequencing Data Management, Providence
Beyond the Genome conference, Harvard Medical School
Clinical Informatics Summit, Harvard Medical School
Isaac Newton Institute for Mathematical Sciences, University of Cambridge, UK
Cancer Bioinformatics Workshop, Cambridge Research Institute, Cambridge, UK

2009 Royal Society of Chemistry, Frontiers in Epigenetics (plenary), London, UK
Department of Biochemistry, University of Oxford, UK
Wellcome Trust Adv Course in Functional Genomics & Systems Biology, Hinxton, UK
Program in Quantitative Genomics, Harvard School of Public Health
The Broad Institute, Cambridge, MA
10th Advances in Genome Biology and Technology Meeting, Marco Island, FL
Annual Meeting of the American Association for Cancer Research, Denver
School of Informatics and Computing, Indiana University

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| | Korea Advanced Institute of Technology (KAIST), Daejeon, Korea<br>Third International Epigenomics and Sequencing Meeting, Boston |
| 2008 | Department of Human Genetics, University of Michigan, Ann Arbor, MI<br>Summer School in Systems, Synthetic & Semantic Biology, University of Trento, Italy |
| 2007 | Division of Endocrinology, Children's Hospital Boston<br>Department of Biostatistics, Harvard School of Public Health<br>Longwood Computational Biology Seminars<br>Annual Meeting of the American Association for Cancer Research, Los Angeles<br>BioKorea Conference and Exhibition, Seoul, Korea<br>International Workshop on Glioma Research and Therapy, Boston |
| 2006 | Cardiovascular Research Center, Massachusetts General Hospital<br>Genomics Interest Group, Joslin Diabetes Center, Boston<br>Dept of Mathematical Sciences, Worcester Polytechnical Institute, Worcester, MA<br>9th Annual Conference on Computational Genomics, Baltimore<br>Statistics for Genome-wide Copy Number Analysis, Palo Alto, CA<br>School of Medicine, Seoul National University, Korea<br>Division of Molecular Life Sciences, Ewha University, Korea<br>Department of Computing, Soongsil University, Seoul, Korea |
| 2005 | Harvard-Partners Center for Genetics and Genomics, Boston<br>Distinguished Lecture Series, Arizona State University, Tempe, AZ<br>Drug Discovery Technology and Development World Congress, Boston<br>International Biometric Society meeting, Austin<br>Department of Informatics, University of Oslo |
| 1999-2004 | Harvard-Partners Center for Genetics and Genomics<br>Harvard Medical International/Asan Medical Center Symposium, Seoul, Korea<br>Division of Genetics Seminar Series, Boston Children's Hospital<br>Applied Mathematics Table, Harvard College<br>NIDDK Diseases Biotechnology Consortium, Washington DC<br>Emerging Technology and the Future of Vascular Research Conf, Washington DC<br>Seoul National Univ School of Medicine, Seoul, Korea<br>European Molecular Biology Organization, Milan, Italy<br>Intelligent Systems for Molecular Biology, Edmonton, Canada<br>Pacific Symposium on Biocomputing, HI<br>Department of Biostatistics, Harvard School of Public Health<br>MIT Lincoln Laboratory, Lexington, MA |

## Trainees

first position after leaving the lab listed

### Postdoctoral Fellows, >30 including

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|---|---|
| 2006-2011 | Peter Kharchenko, Assistant Professor, Harvard Medical School |
| 2009-2012 | Ruibin Xi, Assistant Professor of Statistics, Peking University |
| 2010-2017 | Alice E. Lee, Assistant Professor, Harvard/Boston Children's Hospital |
| 2010-2017 | Lixing Yang, Assistant Professor, University of Chicago |
| 2010-2014 | Francesco Ferrari, Principle Investigator, IFOM, Milan, Italy |
| 2010-2015 | Nils Gehlenborg, Assistant Professor, Harvard Medical School |
| 2016-2019 | Isidro Cortes-Ciriano, Group Leader, European Bioinformatics Institute, UK |
| 2017-2023 | Doga Gulhan, Assistant Professor, Harvard/Massachusetts General Hospital |

Graduate Students, >10 including

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| 2007-2008 | Julie Yoo, Co-founder and Chief Product Officer, Kyruus |
| 2010-2015 | Dan Day, Postdoctoral Fellow, MIT |
| 2016-2020 | Craig Bohrson, Postdoctoral Fellow, Harvard |
| 2016-2021 | Joe Luquette, Postdoctoral Fellow, Harvard |
| 2017-2022 | Joshua Cook, Vertex Pharmaceuticals |
| 2017-2022 | Vinay Viswanadham, Postdoctoral Fellow, Harvard |

Scientific Programmers, >15 including

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| 2003-2004 | Richard Kim, Medical student, UCSF |
| 2004-2006 | Weil Lai, Medical student, Tufts |
| 2008-2014 | Joe Luquette, Graduate student, Harvard Medical School |
| 2016-2018 | Alison Barton, Graduate student, Harvard Medical School |
| 2016-2019 | Max Sherman, Graduate student, MIT |
| 2017-2021 | Alon Galor, Graduate student, Oxford |
| 2019-2021 | Victor Mao, Google |
| 2021-2023 | Antuan Tran, Medical student, Mayo Clinic |

## Key Publications

† denotes co-first authorship; ‡ denote co-corresponding authorship; ⋆ denotes favorites

1. H. Jin, D. C. Gulhan, B. Geiger, D. Ben-Isvy, D. Geng, V. Ljungström, and **P. J. Park**. *Accurate and sensitive mutational signature analysis with MuSiCal.* **Nature Genetics**, in press ★

2. T. Gao, M. E. Kastriti, V. Ljungström, A. Heinzel, A. S. Tischler, R. Oberbauer, P.-R. Loh, I. Adameyko, **P. J. Park**‡, and P. V. Kharchenko‡. *A pan-tissue survey of mosaic chromosomal alterations in 948 individuals.* **Nature Genetics**, in press

3. E. V. Watson†, J. J.-K. Lee†, D. C. Gulhan, G. E. M. Melloni, S. V. Venev, R. Y. Magesh, A. Frederick, K. Chiba, E. C. Wooten, K. Naxerova, J. Dekker, **P. J. Park**‡, and S. J. Elledge‡. *Chromosome evolution screens select tissue-specific tumor aneuploidy patterns.* **Nature Genetics**, in press

4. S. L'Yi, D. Maziec, V. Stevens, T. Manz, V. Veit, M. Berselli, **P. J. Park**‡, D. Glodzik‡, and N. Gehlenborg‡. *Chromoscope: interactive multiscale visualization for structural variation in human genomes.* **Nature Methods**, in press

5. C. Chu, E. W. Lin, A. Tran, H. Jin, N. I. Ho, A. Veit, I. Cortes-Ciriano, K. H. Burns, D. T. Ting, and **P. J. Park**. *The landscape of human SVA retrotransposons.* **Nucleic Acids Res**, in press

6. J. J. Lee‡, Y. L. Jung, T. C. Cheong, J. Espejo Valle-Inclan, C. Chu, D. C. Gulhan, V. m, H. Jin, V. V. Viswanadham, E. V. Watson, I. Cortes-Ciriano, S. J. Elledge, R. Chiarle, D. Pellman, and **P. J. Park**‡. *ER$\alpha$-associated translocations underlie oncogene amplifications in breast cancer.* **Nature** 618.7967, pp. 1024–1032, 2023 ★

7. J. Kim, S. Woo, C. M. de Gusmao, B. Zhao, D. H. Chin, R. L. DiDonato, M. A. Nguyen, T. Nakayama, C. A. Hu, A. Soucy, A. Kuniholm, J. K. Thornton, O. Riccardi, D. A. Friedman, C. M. El Achkar, Z. Dash, L. Cornelissen, C. Donado, K. N. W. Faour, L. W. Bush, V. Suslovitch, C. Lentucci, **P. J. Park**, E. A. Lee, A. Patterson, A. A. Philippakis, B. Margus, C. B. Berde, and T. W. Yu. *A framework for individualized splice-switching oligonucleotide therapy.* **Nature** 619.7971, pp. 828–836, 2023

8. J. Dekker, F. Alber, S. Aufmkolk, B. J. Beliveau, B. G. Bruneau, A. S. Belmont, L. Bintu, A. Boettiger, R. Calandrelli, C. M. Disteche, D. M. Gilbert, T. Gregor, A. S. Hansen, B. Huang, D. Huangfu, R. Kalhor, C. S. Leslie, W. Li, Y. Li, J. Ma, W. S. Noble, **P. J. Park**, J. E. Phillips-Cremins, K. S. Pollard, S. M. Rafelski, B. Ren, Y. Ruan, Y. Shav-Tal, Y. Shen, J. Shendure, X. Shu, C. Strambio-De-Castillia, A. Vertii, H. Zhang, and S. Zhong. *Spatial and temporal*

*organization of the genome: Current state and future aims of the 4D nucleome project.* **Mol Cell** 83.15, pp. 2624–2640, 2023

9. L. J. Luquette[†], M. B. Miller[†], Z. Zhou[†], C. L. Bohrson, Y. Zhao, H. Jin, D. Gulhan, J. Ganz, S. Bizzotto, S. Kirkham, T. Hochepied, C. Libert, A. Galor, J. Kim, M. A. Lodato, J. I. Garay-coechea, C. Gawad, J. West, C. A. Walsh[‡], and **P. J. Park**[‡]. *Single-cell genome sequencing of human neurons identifies somatic point mutation and indel enrichment in regulatory elements.* **Nat Genet** 54.10, pp. 1564–1571, 2022 ★

10. I. Cortes-Ciriano, D. C. Gulhan, J. J. Lee, G. E. M. Melloni, and **P. J. Park**. *Computational analysis of cancer genome sequencing data.* **Nat Rev Genet** 23.5, pp. 298–314, 2022 ★

11. S. B. Reiff, A. J. Schroeder, K. ı, A. Cosolo, C. Bakker, L. Mercado, S. Lee, A. D. Veit, A. K. Balashov, C. Vitzthum, W. Ronchetti, K. M. Pitman, J. Johnson, S. R. Ehmsen, P. Kerpedjiev, N. Abdennur, M. Imakaev, S. U. Ozturk, U. Camoglu, L. A. Mirny, N. Gehlenborg, B. H. Alver, and **P. J. Park**. *The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data.* **Nat Commun** 13.1, p. 2365, 2022

12. C. Chu, R. Borges-Monroy, V. V. Viswanadham, S. Lee, H. Li, E. A. Lee[‡], and **P. J. Park**[‡]. *Comprehensive identification of transposable element insertions using multiple sequencing technologies.* **Nat Commun** 12.1, p. 3836, 2021

13. J. H. Cook[†], G. E. M. Melloni[†], D. C. Gulhan, **P. J. Park**[‡], and K. M. Haigis[‡]. *The origins and genetic interactions of KRAS mutations are allele- and tissue-specific.* **Nat Commun** 12.1, p. 1808, 2021

14. S. Bizzotto[†], Y. Dou[†], J. Ganz[†], R. N. Doan, M. Kwon, C. L. Bohrson, S. N. Kim, T. Bae, A. Abyzov, NIMH Brain Somatic Mosaicism Network, **P. J. Park**[‡], and C. A. Walsh[‡]. *Landmarks of human embryonic development inscribed in somatic mutations.* **Science** 371.6535, pp. 1249–1253, 2021 ★

15. Y. L. Jung, K. Kirli, B. H. Alver, and **P. J. Park**. *Resources and challenges for integrative analysis of nuclear architecture data.* **Curr Opin Genet Dev** 67, pp. 103–110, 2021

16. R. E. Rodin[†], Y. Dou[†], M. Kwon, M. A. Sherman, A. M. D'Gama, R. N. Doan, L. M. Rento, K. M. Girskis, C. L. Bohrson, S. N. Kim, A. Nadig, L. J. Luquette, D. C. Gulhan, Brain Somatic Mosaicism Network, **P. J. Park**[‡], and C. A. Walsh[‡]. *The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing.* **Nat Neurosci** 24.2, pp. 176–185, 2021

17. M. A. Sherman, R. E. Rodin, G. Genovese, C. Dias, A. R. Barton, R. E. Mukamel, B. Berger, **P. J. Park**[‡], C. A. Walsh[‡], and P. R. Loh[‡]. *Large mosaic copy number variations confer autism risk.* **Nat Neurosci** 24.2, pp. 197–203, 2021

18. Y. Dou, M. Kwon, R. E. Rodin, I. Cortes-Ciriano, R. Doan, L. J. Luquette, A. Galor, C. Bohrson, C. A. Walsh, and **P. J. Park**. *Accurate detection of mosaic variants in sequencing data without matched controls.* **Nat Biotechnol** 38.3, pp. 314–319, 2020 ★

19. J. W. Yun, L. Yang, H. Y. Park, C. W. Lee, H. Cha, H. T. Shin, K. W. Noh, Y. L. Choi, W. Y. Park[‡], and **P. J. Park**[‡]. *Dysregulation of cancer genes by recurrent intergenic fusions.* **Genome Biol** 21.1, p. 166, 2020

20. S. Wang, S. Lee, C. Chu, D. Jain, P. Kerpedjiev, G. M. Nelson, J. M. Walsh, B. H. Alver, and **P. J. Park**. *HiNT: a computational method for detecting copy number variations and translocations from Hi-C data.* **Genome Biol** 21.1, p. 73, 2020

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