Christina Curtis

RZ Cao Professor and Professor of Genetics

Medicine - Oncology

Bio

BIO

Christina Curtis, PhD, MSc is the RZ Cao Professor of Medicine, Genetics and Biomedical Data Science at Stanford University where she also serves as Senior Vice Chair of Research in the Department of Medicine and Director of Artificial Intelligence and Cancer Genomics at the Stanford Cancer Institute. Dr. Curtis leads a federally-funded research laboratory focused on AI/ML, computational modeling, high-throughput molecular profiling and experimentation to develop new ways to prevent, diagnose and treat cancer. Her research redefined the molecular map of breast cancer and led to new paradigms in understanding the origins of human cancers, as well as how they evolve and metastasize. Dr. Curtis has been the recipient of numerous awards, including the National Institutes of Health (NIH) Director's Pioneer Award (2018) and the American Association for Cancer Research (AACR) Award for Outstanding Achievement in Basic Science (2022). She received the 2024 AACR-Breast Cancer Research Foundation (BCRF) Award for Outstanding Achievement in Breast Cancer Research and the Susan G. Komen Brinker Award, as well as the 2025 European Society for Molecular Oncology (ESMO) Translational Award and the Paul Marks Prize for Cancer Research. She is a Kavli Fellow of the National Academy of Sciences, a Susan G. Komen Scholar, and a Chan Zuckerberg Biohub Investigator. Dr. Curtis has served as a member of Board of Reviewing Editors at Science, and as a member of the Board of Directors of AACR and Stand Up 2 Cancer (SU2C). She is a scientific advisor to biopharma (Astrazeneca, Genentech, Bristol Myers Squibb, Pfizer), biotech and to VC firms.

ACADEMIC APPOINTMENTS

- Professor, Medicine - Oncology
- Professor, Genetics
- Member, Bio-X
- Member, Stanford Cancer Institute

ADMINISTRATIVE APPOINTMENTS

- Senior Vice Chair, Department of Medicine, Stanford School of Medicine, (2025- present)
- Director, Artificial Intelligence and Cancer Genomics, Stanford Cancer Institute, (2022- present)
- Director, Breast Cancer Translational Research, Stanford Cancer Institute, (2021- present)
- Co-Director, Molecular Tumor Board, Stanford Cancer Institute, (2014-2022)

HONORS AND AWARDS

- Fellow, American Association for Cancer Research (2026)
- Translational Award, European Society for Molecular Oncology (ESMO) (2025)
- Paul Marks Prize for Cancer Research, Memorial Sloan Kettering Cancer Center (2025)

- Outstanding Achievement in Breast Cancer Research, American Association for Cancer Research (AACR) and Breast Cancer Research Foundation (BCRF) (2024)
- Brinker Award, Susan G. Komen (2024)
- Outstanding Achievement in Basic Science, American Association for Cancer Research (AACR) (2022)
- Investigator, Chan Zuckerberg Biohub (2022)
- Julius B Kahn Visiting Professor, Northwestern University, Department of Pharmacology (2021)
- Rising Leader, Life Sciences, In Vivo (2021)
- Stanford Prize in Population Genetics and Society, Stanford University (2020)
- Komen Scholar, Susan G. Komen (2020)
- NIH Director's Pioneer Award, NIH (2018)
- Kavli Frontier of Science Fellow, National Academy of Science (USA) (2016)
- Career Development Award, American Association for Cancer Research (AACR): Triple Negative Breast Cancer Foundation (2016)
- Career Development Award, STOP Cancer (2012)
- V Scholar Award, V Foundation for Cancer Research (2012)
- Scholar-In-Training Award, American Association for Cancer Research (2009)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Scientific Advisor, Bristol Myers Squibb (2025 - present)
- Scientific Advisor, Pfizer (2024 - present)
- Advisor/Consultant, AstraZeneca (2024 - present)
- Scientific Review Board, Genentech (2024 - present)
- Board of Directors, American Association for Cancer Research (AACR) (2022 - 2025)
- Board of Reviewing Editors, Science (2022 - 2024)
- Scientific Advisory Board, ResistanceBio (2020 - 2022)
- Scientific Advisory Board, Columbia University, Herbert Irving Comprehensive Cancer Center (2020 - 2024)
- Editorial Board Member, ASCO Journal of Clinical Oncology: Precision Oncology (2016 - 2025)
- Scientific Advisory Board, Susan G. Komen Big Data Initiative, Share for Cures (2019 - 2023)
- Scientific Advisory Board, Singapore Cancer Science Institute (2023 - present)
- Scientific Advisory Board, NY Genome Center (2023 - present)
- Scientific Advisory Board, DeepCell (2021 - present)
- Scientific Advisory Board, Genentech, Oncology (2020 - present)
- Scientific Advisory Board, Nanostring (2020 - present)
- Scientific Advisory Board, GRAIL (2017 - 2019)
- Scientific Advisory Board, Ontario Institute for Cancer Research, Adaptive Oncology Program (2017 - present)
- Scientific Advisory Board, Cancer Research UK Early Detection Committee (2017 - 2020)
- Editorial Board Member, Cancer Discovery (2020 - present)
- Editorial Board Member, Cell Systems (2019 - present)
- Editorial Board Member, Journal of Computational Biology (2017 - present)
- Associate Editor, Breast Cancer Research (2015 - 2020)

PROFESSIONAL EDUCATION

- Postdoctoral Fellow, University of Cambridge , Computational Biology
- PhD, University of Southern California , Molecular and Computational Biology
- MS, University of Southern California , Bioinformatics and Computational Biology
- MSc, University of Heidelberg, Germany , Molecular Biology

COMMUNITY AND INTERNATIONAL WORK

- ECOG/ACRIN Correlative science
- Stanford Breast Cancer Metastasis Center
- NCI/CTEP Translational Bioinformatics Committee
- Human Tumor Atlas Network
- The Cancer Genome Atlas, Data Analysis Working Groups

LINKS

- Cancer Computational and Systems Biology Lab: http://med.stanford.edu/curtislab.html

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Harnessing AI/ML and computational modeling and multi-modal and perturbational datasets, our research seeks to advance target discovery, diagnostic development and a mechanistic understanding of cancer origins and progression. volutionary dynamics, novel therapeutic targets, and the genotype to phenotype map in cancer. A unifying theme of our research is to exploit ‘omic’ data derived from clinically annotated samples in robust computational frameworks coupled with iterative experimental validation in order to advance our understanding of cancer systems biology. Ongoing projects include
1.) Modeling the evolutionary dynamics of tumor initiation, progression and therapeutic resistance and metastasis
2) Elucidating disease etiology and novel molecular targets through integrative analyses of high-throughput omic data
3) Developing techniques for the systems-level interpretation of genotype-phenotype associations in cancer
4) Establishing robust computational pathology methods and multi-modal spatial foundation models
5) Designing and optimizing small molecule and immune therapies for cancer treatment and interception

Our research is funded by the NIH/NCI, NHGRI, Department of Defense, Breast Cancer Research Foundation, American Association for Cancer Research, Susan G. Komen Foundation, Emerson Collective and V Foundation for Cancer Research.

CLINICAL TRIALS

- Molecular Analysis of Breast Cancer, Not Recruiting
- Study of Infigratinib in Combination With Tamoxifen in Hormone Receptor Positive, HER2 Negative, FGFR Altered Advanced Breast Cancer, Not Recruiting
- Umbrella Trial Testing Integrative Subtype Targeted Therapeutics in Estrogen Receptor Positive, HER2-Negative Breast Cancer, Not Recruiting

Teaching

STANFORD ADVISEES

Med Scholar Project Advisor

Sophia Pribus

Doctoral Dissertation Reader (AC)

Peter Du, Ibtihal Elfaki, Venkat Sankar

Postdoctoral Faculty Sponsor

Cameron Durfee, Artem Lomakin, Lise Mangiante, Seongyeol Park, Maryam Pourmaleki, Debra Van Egeren

Doctoral Dissertation Advisor (AC)

Alvina Adimoelja, Kristle Garcia, Gabriella Reynolds, Brennan Simon

Master's Program Advisor

Ariana Lotfi, Ryan Nayebi

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (Phd Program)
- Cancer Biology (Phd Program)
- Genetics (Phd Program)
- Oncology (Fellowship Program)

Publications

PUBLICATIONS

- **An international framework for clinical translation of molecular classifiers in osteosarcoma.** *NPJ precision oncology*

  Marinoff, A. E., Nathrath, M., Shulman, D. S., Whittle, S. B., Pavisic, J., Spentzos, D., Albert, C. M., Nash, J. O., Shlien, A., Cortes-Ciriano, I., Marchais, A., Lopez-Fuentes, E., Curtis, et al

  2026

- **Temporal and spatial composition of the tumor microenvironment predicts response to immune checkpoint inhibition in metastatic TNBC.** *Nature cancer*

  Greenwald, N. F., Nederlof, I., Sowers, C., Ding, D. Y., Park, S., Kong, A., Houlahan, K. E., Varra, S. R., de Graaf, M., Geurts, V., Liu, C. C., Ranek, J. S., Voorwerk, et al

  2026

- **Polyclonal origins of human premalignant colorectal lesions.** *Nature*

  Van Egeren, D., Schenck, R. O., Khan, A., Horning, A. M., Mo, S., Weiß, C. L., Esplin, E. D., Becker, W. R., Wu, S., Hanson, C., Barapour, N., Jiang, L., Contrepois, et al

  2025

- **Germline-mediated immunoediting sculpts breast cancer subtypes and metastatic proclivity.** *Science (New York, N.Y.)*

  Houlahan, K. E., Khan, A., Greenwald, N. F., Vivas, C. S., West, R. B., Angelo, M., Curtis, C.

  2024; 384 (6699): eadh8697

- **A microwell platform for high-throughput longitudinal phenotyping and selective retrieval of organoids.** *Cell systems*

  Sockell, A., Wong, W., Longwell, S., Vu, T., Karlsson, K., Mokhtari, D., Schaepe, J., Lo, Y., Cornelius, V., Kuo, C., Van Valen, D., Curtis, C., Fordyce, et al

  2023; 14 (9): 764

- **Deterministic evolution and stringent selection during preneoplasia.** *Nature*

  Karlsson, K., Przybilla, M. J., Kotler, E., Khan, A., Xu, H., Karagyozova, K., Sockell, A., Wong, W. H., Liu, K., Mah, A., Lo, Y. H., Lu, B., Houlahan, et al

  2023

- **Germline-mediated immunoediting sculpts breast cancer subtypes and metastatic proclivity.** *bioRxiv : the preprint server for biology*

  Houlahan, K. E., Khan, A., Greenwald, N. F., West, R. B., Angelo, M., Curtis, C.

  2023

- **Spatial proteomic characterization of HER2-positive breast tumors through neoadjuvant therapy predicts response.** *Nature cancer*
  McNamara, K. L., Caswell-Jin, J. L., Joshi, R., Ma, Z., Kotler, E., Bean, G. R., Kriner, M., Zhou, Z., Hoang, M., Beechem, J., Zoeller, J., Press, M. F., Slamon, et al
  2021; 2 (4): 400-413

- **Characterizing the ecological and evolutionary dynamics of cancer.** *Nature genetics*
  Zahir, N. n., Sun, R. n., Gallahan, D. n., Gatenby, R. A., Curtis, C. n.
  2020

- **Pathologic and molecular responses to neoadjuvant trastuzumab and/or lapatinib from a phase II randomized trial in HER2-positive breast cancer (TRIO-US B07).** *Nature communications*
  Hurvitz, S. A., Caswell-Jin, J. L., McNamara, K. L., Zoeller, J. J., Bean, G. R., Dichmann, R., Perez, A., Patel, R., Zehngebot, L., Allen, H., Bosserman, L., DiCarlo, B., Kennedy, et al
  2020; 11 (1): 5824

- **Quantitative evidence for early metastatic seeding in colorectal cancer.** *Nature genetics*
  Hu, Z., Ding, J., Ma, Z., Sun, R., Seoane, J. A., Scott Shaffer, J., Suarez, C. J., Berghoff, A. S., Cremolini, C., Falcone, A., Loupakis, F., Birner, P., Preusser, et al
  2019

- **Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups** *NATURE*
  Rueda, O. M., Sammut, S., Seoane, J. A., Chin, S., Caswell-Jin, J. L., Callari, M., Batra, R., Pereira, B., Bruna, A., Ali, H., Provenzano, E., Liu, B., Parisien, et al
  2019; 567 (7748): 399-+

- **Clonal replacement and heterogeneity in breast tumors treated with neoadjuvant HER2-targeted therapy.** *Nature communications*
  Caswell-Jin, J. L., McNamara, K. n., Reiter, J. G., Sun, R. n., Hu, Z. n., Ma, Z. n., Ding, J. n., Suarez, C. J., Tilk, S. n., Raghavendra, A. n., Forte, V. n., Chin, S. F., Bardwell, et al
  2019; 10 (1): 657

- **Chromatin regulators mediate anthracycline sensitivity in breast cancer.** *Nature medicine*
  Seoane, J. A., Kirkland, J. G., Caswell-Jin, J. L., Crabtree, G. R., Curtis, C. n.
  2019

- **The chromatin accessibility landscape of primary human cancers.** *Science (New York, N.Y.)*
  Corces, M. R., Granja, J. M., Shams, S. n., Louie, B. H., Seoane, J. A., Zhou, W. n., Silva, T. C., Groeneveld, C. n., Wong, C. K., Cho, S. W., Satpathy, A. T., Mumbach, M. R., Hoadley, et al
  2018; 362 (6413)

- **Between-region genetic divergence reflects the mode and tempo of tumor evolution.** *Nature genetics*
  Sun, R., Hu, Z., Sottoriva, A., Graham, T. A., Harpak, A., Ma, Z., Fischer, J. M., Shibata, D., Curtis, C.
  2017

- **A Big Bang model of human colorectal tumor growth.** *Nature genetics*
  Sottoriva, A., Kang, H., Ma, Z., Graham, T. A., Salomon, M. P., Zhao, J., Marjoram, P., Siegmund, K., Press, M. F., Shibata, D., Curtis, C.
  2015

- **Whole-genome doubling drives immune evasion by silencing antigen presentation.** *Cancer cell*
  Foidart, P., Li, Z., Cai, X., Seehawer, M., Brown, D. D., Tawawalla, A., Baldominos, P., Parvin, S., Nishida, J., Rojas-Jimenez, E., Bui, T. M., Diciaccio, B., Kumar, et al
  2026

- **Enforced ZFP281 expression delays breast cancer initiation and can provide lifelong protection against breast cancer metastasis.** *bioRxiv : the preprint server for biology*
  Singh, D. K., Zhou, H., Sherpa, N., Zheng, X. Y., Lomakin, A., Razghandi, P., Hunag, X., Kadamb, R., Shukla, S., Valencia Salazar, L. E., Entenberg, D., Zheng, D., Curtis, et al
  2026

- **Tumor and microenvironmental co-evolution in metastatic triple-negative breast cancer during immunotherapy**
  Park, S., de Graaf, M., Lomakin, A., Ma, Z., Greenwald, N. F., Mangiante, L., Weiss, C. L., Simon, B., Angelo, M., Kok, M., Curtis, C.
  AMER ASSOC CANCER RESEARCH.2026

- **Generative AI improves breast cancer genomic subtype prediction from histology images.**
  Simon, B., Weiss, C. L., Chan, D., Mangiante, L., Smith, N. H., Ma, Z., Karakas, C., Curtis, C.
  AMER ASSOC CANCER RESEARCH.2026

- **In-situ direct single-cell visualization of 3D genome architecture in ER+ and HER2+breast cancer cell lines using PaintScape™ system**
  Nguyen, H., Pribus, S., Ma, Z., King, D., Huynh, J., Tulu, S., Glazer, M., Smart, B., Castillo, D., Chung, K., Chattoraj, S., Dunne, J., Werner, et al
  AMER ASSOC CANCER RESEARCH.2026: 7243

- **Polyclonal origins of human premalignant colorectal lesions.** *bioRxiv : the preprint server for biology*
  Van Egeren, D., Schenck, R. O., Khan, A., Horning, A. M., Mo, S., Weiß, C. L., Esplin, E. D., Becker, W. R., Wu, S., Hanson, C., Barapour, N., Jiang, L., Contrepois, et al
  2025

- **Correction: Analysis of ductal carcinoma in situ by self-reported race reveals molecular differences related to outcome.** *Breast cancer research : BCR*
  Strand, S. H., Houlahan, K. E., Branch, V., King, L. M., Lynch, T., Rivero-Guitiérrez, B., Harmon, B., Couch, F., Gallagher, K., Kilgore, M., Wei, S., DeMichele, A., King, et al
  2025; 27 (1): 153

- **Characterization of breast tumors and the tumor immune landscape in young, diverse participants of the Northern California Breast Cancer Family Registry**
  McClure, M., Mangiante, L., Simon, B. G., Weiss, C., Ma, Z., Koo, J., Ransohoff, J., John, E. M., Curtis, C., Caswell-Jin, J., Kurian, A. W.
  LIPPINCOTT WILLIAMS & WILKINS.2025: E12551

- **Three-dimensional genome landscape of primary human cancers.** *Nature genetics*
  Yost, K. E., Zhao, Y., Hung, K. L., Zhu, K., Xu, D., Corces, M. R., Shams, S., Louie, B. H., Sarmashghi, S., Sundaram, L., Luebeck, J., Clarke, S., Doane, et al
  2025

- **Evolutionary measures show that recurrence of DCIS is distinct from progression to breast cancer.** *Breast cancer research : BCR*
  Fortunato, A., Mallo, D., Cisneros, L., King, L. M., Khan, A., Curtis, C., Ryser, M. D., Lo, J. Y., Hall, A., Marks, J. R., Hwang, E. S., Maley, C. C.
  2025; 27 (1): 43

- **Temporal and spatial composition of the tumor microenvironment predicts response to immune checkpoint inhibition.** *bioRxiv : the preprint server for biology*
  Greenwald, N. F., Nederlof, I., Sowers, C., Ding, D. Y., Park, S., Kong, A., Houlahan, K. E., Varra, S. R., de Graaf, M., Geurts, V., Liu, C. C., Ranek, J. S., Voorwerk, et al
  2025

- **Author Correction: Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis.** *Nature cancer*
  Zhu, Y., Lee, H., White, S., Weimer, A. K., Monte, E., Horning, A., Nevins, S. A., Esplin, E. D., Paul, K., Krieger, G., Shipony, Z., Chiu, R., Laquindanum, et al
  2025

- **Complex rearrangements fuel ER+ and HER2+ breast tumours.** *Nature*
  Houlahan, K. E., Mangiante, L., Sotomayor-Vivas, C., Adimoelja, A., Park, S., Khan, A., Pribus, S. J., Ma, Z., Caswell-Jin, J. L., Curtis, C.
  2025

- **Cancers adapt to their mutational load by buffering protein misfolding stress.** *eLife*
  Tilk, S., Frydman, J., Curtis, C., Petrov, D. A.
  2024; 12

- **Single-cell spatial mapping reveals alteration of cell type composition and tissue microenvironment during early colorectal cancer formation.** *bioRxiv : the preprint server for biology*
  Guha, T. K., Esplin, E. D., Horning, A. M., Chiu, R., Paul, K., Weimer, A. K., Becker, W. R., Laquindanum, R., Mills, M. A., Glen Esplin, D., Shen, J., Monte, E., White, et al
  2024

- **Enhancing transcription-replication conflict targets ecDNA-positive cancers.** *Nature*

Tang, J., Weiser, N. E., Wang, G., Chowdhry, S., Curtis, E. J., Zhao, Y., Wong, I. T., Marinov, G. K., Li, R., Hanoian, P., Tse, E., Mojica, S. G., Hansen, et al

2024; 635 (8037): 210-218

- **Multiomic analysis of familial adenomatous polyposis reveals molecular pathways associated with early tumorigenesis.** *Nature cancer*

  Esplin, E. D., Hanson, C., Wu, S., Horning, A. M., Barapour, N., Nevins, S. A., Jiang, L., Contrepois, K., Lee, H., Guha, T. K., Hu, Z., Laquindanum, R., Mills, et al

  2024

- **Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis.** *Nature cancer*

  Zhu, Y., Lee, H., White, S., Weimer, A. K., Monte, E., Horning, A., Nevins, S. A., Esplin, E. D., Paul, K., Krieger, G., Shipony, Z., Chiu, R., Laquindanum, et al

  2024

- **The G1-S transition is promoted by Rb degradation via the E3 ligase UBR5.** *Science advances*

  Zhang, S., Valenzuela, L. F., Zatulovskiy, E., Mangiante, L., Curtis, C., Skotheim, J. M.

  2024; 10 (43): eadq6858

- **Deletions Rate-Limit Breast and Ovarian Cancer Initiation.** *bioRxiv : the preprint server for biology*

  Houlahan, K. E., Bihie, M., Contreras, J. G., Fulop, D. J., Lopez, G., Huang, H., Van Loo, P., Curtis, C., Boutros, P. C., Huang, K.

  2024

- **Single-cell chromatin accessibility reveals malignant regulatory programs in primary human cancers.** *Science (New York, N.Y.)*

  Sundaram, L., Kumar, A., Zatzman, M., Salcedo, A., Ravindra, N., Shams, S., Louie, B. H., Bagdatli, S. T., Myers, M. A., Sarmashghi, S., Choi, H. Y., Choi, W. Y., Yost, et al

  2024; 385 (6713): eadk9217

- **Analysis of ductal carcinoma in situ by self-reported race reveals molecular differences related to outcome.** *Breast cancer research : BCR*

  Strand, S. H., Houlahan, K. E., Branch, V., Lynch, T., Rivero-Guitiérrez, B., Harmon, B., Couch, F., Gallagher, K., Kilgore, M., Wei, S., DeMichele, A., King, T., McAuliffe, et al

  2024; 26 (1): 127

- **Evolutionary Measures Show that Recurrence of DCIS is Distinct from Progression to Breast Cancer.** *medRxiv : the preprint server for health sciences*

  Fortunato, A., Mallo, D., Cisneros, L., King, L. M., Khan, A., Curtis, C., Ryser, M. D., Lo, J. Y., Hall, A., Marks, J. R., Hwang, E. S., Maley, C. C.

  2024

- **Engineered matrices reveal stiffness-mediated chemoresistance in patient-derived pancreatic cancer organoids.** *Nature materials*

  LeSavage, B. L., Zhang, D., Huerta-López, C., Gilchrist, A. E., Krajina, B. A., Karlsson, K., Smith, A. R., Karagyozova, K., Klett, K. C., Huang, M. S., Long, C., Kaber, G., Madl, et al

  2024

- **Analysis of the sensitivity to endocrine therapy (SET) assay in the PALLAS adjuvant trial of palbociclib in HR+/HER2-breast cancer (ABCSG-42/AFT-05/BIG-14-13)**

  Metzger, O., Ballman, K. V., Gnant, M., Watson, M., Chen, E., Tran, K., O'Brien, P., Hlauschek, D., Martin, M., Balko, J. M., Nowecki, Z., Hahn, O., Denkert, et al

  LIPPINCOTT WILLIAMS & WILKINS.2024

- **Functional screening of amplification outlier oncogenes in organoid models of early tumorigenesis.** *Cell reports*

  Salahudeen, A. A., Seoane, J. A., Yuki, K., Mah, A. T., Smith, A. R., Kolahi, K., De la O, S. M., Hart, D. J., Ding, J., Ma, Z., Barkal, S. A., Shukla, N. D., Zhang, et al

  2023; 42 (11): 113355

- **The G1/S transition is promoted by Rb degradation via the E3 ligase UBR5.** *bioRxiv : the preprint server for biology*

  Zhang, S., Valenzuela, L. F., Zatulovskiy, E., Skotheim, J. M.

  2023

- **Serine starvation silences estrogen receptor signaling through histone hypoacetylation.** *Proceedings of the National Academy of Sciences of the United States of America*

  Li, A. M., He, B., Karagiannis, D., Li, Y., Jiang, H., Srinivasan, P., Ramirez, Y., Zhou, M. N., Curtis, C., Gruber, J. J., Lu, C., Rankin, E. B., Ye, et al

2023; 120 (38): e2302489120

- **Osteosarcoma PDX-Derived Cell Line Models for Preclinical Drug Evaluation Demonstrate Metastasis Inhibition by Dinaciclib through a Genome-Targeted Approach.** *Clinical cancer research : an official journal of the American Association for Cancer Research*

  Schott, C. R., Koehne, A. L., Sayles, L. C., Young, E. P., Luck, C., Yu, K., Lee, A. G., Breese, M. R., Leung, S. G., Xu, H., Shah, A. T., Liu, H. Y., Spillinger, et al

  2023: OF1-OF16

- **PhyloVelo enhances transcriptomic velocity field mapping using monotonically expressed genes.** *Nature biotechnology*

  Wang, K., Hou, L., Wang, X., Zhai, X., Lu, Z., Zi, Z., Zhai, W., He, X., Curtis, C., Zhou, D., Hu, Z.

  2023

- **Author Correction: Combinatorial immunotherapies overcome MYC-driven immune evasion in triple negative breast cancer.** *Nature communications*

  Lee, J. V., Housley, F., Yau, C., Nakagawa, R., Winkler, J., Anttila, J. M., Munne, P. M., Savelius, M., Houlahan, K. E., Van de Mark, D., Hemmati, G., Hernandez, G. A., Zhang, et al

  2022; 13 (1): 7140

- **Molecular classification and biomarkers of clinical outcome in breast ductal carcinoma in situ: Analysis of TBCRC 038 and RAHBT cohorts.** *Cancer cell*

  Strand, S. H., Rivero-Gutierrez, B., Houlahan, K. E., Seoane, J. A., King, L. M., Risom, T., Simpson, L. A., Vennam, S., Khan, A., Cisneros, L., Hardman, T., Harmon, B., Couch, et al

  2022

- **Most cancers carry a substantial deleterious load due to Hill-Robertson interference.** *eLife*

  Tilk, S., Tkachenko, S., Curtis, C., Petrov, D. A., McFarland, C. D.

  2022; 11

- **ZFP281 drives a mesenchymal-like dormancy program in early disseminated breast cancer cells that prevents metastatic outgrowth in the lung.** *Nature cancer*

  Nobre, A. R., Dalla, E., Yang, J., Huang, X., Wullkopf, L., Risson, E., Razghandi, P., Anton, M. L., Zheng, W., Seoane, J. A., Curtis, C., Kenigsberg, E., Wang, et al

  2022

- **"Fateful" encounter: Lineage tracing meets phylogeny to unravel mysteries of cancer progression.** *Developmental cell*

  Wong, W. H., Curtis, C.

  2022; 57 (14): 1680-1682

- **Combinatorial immunotherapies overcome MYC-driven immune evasion in triple negative breast cancer.** *Nature communications*

  Lee, J. V., Housley, F., Yau, C., Nakagawa, R., Winkler, J., Anttila, J. M., Munne, P. M., Savelius, M., Houlahan, K. E., Van de Mark, D., Hemmati, G., Hernandez, G. A., Zhang, et al

  2022; 13 (1): 3671

- **Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer.** *Nature genetics*

  Becker, W. R., Nevins, S. A., Chen, D. C., Chiu, R., Horning, A. M., Guha, T. K., Laquindanum, R., Mills, M., Chaib, H., Ladabaum, U., Longacre, T., Shen, J., Esplin, et al

  2022

- **Patient perspectives on window of opportunity clinical trials in early-stage breast cancer.** *Breast cancer research and treatment*

  Parikh, D. A., Kody, L., Brain, S., Heditsian, D., Lee, V., Curtis, C., Karin, M. R., Wapnir, I. L., Patel, M. I., Sledge, G. W., Caswell-Jin, J. L.

  2022

- **The Mettl3 epitranscriptomic writer amplifies p53 stress responses.** *Molecular cell*

  Raj, N., Wang, M., Seoane, J. A., Zhao, R. L., Kaiser, A. M., Moonie, N. A., Demeter, J., Boutelle, A. M., Kerr, C. H., Mulligan, A. S., Moffatt, C., Zeng, S. X., Lu, et al

  2022

- **MITI minimum information guidelines for highly multiplexed tissue images.** *Nature methods*

  Schapiro, D., Yapp, C., Sokolov, A., Reynolds, S. M., Chen, Y., Sudar, D., Xie, Y., Muhlich, J., Arias-Camison, R., Arena, S., Taylor, A. J., Nikolov, M., Tyler, et al

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