Stanford

Christina Curtis

RZ Cao Professor, Professor of Genetics and of Biomedical Data Science

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 the Director of Artificial Intelligence and Cancer Genomics and of Breast Cancer Translational Research. Dr. Curtis's laboratory leverages computational modeling, high-throughput molecular profiling and experimentation to develop new ways to prevent, diagnose and treat cancer. Her research has 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 is a Kavli Fellow of the National Academy of Sciences, a Susan G. Komen Scholar, and a Chan Zuckerberg Biohub Investigator. Dr. Curtis is a member of Board of Reviewing Editors at Science, the AACR Board of Directors, and is a scientific advisor to biotech/biopharma.

ACADEMIC APPOINTMENTS

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

ADMINISTRATIVE APPOINTMENTS

- 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- present)

HONORS AND AWARDS

- 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 Advisory Board, Singapore Cancer Science Institute (2023 - present)
- Scientific Advisory Board, NY Genome Center (2023 - present)
- Board of Directors, American Association for Cancer Research (AACR) (2022 - present)
- Board of Reviewing Editors, Science (2022 - present)
- Scientific Advisory Board, Bristol Myers Squibb, Oncology/TME (2022 - present)
- Scientific Advisory Board, DeepCell (2021 - present)
- Scientific Advisory Board, Columbia University, Herbert Irving Comprehensive Cancer Center (2020 - present)
- Scientific Advisory Board, ResistanceBio (2020 - present)
- Scientific Advisory Board, Genentech, Oncology (2020 - present)
- Scientific Advisory Board, Nanostring (2020 - present)
- Scientific Advisory Board, Susan G. Komen Big Data Initiative, Share for Cures (2019 - 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)
- Editorial Board Member, ASCO Journal of Clinical Oncology: Precision Oncology (2016 - 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

- 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

We are interested in elucidating tumor evolutionary 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. In particular, we employ advanced genomic techniques, computational and mathematical modeling, and powerful model systems in order to:

1.) Model the evolutionary dynamics of tumor progression and therapeutic resistance and metastasis

2) Elucidate disease etiology and novel molecular targets through integrative analyses of high-throughput omic data

3) Develop techniques for the systems-level interpretation of genotype-phenotype associations in cancer

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

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

Teaching

STANFORD ADVISEES

Emily Shuldiner

Doctoral Dissertation Reader (AC)

Peter Du, Ibtihal Elfaki, Yuanhao Qu, Venkat Sankar, Kiarash Shamardani

Postdoctoral Faculty Sponsor

Michael Heskett, Kathleen Houlahan, Lise Mangiante, Seongyeol Park, Maryam Pourmaleki, Ryan Schenck, Debra Van Egeren

Doctoral Dissertation Advisor (AC)

Kristle Garcia, Brennan Simon

Doctoral Dissertation Co-Advisor (AC)

Alvina Adimoelja, Noah Greenwald, Katherine Liu

Doctoral (Program)

Katherine Liu

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Cancer Biology (Phd Program)
- Genetics (Phd Program)
- Oncology (Fellowship Program)

Publications

PUBLICATIONS

- **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

- **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

2022; 19 (3): 262-267

- **Inter-cellular CRISPR screens reveal regulators of cancer cell phagocytosis.** *Nature*
  Kamber, R. A., Nishiga, Y., Morton, B., Banuelos, A. M., Barkal, A. A., Vences-Catalan, F., Gu, M., Fernandez, D., Seoane, J. A., Yao, D., Liu, K., Lin, S., Spees, et al
  2021
- **Preface.** *Biochimica et biophysica acta. Reviews on cancer*
  Curtis, C., Chin, L.
  2021: 188617
- **Transcriptome and genome evolution during HER2-amplified breast neoplasia.** *Breast cancer research : BCR*
  Lu, P., Foley, J., Zhu, C., McNamara, K., Sirinukunwattana, K., Vennam, S., Varma, S., Fehri, H., Srivastava, A., Zhu, S., Rittscher, J., Mallick, P., Curtis, et al
  2021; 23 (1): 73
- **A CRISPR/Cas9-engineered ARID1A-deficient human gastric cancer organoid model reveals essential and non-essential modes of oncogenic transformation.**
  Lo, Y., Kolahi, K. S., Du, Y., Chang, C., Krokhotin, A., Nair, A., Sobba, W. D., Karlsson, K., Jones, S. J., Longacre, T. A., Mah, A. T., Sockell, A., Seoane, et al
  AMER ASSOC CANCER RESEARCH.2021
- **A tumor "personality" test to guide therapeutic decision making.** *Cancer cell*
  Houlahan, K. E., Curtis, C.
  2021
- **The AMBRA1 E3 ligase adaptor regulates the stability of cyclinD.** *Nature*
  Chaikovsky, A. C., Li, C., Jeng, E. E., Loebell, S., Lee, M. C., Murray, C. W., Cheng, R., Demeter, J., Swaney, D. L., Chen, S., Newton, B. W., Johnson, J. R., Drainas, et al
  2021
- **Integrating Quantitative Approaches in Cancer Research and Oncology** *TRENDS IN CANCER*
  Barker, A. D., Gatenby, R., Finley, S. D., Leggett, S. E., Nelson, C. M., Curtis, C., Mathur, D., Xavier, J. B., Califano, A., Castillo, S. P., Yuan, Y., Davies, P.
  2021; 7 (4): 270–75
- **The oncogene AAMDC links PI3K-AKT-mTOR signaling with metabolic reprograming in estrogen receptor-positive breast cancer.** *Nature communications*
  Golden, E., Rashwan, R., Woodward, E. A., Sgro, A., Wang, E., Sorolla, A., Waryah, C., Tie, W. J., Cuyas, E., Ratajska, M., Kardas, I., Kozlowski, P., Johnstone, et al
  2021; 12 (1): 1920
- **An expanded universe of cancer targets.** *Cell*
  Hahn, W. C., Bader, J. S., Braun, T. P., Califano, A., Clemons, P. A., Druker, B. J., Ewald, A. J., Fu, H., Jagu, S., Kemp, C. J., Kim, W., Kuo, C. J., McManus, et al
  2021; 184 (5): 1142–55
- **Cell of Origin Influences Pancreatic Cancer Subtype** *CANCER DISCOVERY*
  Flowers, B. M., Xu, H., Mulligan, A. S., Hanson, K. J., Seoane, J. A., Vogel, H., Curtis, C., Wood, L. D., Attardi, L. D.
  2021; 11 (3): 660–77
- **Cell of Origin Influences Pancreatic Cancer Subtype.** *Cancer discovery*
  Flowers, B. M., Xu, H., Mulligan, A. S., Hanson, K. J., Seoane, J. A., Vogel, H., Curtis, C., Wood, L. D., Attardi, L. D.
  2021; 11 (3): 660-677
- **Androgen receptor agonists as breast cancer therapeutics.** *Nature medicine*
  Caswell-Jin, J. L., Curtis, C.
  2021
- **The human tumor atlas network (HTAN) breast pre cancer atlas: A multi-omic integrative analysis of ductal carcinoma in situ (DCIS) and correlation with clinical outcomes**
  Hwang, S., Strand, S. H., Rivero, B., King, L., Risom, T., Harmon, B., Couch, F., Gallagher, K., Kilgore, M., Wei, S., DeMichele, A., King, T., McAuliffe, et al
  AMER ASSOC CANCER RESEARCH.2021
- **A CRISPR/Cas9-engineered ARID1A-deficient human gastric cancer organoid model reveals essential and non-essential modes of oncogenic transformation.** *Cancer discovery*

Lo, Y. H., Kolahi, K. S., Du, Y. n., Chang, C. Y., Krokhotin, A. n., Nair, A. n., Sobba, W. D., Karlsson, K. n., Jones, S. J., Longacre, T. A., Mah, A. T., Tercan, B. n., Sockell, et al

2021

- **Molecular Heterogeneity and Evolution in Breast Cancer** *Annual review of cancer biology*

  Caswell-Jin, J. L., Lorenz, C., Curtis, C.

  2021; 5: 79-94

- **A High-Dimensional Window into the Micro-Environment of Triple Negative Breast Cancer.** *Cancers*

  Nederlof, I. n., Horlings, H. M., Curtis, C. n., Kok, M. n.

  2021; 13 (2)

- **Zmat3 Is a Key Splicing Regulator in the p53 Tumor Suppression Program.** *Molecular cell*

  Bieging-Rolett, K. T., Kaiser, A. M., Morgens, D. W., Boutelle, A. M., Seoane, J. A., Van Nostrand, E. L., Zhu, C., Houlihan, S. L., Mello, S. S., Yee, B. A., McClendon, J., Pierce, S. E., Winters, et al

  2020; 80 (3): 452

- **Understanding patient perspectives on window of opportunity clinical trials.**

  Parikh, D., Kody, L., Brain, S., Heditsian, D., Lee, V., Curtis, C., Sledge, G. W., Caswell-Jin, J.

  AMER SOC CLINICAL ONCOLOGY.2020

- **Reprogramming of serine metabolism during breast cancer progression**

  Li, A., Ducker, G. S., Li, Y., Seoane, J. A., Xiao, Y., Melemenidis, S., Zhou, Y., Liu, L., Vanharanta, S., Graves, E. E., Rankin, E. B., Curtis, C., Massague, et al

  AMER ASSOC CANCER RESEARCH.2020

- **Looking backward in time to define the chronology of metastasis.** *Nature communications*

  Hu, Z., Curtis, C.

  2020; 11 (1): 3213

- **Translating Basic Cancer Discoveries to the Clinic** *CANCER CELL*

  Mardis, E. R., Dawson, M. A., Curtis, C., Xu, R., Long, G. V., Scolyer, R. A., Bakhoum, S. F., Nam, D., Garnett, M., Huang, A.

  2020; 37 (6): 735–37

- **Deconstructing the origins of PDAC development.**

  Flowers, B., Xu, H., Hanson, K., Curtis, C., Vogel, H., Wood, L., Attardi., L. D.

  AMER ASSOC CANCER RESEARCH.2020: 19

- **The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution.** *Cell*

  Rozenblatt-Rosen, O., Regev, A., Oberdoerffer, P., Nawy, T., Hupalowska, A., Rood, J. E., Ashenberg, O., Cerami, E., Coffey, R. J., Demir, E., Ding, L., Esplin, E. D., Ford, et al

  2020; 181 (2): 236–49

- **CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities.** *Nature*

  Han, K., Pierce, S. E., Li, A., Spees, K., Anderson, G. R., Seoane, J. A., Lo, Y. H., Dubreuil, M., Olivas, M., Kamber, R. A., Wainberg, M., Kostyrko, K., Kelly, et al

  2020; 580 (7801): 136-141

- **CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities** *NATURE*

  Han, K., Pierce, S. E., Li, A., Spees, K., Anderson, G. R., Seoane, J. A., Lo, Y., Dubreuil, M., Olivas, M., Kamber, R. A., Wainberg, M., Kostyrko, K., Kelly, et al

  2020

- **Characterizing the tumor and immune microenvironment through treatment to predict response to neoadjuvant HER2-targeted therapy using the Digital Spatial Profiler**

  McNamara, K., Caswell-Jin, J. L., Ma, Z., Zoeller, J. J., Kriner, M., Zhou, Z., Reeves, J., Hoang, M., Beechem, J., Slamon, D. J., Press, M. F., Brugge, J., Hurvitz, et al

  AMER ASSOC CANCER RESEARCH.2020

- **Tumor expression and microenvironment in HER2-positive breast cancer before and on HER2-targeted therapy: Analysis of microarray expression data from the TRIO-US B07 trial**

  Caswell-Jin, J. L., McNamara, K. L., Dering, J., Chen, H., Dichmann, R., Perez, A., Patel, R., Kotler, E., Zoeller, J. J., Brugge, J. S., Press, M. F., Slamon, D. J., Curtis, et al

AMER ASSOC CANCER RESEARCH.2020

- **Metabolic Profiling Reveals a Dependency of Human Metastatic Breast Cancer on Mitochondrial Serine and One-Carbon Unit Metabolism.** *Molecular cancer research : MCR*
  Li, A. M., Ducker, G. S., Li, Y. n., Seoane, J. A., Xiao, Y. n., Melemenidis, S. n., Zhou, Y. n., Liu, L. n., Vanharanta, S. n., Graves, E. E., Rankin, E. B., Curtis, C. n., Massague, et al
  2020
- **The m6A RNA demethylase FTO is a HIF-independent synthetic lethal partner with the VHL tumor suppressor.** *Proceedings of the National Academy of Sciences of the United States of America*
  Xiao, Y. n., Thakkar, K. N., Zhao, H. n., Broughton, J. n., Li, Y. n., Seoane, J. A., Diep, A. N., Metzner, T. J., von Eyben, R. n., Dill, D. L., Brooks, J. D., Curtis, C. n., Leppert, et al
  2020
- **Novel insights into breast cancer copy number genetic heterogeneity revealed by single-cell genome sequencing.** *eLife*
  Baslan, T. n., Kendall, J. n., Volyanskyy, K. n., McNamara, K. n., Cox, H. n., D'Italia, S. n., Ambrosio, F. n., Riggs, M. n., Rodgers, L. n., Leotta, A. n., Song, J. n., Mao, Y. n., Wu, et al
  2020; 9
- **CHRISTINA CURTIS COMPUTING CANCER** *NATURE*
  Curtis, C.
  2020; 577 (7791): 586
- **Quantifying mutations in healthy blood.** *Science (New York, N.Y.)*
  Curtis, C. n.
  2020; 367 (6485): 1426–27
- **Deciphering the origins of PDAC development**
  Flowers, B., Xu, H., Hanson, K., Curtis, C., Vogel, H., Wood, L. D., Attardi, L. D.
  AMER ASSOC CANCER RESEARCH.2019
- **Elucidating the role of p53 in the cellular origins of pancreatic cancer development**
  Flowers, B. M., Xu, H., Hanson, K., Curtis, C., Vogel, H., Wood, L. D., Attardi, L. D.
  AMER ASSOC CANCER RESEARCH.2019
- **Chromatin state as a mechanism of anthracycline response in breast cancer**
  Seoane, J. A., Kirkland, J. G., Caswell-Jin, J. L., Crabtree, G. R., Curtis, C.
  AMER ASSOC CANCER RESEARCH.2019
- **Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen** *NATURE COMMUNICATIONS*
  Menden, M. P., Wang, D., Mason, M. J., Szalai, B., Bulusu, K. C., Guan, Y., Yu, T., Kang, J., Jeon, M., Wolfinger, R., Nguyen, T., Zaslavskiy, M., Jang, et al
  2019; 10: 2674
- **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. R., Provenzano, E., Liu, B., Parisien, et al
  2019
- **Assessment of ERBB2/HER2 Status in HER2-Equivocal Breast Cancers by FISH and 2013/2014 ASCO-CAP Guidelines** *JAMA ONCOLOGY*
  Press, M. F., Seoane, J. A., Curtis, C., Quinaux, E., Guzman, R., Sauter, G., Eiermann, W., Mackey, J. R., Robert, N., Pienkowski, T., Crown, J., Martin, M., Valero, et al
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