



Christina Curtis

Professor of Medicine (Oncology), of Genetics and of Biomedical Data Science
Medicine - Oncology

Bio

BIO

Christina Curtis, PhD, MSc is an Endowed Professor of Medicine and Genetics at Stanford University where she leads the Cancer Computational and Systems Biology group. Dr. Curtis also serves as the Director of Breast Cancer Translational Research and Co-Director of the Molecular Tumor Board at the Stanford Cancer Institute. 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 helped to redefine the molecular map of breast cancer and led to new paradigms in understanding how human tumors evolve and metastasize. Dr. Curtis is the recipient of numerous awards, including those from the V Foundation for Cancer Research, STOP Cancer and the American Association for Cancer Research (AACR). She received the National Institutes of Health Director's Pioneer Award in 2018, the Stanford Prize in Population Genetics and Society (2020) and was named an In vivo Rising Leader in the Life Sciences (2021) and the Julius B. Kahn Visiting Professor in the Dept of Pharmacology, at Northwestern University (2020). In 2022 she received the AACR Award for Outstanding Achievement in Basic Science. Dr. Curtis is also Kavli Fellow of the National Academy of Sciences, a Susan G. Komen Scholar and a Chan Zuckerberg Biohub Investigator. Dr. Curtis serves as a scientific advisor to multiple academic institutes and biotech as is a member of the AACR Board of Directors. She also serves on the editorial board of journals spanning computational biology to precision oncology.

ACADEMIC APPOINTMENTS

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

ADMINISTRATIVE APPOINTMENTS

- 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, 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)
- AACR Career Development Award, AACR Triple Negative Breast Cancer Foundation - Carol's Crusade for a Cure Foundation (2016)
- Seed Grant Recipient, American Cancer Society (2013)
- 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

- Board of Directors, AACR (2022 - present)
- Board of Reviewing Editors, Science (2022 - present)
- Scientific Advisory Board, DeepCell (2021 - present)
- Scientific Advisory Board, Genentech, Oncology, Physiological Chemistry (2020 - present)
- Scientific Advisory Board, ResistanceBio (2020 - present)
- Scientific Advisory Board, Nanostring (2020 - present)
- Scientific Advisory Board, GRAIL (2017 - present)
- Scientific Advisory Board, Herbert Irving Comprehensive Cancer Center (2020 - present)
- Scientific Advisory Board, Susan G. Komen Big Data Initiative (2019 - present)
- Scientific Advisory Board, Cancer Research UK Early Detection Committee (2017 - present)
- Scientific Advisory Board, Ontario Institute for Cancer Research, Adaptive Oncology Program (2017 - present)
- Vice Chair, Annual Meeting Program Committee, American Association for Cancer Research (2019 - present)
- Editorial Board Member, Cancer Discovery (2020 - present)
- Editorial Board Member, Cell Systems (2019 - present)
- Editorial Board Member, Carcinogenesis: Integrative Cancer Biology (2018 - 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 particularly 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

- Study of Infigratinib in Combination With Tamoxifen or With Fulvestrant and Palbociclib in Hormone Receptor Positive, HER2 Negative, FGFR Altered Advanced Breast Cancer, Recruiting

Teaching

STANFORD ADVISEES

Emily Shuldiner

Doctoral Dissertation Reader (AC)

Peter Du, Yuanhao Qu

Postdoctoral Faculty Sponsor

Michael Heskett, Kathleen Houlahan, Swathi Karthikeyan, Eran Kotler, Lise Mangiante, Wing Hing Wong, Wenting Yang

Doctoral Dissertation Advisor (AC)

Alexandra Sockell

Doctoral Dissertation Co-Advisor (AC)

Markus Diehl, Noah Greenwald, Katherine Liu, Susanne Tilk

Doctoral (Program)

Katherine Liu, Susanne Tilk

Postdoctoral Research Mentor

Wenting Yang

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **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
- **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
- **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
- **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
- **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., Bakhoun, S. F., Nam, D., Garnett, M., Huang, A.
2020; 37 (6): 735–37
- **Multi-cancer analysis of clonality and the timing of systemic spread in paired primary tumors and metastases.** *Nature genetics*
Hu, Z., Li, Z., Ma, Z., Curtis, C.
2020
- **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 ecological and evolutionary dynamics of cancer.** *Nature genetics*
Zahir, N. n., Sun, R. n., Gallahan, D. n., Gatenby, R. A., Curtis, C. n.
2020
- **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

- **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+
- **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
- **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
- **A role for chromatin regulatory dynamics in breast cancer evolution** *NATURE MEDICINE*
Probert, C., Curtis, C.
2018; 24 (9): 1309-1311
- **Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element.** *Cell*
Cho, S. W., Xu, J., Sun, R., Mumbach, M. R., Carter, A. C., Chen, Y. G., Yost, K. E., Kim, J., He, J., Nevins, S. A., Chin, S., Caldas, C., Liu, et al
2018; 173 (6): 1398
- **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**
Sottoriva, A., Kang, H., Ma, Z., Graham, T. A., Salomon, M., Zhao, J., Marjoram, P., Siegmund, K., Press, M. F., Shibata, D., Curtis, C.
AMER ASSOC CANCER RESEARCH.2015
- **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
- **The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups** *NATURE*
Curtis, C., Shah, S. P., Chin, S., Turashvili, G., Rueda, O. M., Dunning, M. J., Speed, D., Lynch, A. G., Samarajiwa, S., Yuan, Y., Graef, S., Ha, G., Haffari, et al
2012; 486 (7403): 346-352
- **"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., Houlihan, K. E., Van de Mark, D., Hemmati, G., Hernandez, G. A., Zhang, et al
2022; 13 (1): 3671
- **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*
Houlihan, K. E., Curtis, C.
2021
- **The oncogene AAMDC links PI3K-AKT-mTOR signaling with metabolic reprogramming 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 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)
- **Molecular Heterogeneity and Evolution in Breast Cancer** *Annual review of cancer biology*
Caswell-Jin, J. L., Lorenz, C., Curtis, C.
2021; 5: 79-94
- **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
- **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
- **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
- **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
- **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
- **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

● **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

● **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
2019; 5 (3): 366-375

● **Clonal replacement and heterogeneity in breast tumors treated with neoadjuvant HER2-targeted therapy** *NATURE COMMUNICATIONS*

Caswell-Jin, J. L., McNamara, K., Reiter, J. G., Sun, R., Hu, Z., Ma, Z., Ding, J., Suarez, C. J., Tilk, S., Raghavendra, A., Forte, V., Chin, S., Bardwell, et al
2019; 10

● **Clonal replacement of tumor-specific T cells following PD-1 blockade.** *Nature medicine*

Yost, K. E., Satpathy, A. T., Wells, D. K., Qi, Y. n., Wang, C. n., Kageyama, R. n., McNamara, K. L., Granja, J. M., Sarin, K. Y., Brown, R. A., Gupta, R. K., Curtis, C. n., Bucktrout, et al
2019

● **Publisher Correction: 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): 2433

● **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
2018

● **Tumor Molecular Profiling Aids in Determining Tissue of Origin and Therapy for Metastatic Adenocarcinoma in a Patient With Multiple Primary Malignancies.** *JCO precision oncology*

Costa, H. A., Reyes, R., Mills, M., Zehnder, J. L., Sledge, G., Curtis, C., Ford, J. M., Suarez, C. J.
2018; 2: 1-4

● **Tumor Molecular Profiling Aids in Determining Tissue of Origin and Therapy for Metastatic Adenocarcinoma in a Patient With Multiple Primary Malignancies** *JCO PRECISION ONCOLOGY*

Costa, H. A., Reyes, R., Mills, M., Zehnder, J. L., Sledge, G., Curtis, C., Ford, J. M., Suarez, C. J.
2018; 2

● **A role for chromatin regulatory dynamics in breast cancer evolution.** *Nature medicine*

Probert, C., Curtis, C.
2018

● **Quantification of subclonal selection in cancer from bulk sequencing data (vol 50, pg 895, 2018)** *NATURE GENETICS*

Williams, M. J., Werner, B., Heide, T., Curtis, C., Barnes, C. P., Sottoriva, A., Graham, T. A.
2018; 50 (9): 1342

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