Stanford

Aaron Newman

Associate Professor of Biomedical Data Science

Department of Biomedical Data Science

CONTACT INFORMATION

- **Administrative Contact**

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Bio

ACADEMIC APPOINTMENTS

- Associate Professor, Department of Biomedical Data Science
- Member, Bio-X
- Member, Institute for Stem Cell Biology and Regenerative Medicine
- Member, Stanford Cancer Institute

HONORS AND AWARDS

- AACR Trailblazer Cancer Research Grant for Mid-Career Investigators, American Association for Cancer Research (2026-2029)
- 3rd Annual Daisy Ho Memorial Award, Department of Experimental Therapeutics, MD Anderson Cancer Center (2023)
- CZ Biohub Investigator, Chan Zuckerberg Biohub (2022 - 2027)
- Baxter Faculty Scholar Award, Donald E. and Delia B. Baxter Foundation (2020)
- Interdisciplinary Initiatives Seed Grants Program Award, Stanford Bio-X (2018 - 2020)
- Stem Cell Research Award, Stinehart/Reed Foundation (2018 - 2020)
- K99/R00 Pathway to Independence Award, NIH/NCI (2015 - 2020)
- Visionary Postdoctoral Fellowship, Dept. of Defense (2012 - 2015)
- NIH T32 Cancer Biology Training Grant, Stanford University (2012)
- Siebel Fellow, The Siebel Stem Cell Institute (Stanford/UC Berkeley) (2011-2015)
- Graduate Dissertation Fellowship Award, UCSB (2009)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Member, International Society for Computational Biology (ISCB) (2008 - present)
- Associate Member, American Association for Cancer Research (AACR) (2012 - present)

PROFESSIONAL EDUCATION

- PhD, University of California, Santa Barbara , Biomolecular Science and Engineering Program (2010)

LINKS

- Newman Lab: http://newmanlab.stanford.edu
- Google Scholar: https://scholar.google.com/citations?user=gODP8bYAAAAJ&hl=en
- Twitter: https://twitter.com/AaronNewmanLab

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our group combines computational and experimental techniques to study the cellular organization of complex tissues, with a focus on determining the phenotypic diversity and clinical significance of tumor cell subsets and their surrounding microenvironments. We have a particular interest in developing innovative data science tools that illuminate the cellular hierarchies and stromal elements that underlie tumor initiation, progression, and response to therapy. As part of this focus, we develop new algorithms to resolve cellular states and multicellular communities, tumor developmental hierarchies, and single-cell spatial relationships from genomic profiles of clinical biospecimens. Key results are further explored experimentally, both in our lab and through collaboration, with the goal of translating promising findings into the clinic.

As a member of the Department of Biomedical Data Science and the Institute for Stem Cell Biology and Regenerative Medicine, and as an affiliate of graduate programs in Biomedical Informatics, Cancer Biology, and Immunology, we are also interested in the development of impactful biomedical data science tools in areas beyond our immediate research focus, including developmental biology, regenerative medicine, and systems immunology.

Teaching

COURSES

2025-26

- Bioinformatics for Stem Cell and Cancer Biology: BMDS 205, STEMREM 205 (Win)

2024-25

- Bioinformatics for Stem Cell and Cancer Biology: BIODS 205, STEMREM 205 (Win)
- Workshop in Biostatistics: BIODS 260B, STATS 260B (Win)

2023-24

- Bioinformatics for Stem Cell and Cancer Biology: BIODS 205, STEMREM 205 (Win)
- Workshop in Biostatistics: BIODS 260B, STATS 260B (Win)

2022-23

- Bioinformatics for Stem Cell and Cancer Biology: BIODS 205, STEMREM 205 (Win)
- Workshop in Biostatistics: BIODS 260B, STATS 260B (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Jessica Arozqueta Basurto, Quenton Bubb, Maria Korah

Postdoctoral Faculty Sponsor

Wubing Zhang

Doctoral Dissertation Advisor (AC)

Erin Brown, Jeremy D'Silva, Rachel Gleyzer, Minji Kang, Janella Schwab Lizárraga

Master's Program Advisor

Armeen Ahmed

Doctoral (Program)

Ryan Goto, Minji Kang

Postdoctoral Research Mentor

Wubing Zhang

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (Phd Program)
- Cancer Biology (Phd Program)
- Immunology (Phd Program)
- Stem Cell Biology and Regenerative Medicine (Phd Program)

Publications

PUBLICATIONS

- **Improved reconstruction of single-cell developmental potential with CytoTRACE 2.** *Nature methods*

  Kang, M., Gulati, G. S., Brown, E. L., Qi, Z., Avagyan, S., Armenteros, J. J., Gleyzer, R., Zhang, W., Steen, C. B., D'Silva, J. P., Schwab, J., Clarke, M. F., Chaudhuri, et al

  2025

- **Profiling cell identity and tissue architecture with single-cell and spatial transcriptomics.** *Nature reviews. Molecular cell biology*

  Gulati, G. S., D'Silva, J. P., Liu, Y., Wang, L., Newman, A. M.

  2024

- **High-resolution alignment of single-cell and spatial transcriptomes with CytoSPACE.** *Nature biotechnology*

  Vahid, M. R., Brown, E. L., Steen, C. B., Zhang, W., Jeon, H. S., Kang, M., Gentles, A. J., Newman, A. M.

  2023

- **T cell characteristics associated with toxicity to immune checkpoint blockade in patients with melanoma.** *Nature medicine*

  Lozano, A. X., Chaudhuri, A. A., Nene, A., Bacchiocchi, A., Earland, N., Vesely, M. D., Usmani, A., Turner, B. E., Steen, C. B., Luca, B. A., Badri, T., Gulati, G. S., Vahid, et al

  2022

- **Atlas of clinically distinct cell states and ecosystems across human solid tumors.** *Cell*

  Luca, B. A., Steen, C. B., Matusiak, M., Azizi, A., Varma, S., Zhu, C., Przybyl, J., Espín-Pérez, A., Diehn, M., Alizadeh, A. A., van de Rijn, M., Gentles, A. J., Newman, et al

  2021

- **Single-cell transcriptional diversity is a hallmark of developmental potential.** *Science (New York, N.Y.)*

  Gulati, G. S., Sikandar, S. S., Wesche, D. J., Manjunath, A. n., Bharadwaj, A. n., Berger, M. J., Ilagan, F. n., Kuo, A. H., Hsieh, R. W., Cai, S. n., Zabala, M. n., Scheeren, F. A., Lobo, et al

  2020; 367 (6476): 405–11

- **Determining cell type abundance and expression from bulk tissues with digital cytometry.** *Nature biotechnology*

  Newman, A. M., Steen, C. B., Liu, C. L., Gentles, A. J., Chaudhuri, A. A., Scherer, F. n., Khodadoust, M. S., Esfahani, M. S., Luca, B. A., Steiner, D. n., Diehn, M. n., Alizadeh, A. A.

  2019

- **Integrated digital error suppression for improved detection of circulating tumor DNA** *NATURE BIOTECHNOLOGY*

  Newman, A. M., Lovejoy, A. F., Klass, D. M., Kurtz, D. M., Chabon, J. J., Scherer, F., Stehr, H., Liu, C., Bratman, S. V., Say, C., Zhou, L., Carter, J. N., West, et al

  2016

- **Robust enumeration of cell subsets from tissue expression profiles** *NATURE METHODS*

  Newman, A. M., Liu, C., Green, M. R., Gentles, A. J., Feng, W., Xu, Y., Hoang, C. D., Diehn, M., Alizadeh, A. A.

  2015

- **The prognostic landscape of genes and infiltrating immune cells across human cancers** *NATURE MEDICINE*

  Gentles, A. J., Newman, A. M. (co-first author) , Liu, C., Bratman, S. V., Feng, W., Nair, V. S., Xu, Y., Khuong, A., Hoang, C. D., Diehn, M., West, R. B., Plevritis, S. K., Alizadeh, et al

  2015

- **An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage** *NATURE MEDICINE*

  Newman, A. M., Bratman, S. V., To, J., Wynne, J. F., Eclov, N. C., Modlin, L. A., Liu, C. L., Neal, J. W., Wakelee, H. A., Merritt, R. E., Shrager, J. B., Loo, B. W., Alizadeh, et al

  2014; 20 (5): 552-558

- **Identification of a colonial chordate histocompatibility gene** *SCIENCE*

  Voskoboynik, A., Newman, A. M. (co-first author) , Corey, D. M., Sahoo, D., Pushkarev, D., et al

  2013; 341 (6144): 384-387

- **Lab-Specific Gene Expression Signatures in Pluripotent Stem Cells** *CELL STEM CELL*

  Newman, A. M., Cooper, J. B.

  2010; 7 (2): 258-262

- **Blinded clinical validation of LiquidTME, a cell-free DNA assay for predicting response to immunotherapy by noninvasively profiling the tumor microenvironment**

  Chaudhuri, A. A., Chen, D. Y., Hansen, T., Jarosz, M., Miller, V. A., Newman, A. M.

  AMER ASSOC CANCER RESEARCH.2026

- **Liquid biopsy profiling of the tumor microenvironment to determine response to immunotherapy regimens across solid tumors.**

  Brown, E. L., Zhang, W., Usmani, A., Earland, N., Hashmi, A., Olelewe, C., Viswanathan, A., Chauhan, P. S., Kang, M., Steen, C. B., Jeon, H., Avagyan, S., Alahi, et al

  AMER ASSOC CANCER RESEARCH.2026: 94

- **Distinct cell state ecosystems for nodular lymphocyte-predominant Hodgkin lymphoma.** *Nature communications*

  Subramanian, A., Su, S., Flerlage, J., Alig, S., Younes, S., Marks, L. J., Pinnix, C., Vega, F., Steiner, R., Kumar, P., Mocikova, H., Sykorova, A., Prochazka, et al

  2025; 16 (1): 8473

- **A single-cell framework identifies functionally and molecularly distinct multipotent progenitors in adult human hematopoiesis.** *Cell reports*

  Ediriwickrema, A., Nakauchi, Y., Fan, A. C., Köhnke, T., Hu, X., Luca, B. A., Kim, Y., Ramakrishnan, S., Nakamoto, M., Karigane, D., Linde, M. H., Azizi, A., Newman, et al

  2025; 44 (9): 116236

- **Resolving the Microarchitecture of Classic and Transformed Follicular Lymphoma By Single Cell Alignment to Spatial Transcriptomes**

  Noordenbos, T., Schroers-Martin, J. G., Hamilton, M. P., Jun, S., Sugio, T., Sworder, B. J., Steen, C., Olsen, M., Liu, C., Newman, A., Howitt, B., Natkunam, Y., Miklos, et al

  ELSEVIER.2024: 2993-2994

- **Community assessment of methods to deconvolve cellular composition from bulk gene expression.** *Nature communications*

  White, B. S., de Reyniès, A., Newman, A. M., Waterfall, J. J., Lamb, A., Petitprez, F., Lin, Y., Yu, R., Guerrero-Gimenez, M. E., Domanskyi, S., Monaco, G., Chung, V., Banerjee, et al

  2024; 15 (1): 7362

- **Quantification of cerebrospinal fluid tumor DNA in lung cancer patients with suspected leptomeningeal carcinomatosis.** *NPJ precision oncology*

  Azad, T. D., Nanjo, S., Jin, M. C., Chabon, J. J., Kurtz, D. M., Chaudhuri, A. A., Connolly, I. D., Hui, A. B., Liu, C. L., Merriott, D., Ko, R., Yoo, C., Carter, et al

  2024; 8 (1): 121

- **Spatially Segregated Macrophage Populations Predict Distinct Outcomes In Colon Cancer.** *Cancer discovery*

  Matusiak, M., Hickey, J. W., van IJzendoorn, D. G., Lu, G., Kidzinski, L., Zhu, S., Colburg, D. R., Luca, B., Phillips, D. J., Brubaker, S. W., Charville, G. W., Shen, J., Loh, et al

2024

- **Sarcoma microenvironment cell states and ecosystems are associated with prognosis and predict response to immunotherapy.** *Nature cancer*

  Subramanian, A., Nemat-Gorgani, N., Ellis-Caleo, T. J., van IJzendoorn, D. G., Sears, T. J., Somani, A., Luca, B. A., Zhou, M. Y., Bradic, M., Torres, I. A., Oladipo, E., New, C., Kenney, et al

  2024

- **Single Cell Spatial Biology for Precision Cancer Medicine.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*

  Gentles, A. J., Nirmal, A. J., Heiser, L. M., Lundberg, E., Newman, A. M.

  2023; 28: 549-553

- **Single-cell mapping identifies MSI+ cells as a common origin for diverse subtypes of pancreatic cancer.** *Cancer cell*

  Rajbhandari, N., Hamilton, M., Quintero, C. M., Ferguson, L. P., Fox, R., Schürch, C. M., Wang, J., Nakamura, M., Lytle, N. K., McDermott, M., Diaz, E., Pettit, H., Kritzik, et al

  2023

- **Diversity of intratumoral regulatory T cells in B-cell non-Hodgkin lymphoma.** *Blood advances*

  Spasevska, I., Sharma, A., Steen, C. B., Josefsson, S. E., Blaker, Y. N., Kolstad, A., Rustad, E. H., Meyer, S., Isaksen, K. T., Chellappa, S., Kushekhar, K., Beiske, K., Førsund, et al

  2023

- **CD4 T cells and toxicity from immune checkpoint blockade.** *Immunological reviews*

  Earland, N., Zhang, W., Usmani, A., Nene, A., Bacchiocchi, A., Chen, D. Y., Sznol, M., Halaban, R., Chaudhuri, A. A., Newman, A. M.

  2023

- **p53 governs an AT1 differentiation programme in lung cancer suppression.** *Nature*

  Kaiser, A. M., Gatto, A., Hanson, K. J., Zhao, R. L., Raj, N., Ozawa, M. G., Seoane, J. A., Bieging-Rolett, K. T., Wang, M., Li, I., Trope, W. L., Liou, D. Z., Shrager, et al

  2023

- **Profiling Cellular Ecosystems at Single-Cell Resolution and at Scale with EcoTyper.** *Methods in molecular biology (Clifton, N.J.)*

  Steen, C. B., Luca, B. A., Alizadeh, A. A., Gentles, A. J., Newman, A. M.

  2023; 2629: 43-71

- **Multiomic analysis for optimization of combined focal and immunotherapy protocols in murine pancreatic cancer.** *Theranostics*

  Wang, J., Fite, B. Z., Kare, A. J., Wu, B., Raie, M., Tumbale, S. K., Zhang, N., Davis, R. R., Tepper, C. G., Aviran, S., Newman, A. M., King, D. A., Ferrara, et al

  2022; 12 (18): 7884-7902

- **Identification of a minority population of LMO2+ breast cancer cells that integrate into the vasculature and initiate metastasis.** *Science advances*

  Sikandar, S. S., Gulati, G. S., Antony, J., Fetter, I., Kuo, A. H., Ho, W. H., Haro-Acosta, V., Das, S., Steen, C. B., Pereira, T. A., Qian, D., Beachy, P. A., Dirbas, et al

  2022; 8 (45): eabm3548

- **Inferring gene expression from cell-free DNA fragmentation profiles.** *Nature biotechnology*

  Esfahani, M. S., Hamilton, E. G., Mehrmohamadi, M., Nabet, B. Y., Alig, S. K., King, D. A., Steen, C. B., Macaulay, C. W., Schultz, A., Nesselbush, M. C., Soo, J., Schroers-Martin, J. G., Chen, et al

  2022

- **Integrative molecular and clinical profiling of acral melanoma links focal amplification of 22q11.21 to metastasis.** *Nature communications*

  Farshidfar, F., Rhrissorrakrai, K., Levovitz, C., Peng, C., Knight, J., Bacchiocchi, A., Su, J., Yin, M., Sznol, M., Ariyan, S., Clune, J., Olino, K., Parida, et al

  2022; 13 (1): 898

- **Integrated spatial multiomics reveals fibroblast fate during tissue repair.** *Proceedings of the National Academy of Sciences of the United States of America*

  Foster, D. S., Januszyk, M., Yost, K. E., Chinta, M. S., Gulati, G. S., Nguyen, A. T., Burcham, A. R., Salhotra, A., Ransom, R. C., Henn, D., Chen, K., Mascharak, S., Tolentino, et al

  2021; 118 (41)

- **Landscape of innate lymphoid cells in human head and neck cancer reveals divergent NK cell states in the tumor microenvironment.** *Proceedings of the National Academy of Sciences of the United States of America*

  Moreno-Nieves, U. Y., Tay, J. K., Saumyaa, S., Horowitz, N. B., Shin, J. H., Mohammad, I. A., Luca, B., Mundy, D. C., Gulati, G. S., Bedi, N., Chang, S., Chen, C., Kaplan, et al

  2021; 118 (28)

- **The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma.** *Cancer cell*

  Steen, C. B., Luca, B. A., Esfahani, M. S., Azizi, A., Sworder, B. J., Nabet, B. Y., Kurtz, D. M., Liu, C. L., Khameneh, F., Advani, R. H., Natkunam, Y., Myklebust, J. H., Diehn, et al

  2021

- **LEFTY1 Is a Dual-SMAD Inhibitor that Promotes Mammary Progenitor Growth and Tumorigenesis.** *Cell stem cell*

  Zabala, M., Lobo, N. A., Antony, J., Heitink, L. S., Gulati, G. S., Lam, J., Parashurama, N., Sanchez, K., Adorno, M., Sikandar, S. S., Kuo, A. H., Qian, D., Kalisky, et al

  2020

- **Analytical validation of iSort digital cytometry for leukocyte enumeration in clinical tumor specimens.**

  Newman, A. M., Nakao, A., Li, K., Wilson, D., Liu, C., Diehn, M., Alizadeh, A. A.

  LIPPINCOTT WILLIAMS & WILKINS.2020

- **Analytical validation of digital cytometry (iSort) for leukocyte enumeration using stored blood.**

  Newman, A. M., Nakao, A., Li, K., Liu, C., Mathi, K., Sigal, N., Maecker, H., Diehn, M., Alizadeh, A. A.

  AMER SOC CLINICAL ONCOLOGY.2020

- **Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition.** *Cell*

  Nabet, B. Y., Esfahani, M. S., Moding, E. J., Hamilton, E. G., Chabon, J. J., Rizvi, H. n., Steen, C. B., Chaudhuri, A. A., Liu, C. L., Hui, A. B., Almanza, D. n., Stehr, H. n., Gojenola, et al

  2020

- **Molecular and immunological signatures are related to clinical benefit from treatment with Vocimagene amiretrorepvec (Toca 511) and 5-fluorocytosine (Toca FC) in patients with glioma.** *Clinical cancer research : an official journal of the American Association for Cancer Research*

  Accomando, W. P., Rao, A. R., Hogan, D. J., Newman, A. M., Nakao, A. n., Alizadeh, A. A., Diehn, M. n., Diago, O. R., Gammon, D. K., Haghighi, A. n., Gruber, H. E., Jolly, D. J., Ostertag, et al

  2020

- **Multiomic single cell analysis of normal human bone marrow identifies a unique stem and progenitor population that expands in AML** *Proceedings of the Annual Meeting of the American Association for Cancer Research 2020*

  Ediriwickrema, A., Ramakrishnan, S., Nakamoto, M., Ghanekar, S., Luca, B., Newman, A., Gentles, A., Majeti, R.

  2020

- **Profiling Cell Type Abundance and Expression in Bulk Tissues with CIBERSORTx.** *Methods in molecular biology (Clifton, N.J.)*

  Steen, C. B., Liu, C. L., Alizadeh, A. A., Newman, A. M.

  2020; 2117: 135–57

- **Atlas of clinically-distinct cell states and cellular ecosystems across human solid tumors**

  Luca, B., Alizadeh, A., Diehn, M., Newman, A., Gentles, A., Steen, C.

  BMC.2019

- **The Immune Landscape of Cancer.** *Immunity*

  Thorsson, V., Gibbs, D. L., Brown, S. D., Wolf, D., Bortone, D. S., Ou Yang, T., Porta-Pardo, E., Gao, G. F., Plaisier, C. L., Eddy, J. A., Ziv, E., Culhane, A. C., Paull, et al

  2019; 51 (2): 411–12

- **A tumor deconvolution DREAM Challenge: Inferring immune infiltration from bulk gene expression data**

  White, B. S., Gentles, A. J., de Reynies, A., Newman, A. M., Lamb, A., Heiser, L., Waterfall, J. J., Yu, T., Guinney, J.

  AMER ASSOC CANCER RESEARCH.2019

- **Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction.** *Cell*

  Kurtz, D. M., Esfahani, M. S., Scherer, F., Soo, J., Jin, M. C., Liu, C. L., Newman, A. M., Duhrsen, U., Huttmann, A., Casasnovas, O., Westin, J. R., Ritgen, M., Bottcher, et al

  2019

- **A functional subset of CD8+ T cells during chronic exhaustion is defined by SIRPalpha expression.** *Nature communications*
  Myers, L. M., Tal, M. C., Torrez Dulgeroff, L. B., Carmody, A. B., Messer, R. J., Gulati, G., Yiu, Y. Y., Staron, M. M., Angel, C. L., Sinha, R., Markovic, M., Pham, E. A., Fram, et al
  2019; 10 (1): 794
- **Reply to J. Wang et al.** *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*
  Kurtz, D. M., Scherer, F., Jin, M. C., Soo, J., Craig, A. F., Esfahani, M. S., Chabon, J. J., Stehr, H., Liu, C. L., Tibshirani, R., Maeda, L. S., Gupta, N. K., Khodadoust, et al
  2019: JCO1801907
- **Spatial mapping of the immune microenvironment in primary triple-negative breast cancer (TNBC) and association with neoadjuvant therapy response**
  Telli, M. L., Vinayak, S., Khododoust, M. S., Gruber, J. J., Ford, J. M., Sanchez, P., Banayan, N., Azimi, S., Tumeh, P. C., Newman, A. M., Alizadeh, A. A.
  AMER ASSOC CANCER RESEARCH.2019
- **Computational approaches for characterizing the tumor immune microenvironment.** *Immunology*
  Liu, C. C., Steen, C. B., Newman, A. M.
  2019
- **Functional significance of U2AF1 S34F mutations in lung adenocarcinomas** *Nature Communications*
  Shahrokh Esfahani, M.
  2019; 10
- **Circulating tumor DNA analysis for detection of minimal residual disease after chemoradiotherapy for localized esophageal cancer.** *Gastroenterology*
  Azad, T. D., Chaudhuri, A. A., Fang, P. n., Qiao, Y. n., Esfahani, M. S., Chabon, J. J., Hamilton, E. G., Yang, Y. D., Lovejoy, A. n., Newman, A. M., Kurtz, D. M., Jin, M. n., Schroers-Martin, et al
  2019
- **Functional significance of U2AF1 S34F mutations in lung adenocarcinomas.** *Nature communications*
  Esfahani, M. S., Lee, L. J., Jeon, Y. J., Flynn, R. A., Stehr, H. n., Hui, A. B., Ishisoko, N. n., Kildebeck, E. n., Newman, A. M., Bratman, S. V., Porteus, M. H., Chang, H. Y., Alizadeh, et al
  2019; 10 (1): 5712
- **Method of Isolating and Transplanting the Hematopoietic Stem Cell with Its Microenvironment Which Improves Functional Hematopoietic Engraftment**
  Borrelli, M. R., Lopez, M., Gulati, G., Murphy, M. P., Sinha, R., Longaker, M. T., Weissman, I. L., Newman, A. M., Chan, C. K., Sokol, J.
  ELSEVIER SCIENCE INC.2018: E224
- **Circulating tumor DNA (ctDNA) in B-cell lymphoma**
  Scherer, F., Kurtz, D. M., Newman, A. M., Stehr, H., Craig, A. F. M., Esfahani, M. S., Lovejoy, A. F., Chabon, J. J., Klass, D. M., Green, M. R., Liu, C. L., Zhou, L., Glover, et al
  WILEY.2018: 16–17
- **Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma.** *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*
  Kurtz, D. M., Scherer, F., Jin, M. C., Soo, J., Craig, A. F., Esfahani, M. S., Chabon, J. J., Stehr, H., Liu, C. L., Tibshirani, R., Maeda, L. S., Gupta, N. K., Khodadoust, et al
  2018: JCO2018785246
- **Circulating Tumor DNA Quantitation for Early Response Assessment of Immune Checkpoint Inhibitors for Metastatic Non-Small Cell Lung Cancer**
  Chaudhuri, A. A., Nabet, B. Y., Merriott, D. J., Jin, M., Chen, E. L., Chabon, J. J., Newman, A. M., Stehr, H., Say, C., Carter, J. N., Walters, S., Becker, H., Das, et al
  ELSEVIER SCIENCE INC.2018: E1–E2
- **Genomic Feature Selection by Coverage Design Optimization.** *Journal of applied statistics*
  Reid, S., Newman, A. M., Diehn, M., Alizadeh, A. A., Tibshirani, R.
  2018; 45 (14): 2658-2676

- **Profiling Tumor Infiltrating Immune Cells with CIBERSORT.** *Methods in molecular biology (Clifton, N.J.)*
  Chen, B. n., Khodadoust, M. S., Liu, C. L., Newman, A. M., Alizadeh, A. A.
  2018; 1711: 243–59

- **Complex mammalian-like haematopoietic system found in a colonial chordate.** *Nature*
  Rosental, B. n., Kowarsky, M. n., Seita, J. n., Corey, D. M., Ishizuka, K. J., Palmeri, K. J., Chen, S. Y., Sinha, R. n., Okamoto, J. n., Mantalas, G. n., Manni, L. n., Raveh, T. n., Clarke, et al
  2018

- **Circulating tumor DNA levels correlate with response to treatment in LMS patients**
  Przybyl, J., Chabon, J. J., Spans, L., Ganjoo, K., Vennam, S., Newman, A. M., Forgo, E., Varma, S., Zhu, S., Debiec-Rychter, M., Alizadeh, A., Diehn, M., van de Rijn, et al
  AMER ASSOC CANCER RESEARCH.2018: 38–39

- **Combination approach for detecting different types of alterations in circulating tumor DNA in leiomyosarcoma.** *Clinical cancer research : an official journal of the American Association for Cancer Research*
  Przybyl, J. n., Chabon, J. J., Spans, L. n., Ganjoo, K. n., Vennam, S. n., Newman, A. M., Forgó, E. n., Varma, S. n., Zhu, S. n., Debiec-Rychter, M. n., Alizadeh, A. A., Diehn, M. n., van de Rijn, et al
  2018

- **Early B cell changes predict autoimmunity following combination immune checkpoint blockade.** *The Journal of clinical investigation*
  Das, R. n., Bar, N. n., Ferreira, M. n., Newman, A. M., Zhang, L. n., Bailur, J. K., Bacchiocchi, A. n., Kluger, H. n., Wei, W. n., Halaban, R. n., Sznol, M. n., Dhodapkar, M. V., Dhodapkar, et al
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