Noah F. Greenwald

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EDUCATION

Stanford University School of Medicine — Stanford, CA
Ph.D. in Cancer Biology — 2024

Harvard College — Cambridge, MA
A.B. in Biophysics. High Honors, *magna cum laude.* GPA 3.88 — 2015

RESEARCH EXPERIENCE

Postdoctoral Research Fellow — San Francisco, CA
University of California San Francisco School of Pharmacy — 2024-Present
Advisor: Dr. Willow Coyote-Maestas

- Used deep mutational scanning and computational analysis to understand the biophysical determinants of cancer-immune interactions.

Angelo Lab Computational Team Lead — Stanford, CA
Stanford University School of Medicine — 2020-2024

- Conceptualized and supervised the creation of the open-source image analysis pipeline which forms the backbone for all imaging projects in the Angelo lab. [GitHub]
- Managed and directed team of computational research assistants, undergraduate interns, and high school students to design algorithms for image processing, clustering, and spatial analyses.

Graduate Researcher — Stanford, CA
Stanford University School of Medicine — 2017-2024
Advisors: Dr. Michael Angelo and Dr. Christina Curtis
Thesis Committee: Dr. Edgar Engleman, Dr. Andrew Gentles, Dr. Nima Aghaeepour

- Developed a deep-learning algorithm to identify the location of cells in image data across a range of tissue types and microscope platforms. [Nature Biotechnology]
- Integrated multiplexed imaging and sequencing data of triple negative breast cancer patient samples from an immunotherapy clinical trial to predict patient responses. [bioRxiv]
- Designed a deep learning algorithm to classify staining patterns in image data across distinct cell types and markers. [bioRxiv]

Research Assistant Boston, MA
Harvard Medical School 2015-2017
Advisors: Dr. Rameen Beroukhim and Dr. Ian Dunn

- Profiled large cohort of pituitary adenomas with whole-exome sequencing to define landscape of mutations and copy-number alterations. [Clinical Cancer Research]
- Investigated the driver alterations which distinguish low- and high-grade meningiomas by integrating whole-genome, whole-exome, and targeted sequencing. [Genomic Medicine]

Undergraduate Research Assistant Cambridge, MA
Harvard University Department of Chemistry 2014
Advisor: Dr. George Whitesides

- Explored the hydrophobic effect in protein-ligand binding through bacterial production of proteins followed by analysis of binding kinetics.
- Investigated whether nanofabrication of antennas by photolithography could aid in detection of binding events of immobilized proteins through signal amplification.

Summer Intern Cambridge, MA
Vaxess Technologies 2014

- Implemented, ran, and optimized potency assay to measure vaccine activity after long-term storage, then scaled up from bench scale.
- Researched and presented competitive analysis of other vaccine preservation companies.

Summer Intern Santiago, Chile
Chilean Ministry of Energy 2013

- Helped draft preliminary analytical framework for assessing volatility in fuel storage levels.
- Revamped template for subsequent analysis of entire energy sector to guide creation of federal storage level minimums.

HONORS AND AWARDS

Best Poster Award 2023
Stanford Pathology Department Retreat

Best Talk Award 2022
Stanford Cancer Biology Program Retreat

Lucille P. Markey Biomedical Research Fellow 2017-2020
Stanford Graduate Fellowship Program

RESEARCH FUNDING

NIH/NCI F99/K00 CA264307 (PI Greenwald) 2021-2028
"Comprehensive profiling of the tumor microenvironment to predict patient response to immunotherapy."
Role: PI.
Summary: Using sequencing, multiplexed imaging, and experimental models to better understand the mechanism of immunotherapy in breast cancer.

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DOD W81XWH2110143 (PI Angelo) 2021-2025
"Relating the interplay of tumor function and host response to clinical outcome in triple negative breast cancer."
Role: Co-wrote Aims.
Summary: Identifying the underlying features of the tumor microenvironment which modulate response to therapy in breast cancer across disease subtypes and treatment regimes.

NIH/NCI F31 CA246880 (PI Greenwald) 2020-2021
"Predicting response to anti-PD-1 therapy in triple negative breast cancer by comprehensive profiling of the tumor microenvironment."
Role: PI.
Summary: Integrated analysis of the tumor microenvironment by combining sequencing and multiplexed imaging to better understand response to immunotherapy.

NIH/NCI UH3 CA246633 (PI Angelo) 2019-2022
"A robust platform for multiplexed, subcellular proteomic imaging in human tissue."
Role: Co-wrote Aim 1.
Summary: Develop robust analytical pipelines and reagents to enable large-scale adoption of MIBI technology across a wide range of normal and diseased tissue types.

MENTORSHIP

Post-doctoral fellow 2023-2024
Guided analysis of imaging data to predict breast cancer patient outcome

Post-doctoral fellow 2023-2024
Guided analysis of sequencing and imaging data to understand breast cancer evolution

Visiting PhD student 2022-2024
Supervised design of deep learning algorithm for cell classification

Computational research associate 2022-2024
Supervised implementation of algorithms for spatial analysis

Computational research associate 2022-2024
Supervised creation of tools for reproducible computational analysis

Rotation student 2022
Supervised segmentation and phenotyping of cells in pre-invasive breast cancer

Computational research associate 2021
Supervised optimization of spatial algorithms

Rotation student 2020
Guided analysis of sequencing data to predict patient outcome

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High school student 2020
Supervised creation of user-friendly image data visualizations

Undergraduate student 2020
Supervised optimization of spatial analysis code

Computational research associate 2020-2024
Supervised creation of user-friendly image analysis pipelines

Computational research associate 2020-2022
Supervised design of algorithms for spatial analysis

High school students 2019
Supervised creation of ground-truth data for training deep learning models

Rotation student 2019
Supervised application of denoising algorithms to MIBI data

Rotation student 2019
Supervised optimization of segmentation algorithm parameters

TEACHING

Stanford University

CBIO 275: Tumor Immunology 2021
Teaching Assistant

"Profiling the tumor microenvironment with high-dimensional imaging" 2021
CBIO 275 Guest Lecture

"How to analyze multiplexed imaging data" 2021
Immunology 206 Guest Lecture

PROFESSIONAL DEVELOPMENT

UCSF

Developing Your Negotiation Strategy 2024
A hands-on seminar to demonstrate and practice negotiation skills in different professional settings

Stanford University

Coaching High Performance Teams 2022
A week-long workshop on how to effectively coach and manage teams

LAW 7807: Facilitation 2021
A three-day workshop introducing key techniques for effective facilitation

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SGSI: Negotiation 2021
A week-long workshop detailing how to approach multi-party negotiations

Effective Negotiation 2020
A full-day workshop on structuring productive negotiations

Alda Science Communication Workshop 2019
A half-day workshop on delivering dynamic and engaging presentations

Grant Writing Academy 2018
An eight-week class to develop core grant writing skills

PEER REVIEW

Invited Reviewer

Journals: Computational and Structural Biotechnology Journal, IEEE Transactions on Image Processing, IEEE Transactions on Medical Imaging, Scientific Reports.

Conferences: Neural Information Processing Systems (NeurIPS) LMRL Workshop.

Reviewer

Journals: Cancer Cell, Cancer Discovery, Cell, Cell Reports Methods, Cell Systems, Genome Biology, Nature, Nature Cancer, Nature Communications, Nature Immunology, Nature Methods, PLoS ONE

SERVICE AND LEADERSHIP

Single-Cell Cancer Biology Gordon Research Seminar Discussion Leader 2024
- Moderated discussion and facilitated Q&A for session on emerging technologies and methods

Skype a Scientist Volunteer 2023-present
- Gave presentations to middle school and high school students about what it's like to be a scientist and answered questions about cancer research, genetics, and science.

Spatial Biology Summit Co-Chair 2022 & 2023
- Conceptualized the event, designed the agenda, and invited external speakers for the first two years of our annual summit dedicated to the spatial analysis of biological data.
- Ran the sessions and moderated Q&A from the over 1,100 registered participants.

Stanford Cancer Biology Seminar Series Co-organizer 2021
- Solicited program input to create schedule of external faculty speakers.
- Worked with the Cancer Biology Racial Justice group to add talks from post-docs from historically under-represented populations.

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Advance Undergraduate Institute Mentor 2021

- Provided guidance on applying to graduate school for students from under-represented backgrounds via panel discussions and mock interviews, as well as one-on-one mentoring.

SSRP Admissions Committee Member 2020 & 2021

- Reviewed applications for Stanford's summer undergraduate research program, which is geared towards preparing members of historically under-represented groups for STEM PhD programs.

EPATT Tutor 2019-2022

- Met one-on-one twice a week with students from East Palo Alto Middle School to help with specific coursework, as well as establish good academic habits and study skills.

Stanford Cancer Biology Recruitment, Social Committee Chair 2018-2020

- Organized and ran activities for prospective graduate students during interview week.

Stanford Biosciences Student Association Grants Committee Co-Chair 2018

- Planned and ran informational workshops with grant writing tips and advice on applications.
- Organized peer-to-peer advising to provide feedback on NSF and NIH fellowships.

PRESENTATIONS

Invited Talks

Greenwald NF, Nederlof I, Ding D, Houlahan K, Horlings H, Kok M, Curtis C, Angelo M. The temporal influence of the tumor microenvironment in response to checkpoint blockade. **Center for Cancer Systems Biology Symposium**. April 2024; Stanford, California.

Greenwald NF, Rumberger L, Angelo M. An integrated toolkit for analyzing high-dimensional imaging data. **Quantitative Bioimaging Society MIA Workshop**. October 2023; San Diego, California.

Talks

Greenwald NF, Nederlof I, Ding D, Houlahan K, Horlings H, Kok M, Curtis C, Angelo M. Temporal and spatial composition of the tumor microenvironment predicts response to immune checkpoint inhibition. **Spatial Biology Summit**. September 2024; Stanford, California

Greenwald NF, Nederlof I, Ding D, Houlahan K, Horlings H, Kok M, Curtis C, Angelo M. The temporal influence of the tumor microenvironment in response to checkpoint blockade. **Single-Cell Cancer Biology Gordon Research Conference**. June 2024; Manchester, New Hampshire

Greenwald NF, Nederlof I, Ding D, Houlahan K, Horlings H, Kok M, Curtis C, Angelo M. The temporal influence of the tumor microenvironment in response to checkpoint blockade. **American Association for Cancer Research Annual Meeting**. April 2024; San Diego, California

Greenwald NF, Nederlof I, Ding D, Houlahan K, Horlings H, Kok M, Curtis C, Angelo M. The temporal influence of the tumor microenvironment in response to checkpoint blockade. **Computational Systems Immunology Symposium**. October 2023; Stanford, California.

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Greenwald NF. Segmentation of multiplexed imaging data. **Spatial Biology Summit**. August 2023; Stanford, CA

Greenwald NF, Nederlof I, Houlahan K, Kagel A, Kong A, Horlings H, Kok M, Curtis C, Angelo M. Mapping the evolution of the tumor microenvironment in triple-negative breast cancer. **Stanford Cancer Biology Program Retreat**. October 2022; San Jose, California.

Greenwald NF. Quantifying MIBI sensitivity. **Spatial Biology Summit**. August 2022; Stanford, CA

Greenwald NF*, Miller G*, Moen E, Dougherty T, Singh J, Fong M, Chaudhry G, Abraham Z, Mosely J, Soon E, Greenbaum S, Keren L, Graf W, Angelo M§, Van Valen D§. Accurate whole-cell segmentation by combining convolutional neural networks and high-dimensional imaging. **Keystone Symposia: Single Cell Biology**. March 2020; Virtual.

Bi WL, Horowitz P, **Greenwald NF**, Abedalthagafi M, Agarwalla PK, Schumacher S, Mei Y, Brastianos P, Santagata S, Laws ER Jr., Beroukhim R, Dunn IF. Landscape of genomic alterations in pituitary adenoma. **New England Neurosurgical Society Annual Meeting**. June 2016; Cape Cod, MA.

Bi WL, **Greenwald NF**, Abedalthagafi M, Agarwalla PK, Horowitz P, Gibson WJ, Al-Mefty O, Santagata S, Beroukhim R, Dunn IF. Landscape of genomic alterations in high-grade meningioma. **Society for Neuro-Oncology Conference on Meningioma**. June 2016; Toronto, Canada.

Posters

Greenwald NF, Nederlof I, Ding D, Houlahan K, Horlings H, Kok M, Curtis C, Angelo M. The temporal influence of the tumor microenvironment in response to checkpoint blockade. **Stanford Pathology Department Retreat**. November 2023; Stanford, California.

Greenwald NF, Keren L , Greenbaum S, Fong M, Chaudry G, Abraham Z, Moseley J, Van Valen D, Angelo M. Accurate whole-cell segmentation in clinical tissue samples by combining convolutional neural networks and multiplexed imaging. **Allen Institute Bioimage Informatics**. October 2019; Seattle, WA.

Greenwald NF, Keren L, Angelo M. Harnessing deep learning to enable multiplexed in situ cellular segmentation and morphological characterization. **Stanford Cancer Biology Program Retreat**. September 2018; San Jose, CA.

Bi WL, Coroller T, **Greenwald NF**, Beroukhim R, Dunn IF, Huang R, Aerts H. Radiographic prediction of meningioma grade and genotype. **Broad Cancer Program Retreat**. December 2016; Cambridge, MA.

Greenwald NF, Bi WL, Beroukhim R. Liquid Biopsies: Circulating Tumor DNA as a Clinical Marker. **Broad Research Assistants and Technicians Poster Session**. November 2015; Cambridge, MA.

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PUBLICATIONS

* indicates equal contribution | § indicates co-corresponding

Selected Articles

Rumberger JL*, **Greenwald NF***§, Ranek JS, Boonrat P, Walker C, Franzen J, Varra SR, Kong A, Sowers C, Liu CC, Averbukh I, Piyadasa H, Vanguri R, Nederlof I, Wang XJ, Van Valen D, Kok M, Hollmann TJ, Kainmueller D, Angelo M§. Automated classification of cellular expression in multiplexed imaging data with Nimbus.

- Preprint: bioRxiv (2024). DOI: 10.1101/2024.06.02.597062

Greenwald NF*, Miller G*, Moen E, Kong A, Kagel A, Fullaway CC, McIntosh BJ, Leow K, Schwartz MS, Dougherty T, Pavelchek C, Cui S, Camplisson I, Bar-Tal O, Singh J, Fong M, Chaudhry G, Abraham Z, Mosely J, Warshawsky S, Soon E, Greenbaum S, Risom T, Hollmann T, Keren L, Graf W, Angelo M§, Van Valen D§. Whole-cell segmentation of tissue images with human-level performance using large-scale data annotation and deep learning. **Nature Biotechnology** (2021). DOI: 10.1038/s41587-021-01094-0

- Preprint: bioRxiv (2021). DOI: 10.1101/2021.03.01.431313

Bi WL*, **Greenwald NF***, Abedalthagafi M*, Wala J, Gibson WJ, Agarwalla PK, Horowitz P, Schumacher S, Artomov M, Esaulova E, Chevalier A, Ducar M, Thorner A, van Hummelin P, Brastianos P, Al-Mefty O, Dunn GP, Santagata S§, Dunn IF§, Beroukhim R§. Genomic landscape of high-grade meningioma. **npj Genomic Medicine** (2017). DOI: 10.1038/s41525-017-0014-7

Bi WL*, Horowitz P*, **Greenwald NF***, Abedalthagafi M, Agarwalla PK, Gibson WJ, Mei Y, Schumacher S, Ben-David U, Chevalier A, Carter S, Tiao G, Brastianos P, Ligon AH, Laws ER Jr., Santagata S, Beroukhim R§, Dunn IF§. Landscape of genomic alterations in pituitary adenoma. **Clinical Cancer Research** (2016). DOI: 10.1158/1078-0432.CCR-16-0790

Research Articles

Ghosh HS*, Patel RV*, Woodward E, **Greenwald NF**, Bhave VM, Maury EA, Cello G, Hoffman SE, Li Y, Gupta H, Youssef G, Spurr LF, Vogelzang J, Touat M, Dubois F, Cherniack AD, Guo X, Tavakol S, Cioffi G, Lindeman NI, Ligon AH, Chiocca EA, Reardon DA, Wen PY, Meredith D, Santagata S, Barnholtz-Sloan JS, Ligon KL, Beroukhim R, Bi WL. Contemporary Prognostic Signatures and Refined Risk Stratification of Gliomas: An Analysis of 4,400 Tumors. **Neuro-Oncology** (2024). DOI: 10.1093/neuonc/noae164

Rumberger JL*, **Greenwald NF***§, Ranek JS, Boonrat P, Walker C, Franzen J, Varra SR, Kong A, Sowers C, Liu CC, Averbukh I, Piyadasa H, Vanguri R, Nederlof I, Wang XJ, Van Valen D, Kok M, Hollmann TJ, Kainmueller D, Angelo M§. Automated classification of cellular expression in multiplexed imaging data with Nimbus.

- Preprint: bioRxiv (2024). DOI: 10.1101/2024.06.02.597062

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Houlahan KE, Khan A, **Greenwald NF**, Vivas CS, West RB, Angelo M, Curtis C. Germline-mediated immunoediting sculpts breast cancer subtypes and metastatic proclivity. **Science** (2024). DOI: 10.1126/science.adh8697

- Preprint: bioRxiv (2023). DOI: 10.1101/2023.03.15.532870
- Related coverage: Science

Ma J, Xie R, Ayyadhury S, Ge C, Gupta A, Gupta R, Gu S, Zhang Y, Lee G, Kim J, Lou W, Li H, Upschulte E, Dickscheid T, de Almeida JG, Wang Y, Han L, Yang X, Labagnara M, Gligorovski V, Scheder M, Rahi SJ, Kempster C, Pollitt A, Espinosa L, Mignot T, Middeke JM, Eckardt JN, Li W, Li Z, Cai X, Bai B, **Greenwald NF**, Van Valen D, Weisbart E, Cimini BA, Cheung T, Brück O, Bader GD, Wang B. The multimodality cell segmentation challenge: toward universal solutions. **Nature Methods** (2024). DOI: 10.1038/s41592-024-02233-6

- Preprint: arXiv (2023). DOI: 10.48550/arXiv.2308.05864

Ferrian S, Cao A, McCaffrey EF, Saito T, **Greenwald NF**, Nicolls MR, Bruce T, Zamanian RT, Del Rosario P, Rabinovitch M, Angelo M. Single-Cell Imaging Maps Inflammatory Cell Subsets to Pulmonary Arterial Hypertension Vasculopathy. **American Journal of Respiratory and Critical Care Medicine** (2024). DOI: 10.1164/rccm.202209-1761OC

- Related coverage: American Journal of Respiratory and Critical Care Medicine

Rauch PJ, Gopakumar J, Silver AJ, Nachun D, Ahmad H, Mcconkey M, Nakao T, Bosse M, Rentz T, Gonzalez N, **Greenwald NF**, Mccaffrey EF, Khair Z, Gopakumar M, Rodrigues KB, Lin AE, Sinha E, Fefer M, Cohen DN, Vromman A, Shvartz E, Sukhova G, Bendall S, Angelo M, Libby P, Ebert BL, Jaiswal S. Loss-of-function mutations in Dnmt3a and Tet2 lead to accelerated atherosclerosis and concordant macrophage phenotypes**. Nature Cardiovascular Research** (2023). DOI: 10.1038/s44161-023-00326-7

Liu CC, **Greenwald NF**, Kong A, McCaffrey EF, Leow KX, Mrdjen D, Cannon BJ, Rumberger JL, Varra SR, Angelo M. Robust phenotyping of highly multiplexed tissue imaging data using pixel-level clustering. **Nature Communications** (2023). DOI: 10.1038/s41467-023-40068-5

- Preprint: bioRxiv (2022). DOI: 10.1101/2022.08.16.504171

Greenbaum S*, Averbukh I*, Soon E*, Rizzuto G, Baranski A, **Greenwald NF**, Kagel A, Bosse M, Jaswa EG, Khair Z, Kwok S, Warshawsky S, Piyadasa H, Goldston M, Spence A, Miller G, Schwartz M, Graf W, Van Valen D, Winn VD, Hollmann T, Keren L, van de Rijn M, Angelo M. A spatially resolved timeline of the human maternal-fetal interface. **Nature** (2023). DOI: 10.1038/s41586-023-06298-9

- Preprint: bioRxiv (2022). DOI: 10.1101/2021.09.08.459490
- Related coverage: Nature, Nature

Bai Y, Zhu B, Oliveria JP, Cannon BJ, Feyaerts D, Bosse M, Vijayaragavan K, **Greenwald NF**, Phillips D, Schürch CM, Naik SM, Ganio EA, Gaudilliere B, Rodig SJ, Miller MB, Angelo M, Bendall SC, Rovira-Clavé X§, Nolan GP§, Jiang S§. Expanded vacuum-stable gels for multiplexed high-resolution spatial histopathology. **Nature Communications** (2023). DOI: 10.1038/s41467-023-39616-w

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Vijayaragavan K*, Cannon BJ*, Tebaykin D, Bossé M, Baranski A, Oliveria JP, Bukhari SA, Mrdjen D, Corces MR, McCaffrey EF, **Greenwald NF**, Sigal Y, Marquez D, Khair Z, Bruce T, Goldston M, Bharadwaj A, Montine KS, Angelo RM, Montine TJ, Bendall SC. Single-cell spatial proteomic imaging for human neuropathology. **Acta Neuropathologica Communications** (2022). DOI: 10.1186/s40478-022-01465-x

- Preprint: bioRxiv (2022). DOI: 10.1101/2022.03.02.482730

Rovira-Clavé X*, Drainas AP*, Jiang S*, Bai Y, Baron M, Zhu B, Dallas AE, Lee MC, Chu TP, Holzem A, Ayyagari R, Bhattacharya D, McCaffrey EF, **Greenwald NF**, Markovic M, Coles GL, Angelo M, Bassik MC, Sage J§, Nolan GP§. Spatial epitope barcoding reveals clonal tumor patch behaviors. **Cancer Cell** (2022). DOI: 10.1016/j.ccell.2022.09.014

- Preprint: bioRxiv (2022). DOI: 10.1101/2021.06.29.449991

Dubois FPB, Shapira O, **Greenwald NF**, Zack T, Wala J, Tsai JW, Crane A, Baguette A, Hadjadj D, Harutyunyan AS, Kumar KH, Blattner-Johnson M, Vogelzang J, Sousa C, Kang KS, Sinai C, Wang DK, Khadka P, Lewis K, Nguyen L, Malkin H, Ho P, O'Rourke R, Zhang S, Gold R, Deng D, Serrano J, Snuderl M, Jones C, Wright KD, Chi SN, Grill J, Kleinman CL, Goumnerova LC, Jabado N, Jones DTW, Kieran MW, Ligon KL§, Beroukhim R§, Bandopadhayay P§. Structural variants shape driver combinations and outcomes in pediatric high-grade glioma. **Nature Cancer** (2022). DOI: 10.1038/s43018-022-00403-z

- Related coverage: Nature Cancer

Ghahremani P, Li Y, Kaufman A, Vanguri R, **Greenwald NF**, Angelo M, Hollmann TJ, Nadeem S. Deep learning-inferred multiplex immunofluorescence for immunohistochemical image quantification. **Nature Machine Intelligence** (2022). DOI: 10.1038/s42256-022-00471-x

Jiang S*, Chan CN*, Rovira-Clavé X*, Chen H, Bai Y, Zhu B, McCaffrey E, **Greenwald NF**, Liu C, Barlow GL, Weirather JL, Oliveria JP, Nakayama T, Lee IT, Matter MS, Carlisle AE, Philips D, Vazquez G, Mukherjee N, Busman-Sahay K, Nekorchuk M, Terry M, Younger S, Bosse M, Demeter J, Rodig SJ, Tzankov A, Goltsev Y, McIlwain DR, Angelo M, Estes JD§, Nolan GP§. Combined protein and nucleic acid imaging reveals virus-dependent B cell and macrophage immunosuppression of tissue microenvironments. **Immunity** (2022). DOI: 10.1016/j.immuni.2022.03.020

- Preprint: bioRxiv (2021). DOI: 10.1101/2021.05.21.444548

Khadka P*, Reitman ZJ*, Lu S, Buchan G, Gionet G, Dubois F, Carvalho DM, Shih J, Zhang S, **Greenwald NF**, Zack T, Shapira O, Pelton K, Hartley R, Bear H, Georgis Y, Jarmale S, Melanson R, Bonanno K, Schoolcraft K, Miller PG, Condurat AL, Gonzalez EM, Qian K, Morin E, Langhnoja J, Lupien LE, Rendo V, Digiacomo J, Wang D, Zhou K, Kumbhani R, Guerra Garcia ME, Sinai CE, Becker S, Schneider R, Vogelzang J, Krug K, Goodale A, Abid T, Kalani Z, Piccioni F, Beroukhim R, Persky NS, Root DE, Carcaboso AM, Ebert BL, Fuller C, Babur O, Kieran MW, Jones C, Keshishian H, Ligon KL, Carr SA, Phoenix TN§, Bandopadhayay P§. PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. **Nature Communications** (2022). DOI: 10.1038/s41467-022-28198-8

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Risom T, Glass DR, Averbukh I, Liu CC, Baranski A, Kagel A, McCaffrey EF, **Greenwald NF**, Rivero-Gutiérrez B, Strand SH, Varma S, Kong A, Keren L, Srivastava S, Zhu C, Khair Z, Veis DJ, Deschryver K, Vennam S, Maley C, Hwang ES, Marks JR, Bendall SC, Colditz GA, West RB, Angelo M. Transition to invasive breast cancer is associated with progressive changes in the structure and composition of tumor stroma. **Cell** (2022). DOI: 10.1016/j.cell.2021.12.023

- Preprint: bioRxiv (2021). DOI: 10.1101/2021.01.05.425362

McCaffrey EF, Donato M, Keren L, Chen Z, Delmastro A, Fitzpatrick MB, Gupta S, **Greenwald NF**, Baranski A, Graf W, Kumar R, Bosse M, Fullaway CC, Ramdial PK, Forgó E, Jojic V, Van Valen D, Mehra S, Khader SA, Bendall SC, van de Rijn M, Kalman D, Kaushal D, Hunter RL, Banaei N, Steyn AJC, Khatri P, Angelo M. The immunoregulatory landscape of human tuberculosis granulomas. **Nature Immunology** (2022). DOI: 10.1038/s41590-021-01121-x

- Preprint: bioRxiv (2020). DOI: 10.1101/2020.06.08.140426

Greenwald NF*, Miller G*, Moen E, Kong A, Kagel A, Fullaway CC, McIntosh BJ, Leow K, Schwartz MS, Dougherty T, Pavelchek C, Cui S, Camplisson I, Bar-Tal O, Singh J, Fong M, Chaudhry G, Abraham Z, Mosely J, Warshawsky S, Soon E, Greenbaum S, Risom T, Hollmann T, Keren L, Graf W, Angelo M§, Van Valen D§. Whole-cell segmentation of tissue images with human-level performance using large-scale data annotation and deep learning. **Nature Biotechnology** (2021). DOI: 10.1038/s41587-021-01094-0

- Preprint: bioRxiv (2021). DOI: 10.1101/2021.03.01.431313

Driver J, Hoffman SE, Tavakol S, Woodward E, Maury EA, Bhave V, **Greenwald NF**, Nassiri F, Aldape K, Zadeh G, Choudhury A, Vasudevan HN, Magill ST, Raleigh DR, Abedalthagafi M, Aizer AA, Alexander BM, Ligon KL, Reardon DA, Wen PY, Al-Mefty O, Ligon AH, Dubuc AM, Beroukhim R, Claus EB, Dunn IF, Santagata S§, Bi WL§. A molecularly integrated grade for Meningioma. **Neuro Oncology** (2021). DOI: 10.1093/neuonc/noab213

Bannon D, Moen E, Schwartz M, Borba E, Kudo T, **Greenwald NF**, Vijayakumar V, Chang B, Pao E, Osterman E, Graf W, Van Valen D. DeepCell Kiosk: Scaling deep learning-enabled cellular image analysis with Kubernetes. **Nature Methods** (2021). DOI: 10.1038/s41592-020-01023-0

- Preprint: bioRxiv (2020). DOI: 10.1101/505032

Hartmann FJ, Mrdjen D, McCaffrey E, Glass DR, **Greenwald NF**, Bharadwaj A, Khair Z, Verberk SGS, Baranski A, Baskar R, Graf W, Van Valen D, Van den Bossche J, Angelo M, Bendall SC. Single-cell metabolic profiling of human cytotoxic T cells. **Nature Biotechnology** (2020). DOI: 10.1038/s41587-020-0651-8

- Preprint: bioRxiv (2019). DOI: 10.1101/2020.01.17.909796
- Related coverage: Nature Methods

Jaimes C, Vajapeyam S, Brown D, Kao PC, Ma C, Greenspan L, Gupta N, Goumnerova L, Bandopahayay P, Dubois F, **Greenwald NF**, Zack T, Shapira O, Beroukhim R, Ligon KL, Chi S, Kieran MW, Wright KD, Poussaint TY**.** MR Imaging Correlates for Molecular and Mutational Analyses in Children with Diffuse Intrinsic Pontine Glioma. **American Journal of Neuroradiology** (2020). DOI: 10.3174/ajnr.A6546

Peter Brown P, **RELISH Consortium**, Zhou Y. Large expert-curated database for benchmarking document similarity detection in biomedical literature search. **Database** (2019). DOI: 10.1093/database/baz085

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