

Noah F. Greenwald
ngreenwald.github.io
nfgreen@stanford.edu | (310) 387-1326

EDUCATION

Stanford University School of Medicine Ph.D. Candidate in Cancer Biology	Stanford, CA 2017-Present
------------------------------------------------------------------------------------	------------------------------

Harvard College A.B. in Biophysics. High Honors, <i>magna cum laude</i> . GPA 3.88	Cambridge, MA 2015
----------------------------------------------------------------------------------------------	-----------------------

RESEARCH EXPERIENCE

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

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

Stanford University School of Medicine Graduate Researcher	Stanford, CA 2017-Present
----------------------------------------------------------------------	------------------------------

Advisors: [Dr. Michael Angelo](#) and [Dr. Christina Curtis](#)

Thesis Committee: Dr. Edgar Engleman, Dr. Andrew Gentles, Dr. Nima Aghaeepour

- Developed a novel deep-learning algorithm to identify the location of cells in image data across a range of tissue types and microscope platforms.
- Integrated genomics with multiplexed imaging to predict response to immunotherapy in triple negative breast cancer.

Harvard Medical School Research Assistant	Boston, MA 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.
- Investigated the patterns of driver alterations which distinguish low- and high-grade meningiomas by integrating whole-genome, whole-exome, and targeted sequencing.

Harvard University Department of Chemistry Undergraduate Research Assistant	Cambridge, MA 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.

Vaxess Technologies

Cambridge, MA

Summer Intern

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.

Chilean Ministry of Energy

Santiago, Chile

Summer Intern

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 Talk Award**

2022

Stanford University Cancer Biology Program Retreat

Lucille P. Markey Biomedical Research Fellow

2017-2020

Stanford University 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.

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 CA24663301 (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-present

“Identifying spatial determinants of outcome in TNBC”

Post-doctoral fellow

2023-present

“Characterizing the genomic and microenvironmental evolution of TNBC”

Visiting PhD student

2022-present

“Automated classification of cell types in multiplexed imaging data”

Computational research associate

2022-present

“Developing algorithms for spatial analysis of image data”

Computational research associate

2022-present

“Building tools for robust and reproducible computational workflows”

Rotation student

2022

“Analysis of imaging data from pre-invasive breast cancer”

Computational research associate

2021

“Optimization of algorithms to identify the spatial organization of cells”

Rotation student

2020

“Predicting response to checkpoint blockade from DNA sequencing data”

High school student

2020

“Visualizing cell populations in multiplexed images”

Undergraduate student

2020

“Calculating spatial enrichment of distinct cell subtypes”

Computational research associate

2020-present

“Building a user-friendly pipeline for image analysis”

Computational research associate

2020-2022

“Developing algorithms for spatial analysis of image data”

High school students

2019

“Curating image data to train machine learning algorithms”

Noah F. Greenwald	<i>Curriculum Vitae</i>	4
Rotation student		2019
“Using convolutional neural networks to predict high resolution imaging data”		
Rotation student		2019
“Assessing the accuracy of cell segmentation algorithms”		

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

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	
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

Journals

IEEE Transactions on Medical Imaging.

Conferences

Neural Information Processing Systems (NeurIPS) LMRL Workshop (2022).

SERVICE AND LEADERSHIP**Skype a Scientist Volunteer** 2023

- Gave presentations to elementary and middle school students about what it's like to be a scientist and answered questions about cancer research, genetics, and science.

Stanford University MIBI Workshop Co-Chair 2022

- Set agenda, organized presentations, and invited external speakers for the first annual workshop dedicated to the generation and analysis imaging data.
- Moderated sessions and handled Q&A from the over 300 registered participants.

Stanford Cancer Biology Seminar Series Co-organizer 2021-2022

- 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.

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 2018-2019

- 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, 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. The temporal influence of the tumor microenvironment in response to checkpoint blockade. **Computational Systems Immunology Symposium**. October 2023; Stanford, California.

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*, 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, 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.

PUBLICATIONS

* indicates equal contribution | § indicates co-corresponding

Selected Articles

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](https://doi.org/10.1038/s41587-021-01094-0).

- Preprint: bioRxiv (2021). DOI: [10.1101/2021.03.01.431313](https://doi.org/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](https://doi.org/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](https://doi.org/10.1158/1078-0432.CCR-16-0790).

Research Articles

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](https://doi.org/10.1038/s41467-023-40068-5).

- Preprint: bioRxiv (2022). DOI: [10.1101/2022.08.16.504171](https://doi.org/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](https://doi.org/10.1038/s41586-023-06298-9)

- Preprint: bioRxiv (2022). DOI: [10.1101/2021.09.08.459490](https://doi.org/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](https://doi.org/10.1038/s41467-023-39616-w).

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](https://doi.org/10.1186/s40478-022-01465-x).

- Preprint: bioRxiv (2022). DOI: [10.1101/2022.03.02.482730](https://doi.org/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](https://doi.org/10.1016/j.ccell.2022.09.014)

- Preprint: bioRxiv (2022). DOI: [10.1101/2021.06.29.449991](https://doi.org/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[§], Bandopadhyay P[§]. Structural variants shape driver combinations and outcomes in pediatric high-grade glioma. **Nature Cancer** (2022). DOI: [10.1038/s43018-022-00403-z](https://doi.org/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](https://doi.org/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](https://doi.org/10.1016/j.immuni.2022.03.020).

- Preprint: bioRxiv (2021). DOI: [10.1101/2021.05.21.444548](https://doi.org/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[§], Bandopadhyay P[§]. PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. **Nature Communications** (2022). DOI: [10.1038/s41467-022-28198-8](https://doi.org/10.1038/s41467-022-28198-8)

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](https://doi.org/10.1016/j.cell.2021.12.023).

- Preprint: bioRxiv (2021). DOI: [10.1101/2021.01.05.425362](https://doi.org/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](https://doi.org/10.1038/s41590-021-01121-x).

- Preprint: bioRxiv (2020). DOI: [10.1101/2020.06.08.140426](https://doi.org/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](https://doi.org/10.1038/s41587-021-01094-0).

- Preprint: bioRxiv (2021). DOI: [10.1101/2021.03.01.431313](https://doi.org/10.1101/2021.03.01.431313)

Driver J, Hoffman SE, Tavakol S, Woodward E, Maury EA, Bhavé 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, Beroukheim R, Claus EB, Dunn IF, Santagata S[§], Bi WL[§]. A molecularly integrated grade for Meningioma. **Neuro Oncology** (2021). DOI: [10.1093/neuonc/noab213](https://doi.org/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](https://doi.org/10.1038/s41592-020-01023-0).

- Preprint: bioRxiv (2020). DOI: [10.1101/505032](https://doi.org/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](https://doi.org/10.1038/s41587-020-0651-8).

- Preprint: bioRxiv (2019). DOI: [10.1101/2020.01.17.909796](https://doi.org/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, Beroukheim 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](https://doi.org/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](https://doi.org/10.1093/database/baz085).

Keren L*, Bosse M*, Thompson S, Risom T, Vijayaragavan K, McCaffrey E, Marquez D, Angoshtari R, **Greenwald NF**, Fienberg H, Wang J, Kambham N, Kirkwood D, Nolan G, Montine TJ, Galli SJ, West R, Bendall SC, Angelo M. MIBI-TOF: A multiplexed imaging platform relates cellular phenotypes and tissue structure. **Science Advances** (2019). DOI: [10.1126/sciadv.aax5851](https://doi.org/10.1126/sciadv.aax5851).

Bandopadhyay P, Piccioni F, O'Rourke R, Ho P, Gonzalez EM, Buchan G, Qian K, Gionet G, Girard E, Coxon M, Rees MG, Brenan L, Dubois F, Shapira O, **Greenwald NF**, Pages M, Balboni Iniguez A, Paoletta BR, Meng A, Sinai C, Roti G, Dharia NV, Creech A, Tanenbaum B, Khadka P, Tracy A, Tiv HL, Hong AL, Coy S, Rashid R, Lin JR, Cowley GS, Lam FC, Goodale A, Lee Y, Schoolcraft K, Vazquez F, Hahn WC, Tsherniak A, Bradner JE, Yaffe MB, Milde T, Pfister SM, Qi J, Schenone M, Carr SA, Ligon KL, Kieran MW, Santagata S, Olson JM, Gokhale PC, Jaffe JD, Root DE, Stegmaier K, Johannessen CM[§], Beroukhim R[§]. Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in MYC-driven medulloblastoma. **Nature Communications** (2019). DOI: [10.1038/s41467-019-10307-9](https://doi.org/10.1038/s41467-019-10307-9).

Wala JA, Bandopadhyay P, **Greenwald NF**, O'Rourke R, Sharpe T, Stewart C, Schumacher S, Li Y, Weischenfeldt J, Yao X, Nusbaum C, Campbell P, Getz G, Meyerson M, Zhang CZ, Imielinski M[§], Beroukhim R[§]. SvABA: genome-wide detection of structural variants and indels by local assembly. **Genome Research** (2018). DOI: [10.1101/gr.221028.117](https://doi.org/10.1101/gr.221028.117).

Coroller TP*, Bi WL*, Huynh E, Abedalthagafi M, Aizer AA, **Greenwald NF**, Parmar C, Narayan V, Wu WW, Miranda de Moura S, Gupta S, Beroukhim R, Wen PY, Al-Mefty O, Dunn IF, Santagata S, Alexander BM, Huang RY[§], Aerts HJWL[§]. Radiographic Prediction of Meningioma Grade by Semantic and Radiomic features. **PLoS One** (2017). DOI: [10.1371/journal.pone.0187908](https://doi.org/10.1371/journal.pone.0187908).

Ben-David U, Ha G, Tseng YY, **Greenwald NF**, Oh C, Shih J, McFarland JM, Wong B, Boehm JS, Beroukhim R[§], Golub TR[§]. Patient-derived xenografts undergo mouse-specific tumor evolution. **Nature Genetics** (2017). DOI: [10.1038/ng.3967](https://doi.org/10.1038/ng.3967).

- Related coverage: [Nature Genetics](#), [Nature](#)

Mei Y, Du Z, Hu C, **Greenwald NF**, Abedalthagafi M, Agar NYR, Dunn GP, Bi WL, Santagata S, Dunn IF. Osteoglycin promotes meningioma development through downregulation of NF2 and activation of mTOR signaling. **Cell Communication & Signaling** (2017). DOI: [10.1186/s12964-017-0189-7](https://doi.org/10.1186/s12964-017-0189-7).

Mei Y, Bi WL, **Greenwald NF**, Agar NY, Beroukhim R, Dunn GP, Dunn IF. Genomic profile of human meningioma cell lines. **PLoS One** (2017). DOI: [10.1371/journal.pone.0178322](https://doi.org/10.1371/journal.pone.0178322).

Bi WL*, **Greenwald NF***, Ramkissoon SH, Abedalthagafi M, Coy SM, Ligon KL, Mei Y, MacConaill L, Ducar M, Min L, Santagata S, Kaiser UB, Beroukhim R, Laws ER Jr, Dunn IF. Clinical identification of oncogenic drivers and copy number alterations in pituitary tumors. **Endocrinology** (2017). DOI: [10.1210/en.2016-1967](https://doi.org/10.1210/en.2016-1967).

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](https://doi.org/10.1038/s41525-017-0014-7).

Ramkissoon SH*, Bandopadhyay P*, Hwang J*, Ramkissoon LA*, **Greenwald NF**, Schumacher SE, O'Rourke R, Pinches N, Ho P, Malkin H, Sinai C, Filbin M, Plant A, Bi WL, Chang MS, Yang E, Wright KD, Manley PE, Ducar M, Alexandrescu S, Lidov H, Delalle I, Goumnerova LC, Church AJ, Janeway KA, Harris MH, MacConaill LE, Folkerth RD, Lindeman NI, Stiles CD, Kieran MW, Ligon AH, Santagata S, Dubuc AM, Chi SN[§], Beroukhi R[§], Ligon KL[§]. Clinical targeted exome-based sequencing in combination with genome-wide copy number profiling: Precision medicine analysis of 203 pediatric brain tumors. **Neuro Oncology** (2017). DOI: [10.1093/neuonc/now294](https://doi.org/10.1093/neuonc/now294).

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, Beroukhi R[§], Dunn IF[§]. Landscape of genomic alterations in pituitary adenoma. **Clinical Cancer Research** (2016). DOI: [10.1158/1078-0432.CCR-16-0790](https://doi.org/10.1158/1078-0432.CCR-16-0790).

Mei Y*, Bi WL*, **Greenwald NF**, Du Z, Agar NYR, Kaiser UB, Woodmansee WW, Reardon DA, Freeman GJ, Fecci PE, Laws ER Jr., Santagata S, Dunn GP, Dunn IF. Increased expression of programmed death ligand 1 (PD-L1) in human pituitary tumors. **Oncotarget** (2016). DOI: [10.18632/oncotarget.12088](https://doi.org/10.18632/oncotarget.12088).

Review Articles

Liu CC, McCaffrey EF, **Greenwald NF**, Soon E, Risom T, Vijayaragavan K, Oliveria JP, Mrdjen D, Bosse M, Tebaykin D, Bendall SC, Angelo M. Multiplexed Ion Beam Imaging: Insights into Pathobiology. **Annual Review of Pathology** (2021). DOI: [10.1146/annurev-pathmechdis-030321-091459](https://doi.org/10.1146/annurev-pathmechdis-030321-091459).

Taube JM, Akturk G, Angelo M, Engle EL, Gnjjatic S, Greenbaum S, **Greenwald NF**, Hedvat CV, Hollmann TJ, Juco J, Parra ER, Rebelatto MC, Rimm DL, Rodriguez-Canales J, Schalper KA, Stack EC, Ferreira CS, Korski K, Lako A, Rodig SJ, Schenck E, Steele KE, Surace MJ, Tetzlaff MT, von Loga K, Wistuba II, Bifulco CB, Society for Immunotherapy of Cancer (SITC) Pathology Task Force. The Society for Immunotherapy in Cancer statement on best practices for multiplex immunohistochemistry (IHC) and immunofluorescence (IF) staining and validation. **Journal for Immunotherapy of Cancer** (2020). DOI: [10.1136/jitc-2019-000155](https://doi.org/10.1136/jitc-2019-000155).

Other Articles

Averbukh I, **Greenwald NF**, Liu CC, Angelo M. Evaluation of Geuenich et al.: Targeting a crucial bottleneck for analyzing single-cell multiplexed imaging data. **Cell Systems** (2021). DOI: [10.1016/j.cels.2021.11.003](https://doi.org/10.1016/j.cels.2021.11.003)

Cable J, Elowitz MB, Domingos AI, Habib N, Itzkovitz S, Hamidzada H, Balzer MS, Yanai I, Liberali P, Whited J, Streets A, Cai L, Stergachis AB, Hong CKY, Keren L, Williams M, Alon U, Shalek AK, Hamel R, Pfau SJ, Raj A, Quake SR, Zhang NR, Fan J, Trapnell C, Wang B, **Greenwald NF**, Vento-Tormo R, Santos SDM, Spencer SL, Garcia HG, Arekatla G, Gaiti F, Arbel-Goren R, Rulands S, Junker JP, Klein AM, Morris SA, Murray JI, Galloway KE, Ratz M, Romeike M. Single-cell biology-a Keystone Symposia report. **Annals of The New York Academy of Sciences** (2021). DOI: [10.1111/nyas.14692](https://doi.org/10.1111/nyas.14692)

Greenwald NF, Bandopadhyay P, Beroukhi R. Open data: Spot data glitches before publication. **Nature** (2017). DOI: [10.1038/550333c](https://doi.org/10.1038/550333c).

Musib M, Wang F, Tarselli MA, Yoho R, Yu KH, Andrés RM, **Greenwald NF**, Pan X, Lee CH, Zhang J, Dutton-Regester K, Johnston JW, Sharafeldin IM. Artificial intelligence in research. **Science** (2017). DOI: [10.1126/science.357.6346.28](https://doi.org/10.1126/science.357.6346.28).