Gregory P. Way, Ph.D.

ASSISTANT PROFESSOR

Center for Health Artificial Intelligence • University of Colorado Cancer Center• University of Colorado Anschutz Medical School 1890 N Revere Ct. Aurora, CO 80045 gregory.way@gmail.com • https://github.com/gwaygenomics • https://waysciencelab.com

RESEARCH EXPERIENCE

Principal Investigator, Way Lab, University of Colorado Anschutz, Aurora, CO. Sept 2021 – Present. *Developing cell morphology as a systems biology readout of disease state.* I lead a biomedical data science lab currently interested in developing the field of systems morphology. Our overall mission is to reduce human suffering by integrating high-dimensional biomedical data science into clinical decision making to improve patient outcomes. We develop new methods, approaches, assays, and software for analyzing high-dimensional genomic, molecular, and morphological data.

Postdoctoral research, *Advisor: Anne E. Carpenter*, Broad Institute of MIT and Harvard, Cambridge, MA. March 2019 – 2021. *High-throughput morphology profiling, machine learning, data science, software engineering, and CRISPR to probe the morphological responses of genomic and drug perturbations.* I developed a suite of software tools to process and analyze image-based profiling experiments. I started a data science team, and led five researchers on advanced projects including data integration and software development.

Scientific advisory board, *CEO: Herb Sarnoff*, Infixion Biosciences, San Diego, CA. January 2019 - Present. *Finding a cure for Neurofibromatosis Type 1 (NF1)*. I advise the company in data science, data management, machine learning, and experimental design.

Ph.D. research, *Advisor: Casey S. Greene*, University of Pennsylvania, Philadelphia, PA. August 2014 - February 2019. *Supervised and unsupervised machine learning to reveal biological pathway function.* I developed computational approaches to identify aberrant signalling patterns in cancer transcriptomes. I led the Ras pathway signalling working group as part of The Cancer Genome Atlas (TCGA), and I identified Selumetinib as a potentially viable treatment for tumors with Ras misregulation.

Research internship, Discovery Oncology, Genentech, South San Francisco, CA. Summer 2018. Probing the impact of mutant allele specific expression in TCGA RNAseq data.

Research internship, *Antibody Development Unit*, Morphotek Inc., Exton, PA. Summer 2014. *Determining the cell killing efficacy and mechanisms of antibody treatments in cancer cell lines.*

Masters research, *Advisor: Scott McRobert*, Saint Joseph's University, Philadelphia, PA. August 2012 - May 2014. *Discovering a boldness and aggression behavioral syndrome, and comparing aggression assays in zebrafish.*

Undergraduate research, *Advisor: Matthew Wund*, The College of New Jersey, Ewing, NJ. August 2007 - May 2011. Behavioral syndromes and ecological field research in threespine stickleback fish.

EDUCATION

- **Postdoctoral Associate; Imaging Platform** Broad Institute of MIT and Harvard, Cambridge, MA
- Ph.D. in Genomics and Computational Biology
- University of Pennsylvania, Philadelphia, PA

M.S. in Biology

Saint Joseph's University, Philadelphia, PA

B.S in Biology, Environmental Studies; Minor in Philosophy

The College of New Jersey, Ewing, NJ

HONORS AND FELLOWSHIPS

- 2021 Manager to Leader Program, Broad Institute of MIT and Harvard
- 2020 Team Science Award, American Association for Cancer Research
- 2019 Elected to Advisory Board, CytoData Society
- 2018 1st Place, NHGRI Graduate Poster Competition, University of Pennsylvania
- 2018 Travel Award, Pacific Symposium on Biocomputing, University of Pennsylvania
- 2017 Travel Award, Neural Information Processing Systems, University of Pennsylvania
- 2017 T32 COMP-GEN Training Grant, NHGRI, University of Pennsylvania
- 2017 Student Member, Admissions Committee, University of Pennsylvania
- 2017 Student Member, Curriculum Committee, University of Pennsylvania
- 2015 2nd Place, Norris Cotton Cancer Center Poster Competition, Dartmouth
- 2015 Travel Award, Graduate Student Council Conference Grant, Dartmouth

Predoctoral/undergraduate:

- 2014 Phi Beta Kappa Honor Society Fellowship, Saint Joseph's University
- 2012 Howard Hughes Medical Institute Research Fellowship, Saint Joseph's University
- 2012 Promoted to Online Store Manager at Samzies Uniforms, Ewing, NJ
- 2010 MUSE fellowship, The College of New Jersey
- 2007 Edward J. Bloustein New Jersey Scholarship
- 2007 TCNJ Chairman of the Board Scholarship, The College of New Jersey
- 2007 National Hispanic Scholar

GRANTS AWARDED

2021 BroadIgnite Award, Broad Institute of MIT and Harvard *A deep, multi-modal characterization of a simulatedpatient reveals effective therapeutic strategies* Role: Principal Investigator

MAJOR SOFTWARE PROJECTS AND OTHER RESEARCH PRODUCTS

Cytominer Ecosystem: Open source software for image-based profiling data processing ensuring computational reproducibility. (<u>https://github.com/cytomining</u>)

BioBombe: Open source software and approaches to use unsupervised machine learning to discover novel, data-driven gene expression signatures in transcriptomics compendia. (<u>https://github.com/greenelab/biobombe</u>)

Tybalt: Open source software representing the first application of variational autoencoders to human gene expression data. (<u>https://github.com/greenelab/tybalt</u>)

Project Cognoma: Open source software and community-led project to bring machine learning algorithms to cancer biologists. (<u>http://cognoma.org/#!/home</u>)

PROFESSIONAL SOCIETY MEMBERSHIPS

The Society of Biomolecular Imaging and Informatics, 2021-Present Cancer Systems Biology Consortium, National Cancer Institute, 2021-Present CytoData Society, 2019-Present The Cancer Genome Atlas, National Cancer Institute, 2017-2018 NSF: Penn Pathfinders, University of Pennsylvania, 2015-2017 American Society for Human Genetics, 2017 International Society for Computational Biologists, 2016 American Association for Cancer Research, 2015

TEACHING EXPERIENCE

Lecturer, CPBS 7711: Methods and Tools in Biomedical Informatics, University of Colorado Anschutz, Aurora, CO, November 16, 2021

Guest lecturer, Saint Joseph's University Research Techniques, Philadelphia, PA, November, 16, 2020

Guest speaker, Hampden Sydney College, Hampden Sydney, VA, June 15, 2020

Workshop Lead, Proteome-Targeted Drug Discovery Summit Machine Learning, June 26, 2019, Boston, MA

Teaching Assistant, GCB535: Introduction to Bioinformatics, Mentored biologists with little computational training in bioinformatics applications and independent research project design. University of Pennsylvania, Spring 2018

Teaching Assistant, BIO405: Biomechanics. Saint Joseph's University, Spring 2014

Teaching Assistant, BIO407: Developmental Biology. Saint Joseph's University, Fall 2013

Teaching Assistant, BIO414: Plant Systematics. Saint Joseph's University, Spring 2013

Teaching Assistant, BIO201: Organismic Biology. Saint Joseph's University, Fall 2012

GRADUATE RESEARCH SUPERVISED

- 2021: Hillary Tsang, Master of Science in Health Data Science, Harvard T.H. Chan School of Public Health; Subsequently Bioinformatician at Watershed Informatics
- 2021: Maria Lozada, Research Associate in J.T. Neal's lab at Broad Institute of MIT and Harvard
- 2021: Adeniyi Adeboye, Master of Science in Data Science and Analytics, Grand Valley State University; Subsequently Database Engineer at Amazon
- 2020: Frances Hubis, Master of Science in Quantum Computing and Classical Learning Theory, ETH Zurich; Subsequently AI resident at Google Brain
- 2019: Ariel Hippen Anderson, PhD Genomics and Computational Biology Rotation Student, University of Pennsylvania
- 2017: Alex Lee, Ph.D. Genomics and Computational Biology Rotation Student, University of Pennsylvania
- 2014: Sarah Moss, M.A. of Biology, Saint Joseph's University; Subsequently Finance Manager at Saint Christopher's Inn

UNDERGRADUATE AND HIGH SCHOOL RESEARCH SUPERVISED

2022: Yuen Ler Chow, Intern from Brookline High School, Brookline, MA; Subsequently Undergraduate at Harvard 2020: Saketh Mynampati, Intern from Billerica High School, Billerica, MA; Subsequently Undergraduate at Harvard 2017: Amy Campbell, University of Pennsylvania Postbac from Oberlin College, Oberlin Ohio; Subsequently

Genomics and Computational Biology PhD Candidate at University of Pennsylvania

2017: Timothy Chang, Undergraduate researcher, University of Pennsylvania; Subsequently Strategic Analyst at Uber

- 2014: Stephanie Tittaferrante, Undergraduate researcher, Saint Joseph's University; Subsequently M.D. internal medicine at Temple University Hospital
- 2013: Timothy Kui, Undergraduate researcher, Saint Joseph's University; Subsequently Business Development

Associate at HSBC, Hong Kong

2013: Mechela Carnevale, Undergraduate researcher, Saint Joseph's University; Subsequently D.V.M. Andover Animal Hospital

PROFESSIONAL SERVICE

Board and advisory group membership

The Society of Biomolecular Imaging and Informatics, Board of Directors, 2021 - Present CytoData Society, Operations Officer, 2020 – Present CytoData Society, Resource Officer, 2019 – 2020 Infixion Biosciences, Scientific Advisory Board Member, 2019 – Present

Conferences organized

Workshop: Image-Based Profiling: A Powerful and Challenging New Data Type; Pacific Symposium on Biocomputing, January 3, 2022

Journal reviewer (ad-hoc) Bioinformatics

Cancer Management and Research Cell Systems Critical Reviews in Oncology/Hematology Genome Medicine Gigascience IEEE Transactions on Medical Imaging Journal of the National Cancer Institute Nature Communications Nature Methods Nature Reviews Genetics Patterns Scientific Reports PLoS Computational Biology PLoS One

INVITED LECTURES

Vanderbilt, Quantitative Systems Biology Center, Nov 3, 2021, Nashville, TN Inzen Therapeutics Invited Seminar, July 6, 2021, Cambridge, MA Broad Institute of MIT and Harvard Seminar in Gad Getz Lab Meeting, March 4, 2021, Cambridge, MA Dependency Map Consortium Symposium, Nov 2, 2020, Cambridge, MA Cytodata Conference 2020 (Virtual), Oct 21, 2020, Salt Lake City, UT RIDGE Meeting, Broad Institute of MIT and Harvard, July 10, 2020 Pfizer Cell Painting Consortium, April 10, 2020, Cambridge, MA Broad Institute of MIT and Harvard Seminar in Paquita Vazquez Group Meeting, Feb 10, 2020, Cambridge, MA Models, Inference and Algorithms, Broad Institute of MIT and Harvard, Oct 2, 2019, Cambridge, MA University of California San Francisco Seminar at Arun Wiita Lab Meeting, Aug 9, 2018, San Francisco, CA Genentech Seminar, August 2018, South San Francisco, CA

CONFERENCE TALKS

Rocky Mountain Bioinformatics Conference, Dec 3, 2021, Snowmass CO

Cytodata Conference 2020, Oct 22, 2020, Salt Lake City, UT Open Science Symposium, Carnegie Mellon University, Nov 7, 2019, Pittsburgh, PA Cytodata Conference Open Science Workshop, Oct 27, 2019, Heidelberg, Germany Collaborative Computational Tools for the Human Cell Atlas, Chan-Zuckerberg Initiative, Apr 24, 2018, Aptos, CA Pacific Symposium on Biocomputing, Jan 4, 2017, Big Island, HI Computational Systems for Integrative Genomics, April 4, 2016, Philadelphia, PA Rocky Mountain Bioinformatics Conference, Dec 10, 2015, Snowmass CO

PUBLICATIONS

Google Scholar page (with citation metrics):

https://scholar.google.com/citations?user=iDKZaA4AAAJ&hl=en

(h-index = 17; total citations = >3,200)

31. **Way, G.P.***, Natoli, T.*, Adeboye, A.*, Litichevskiy, L., Yang, A.X., Lu, X., Caicedo, J., Cimini, B.C., Karhohs, K., Logan, D.J., Rohban, M., Kost-Alimova, M., Hartland, K., Bornholdt, M., Chandrasekaran, N., Haghighi, M., Singh, S., Subramanian, A., Carpenter A.E., (2021) Morphology and gene expression profiling provide complementary information for mapping cell state. *bioRxiv*: https://doi.org/10.1101/2021.10.21.465335 (Research Article; preprint)

30. Chow Y., Singh, S., Carpenter, A.E., **Way, G.P.** (2021) Predicting drug polypharmacology from cell morphology readouts using variational autoencoder latent space arithmetic. *bioRxiv*: https://doi.org/10.1101/2021.09.02.458673 (Research Article; preprint)

29. **Way, G.P.**, Greene, C.S., Carninci, P., Carvalho, B.S., de Hoon, M., Finley, S., Gosline, S.J.C., Lê Cao, K., Lee, J.S.H., Marchionni, L., Robine, N., Sindi, S.S., Theis, F.J., Yang, J.Y.H., Carpenter, A.E., Fertig E.J. (2021). A field guide to cultivating computational biology. *PLoS Biology* 19 (10), PMID: 34618807 (Essay)

28. Wilson, S.L., **Way, G.P.**, Bittremieux, W., Armache, J.P., Haendel, M.A., Hoffman, M.M. (2021). Sharing biological data: why, when, and how. *FEBS Letters* 595 (7), 847-863, PMID: 33843054. (Review Article)

27. Way, G.P.*, Kost-Alimova, M.*, Shibue, T., Harrington, W.F., Gill, S., Piccioni, F., Becker, T., Hahn, W.C., Carpenter, A.E., Vazquez, F., Singh, S. (2021) Predicting cell health phenotypes using image-based morphology profiling. *Molecular Biology of the Cell* E20-12-0784, PMID: 33534641. *Co-First Authors (Research Article)

26. Cousminer, D.L., Wagley, Y., Pippin, J., Elhakeem, A., **Way, G.P.,** McCormack, S., Chesi, A., Mitchell, J., Kindler, J., Baird, D., Hartley, A., Howe, L.D., Kalkwarf, H., Lappe, J., Lu, S., Leonard, M., Johnson, M., Hakonarson, H., Gilsanz, V., Shepherd, J., Oberfield, S., Greene, C., Kelly, A., Lawlor, D., Voight, B.F., Wells, A., Zemel, B., Hankenson, K., Grant S. (2021). Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual through variant-to-gene mapping. *Genome Biology* 22 (1), 1-32, PMID: 33397451 (Research Article)

25. **Way, G.P.**, Zietz, M., Rubinetti, V., Himmelstein, D.S., Greene, C.S. (2020) Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. *Genome Biology* 21, 109. PMID: 32393369 (Research Article)

24. Upton, K., Modi, A., Patel, K., Kendersersky, N.M., Conkrite, K.L., Sussman, R.T., **Way, G.P.**, Adams, R.N., Sacks, G.I., Fortina, P., Diskin, S.J., Maris, J.M., Rokita, J.L. (2020) Epigenomic profiling of neuroblastoma cell lines. *Scientific Data*. 7 (1), 1-13. PMID: 32286315 (Research Article)

23. Cousminer, D.L., Wells, A., Wagley, Y., Hankenson, K., **Way, G.P.,** Greene, C., Voight, B., McCormack, S., Chesi, A., Mitchell, J., Kindler, J., Johnson, M., Pippin, J., Hakonarson, H., Zemel, B., Grant, S., Kalkwarf, H., Lappe, J., Gilsanz, V., Shepherd, J., Oberfield S., (2019) Longitudinal genome-wide association study implicates novel loci and candidate genes for pediatric bone accrual. *Journal of Bone and Mineral Research* 34, 5-5

22. Lin, Y.T., **Way, G.P.**, Barwick, B.G., Mariano, M.C., Marcoulis, M., Ferguson, I.D., Driessen, C., Boise, L.H., Greene, C.S., Wiita, A.P., (2019) Integrated Phosphoproteomics and Transcriptional Classifiers Reveal Hidden RAS Signaling Dynamics in Multiple Myeloma. *Blood Advances.* 3 (32): 3214-3227. PMID: 31698452 (Research Article)

21. Martinez-Lage, M., Lynch, T.M., Bi, Y.*, Cocito, C.*, **Way, G.P.***, Pal, S., Haller, J., Yan, R.E., Ziober, A., Nguyen, A., Kandpal, M., O'Rourke, D.M., Greenfield, J.P., Greene, C.S., Davuluri, R.V., Dahmane, N. (2019) Immune landscapes associated with different glioblastoma molecular subtypes. *Acta Neuropathologica Communications*. 7 (1): 1-12. PMID: 31815646 (Research Article) *Co-Second Authors (Research Article)

Rokita, J.L., Rathi, K.S., Cardenas, M.F., Upton, K.A., Jayaseelan, J., Cross, K.L., Pfeil, J., Egolf, L.E., Way, G.P. Farrel, A., Kendsersky, N.M., Patel, K., Gaonkar, K.S., Modi, A., Berko, E.R., Lopez, G., Vaksman, Z., Mayoh, C., Nance, J., McCoy, K., Haber, M., Evans, K., McCalmont, H., Bendak, K., Böhm, J.W., Marshall, G.M., Tyrrell, V., Kalletla, K., Braun, F.K., Qi, L., Du, Y., Zhang, H., Lindsay, H.B., Zhao, S., Shu, J., Baxter, P., Morton, C., Kurmashev, D., Zheng, S., Chen, Y., Bowen, J., Bryan, A.C., Leraas, K.M., Coppens, S.E., Doddapaneni, H.V., Momin, Z., Zhang, W., Sacks, G.I., Hart, L.S., Krytska, K., Mosse, Y.P., Gatto, G.J., Sanchez, Y., Greene, C.S., Diskin, S.J., Vaske, O.M., Haussler, D., Gastier-Foster, J.M., Kolb, E.A., Gorlick, R., Li, X.N., Reynolds, C.P., Kurmasheva, R.T., Houghton, P.J., Smith, M.A., Lock, R.B., Raman, P., Wheeler, D.A., Maris, J.M. (2019) Genomic profiling of childhood tumor patient-derived xenograft models to enable rational clinical trial design. *Cell Reports*. 29 (6), 1675-1689. PMID: 31693904 (Research Article)

19. Way, G.P., Greene, C.S. (2019) Discovering pathway and cell-type signatures in transcriptomic compendia with machine learning. *Annual Review of BiomedicalData Science*. 2, 1-17. (Review Article)

18. **Way, G.P.**, Sanchez-Vega, F. La, K. Armenia, J. Chatila, W.K., Luna, A. Sander, C., Cherniack, A.D., Mina, M, Ciriello, G., Schultz, N. The Cancer Genome Atlas Research Network, Sanchez, Y., Greene, C.S. (2018) Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*. Apr 3;23(1):172-180.e3. PMID: 29617658 (Research Article)

17. **Way, G.P.**, Greene, C.S. (2018) Extracting a Biologically Relevant Latent Space from Cancer Transcriptomes with Variational Autoencoders. *Pacific Symposium on Biocomputing*. 23:80-91. PMID: 29218871 (Research Article)

16. **Way, G.P.**, Greene, C.S. (2018) Bayesian deep learning for single-cell analysis. *Nature Methods*. 15 (12), 1009-1010. PMID: 30504887 (Review)

15. Ching, T., Himmelstein, D.S., Beaulieu-Jones, B.K., Kalinin, A.A., Do, B.T., **Way, G.P.+**, Ferrero, E., Agapow, P., Xie, W., Rosen, G.L., Lengerich, B.J., Israeli, J., Lanchantin, J., Woloszynek, S., Carpenter, A.E., Shrikumar, A., Xu, J., Cofer, E.M., Harris, D.J., DeCaprio, D., Qi, Y., Kundaje, A., Peng, Y., Wiley, L.K., Segler, M.H.S., Gitter, A., Greene, C.S. (2018) Opportunities And Obstacles For Deep Learning In Biology And Medicine. *Journal of the Royal Society Interface*. Apr;15(141). PMID: 29618526 (Review) +Randomized author order

14. Knijnenburg T.A., Wang L., Zimmermann M.T., Chambwe N., Gao G.F., Cherniack A.D., Fan H., Shen H., **Way G.P.**, Greene C.S., Liu Y., Akbani R., Feng B., Donehower L.A., Miller C., Shen Y., Karimi M., Chen H., Kim P., Jia P., Shinbrot E., Zhang S., Liu J., Hu H., Bailey M.H., Yau C., Wolf D., Zhao Z., Weinstein J.N., Li L., Ding L., Mills G.B., Laird P.W., Wheeler D.A., Shmulevich I., Cancer Genome Atlas Research Network, Monnat R.J.,

Xiao Y., Wang C. (2018) Genomic and molecular landscape of DNA damage repair deficiency across The Cancer Genome Atlas. *Cell Reports* 23 (1), 239-254. e6. PMID: 29617664 (Research Article)

13. Sanchez-Vega F., Mina M., Armenia J., Chatila W.K., Luna A., La K.C., Dimitriadoy S., Liu D.L., Kantheti H.S., Saghafinia S., Chakravarty D., Daian F., Gao Q., Bailey M.H., Liang W.W., Foltz S.M., Shmulevich I., Ding L., Heins Z., Ochoa A., Gross B., Gao J., Zhang H., Kundra R., Kandoth C., Bahceci I., Dervishi L., Dogrusoz U., Zhou W., Shen H., Laird P.W., **Way G.P.**, Greene C.S., Liang H., Xiao Y., Wang C., Iavarone A., Berger A.H., Bivona T.G., Lazar A.J., Hammer G.D., Giordano T., Kwong L.N., McArthur G., Huang C., Tward A.D., Frederick M.J., McCormick F., Meyerson M., Cancer Genome Atlas Research Network, Van Allen E.M., Cherniack A.D., Ciriello G., Sander C., Schultz N. (2018) Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell* 173 (2), 321-337. e10. PMID: 29625050 (Research Article)

12. Chen K.M., Tan J, **Way G.P.**, Doing G, Hogan D.A., Greene C.S. (2018) PathCORE-T: identifying and visualizing globally co-occurring pathways in large transcriptomic compendia. *BioData mining* 11 (1), 14. PMID: 29988723 (Research Article)

11. Harrington, L.X., **Way, G.P.**, Doherty, J.A., Greene, C.S. (2018) Functional network community detection can disaggregate and filter multiple underlying pathways in enrichment analyses. *Pacific Symposium on Biocomputing*. 23:157-167. PMID: 29218878 (Research Article)

10. **Way, G.P.***, Allaway, R.J.*, Bouley, S.J., Fadul, C.E., Sanchez, Y., Greene, C.S. (2017) A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. *BMC Genomics*. BMC genomics 18 (1), 1-11. PMID: 28166733 (Research Article) *Co-First Authors

9. **Way, G.P.**, Youngstrom, D.W., Hankenson, K.D., Greene, C.S., Grant, S.F.A. (2017) Implicating candidate genes at GWAS signals by leveraging topologically associating domains. *European Journal of Human Genetics*.25 (11), 1286-1289 PMID: 28792001 (Research Article)

8. Titus, A.J.*, **Way, G.P.***, Johnson, K.C., Christensen, B.C. (2017) Deconvolution of DNA methylation identifies differentially methylated gene regions on 1p36 across breast cancer subtypes. *Scientific Reports*. 7 (1) PMID: 28912426 (Research Article) *Co-First Authors

7. **Way, G.P.**, Greene C.S. (2017) Evaluating deep variational autoencoders trained on pan-cancer gene expression. **arXiv** preprint arXiv:1711.04828 (Research Article - Not Peer Reviewed).

6. Doherty, J.A., Peres, L.C., Wang, C., **Way, G.P.**, Greene, C.S., Schildkraut, J.M. (2017) Challenges and Opportunities in Studying the Epidemiology of Ovarian Cancer Subtypes. *Current Epidemiology Reports*. Current epidemiology reports 4 (3), 211-220. PMID: 29226065 (Review)

5. **Way, G.P.**, Rudd, J., Wang, C., Hamidi, H., Fidley, B.L., Konecny, G.E., Goode, E.L., Greene, C.S., Doherty, J.A. (2016) Cross-population analysis of high-grade serous ovarian cancer reveals only two robust subtypes. *G3: Genes, Genomes, Genetics.* 6 (12), 4097-4103. PMID: 27729437 (Research Article)

4. **Way, G.P.**, Southwell, M., McRobert, S.P. (2016) Boldness, aggression, and shoaling assays for zebrafish behavioral syndromes. *JoVE (Journal of VisualizedExperiments)*, e54049. PMID: 27684060 (Visual Review Article)

3. Moss, S., Tittaferrante, S., **Way, G.P.**, Fuller, A., Sullivan, N., Ruhl, N., McRobert. S.P. (2015) Interactions between aggression, boldness and shoaling within a brood of convict cichlids (Amatitlania nigrofasciatus). *Behavioural Processes,* 121, 63-69. PMID: 26497098 (Research Article)

2. Way, G.P., Ruhl, N., Snekser, J.L., Kiesel, A.L., McRobert, S.P. (2015) A comparison of methodologies to test aggression in zebrafish. *Zebrafish* 12 (2), 144-151. PMID: 25621988 (Research Article)

1. **Way, G.P.**, Kiesel, A.L., Ruhl, N., Snekser, J.L, McRobert, S.P. (2015) Sex differences in a shoaling-boldness behavioral syndrome, but no link with aggression. *Behavioral Processes*, 113: 7-12. PMID: 25562194 (Research Article)