

# SHELLY A. TRIGG, Ph.D.

(339) 368-0029 • shellywanamaker@gmail.com • ORCID ID: 0000-0001-6904-4149 • <https://shellytrigg.github.io>  
University of Washington School of Aquatic and Fishery Sciences, 1122 NE Boat Street Room 234, Seattle, WA 98105

## SUMMARY OF QUALIFICATIONS

- Systems Biologist/Genomicist with 10+ years of experience and an established record of scientific contribution to the fields of plant and marine animal genomics
- Experienced in developing and optimizing innovative assays using a broad range of approaches and techniques to elucidate molecular pathways underlying organism health
- Experienced in written and oral communication to various audiences through technical reports, peer reviewed scientific journal articles, public presentations, and community outreach
- Demonstrated abilities to collaborate and take leadership through team and project management, and volunteer activities with government agencies, tribal organizations, commercial fisheries, and non-profit institutions

## EXPERIENCE

### University of Washington School of Aquatic and Fishery Sciences, Seattle, WA

Postdoctoral Research Associate.....Sept 2018 - Present

Advisor: Steven Roberts, Ph.D.

- Assess epigenetic variation and identify epigenetic marks that differ within Atlantic salmon and Pacific geoduck clam populations exposed to different environmental conditions through analyzing and interpreting genome-wide methylation bisulfite sequencing data
- Develop a qPCR assay to assess reproductive development of Pacific geoduck exposed to different seawater pH using non-lethal, temporally-collected hemolymph samples
- Identify and interpret temporal proteome variation in metamorphosing Pacific oysters exposed to different temperatures
- Assess resilience in pteropods to low oxygen and pH conditions through survival, development, and metabolomics analysis
- Lead cooperative field, hatchery, and laboratory research in collaboration with Jamestown-S'klallam Tribe Fisheries Division, Taylor Shellfish Hatchery, and NOAA NWFSC Conservation Biology Division

### NOAA Northwest Fisheries Science Center, Conservation Biology, Seattle, WA

NSF Graduate Research Internship Program Fellow.....Jun 2017 - May 2018

Advisors: Krista Nichols Ph.D. and Paul McElhany Ph.D.

- Assess physiological impacts of ocean acidification on Dungeness crabs through metabolomics analysis
- Develop and implement bioinformatics pipelines for analyzing complex metabolomics data sets from differentially conditioned Dungeness crabs
- Carried out time-course high throughput laboratory ocean acidification exposure experiments on Dungeness crab larvae
- Did field collection and laboratory rearing of Dungeness crab larvae, juveniles and adults

### Salk Institute for Biological Studies, Ecker Lab, Genomic Analysis Section, La Jolla, CA

Graduate Student Researcher .....Aug 2013 - Sept 2018

Research Assistant II .....Jul 2012 - Aug 2013

Research Assistant I .....Nov 2011 - Jun 2012

Ph.D. dissertation: High-resolution molecular networks from novel 'omics' approaches elucidate survival strategies in organisms from land to sea

Advisor: Joseph Ecker, Ph.D.

- Developed a DNA sequencing assay (CrY2H-seq) for high throughput protein-protein interaction mapping and coded a bioinformatics analysis pipeline to identify and quantify interactions from large sequence datasets
- Performed network simulations for observed network validation

- Generated model predictions to evaluate assay performance
- Performed quality control, network analysis, data integration, and functional analysis to interpret biological significance of protein interaction networks
- Generated comprehensive protein-protein interactome map for Arabidopsis thaliana using CrY2H-seq to iteratively screen billions of interactions en masse
- Did high throughput engineering of thousands of expression clones

### **Dana Farber Cancer Institute, Center for Cancer Systems Biology, Vidal Lab, Boston, MA**

Research Technician I .....Aug 2010 - Oct 2011

Research Trainee .....Jan 2010 - Aug 2010

- Generated comprehensive human protein-protein interactome map from high throughput yeast two-hybrid screening, protein complementation assay, and well-nucleic-acid-programmable-protein-array assay
- Developed a high throughput well-nucleic-acid-programmable-protein-array validation assay
- Generated protein-protein interactome map from high throughput yeast two-hybrid screening of autism genes and isoforms against a human ORFeome
- Constructed clone collections of Kaposi's Sarcoma and Epstein-Barr viral genes by high throughput gateway cloning for yeast two-hybrid screening against a human ORFeome to further define potential cancer driver and passenger proteins

### **Simmons College, Department of Chemistry, Roecklein-Canfield Lab, Boston, MA**

Undergraduate Researcher.....July 2009 - June 2010

B.S. Honors Thesis: The effectiveness of the GST fusion system for isolating Epstein-Barr viral thymidine kinase, a potential target for antiviral antitumor therapies.

- Developed and optimized a GST immunoprecipitation assay for isolation of Epstein-Barr viral proteins

## **EDUCATION**

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Ph.D. in Biological Sciences.....Sept 2018

University of California San Diego, La Jolla, CA

B.S. in Biochemistry.....May 2010

Magna Cum Laude and honors thesis, Simmons College, Boston, MA

## **TECHNICAL SKILLS AND TRAINING**

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**Molecular and Cellular Biology:** Illumina and Oxford Nanopore DNA sequencing, whole genome, RNAseq and Bisulfite sequencing library preparation, PCR, qPCR, oligo design, ELISA, immuno-blotting and precipitation, recombinant DNA techniques, nucleic acid and protein purification, cell culture and transfection, histological techniques

**Marine Biology:** respirometry measurement with PreSens equipment, animal rearing systems design, construction and implementation, seawater chemistry analysis

**Laboratory Automation:** Tecan liquid handling robots and plate readers

**Computation:** Genomics, epigenomics, proteomics, and metabolomics data analysis, data reduction and integration, molecular network analysis (Cytoscape, Qiagen IPA), Linux environment familiarity, Bash and Python/Jupyter scripting, R, data management, supercomputing, GitHub (<https://github.com/shellytrigg>), Slack, Google Suite applications, Microsoft Office applications

**Training:** LC-MS Data processing and statistics course, UC Davis (Jan 2018); Visiting Scientist Network Analysis Training Program, Broad Institute (Jan-Feb 2016); NSF Graduate Data Science Workshop, University of Washington (Aug 2015); Biostatistics Refresher Course, UC San Diego (Aug 2015); Software Carpentry, Salk Institute (Jun 2013, Jan 2014); Tecan EVO Training Course (Aug 2012)

## LEADERSHIP ACTIVITIES

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### Management:

- Trained, supervised, and managed 4 research assistants, 2 technicians, and 8 students from various backgrounds
- Mentored 2 graduate students at UC San Diego, 2 undergraduate and 3 graduate students at University of Washington, and 1 undergraduate student at NOAA NW Fishery Science Center

### Committees:

- Postdoctoral representative of UW SAFS Communications Committee, 2018 - present
- Chair of UC San Diego Biology Department Peer Mentoring Committee, 2015-2016
- Chair of UC San Diego Quantitative Biology graduate seminar series, 2015-2016
- Member of the Salk Institute Partnerships in Science committee 2014-2016
- Member of UC San Diego STEM Education and Diversity group 2014-2016
- Member of Association of Women in Science San Diego Outreach Committee, 2012-2016

## PUBLICATIONS

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Shelly A. Trigg, P McElhany, M Maher, D Perez, DS Busch, and KM Nichols. (2019) Uncovering mechanisms of global ocean change effects on Dungeness crab (*Cancer magister*) through metabolomics analysis. **Scientific Reports**. <https://doi.org/10.1101/574798>.

Shelly A. Trigg, RM Garza, A MacWilliams, JR Nery, A Bartlett, R Castanon, A Goubil, J Feeney, R O'Malley, SC Huang, ZZ Zhang, M Galli, and JR Ecker (2017) CrY2H-seq: a massively multiplexed assay for deep coverage interactome mapping. **Nature Methods**. 14(8):819-825.

Shelly A. Trigg, RM Garza, A MacWilliams, JR Nery, A Bartlett, R Castanon, A Goubil, J Feeney, R O'Malley, SC Huang, ZZ Zhang, M Galli, and JR Ecker (2017) CrY2H-seq interactome screening. **Protocol Exchange**. doi:10.1038/protex.2017.058.

X Yang, [15 others], Shelly A. Trigg, [20 others], and M Vidal. (2016) Widespread expansion of protein interaction capabilities by alternative splicing. **Cell**. 164(4):805-817.

T Rolland, [53 others], Shelly A. Trigg, [14 others], and M Vidal. (2014) A proteome-scale map of the human interactome network. **Cell**. 159(5):1212-1226.

R Corominas, [8 others], Shelly A. Trigg, [18 others], M Vidal, and LM Iakoucheva. (2014) Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. **Nature communications**. 5:3650.

Rozenblatt-Rosen, [36 others], Shelly Wanamaker, [13 others], and M Vidal. (2012) Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. **Nature**. 487(7408):491-495.

## MANUSCRIPTS IN PREPARATION/REVIEW

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Shelly A. Trigg, KM Mitchell, R Elliot, B Eudeline, B Vadopalas, EB Timmins-Schiffman, SB Roberts. (2020) Temporal proteomic profiling reveals insight into critical developmental processes and temperature-influenced physiological response differences in a bivalve mollusc. <https://doi.org/10.1101/2020.06.05.137059>. (In review, **BMC Genomics**)

Shelly A. Trigg, G Nunez-Acuna, V Valenzuela-Munoz, D Valenzuela-Miranda, C Gallardo-Escárate, and SB Roberts. (2020) Epigenomic and transcriptomic relationships in Atlantic salmon infested with sea lice under a changing environment. (In preparation)

Shelly A. Trigg, DS Busch, P McElhany, M Maher, D Perez, C O'Brien, and KM Nichols. (2020) Searching for signs of resilience in over-wintering juvenile pteropods to ocean acidification and deoxygenation. (In preparation)

HM Putnam, Shelly A. Trigg, SJ White, LH Spencer, B Vadopalas, A Natarajan, J Hetzel, E Jaeger, J Soohoo, C Gallardo-Escárate, FW Goetz, and SB Roberts. (2020) Environmental memory through dynamic DNA methylation provides acclimatization of geoduck clams to ocean acidification. (*In preparation*)

## **SELECT CONFERENCE PRESENTATIONS (5 of 20)**

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Shelly A. Trigg. (Apr 2020) Searching for signs of resilience in over-wintering juvenile pteropods to ocean acidification and deoxygenation. NOAA Northwest Fisheries Science Center Science Symposium 2020, talk. <https://doi.org/10.6084/m9.figshare.12440192.v1>

Shelly A. Trigg. (Jan 2020) Influence of ocean acidification on DNA methylation patterns in geoduck clams. Plant and Animal Genome Conference XXVIII, San Diego, CA, talk. <https://github.com/shellytrigg/talk-pag2020>.  
**Recipient of PAG XXVIII USDA NRSP8 Aquaculture Travel Grant.**

Shelly A. Trigg. (Nov 2019) Environmental influence on the Atlantic salmon epigenome during sea lice infestation. International Conference on Integrative Salmonid Biology, Edinburgh, UK, talk. <https://doi.org/10.6084/m9.figshare.10882775.v1>. **Recipient of University of Washington College of the Environment Travel Award.**

Shelly A. Trigg. (Sept 2019) A protein inventory reveals mechanisms of temperature impact on oyster development. Pacific Coast Shellfish Growers Association 2019 Conference, Portland, OR, talk. <https://doi.org/10.6084/m9.figshare.11839359.v1>

Shelly A. Trigg, P McElhany, M Maher, D Perez, DS Busch, and KM Nichols. (May 2019) What happens to Dungeness crab in high CO<sub>2</sub>: experiments and questions. 2019 WOAC Ocean Acidification Science Symposium, Seattle, WA, talk and poster. **Invited speaker.**

## **GRANTS AND FELLOWSHIPS**

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USDA NRSP8 Small Funding Award (\$10K), 2020

USDA NRSP8 PAGXXVIII Aquaculture Travel Award (\$1K), 2020

UW Data Science Postdoctoral Fellowship (\$7K), 2019 - present

UW College of the Environment Travel Award (\$1K), 2019

NSF GRIP Fellowship with NOAA Northwest Fisheries Science Center (\$5K), 2017- 2018

NSF PAMP EAGER: Using novel, clone-free sequencing methods to discover host-microbe protein-protein interactions (Co-authors: Shelly Trigg, Paulo Teixeira, Jeff Dangl (CO-PI), and Joseph Ecker (CO-PI); \$300K), 2016

NSF Graduate Research Fellowship (\$138K), 2014-2018