BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors. Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: William Browne

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Associate Professor

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
University of Chicago, Chicago, Illinois, United States	BA	05/1994	Biological Sciences
University of Chicago, Chicago, Illinois, United States	PHD	03/2003	Molecular Genetics and Cell Biology
Kewalo Marine Laboratory, University of Hawaii, Honolulu, Hawaii, United States	NSF Postdoctoral Fellow	2003-2006	Developmental & Evolutionary Biology
Kewalo Marine Laboratory, University of Hawaii, Honolulu, Hawaii, United States	NAS/NRC Postdoctoral Fellow	2006-2007	Developmental & Evolutionary Biology

A. Personal Statement

Among marine phyla, ctenophores or "comb jellies", represent the most ancient branch of the animal tree of life. The emergence of immunity, the ability to recognize self vs nonself, is integral to the evolution of animal multicellularity. The innate immune system, which includes immune cells and inflammatory molecules, represents the first line of defense against invading pathogens and plays a central role in initiating repair of tissue damage and also protection against tumorigenicity. In humans, the dysregulation of innate immune responses is causally associated with chronic inflammatory diseases and autoimmune disorders. We use the model ctenophore, *Mnemiopsis leidvi*, to shed light on the early evolution of innate immunity in animals by applying molecular genetic, cell biological and whole organism experimental approaches. Our work characterizing immune cells and their responses to pathogens seeks to reveal both conserved and novel aspects of pathogen defense mechanisms and immune cell type specification. For example, our recent work identified ETosis as a deeply conserved metazoan defense against pathogens. Mnemiopsis habitat includes warm water harbors and estuaries that are often polluted with highly pathogenic microbes, including choleragenic and flesh-eating forms of zoonotic gram-negative Vibrio, significant E. coli exposure, and pathogenic marine fungal species. Characterization of novel *Mnemiopsis* immune cell responses to coastal waterborne microbial pathogens may inform AMP based antibiotic/antimicrobial design, with potential therapeutic applications.

B. Positions, Scientific Appointments, and Honors

- 2009 present Associate Professor, University of Miami, Coral Gables, Florida, United States
- 2021 present Adjunct Professor, Rosenstiel School of Marine and Atmospheric Science, University of Miami, Miami, Florida, United States
- 2011 present Research Collaborator, Smithsonian Institution National Museum of Natural History, Washington DC, District of Columbia, United States
- 2007 2009 Assistant Researcher, Kewalo Marine Laboratory, University of Hawaii, Honolulu, Hawaii, United States

- 2006 2007 NAS/NRC Postdoctoral Fellow, Kewalo Marine Laboratory, University of Hawaii, Honolulu, Hawaii, United States
- 2003 2006 NSF Postdoctoral Fellow, Kewalo Marine Laboratory, University of Hawaii, Honolulu, Hawaii, United States

C. Closely Related Contributions

- Vandepas, L. E., Stefani, C., Domeier, P. P., Traylor-Knowles, N., Goetz, R. W., Browne, W. E., Lacy-Hulbert, A.. (2024) Extracellular DNA traps in a ctenophore demonstrate immune cell behaviors present in a non-bilaterian. *Nature Communications* 15, 2990. <u>https://doi.org/10.1038/s41467-024-46807-6</u>
- 2) Boohar, R. T., Vandepas, L. E., Traylor-Knowles, N., Browne, W. E. (2023) Phylogenetic and protein structure analyses provide insight into the evolution and diversification of the CD36 domain "apex" among scavenger receptor class B proteins across Eukarya. *Genome Biology and Evolution* 15 evad218. <u>https://doi.org/10.1093/gbe/evad218</u>
- Dieter A.C., True, A.B.K., Gilbertson, E.A., Snyder, G., Lacy-Hulbert, A., Traylor-Knowles, N., Browne, W. E., Vandepas, L. E.. (2023) Flow cytometry methods for targeted isolation of ctenophore cells. *Frontiers in Marine Science* 10:1276041. <u>https://doi.org/10.3389/fmars.2023.1276041</u>
- 4) Presnell, J. S., Bubel, M., Knowles, T., Patry, W., Browne, W. E.. (2022) Multigenerational laboratory culture of pelagic ctenophores and CRISPR/Cas9 genome editing in the lobate, *Mnemiopsis leidyi*. *Nature Protocols* 17, 1868-1900. <u>https://doi.org/10.1038/s41596-022-00702-w</u>
- 5) Dieter A.C., Vandepas L.E., Browne W.E. (2022) Isolation and maintenance of in vitro cell cultures from the ctenophore *Mnemiopsis leidyi*. In: Blanchoud S., Galliot B. (eds) *Whole-Body Regeneration. Methods in Molecular Biology*, vol 2450, 347-358. Humana, New York, NY. <u>https://doi.org/10.1007/978-1-0716-2172-</u> <u>1_18</u>
- 6) Presnell, J. S., Browne, W. E.. (2021) Krüppel-like factor gene function in the ctenophore Mnemiopsis leidyi assessed by CRISPR/Cas9-mediated genome editing. Development 148, dev199771. <u>https://doi.org/10.1242/dev.199771</u>
- Traylor-Knowles N., Vandepas, L. E., Browne, W. E.. (2019) Still enigmatic: innate immunity in *Mnemiopsis* leidyi. Integrative and Comparative Biology 59, 811-818. <u>https://doi.org/10.1093/icb/icz116</u>
- Vandepas, L. E., Warren, K. J., Amemiya, C. T., Browne, W. E. (2017) Establishing and maintaining primary cell cultures from the ctenophore *Mnemioposis leidyi*. *Journal of Experimental Biology* 220, 1197-1201. <u>http://dx.doi.org/10.1242/jeb.152371</u>
- 9) Presnell, J. S., Vandepas, L. E., Warren, K. J., Swalla, B. J., Amemiya, C. T., Browne, W. E. (2016) The presence of a functionally tripartite through-gut in Ctenophora has implications for metazoan character trait evolution. *Current Biology*, 26, 2814-2820. <u>http://dx.doi.org/10.1016/j.cub.2016.08.019</u>
- Presnell, J. S., Schnitzler, C. E., Browne, W. E.. (2015) KLF/SP transcription factor family evolution: expansion, diversification, and innovation in the Eukaryota. *Genome Biology and Evolution* 7, 2289-2309. <u>http://dx.doi.org/10.1093/gbe/evv141</u>