

**JOSEPH F. RYAN, Ph.D.**  
Associate Professor of Biology



I am a bioinformatician trained in evolutionary genomics. I received a bachelor's degree in computer science from University of Maryland University College, and a Ph.D. in bioinformatics at Boston University. I completed a postdoc at the National Human Genome Research Institute and a second postdoc at the Sars International Centre for Marine Molecular Biology in Norway.

I joined the Whitney Laboratory as an Assistant Professor in 2014 and received tenure and promotion to Associate professor in 2020. My laboratory focuses on applying phylogenetics and genomics to fundamental questions in animal biology to understand the evolution of biodiversity. Emphasis is currently on: (1) understanding the nervous system of ctenophores, (2) understanding the biogeography of *Mnemiopsis* ctenophores, (3) genomic sequencing, annotation, and analyses of many invertebrate genomes including ctenophores, cnidarians, sea cucumbers, bryozoans, and doliolids, and (4) regeneration in ctenophores.

My laboratory currently consists of one senior researcher Yuriy Bobkov, Ph.D. (1/2 time shared with Strother Laboratory), two postdocs Remi Ketchum, Ph.D. and Adolfo Lara, Ph.D., one Ph.D. student Natalia Padillo (UF Genetics and Genomics) and one undergraduate researcher Nina Castillo (UF Biology).

I continue to participate in Whitney Lab's IDEA Committee. IDEA conducted the second ever climate survey in March 2022 and engaged the community and administration based on trends that were evident from the survey. I continue to serve as the co-faculty adviser to the University of Florida's chapter of the Society for Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS).

**Education:**

2001-2007	Boston University, Boston, MA Ph.D. in Bioinformatics (with John Finnerty, Ph.D. & Andreas Baxevanis, Ph.D.)
2001	University of Maryland University College, Adelphi, MD B.S. in Computer Science

**Professional Experience:**

2020-present	Associate Professor, Whitney Laboratory for Marine Bioscience, St Augustine, FL
2014-2020	Assistant Professor, Whitney Laboratory for Marine Bioscience, St Augustine, FL
2011-2013	Postdoctoral Fellow, Sars International Centre for Marine Molecular Biology, Bergen, Norway. (with Andreas Hejnol, Ph.D.)
2007-2011	Postdoctoral Fellow, National Human Genome Research Institute/NIH, Bethesda, MD (with Andreas Baxevanis, Ph.D.)
1996-2001	Bioinformatics Software Programmer, National Human Genome Research Institute/NIH, Bethesda, MD

**Research Interests:**

- Evolutionary genomics
- Marine invertebrate zoology
- Biodiversity
- Phylogenetics
- Embryology
- Neurobiology
- Ecology

### Membership in Professional Societies:

- Society for Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS)
- Society for Systematic Biology
- Society for Integrative and Comparative Biology
- Society for Ctenophorology

### Recent Publications (2011-2022):

Ketchum, R.N., Davidson, P.L., Smith, E.G., Wray, G.A., Burt, J.A., **Ryan, J.F.**, Reitzel, A.M. 2022. A chromosome-level genome assembly of the highly heterozygous sea urchin *Echinometra* sp. *EZ* reveals adaptation in the regulatory regions of stress response genes. *Genome Biology and Evolution*, doi:10.1093/gbe/evac144

Tekle, Y.I., Wang, F., Tran, H., Hayes, D., **Ryan, J.F.** 2022. The Draft Genome of *Cochliopodium minus* reveals a complete meiosis toolkit and provides insight into the evolution of sexual mechanisms in Amoebozoa. *Scientific Reports*. doi:10.1038/s41598-022-14131-y

Santander, M.D., Maronna, M.M., **Ryan, J.F.**, da Silva, S.C. 2022. The state of Medusozoa genomics: current evidence and future challenges. *GigaScience*. doi:10.1093/gigascience/giac036

Babonis, L.S., Enjolras, C., **Ryan, J.F.**, Martindale, M.Q. 2022. A novel regulatory gene promotes novel cell fate by suppressing ancestral fate in the sea anemone *Nematostella vectensis*. *Proceedings of the National Academy of Sciences*. doi:10.1073/pnas.2113701119

Almazan, E.M.P., **Ryan, J.F.**, Rouhana, L. 2021. Regeneration of planarian auricles and reestablishment of chemotactic ability. *Frontier in Cell and Developmental Biology*. doi:10.3389/fcell.2021.777951

Hernandez, A.M., **Ryan, J.F.** 2021. Six-state Amino Acid Recoding is not an Effective Strategy to Offset Compositional Heterogeneity and Saturation in Phylogenetic Analyses. *Society of Systematic Biologists*. doi:10.1093/sysbio/syab027

Medina-Feliciano, J.G., Pirro, S., Garcia-Arraras, J.E., Mashanov, V., **Ryan, J.F.** 2021. Draft genome of the sea cucumber *Holothuria glaberrima*, a model for the study of regeneration. *Frontiers in Marine Science*. doi:10.3389/fmars.2021.603410

Ketchum, R.N., Smith, E.G., DeBiasse, M.B., Vaughan, G.O., McParland, D., Leach, W.B., Al-Mansoori, N., **Ryan, J.F.**, Burt, J.A., Reitzel, A.M. 2020. Population genomic analysis of a sea urchin across an extreme environmental gradient. *Genome Biology and Evolution*. 12(10):1819-29.

Kenny, N.J., Francis, W.R., Rivera-Vicéns, R.E., Juravel, K., de Mendoza, A., Díez-Vives, C., Lister, R., Bezares-Calderon, L., Grombacher, L., Roller, M., Barlow, L.D., Camilli, S., **Ryan, J.F.**, Wörheide, G., Hill, A.L., Riesgo, A., Leys, S. 2020. Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge *Ephydatia muelleri*. *Nature Communications*. 11(1):3676.

DeBiasse, M.B., Colgan, W.N., Harris, L., Davidson, B., **Ryan, J.F.** 2020. Inferring tunicate relationships and the evolution of the tunicate Hox cluster with the genome of *Corella inflata*. *Genome Biology and Evolution*. 12(6):948-964.

Moreland, M.T., Nguyen, A.D., **Ryan, J.F.**, Baxeavanis, A.D. 2020. The Mnemiopsis Genome Project Portal: integrating new gene expression resources and improving data visualization. *Database (Oxford)*. 2020:baaa029.

Dardaillon, J., Dauga, D., Simion, P., Faure, E., Onuma, T.A., DeBiasse, M.B., Louis, A., Nitta, K.R., Naville, M., Besnardeau, L., Reeves, Wang, K., Fagotto, M., Guérault-Bellone, M(g)., Fujiwara, S., Dumollard, R., Veeman, M., Volff, J.N., Roest, Crollius, H., Douzery, E., **Ryan, J.**, Davidson, B., Nishida, H., Dantec, C., Lemaire, P. W. 2020. ANISEED 2019: 4D exploration of genetic data for an extended range of tunicates. *Nucleic acids research*. Jan 8;48(D1):D668-75.

Babonis, Leslie S., et al. Genomic analysis of the tryptome reveals molecular mechanisms of gland cell evolution. 2019. *EvoDevo* 10.1, 1-18.

Colgan, W., Leanza, A., Hwang, A., DeBiasse, M.B., Llosa, I., Rodrigues, D., Adhikari, H., Corona, G.B., Bock, S., Carillo-Perez, A., Currie, M., Colgan, W., Leanza, A., Hwang, A., DeBiasse, M.B., Llosa, I., Rodrigues, D., Adhikari, H., Corona, G.B., Bock, S., Carillo-Perez, A., Currie, M., Darkoa-Larbi, S., Dellal, D., Gutow, H., Hokama, P., Kibby, E., Linhart, N., Moody, S., Naganuma, A., Nguyen, D., Stanton, R., Stark, S., Tumey, C., Velleca, A., **Ryan, J.F.**, Davidson, B. 2019. Variable levels of drift in tunicate cardiopharyngeal gene regulatory elements. *EvoDevo*. Dec;10(1):1-7.

Ohdera, A., Ames, C.L., Dikow, R.B., Kayal, E., Chiodin, M., Busby, B., La, S., Pirro, S., Collins, A.G., Medina, M., **Ryan, J.F.** 2019. Box, stalked, and upside-down? Draft genomes from diverse jellyfish (Cnidaria, Acraspeda) lineages: *Alatina alata* (Cubozoa), *Calvadosia cruxmelitensis* (Staurozoa), and *Cassiopea xamachana* (Scyphozoa). *GigaScience*. Jul;8(7):giz069.

Jiang, J.B., Quattrini, A.M., Francis, W.R., **Ryan, J.F.**, Rodríguez, E., McFadden, C.S. 2019. A hybrid de novo assembly of the sea pansy (*Renilla muelleri*) genome. *GigaScience*. Apr;8(4):giz026.

Pastrana, C.C., DeBiasse, M.B., **Ryan, J.F.** 2019. Sponges lack ParaHox genes. *Genome biology and evolution*. Apr;11(4):1250-7.

DuBuc, T.Q., **Ryan, J.F.**, Martindale, M.Q. 2019. “Dorsal–Ventral” Genes Are Part of an Ancient Axial Patterning System: Evidence from *Trichoplax adhaerens* (Placozoa). *Molecular biology and evolution*. May 1;36(5):966-73.

DeBiasse, M.B., **Ryan, J.F.** 2019. Phylotocol: Promoting transparency and overcoming bias in phylogenetics. *Systematic biology*. Jul 1;68(4):672-8.

Hernandez, A.M., **Ryan, J.F.** 2018. Horizontally transferred genes in the ctenophore *Mnemiopsis leidyi*. *PeerJ*. ;6.

Kayal, E., Bentlage, B., Pankey, M.S., Ohdera, A.H., Medina, M., Plachetzki, D.C., Collins, A.G., **Ryan, J.F.** 2018. Phylogenomics provides a robust topology of the major cnidarian lineages and insights on the origins of key organismal traits. *BMC Evolutionary Biology*. Dec;18(1):68.

Sasson, D.A., Jacquez, A.A., **Ryan, J.F.** 2018. The ctenophore *Mnemiopsis leidyi* regulates egg production via conspecific communication. *BMC ecology*. Dec;18(1):12.

Haddock, S.H.D., Christianson, L.M., Francis, W.R., Martini, S., Dunn, C.W., Pugh, P.R., Mills, C.E., Osborn, K.J., Seibel, B.A., Choy, C.A., Schnitzler, C.E., Matsumoto, G.I., Messié, M., Schultz, D.T., Winnikoff, J.R., Powers, M.L., Gasca, R., Browne, W.E., Johnsen, S., Schlining, K.L., Thun, S.V., Erwin, B.E., **Ryan, J.F.**, Thuesen, E.V. BIODIVERSITY, BEHAVIOR, AND BIOLUMINESCENCE OF DEEP-SEA ORGANISMS. *Oceanography*.;30(4):38.

Sasson, D.S. & **Ryan, J.F.** 2017. A reconstruction of sexual modes throughout animal evolution. *BMC Evolutionary Biology*, doi:10.1186/s12862-017-1071-3

Martin-Duran, J.M.\*, **Ryan, J.F.\***, Vellutini, B.C.C., Pang, K., and Hejzol, A. 2017. Increased taxon sampling reveals thousands of hidden orthologs in flatworms. *Genome Research*, doi:10.1101/gr.216226.116

**Ryan, J.F.**, Schnitzler, C.E., and Tamm, S.L. 2016. Meeting report of Ctenopalooza: The first international meeting of ctenophorologists. *EvoDevo*, doi:10.1186/s13227-016-0057-3

Ames, C.L., **Ryan, J.F.**, Bely, A.E., Cartwright, P., and Collins, A.G., 2016. A new transcriptome and transcriptome profiling of adult and larval tissue in the box jellyfish *Alatina alata*: an emerging model for studying venom, vision and sex. *BMC Genomics*, doi:10.1186/s12864-016-2944-3

Babonis, L.S., Martindale, M.Q., and **Ryan, J.F.**, 2016. Do novel genes drive morphological novelty? An investigation of the nematosomes in the sea anemone *Nematostella vectensis*. *BMC Evolutionary Biology*, 2016, doi:10.1186/s12862-016-0683-3.

Battelle, B.A., **Ryan, J.F.**, Kempler, K., Spencer, S., Marten, C., Warren, W., Minx, P., Montague, M., Green, P., Schmidt, S., Fulton, L., Patel, N., Protas, M., Wilson, R., and Porter, M. Opsin repertoire and expression patterns in horseshoe crabs: evidence from the genome of *Limulus polyphemus*. *Genome Biology and Evolution*, doi:10.1093/gbe/evw100.

Long, K.A., Nossa, C.W., Sewell, M.A., Putnam, N.H., and **Ryan, J.F.** 2016. Low coverage sequencing of three echinoderm genomes: the brittle star *Ophionereis fasciata*, the sea star *Patiriella regularis*, and the sea cucumber *Australostichopus mollis*. *GigaScience*, doi:10.1186/s13742-016-0125-6.

Sasson, D.S. and **Ryan, J.F.** 2016. The sex lives of ctenophores: the influence of light, body size, and self-fertilization on the reproductive output of the sea walnut, *Mnemiopsis leidyi*. *PeerJ*, 2016, doi.org/10.7717/peerj.1846.

Levin, M., Anavy, L., Cole, A.G., Winter, E., Mostov, N., Khair, S., Senderovich, N., Kovalev, E., Silver, D.H., Feder, M., Fernandez-Valverde, S.L., Nakanishi, N., Simmons, D., Simakov, O., Larsson, T., Liu, S.Y., Jerafi-Vider, A., Yaniv, K., **Ryan, J.F.**, Martindale, M.Q., Rink, J.C., Arendt, D., Degnan, S.M., Degnan, B.M., Hashimshony, T., & Yanai, I. 2016. The mid-developmental transition and the evolution of animal body plans. *Nature*, doi:10.1038/nature16994.

Zwarycz, A.S., Nossa, C.W., Putnam, N., & **Ryan, J.F.** 2016. Timing and scope of genomic expansion within Annelida: evidence from homeoboxes in the genome of the earthworm *Eisenia fetida*. *Genome Biology and Evolution*, doi:10.1093/gbe/evv243.

**Ryan, J.F.** and Chiodin, M. 2015. Where is my mind? How sponges and placozoans may have lost neural cell types. *Philosophical Transactions of the Royal Society, Series B*, doi:10.1098/rstb.2015.0059.

Dunn, C.W. and **Ryan, J.F.** 2015. The evolution of animal genomes. *Current Opinion in Genetics & Development*, doi:10.1016/j.gde.2015.08.006

Church, S.H., **Ryan, J.F.** and Dunn, C.W. 2015. Automation and Evaluation of the SOWH Test of Phylogenetic Topologies with SOWHAT. *Systematic Biology* doi:10.1093/sysbio/syv055.

**Ryan, J.F.** (2014). Did the ctenophore nervous system evolve independently?. *Zoology*, doi:10.1016/j.zool.2014.06.001.

Moreland, R.T., Nguyen, A.D., **Ryan, J.F.**, Schnitzler, C.E., Koch, B.J., Siewert, K., Wolfsberg, T.G., Baxevanis, A.D. 2014. A customized Web portal for the genome of the ctenophore *Mnemiopsis leidyi*. *BMC Genomics*, Apr 28;15:316.

GIGA Community of Scientists. Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. *Journal of Heredity*, 2014. Jan-Feb;105(1):1-18.

**Ryan, J.F.**, Pang, K., Schnitzler, C.E., Nguyen, A.D., Moreland, R.T., Simmons, D.K., Koch, B.J., Francis, W.R., Havlak, P.; NISC Comparative Sequencing Program, Smith, S.A., Putnam, N.H., Haddock, S.H., Dunn, C.W., Wolfsberg, T.G., Mullikin, J.C., Martindale, M.Q., Baxeavanis, A.D. 2013. The Genome of the Ctenophore *Mnemiopsis leidyi* and its implications on cell type evolution. *Science*, Dec 13;342(6164):1242592.

Flot, J.F., Aury, J., Couloux, A., Hespeels, B., Xiang, L., Arkhipova, I., Bast, J., Danchin, E., da Rocha, M., da Silva, C., Gladyshev, E., Gouret, P., Hecox-Lea, B., Henrissat, B., Hejnal, A., Manolis, K., Kondrashov, A., Koszul, R., Mark Welch D., Noel B., Piskurek, O., Pontarotti, P., **Ryan, J.F.**, Vakhrusheva, O., Wincker, P., Jaillon, O., and Van Doninck, K. 2013. Genomic evidence for ameiotic evolution in the bdelloid rotifer *Adineta vaga*. *Nature*, Aug 22;500(7463):453-7.

Schnitzler, C.E., Pang, K., Powers, M., Reitzel, A.M., **Ryan, J.F.**, Simmons, D., Tada, T., Park, M., Gupta, J., Brooks, S.Y., Blakesley, R.W., Yokoyama, S., Haddock, S.H.D., Martindale, M.Q., and Baxeavanis, A.D. 2012. Genomic organization, evolution, and expression of photoprotein and opsin genes in *Mnemiopsis leidyi*: a new view of ctenophore photocytes. *BMC Biology*, Dec 21;10:107.

Maxwell, E.K., **Ryan, J.F.**, Schnitzler, C.E., Browne, W.E., Baxeavanis, A.D. 2012. MicroRNAs and essential components of the microRNA processing machinery are not encoded in the genome of the ctenophore *Mnemiopsis leidyi*. *BMC Genomics*, Dec 20;13:714.

Dubuc, T.Q.\*, **Ryan, J.F.\***, Shinzato, C., Satoh, N., Martindale, M.Q. 2012. Coral comparative genomics reveal extensive Hox cluster in the cnidarian-bilaterian ancestor. *Integrative and Comparative Biology*, Jul 4.

Koch, B.\*, **Ryan, J.F.\***, Baxeavanis, A.D. 2012. The Diversification of the LIM superclass at the Base of the Metazoa Increased Subcellular Complexity and Promoted Multicellular Specialization. *PLoS One*, March 15;7(3):e33261.

Kelada, S.N., Aylor, D.L., Peck Bailey, C.E., **Ryan, J.F.**, Tavarez, U., Buus, R.J., Miller, D.R., Chesler, E.J., Threadgill, D.W., Churchill, G.A., Pardo-Manuel de Villena, F., and Collins, F.S. 2012. Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross. *G3*, Feb; 2:157-165.

Reitzel, A.M., **Ryan, J.F.**, Tarrant, A.M. 2011. Establishing a model organism: A report from the first annual *Nematostella* meeting. *Bioessays*, Nov 18.

Pang, K., **Ryan, J.F.**, Baxeavanis, A.D., and Martindale, M.Q. 2011. Evolution of the TGF- $\beta$  signaling pathway and its potential role in the ctenophore *Mnemiopsis leidyi*. *PLOS One*, Sep 8;6(9):e24152.

Pett, W., **Ryan, J.F.**, Pang, K. 2011. NISC Comparative Sequencing Program, Martindale MQ, Mullikin J, Baxeavanis AD, and Lavrov D. Extreme Mitochondrial Genome Evolution in the Ctenophore *Mnemiopsis leidyi*. *Mitochondrial DNA*, Aug;22(4):130-42.

Reitzel, A.M., Pang, K., **Ryan, J.F.**, Mullikin, J.C., Baxeavanis, A.D., Martindale, M.Q., and Tarrant, A.M. 2011. Nuclear Receptors from the Ctenophore *Mnemiopsis leidyi* Lack a Zinc-Finger DNA-Binding Domain: Lineage-Specific Loss or Ancestral Condition in the Emergence of the Nuclear Receptor Superfamily? *BMC Evodevo*, Feb 3;2(1):3.

Hurle, B., Marques-Bonet, T., Antonacci, F., Hughes, I., **Ryan, J.F.**, NISC Comparative Sequencing Program, Eichler, E.E., Ornitz, D.M., and Green, E.D. 2011. Lineage-Specific Evolution of the Vertebrate Otopetrin Gene Family Revealed by Comparative Genomic Analyses. *BMC Evolutionary Biology*, Jan 24;11(1):23.

### **Research Support:**

PI, Allen Distinguished Investigator Award (12/1/2021 — 11/31/2024) “Reconstructing the development and functional architecture of the motor neural circuits of the last common animal ancestor” (\$1,500,000)

PI, NSF (6/1/2020 – 5/31/2023) “ANT LIA Collaborative Research: Interrogating Molecular and Physiological Adaptations in Antarctic Marine Animals” (\$130,765)

PI, NSF (3/6/2020 – 3/5/2023) “EAGER: Exploration of evolutionary mechanisms across multiple scales” (\$299,600)

PI, NSF (09/15/2015 – 09/14/2020) “Dimensions: Collaborative Research: Life at extremes: Linking the phylogenetic and genomic diversity of ctenophores to ecophysiological adaptations in the deep sea” (\$596,549)

PI, NSF (03/01/2016 – 02/28/2023) “REU Site: Marine Biodiversity: lessons from molecules, development and behavior” (\$340,259)

PI, UF Biodiversity Institute, (4/15/2019–12/31/2020) “Developing a genomic foundation to assess the biodiversity & evolutionary dynamics of sea cucumber across the marine biosphere” (\$40,000)

PI, UF Office of Research (2/1/2020 – 2/1/2021) “Southeast SACNAS regional conference” (\$3,000)

PI, NSF (02/15/2016 – 01/31/2017) “Meeting: Ctenopalooza - A Workshop on Ctenophore Biology, March 14-15, 2015, Saint Augustine, Florida” (\$21,710)

PI, UF Office of Research (12/9/2015 – 12/8/2016) “Ctenopalooza, The First Meeting of Ctenophore Biologists” (\$3,000)