

# Graham Larue

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## SUMMARY

I am a computational biologist/bioinformatician specializing in comparative genomics and molecular evolution. I am finishing a PhD in Quantitative and Systems Biology from UC Merced (anticipated Spring 2022), and have published first-author bioinformatics research in prominent scientific journals including *Nucleic Acids Research* and *Current Biology*. I am interested in building tools for/answering biological questions in the areas of genomics and next-generation sequencing technologies.

## EDUCATION

- 2016 – 2022 **Ph.D. (anticipated)**  
Quantitative and Systems Biology  
University of California Merced
- 2013 – 2015 **M.S.**  
Cell and Molecular Biology  
San Francisco State University
- 2002 – 2008 **B.S.**  
Biology  
University of California Santa Cruz

## WORK EXPERIENCE

- AUG. 2016 - PRESENT  
University of California Merced  
**Graduate student**  
Bioinformatics/molecular evolution doctoral research focused around sequence-based classification and comparative genomics of spliceosomal introns.
- JUN. 2019 – SEP. 2019  
DOE Joint Genome Institute  
**Summer Graduate Intern**  
Big data comparative genomic analysis of intron lengths in fungi.
- JUL. 2011 – JUL. 2013  
University of California Berkeley  
**Staff Research Associate I - Depts. of Neurobiology & Electrical Engineering**  
Electrophysiological investigation of mammalian retinal architecture in the labs of Professor Frank Werblin (Neurobiology) and Dr. Long-Sheng Fan (EE).
- JAN. 2009 – NOV. 2010  
Santa Cruz Biotechnology  
**Research Assistant**  
Microarray screening and sample prep. in hybridoma monoclonal antibody production group.

## PROGRAMMING LANGUAGES

BASIC R, Julia, Perl, SQL, C++  
ADVANCED Python, Bash

## TECHNICAL EXPERIENCE

**Bioinformatics:** Novel machine-learning based intron sequence classification algorithm (intronIC), *de novo* transcriptome assembly, NGS-based eukaryotic gene annotation, custom gene orthology and intron homology identification, BLAST, DIAMOND, HISAT, bowtie, StringTie, STAR, AUGUSTUS, Trinity, PASA, Kallisto, Salmon, samtools, bedtools, fastq-dump  
**Computing:** Linux system administration, GNU coreutils, grep, sed, awk, Slurm  
**Data visualization:** Matplotlib, Seaborn  
**Wet lab:** ELISA, microarray, confocal and two-photon microscopy, multi-electrode array, retinal tissue culture and dissection, patch-clamp, rodent husbandry and euthanasia, sterile technique.

## SELECTED PUBLICATIONS

- Larue, G.E., Eliáš, M., Roy, S.W., 2021. "Expansion and transformation of the minor spliceosomal system in the slime mold *Physarum polycephalum*." *Curr. Biol.* o. <https://doi.org/10.1016/j.cub.2021.04.050>
- Moyer, D.C.\*, Larue, G.E.\*, Hershberger, C.E., Roy, S.W., Padgett, R.A., 2020. "Comprehensive database and evolutionary dynamics of U12-type introns." *Nucleic Acids Res.* <https://doi.org/10.1093/nar/gkaa464>. (\*co-first author)
- Hudson, A.J., McWatters, D.C., Bowser, B.A., Moore, A.N., Larue, G.E., Roy, S.W., Russell, A.G., 2019. "Patterns of conservation of spliceosomal intron structures and spliceosome divergence in representatives of the diplomonad and parabasalid lineages." *BMC Evol. Biol.* 19, 162. <https://doi.org/10.1186/s12862-019-1488-y>.
- Slabodnick, M.M., Ruby, J.G., Reiff, S.B., Swart, E.C., Gosai, S., Prabakaran, S., Witkowska, E., Larue, G.E., Fisher, S., Freeman, R.M., Gunawardena, J., Chu, W., Stover, N.A., Gregory, B.D., Nowacki, M., Derisi, J., Roy, S.W., Marshall, W.F., Sood, P., 2017. "The Macronuclear Genome of *Stentor coeruleus* Reveals Tiny Introns in a Giant Cell." *Curr. Biol.* 27, 569–575. <https://doi.org/10.1016/j.cub.2016.12.057>.

## REFERENCES

References available on request