

## EDUCATION

**PhD cum laude** in Plant Biotechnology  
University of Barcelona, Spain

**Master of Arts** in Plant Biology  
University of Texas, Austin

**Bachelor of Science** in Computer Science  
University of Texas, Austin

**International Baccalaureate** with honors  
Lycee Jeanne d'Albret, St Germain-en-Laye,  
France

ELIZABETH HÉNAFF

elizabeth.m.henaff@gmail.com

150 Graham Ave. #4  
Brooklyn, NY 11206

elizabeth-henaff.net

## COMPUTATIONAL SKILLS

Python, bash, Processing | \*nix cluster and workstation | NGS analysis (BWA, samtools, bedtools, IGV), sequence search, alignment and clustering (BLAST, vmatch, MUSCLE, UCLUST, SILIX) | transposon annotation (LTR\_finder, MITE\_hunter, RepeatMasker) | data visualization (Circos, UGENE, matplotlib, Processing)

## DIGITAL FABRICATION

CAD design (Blender, OpenSCAD) | 3D printing

## AWARDS

2015 MipTec Travel Grant  
2009-2013 Fully Funded PhD Scholarship  
2013 Best Student Presentation, CNET  
2008 ASPB Travel Grant  
2005 Excellence in Biology Research,  
UT Undergraduate Poster Session  
2002 Honor List, UT Austin  
2001 Dean's List, UT Austin

## LANGUAGES

English and French (native), Spanish (fluent),  
Catalan (basic)

## OTHER INTERESTS

Rock climbing, interactive installations and  
creative coding, photography

## EXPERIENCE

**How to Grow (Almost) Anything** Sep 2015 - Jan 2016  
bio.academany.org | MIT  
*Instructor training*

**Postdoctoral Research Associate** Sep 2014 - Present  
Weill Cornell Medical College, New York | PI: Chris Mason  
*Environmental metagenomics.*

**Postdoctoral Research Associate** Sep 2014 - Sep 2015  
Memorial Sloan Kettering Cancer Center, New York | PI: Alex  
Kentsis  
*Impact of transposition in pediatric cancers.*

**PhD Fellow** Sep 2009 - Aug 2013  
Center for Research in Agricultural Genomics (CRAG), Barcelona,  
Spain  
*Genome-wide transposon analyses: annotation, movement and  
impact on genome structure and evolution*

**Internship** March - May 2012  
Computational Biology Research Center (CBRC), Tokyo, Japan  
*Detection of transposon-related polymorphisms using whole-genome  
alignments.*

**EMBO Doctoral Course** June - July 2011  
Institut Pasteur, Paris, France  
*Practical Course: Bioinformatics and Comparative Genomics  
Analyses*

**Research / Teaching Assistant** Sep 2006 - Dec 2008  
University of Texas at Austin | PI: Stanley Roux  
*Master's thesis: The role of extracellular ATP in regulating growth by  
cell elongation.*

**Undergraduate Research Assistant** 2002 - 2005  
University of Texas at Austin | PIs: Robin Gutell, Stanley Roux, David  
Hillis.  
*Prediction of two-dimensional RNA structure, genetic algorithms for  
phylogeny reconstruction*

## PUBLICATIONS

1. Hénaff E, Zapata L, Casacuberta JM, Ossowski S. Jitterbug: somatic and germline transposon insertion detection at single-nucleotide resolution. *BMC Genomics*. 2015;16(1):768. doi:10.1186/s12864-015-1975-5.
2. Henssen AG, Hénaff E, Jiang E, et al. Genomic DNA transposition induced by human PGBD5. *Elife*. 2015;4:e10565. doi:10.7554/eLife.10565.
3. Sanseverino W, Hénaff E, Vives C, et al. Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. *Mol Biol Evol*. 2015;32(10):2760-2774. doi:10.1093/molbev/msv152.
4. Afshinnekoo E, Meydan C, Chowdhury S, et al. Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. *Cell Syst*. 2015. doi:10.1016/j.cels.2015.01.001.
5. Hénaff E, Vives C, Desvoyes B, et al. Extensive amplification of the E2F transcription factor binding sites by transposons during evolution of Brassica species. *Plant J*. 2014;77(6):852-862.
6. Yang L, Koo DH, Li D, et al. Next-generation sequencing, FISH mapping and synteny-based modeling reveal mechanisms of decreasing dysploidy in Cucumis. *Plant J*. 2014;77(1):16-30.
7. Hernández-Pinzón I, Cifuentes M, Hénaff E, Santiago N, Espinás ML, Casacuberta JM. The Tnt1 retrotransposon escapes silencing in tobacco, its natural host. *PLoS One*. 2012;7(3).
8. Garcia-Mas J, Benjak A, Sanseverino W, et al. The genome of melon (*Cucumis melo* L.). *Proc Natl Acad Sci*. 2012;109(29):11872-11877. doi:10.1073/pnas.1205415109.
9. González VM, Benjak A, Hénaff EM, et al. Sequencing of 6.7 Mb of the melon genome using a BAC pooling strategy. *BMC Plant Biol*. 2010;10:246. doi:10.1186/1471-2229-10-246.
10. Jeter CR, Tang W, Hénaff E, Butterfield T, Roux SJ. Evidence of a novel cell signaling role for extracellular adenosine triphosphates and diphosphates in *Arabidopsis*. *Plant Cell*. 2004;16(10):2652-2664.

## SELECTED TALKS

- 2015-11-05 *Hacking the Genetic Heritage of a Superfund Site*, Hacking the Human Body, Digital Garage, San Francisco, USA
- 2015-09-20 *Benchmarking and Standardization of Structural Variation Detection Methods*, MipTec, Basel Life Science Week, Basel, Switzerland
- 2015-08-27 *Developing a Benchmark Dataset for Transposon Insertion Detection*, Genome in a Bottle Consortium Meeting, National Institute of Standards and Technology, Washington DC, USA
- 2015-06-18 *The Gowanus Canal Microbiome: Exploring the Microbial Ecosystem of a Superfund Site*, Microbes in the City, New York Academy of Sciences, New York, USA
- 2015-06-19 *A Feeling for the Organism: DNA Sequencing as Digital Insight into Biological Beings*, Genspace, New York, USA
- 2012-04-21 *High transposition activity in recent evolution the of the melon genome*, International Conference on Transposable Elements, St. Malo, France
- 2008-06-22 *Visualization of extracellular ATP in transgenic lines of Arabidopsis expressing a wall localized luminescent reporter*, American Society of Plant Biologists Meeting, Merida, Mexico