

SARAH Z. DUNGAN

*Portfolio*

**Medical & Technical  
Communication**

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# Sarah Z. Dungan, PhD



I'm a newly certified professional technical communicator (CPTC) with an academic background in the life sciences.

As a biologist turned technical writer, I have a strong appreciation for the highly specialized people who use the documentation I compose. I've experienced the stress of peer-review and the frustration of following a vaguely written lab protocol. I too have frantically searched the manual for that extremely expensive new ultra-centrifuge, desperate to find the meaning of the error code it won't stop displaying.

In other words, I know firsthand how important high-quality scientific and technical writing is.

Each piece of content I produce is bespoke to the user and their context, whether they're graduate students, lab technicians, or principle investigators.

At heart, I am a scientist first and a writer second, but that only means my reverence for knowledge and my affection for the people who create it are central to my production process.

### *Is there a difference between technical and medical writing?*

Yes and no.

Medical writing is an umbrella term that refers to technical and scientific writing in health, medicine, and other life science disciplines. Technical writing is more broadly a set of core production and design competencies that emphasize transforming complex information into usable knowledge.

Though medical writers can have all kinds of audiences, I typically write for other medical, health, and science professionals.

The kinds of writing I specialize in include:

- [Peer-reviewed articles and abstracts](#)
- [Whitepapers](#)
- [Conference posters and slide decks](#)
- [UX design for STEM users](#)
- [Software and device documentation \(print and online\)](#)
- [Standard operating procedures \(SOPs\)](#)

# Whitepaper

## *Advocating for ground-breaking DNA sequencing technology*

The purpose of this whitepaper is to make a case for using portable sequencers in wildlife forensics. The target audiences include a variety of stakeholders involved in combating illegal wildlife trade. As such, the writing in this whitepaper had to appeal *both* to experts and non-experts. **Appealing to one does not mean alienating the other!**



A typical workflow with the MinION (Figure 2) can take under three hours and consists of four phases:

1. Break open cells to extract genetic material.
2. Attach Oxford Nanopore Technologies' motor proteins to prepare the sample for sequencing.
3. Generate multiple sequence reads in real-time.
4. Analyze the sequence reads to identify the species.

Additional software compiles all sequence reads together to form a "consensus sequence". Comparing this consensus to a reference database allows an investigator to match the sample with species' genetic barcodes (Ogden et al.).

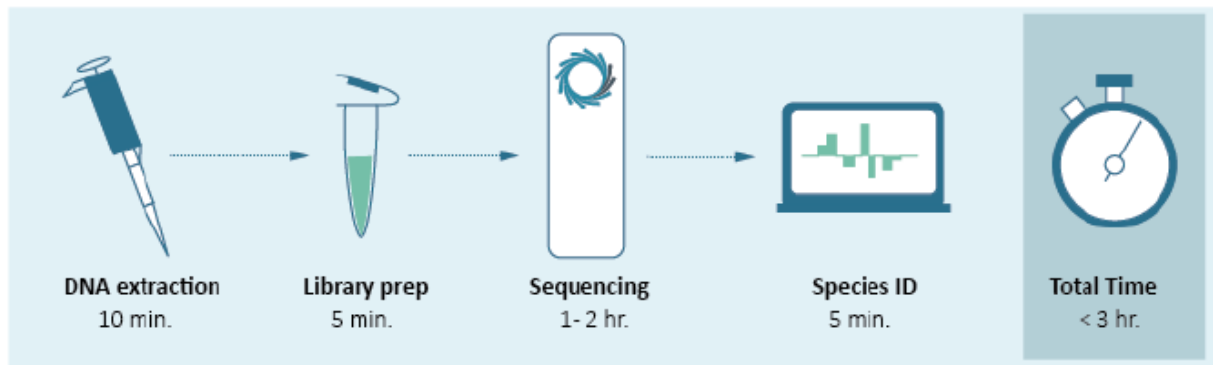


Figure 2. The total workflow of MinION sequencing from DNA extraction to species ID can take under 3 hours!

## Abstract

Illegal wildlife trade (IWT) is a global criminal industry worth billions of dollars annually. The import and export of products derived from endangered species not only threatens biodiversity and the environment, but also creates national security and human health risks.

Unfortunately, the majority of IWT goes undetected and unenforced due to wildlife forensics' limited capacity to genetically profile suspicious products. Operating and analysing the output of standard DNA sequencing technologies requires a high level of expertise, and these technologies are unaffordable for wildlife forensics applications.

On the other hand, portable sequencers like Oxford Nanopore's MinION may provide an equalizing influence on wildlife forensics in the coming decades. By bringing DNA sequencing out of the laboratory and directly into the hands of law-enforcement officials in the field, portable sequencers could unlock the capacity-building potential that wildlife forensics desperately needs.

## *Persuasion with facts and evidence, not rhetoric*

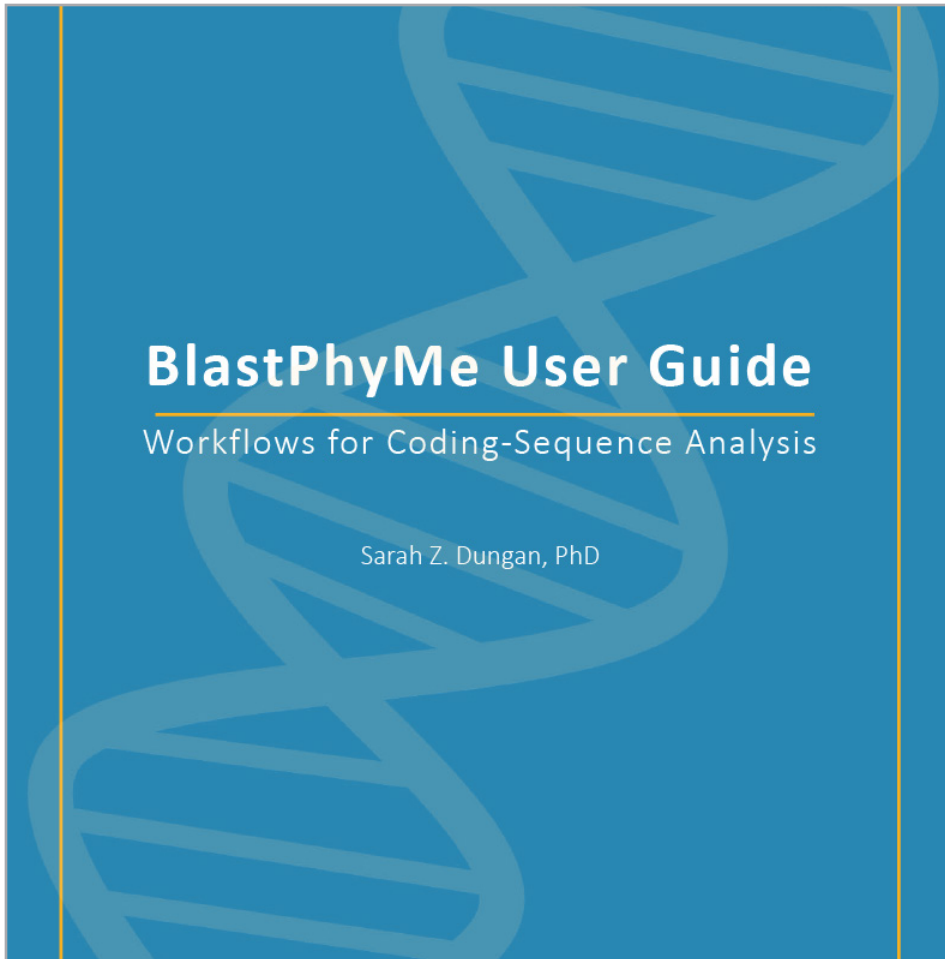
I wrote this piece in a technical communication class to practice a persuasive writing style in a technical context. As a scientist, information accuracy is very important to me.

**As a technical writer, my job is to convey complex information *without* sacrificing accuracy.**

## *Result*

Precise, information-rich content that can also be appreciated by readers who don't have a genetics background.

# Print & Online Manual



never used the software before.

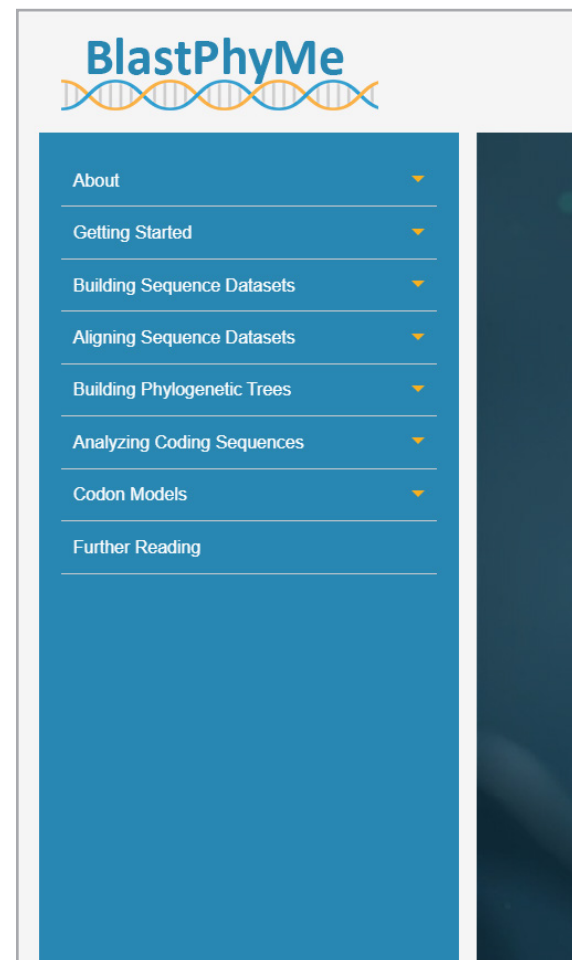
At the same time, my familiarity with the software allowed me to write with an understanding of the kinds of problem-spaces people who use it want to explore.

**I now see myself as an expert who writes for other kinds of experts.**

## *Writing a user manual for open-source bioinformatics software*

Two of my former colleagues developed the program, BlastPhyMe, to help with our lab's computational workflows. At the time, all of us were too busy to write a proper manual for it. As such, I was happy to give this program the documentation it deserves as part of a technical writing class.

The challenge was removing myself from my perspective as an expert user and into the shoes of someone who'd





# CHAPTER 2 Getting Started with BlastPhyMe



*In this chapter*

- Installing BlastPhyMe.....6
- BlastPhyMe Database Structure.....6
- Creating Your First BlastPhyMe Database.....7

To use BlastPhyMe, you will need a Windows desktop computer running Windows 7 at a minimum. Because BlastPhyMe is a workflow tool, you will also need additional 3rd-party software to accomplish specific tasks:

**Sequence alignment software**—BlastPhyMe uses [PRANK](#), [MUSCLE](#), and [MEGA](#) to generate multiple sequence alignments.

**Tree-building and editing software**—BlastPhyMe uses [PhyML](#) to build gene trees, but you will also need a tree editing program to manipulate tree files. See “Editing Tree Files with an External Editor” on page 24 for recommendations.

## Leveraging FrameMaker and MadCap Flare


I wrote the print version in FrameMaker and imported the final book file into MadCap Flare to design an online version as well.

### Result

The same manual in two different formats, written by someone who deeply understands the user-base.


## Welcome to the BlastPhyMe Online Guide

Search our help and documentation




**Getting Started**

Install BlastPhyMe and create your first database.




**Sequence Datasets**

Build coding-sequence datasets and multiple sequence alignments.



**Phylogenetic Trees**

Build gene trees out of your alignment datasets and format them for PAML.



**PAML Analysis**

Analyze your sequences with codon models and test for positive selection.

# User-Centred Prototype Help Site

## Cosima Torkian The over-worked PhD student



*"I love anything that makes writing easier!"*

**Age:** 29  
**Work:** Cell biology PhD  
**Family:** Co-habiting partner  
**Location:** Canada

**Tone of Voice:** Rational, knowledgeable, and reserved  
**Decision-Making Style:** Methodical

### Goals

- Complete my dissertation in time to defend this semester
- Win a prestigious postdoctoral grant
- Start a family

### Frustrations

- I don't have a lot of disposable income
- I'm so busy! I don't have time to learn new software
- My PI is overbearing and very critical of my work

### Key Content to Inform Decisions

- Clear step-by-step instructions
- Feature demonstrations
- Detailed product specifications

### Biography

Cosima is in the 5th year of her PhD in cell biology. She's writing her dissertation in the hopes of defending before the semester ends. She spends long hours in her graduate student office (and occasionally the campus library stacks) writing and making edits.

The writing process is stressful because her PI is notoriously fussy with corrections and often doesn't get back to her until the last minute. Cosima often brings this stress home, which causes her common-law partner to worry about her mental health. They're thinking about starting a family in the next couple of years, but Cosima fears balancing parenthood and an early academic career will be very difficult.

### Personality

- Analytical
- Efficient
- Determined
- Ethical

### Writing Habits

- Windows laptop
- Uses a reference manager all the time
- Relies on Microsoft Word

### Buying Incentives

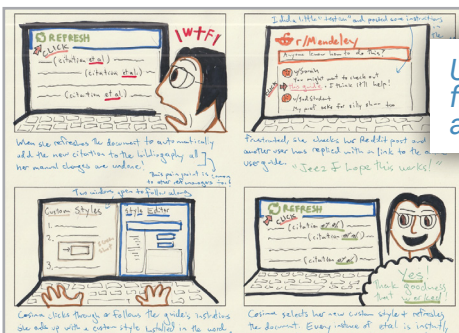
- Low-cost
- Easy/quick to learn
- Ethical company

### Turn-offs

- Lack of detail
- "Feelings over facts"
- Sloppiness

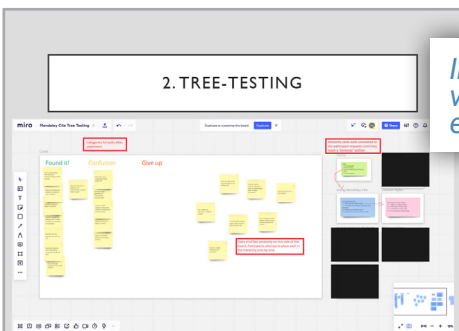
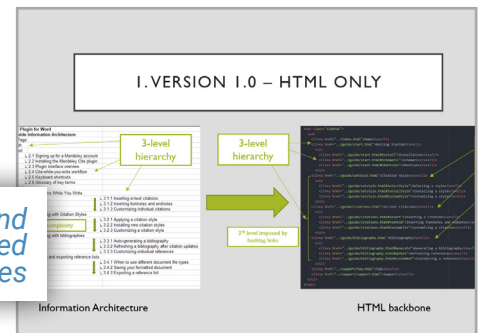
*Every design phase informed by user research*

Mendeley is a reference manager widely used by STEM academics (including myself!) but its existing documentation is currently bare-bones. For a UX design class, I built a help site for the browser plugin tool.



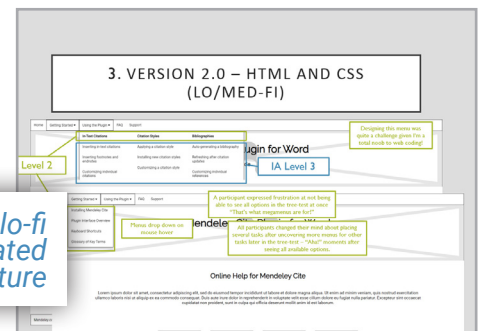
*User personas and story maps from surveys and interviews with academic users*

*Information architecture and HTML backbone emerged from card-sorting exercises*



*Information architecture validated by tree-testing exercises.*

*Navigation design and lo-fi wireframes from user-validated information architecture*



# WORK SAMPLES

### 4. NAVIGATION-TESTING FOR TRICKY TASKS

Key insights from navigation test results (see research documentation for details)

- The importance of **redundancy in FAQ** confirmed for Task 11. Newer users may be more inclined to explore a page, while veteran users want to find the information they need as fast as possible
- Task 13 isn't well-suited for a tip within a contextual topic but **works well in FAQ**. I could also incorporate it into more general workflow instructions (e.g., within the instructions for making in-text citations).
- Consider moving the glossary to the citations section, and putting it in a more prominent position...test?
- Dropdown menu visibility on hover (as opposed to click) seems to encourage site exploration?
- Shrink the placeholder images in the next revision (I agree that they are uncomfortably big)

*Additional topic placement decided by navigation tests*

### 5. VERSION 2.1 – HTML AND CSS (LO/MED-FI)

*Med-fi wireframes designed with HTML and CSS*

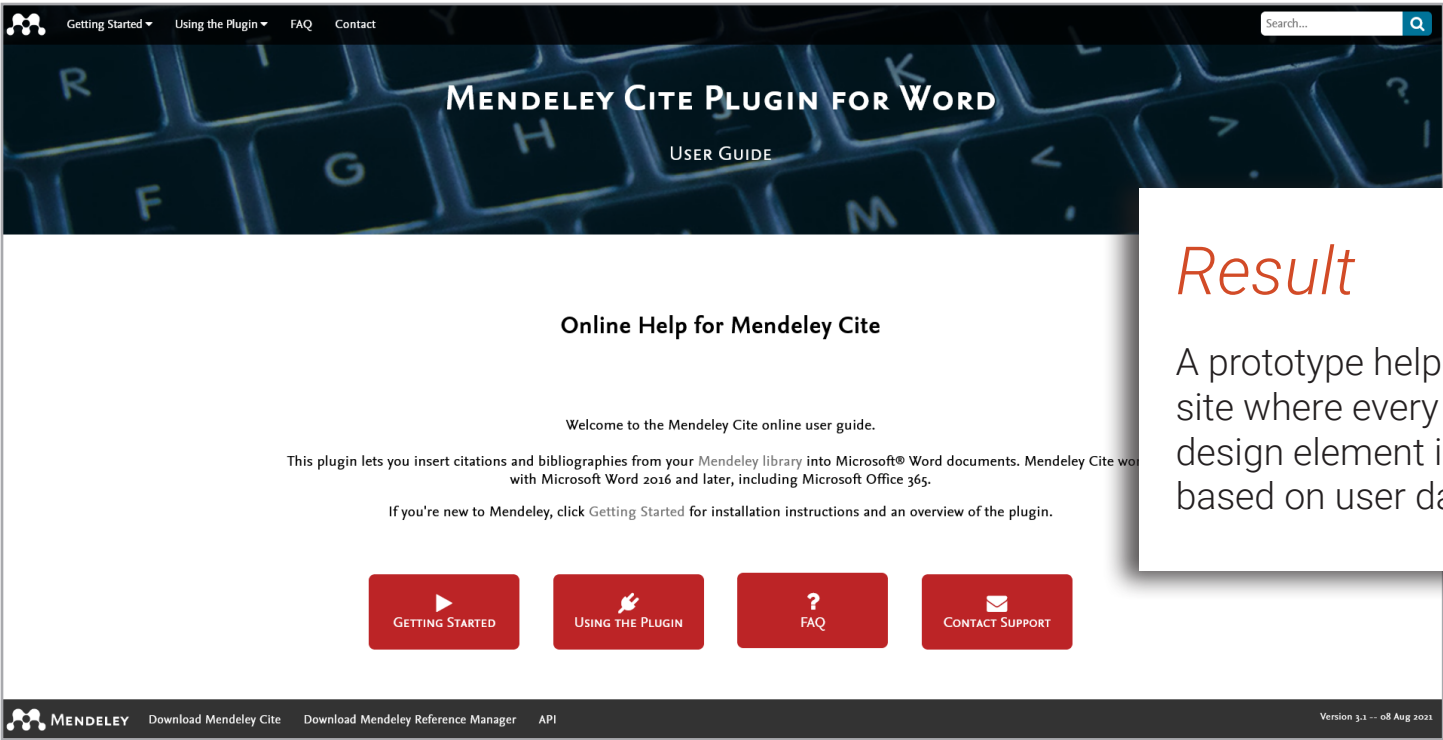
### 6. A/B TESTING

*Final navigation scheme decided by A/B testing*

*Final navigation scheme decided by A/B testing*

*Hi-fi wireframes with filler text, placeholder images and Javascript interactivity*

*Hi-fi wireframes with filler text, placeholder images and Javascript interactivity*



*Result*

A prototype help site where every design element is based on user data.

## *Built from scratch in HTML, CSS, and Javascript*

A major challenge in this project was learning UX research methods at the same time as learning to code. As such, the final design is constrained by my technical abilities. **If I could do this project over again, I'd create a more modern design with the coding and design skills I've continued to develop.**

# Standard Operating Procedure

*From messy lab  
notebooks to clean  
standardized protocol*

Many of the molecular biology protocols I once used were cobbled together through trial and error and shadowing senior lab members. While learning to write instructions using technical writing principles, I decided to give my old bacterial transformation protocol a proper SOP overhaul. **I believe even complex protocols should be easeful, not intimidating.**

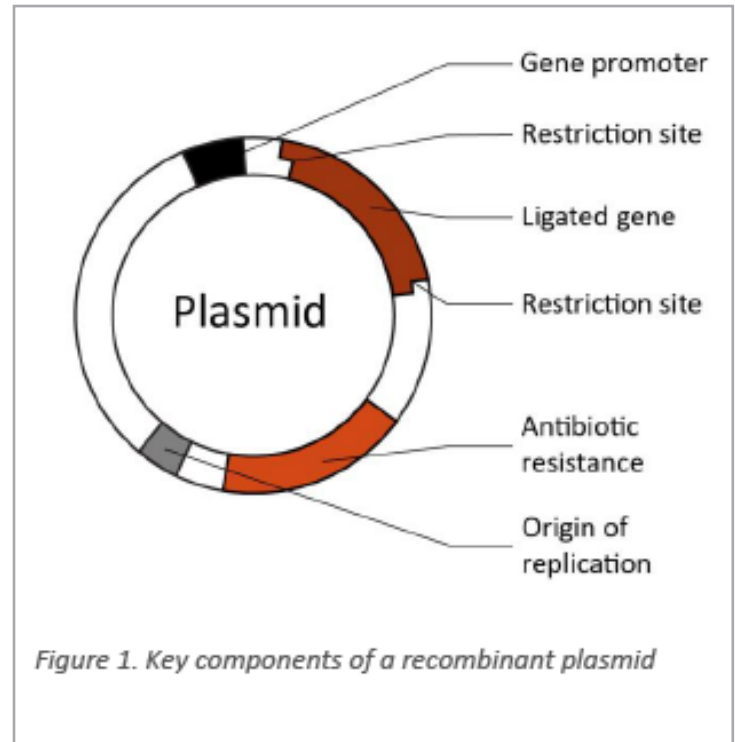


Figure 1. Key components of a recombinant plasmid

## Preparing the Plating Station

While the cells are incubating in the shaker, prepare the plating station by disinfecting all surfaces and arranging all supplies and equipment near the Bunsen burner sterile field.

1. Wipe down the counter-top and turntable with 70% isopropyl alcohol
2. Rest the glass spreader inside a clean 250 mL beaker
3. Fill the beaker with a few mL of 95% ethyl alcohol, just enough to submerge the spreader arm
4. Get the agar plates from the incubator and label each with the date and your initials
5. Turn off the mini-shaker and bring the cell tubes to the plating station
6. Turn on the gas and start the Bunsen burner with a modest flame



**Danger – Explosion and Burn Risk: Ethyl alcohol is flammable. Keep the ethanol beaker away from the open flame and do not put an ignited spreader in the beaker!**

## Plating Transformed Cells

While plating, keep the turntable and glass spreader within the sterile field of the Bunsen burner.

For each plate and cell tube

1. Place the plate on the turntable
2. Aspirate the cell sample (about 300  $\mu$ L, but set pipette to 350  $\mu$ L to ensure you aspirate the whole sample)

## BestBio Labs Standard Operating Procedure

Bacterial Transformation Protocol with  
BioLine™ Gold Competent Cells

Revision: 01

Effective Date: 18-Jun-2021

Author: Sarah Dungan

For: Lab technicians and students

### Lab Safety and Aseptic Technique

Before performing laboratory work, please review BestBio Labs safety guidelines and material safety data sheets (MSDS) for all reagents used in this protocol.

To work safely, you should

- Keep your work areas de-cluttered.
- Wipe down your work areas with 70% isopropyl alcohol.
- Keep all supplies within or near the Bunsen burner's sterile field while plating cells ([Figure 2](#)).
- Loosen reagent screw caps for easy one-handed opening.
- Wash your hands thoroughly with antibacterial soap before and after working with bacteria.
- Wear personal protective equipment (PPE).

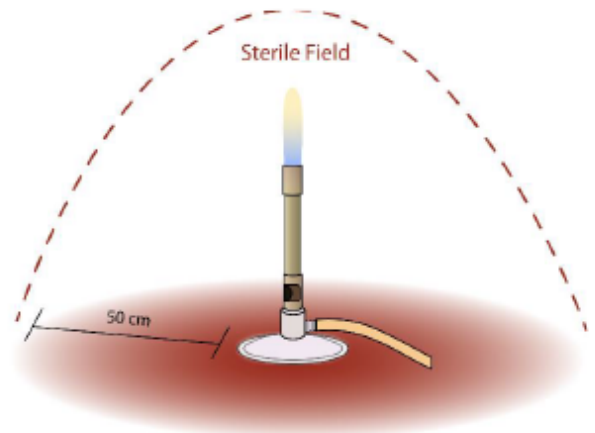


Figure 2. The sterile field created by the flame updraft has a radius of about 50 cm around the Bunsen burner

## Graphics are for medical writers too

As I began to draft the protocol, I thought about the concepts that were difficult for me to grasp until I'd actually been physically at the bench for awhile—small things like the easiest way to hold something and tips for making steps more efficient or less error-prone. **But certain concepts simply require visual clarification.**

For this protocol, I designed simple illustrations to clearly convey critical concepts that are difficult to describe solely in words. For example, conducting a bacterial transformation safely and successfully depends on visually understanding the Bunsen burner sterile field.

### Result

A visually pleasing, easy-to-follow laboratory protocol written by someone who's actually done the procedure before.

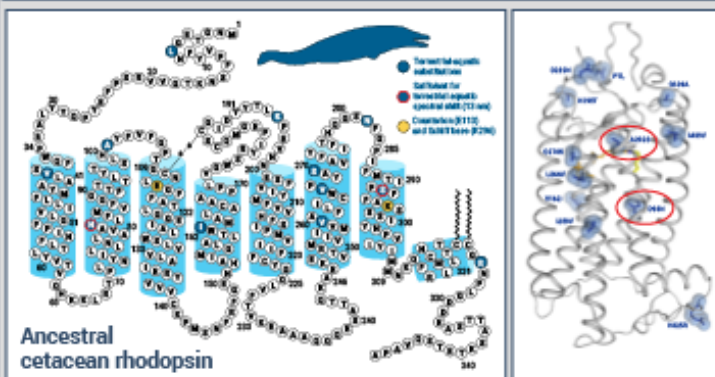


# Tracing ancient whale rhodopsin: Adaptations in vision over a major evolutionary transition

Sarah Z. Dungan<sup>1</sup> and Belinda S. W. Chang<sup>1,2,3</sup>

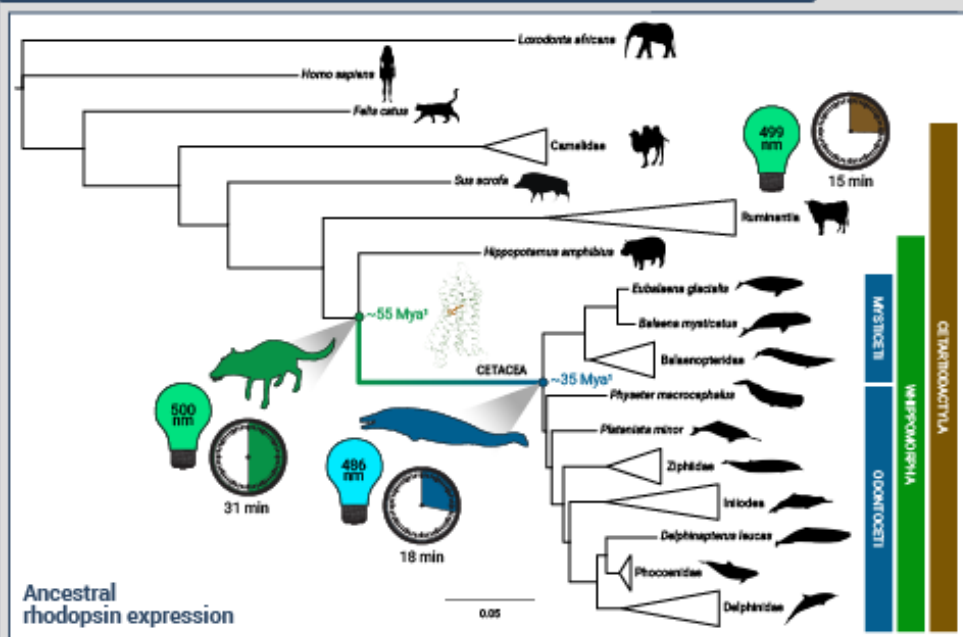
<sup>1</sup>Department of Evolutionary Biology, University of Toronto, <sup>2</sup>Department of Cell and Systems Biology, University of Toronto, <sup>3</sup>Centre for the Analysis of Genome Evolution and Function, University of Toronto

## Twelve substitutions over the terrestrial-aquatic transition



Across the codon models we implemented, the resulting reconstructions of the rhodopsin sequences from the ancestral nodes were nearly identical. According to these models, 12 sites experienced substitutions over the terrestrial-aquatic transition. Most of these (7 sites) occurred in transmembrane helical regions, two of which (sites 83 and 292) are known to affect both spectral tuning and retinal release [5, 6].

## Ancestral shifts in spectral tuning and retinal release

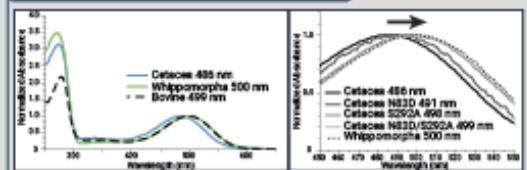


While the Whippomorpha rhodopsin had a spectral peak comparable to terrestrial outgroups, the Cetacea rhodopsin was blue-shifted by ~14 nm. The opposite was the case for the retinal release rates (the first step in regenerating the dark state); the  $t_{1/2}$  for Cetacea rhodopsin was similar to terrestrial outgroups, but the Whippomorpha rhodopsin was significantly slower.

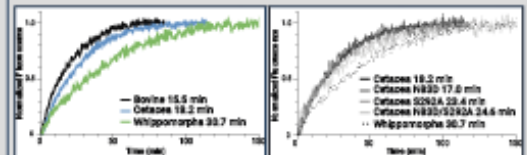
## Acknowledgements

This work was supported by a Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Grant (BSC), a General Motors Women in Science Award (SZD), and a Vision Science Research Program (VSRP) (SZD). Chromophore used in rhodopsin expression experiments was generously provided by Dr. Rosalie Cross.

## Backwards mutations



We created backwards mutations at sites 83 and 292 in the Cetacea rhodopsin to determine whether they could replicate the functional phenotype of the Whippomorpha rhodopsin. Single mutations at each of these sites red-shifted spectral tuning, though the effect of 292 was considerably greater. When combined in a double mutant, sites 83 and 292 were sufficient to shift the spectral peak of Cetacea to match Whippomorpha.



For retinal release, the shifts were minor (1-5 min) though still significant for site 292. When combined in a double mutant, sites 83 and 292 did not recover the Whippomorpha retinal release rate, indicating the involvement of one or more other sites.

## Conclusions

- Dim-light vision in ancient whales
- 486 nm is similar to modern deep divers [4]
  - Faster retinal release could mean faster rod recovery after bleaching (surface-to-depth transition) [7]
  - Greater reliance on vision relative to modern species (no sophisticated acoustic abilities) [8]
- Some of the first fully oceanic cetaceans may have been deep divers

## Sequence reconstruction



## References

Dungan, S. Z. W. Chang, Proc. R. Soc. B 284, 20170117 (2017).  
 Dungan, S. Z. W. Chang, Proc. R. Soc. B 284, 20170117 (2017).  
 Dungan, S. Z. W. Chang, Proc. R. Soc. B 284, 20170117 (2017).

## Result

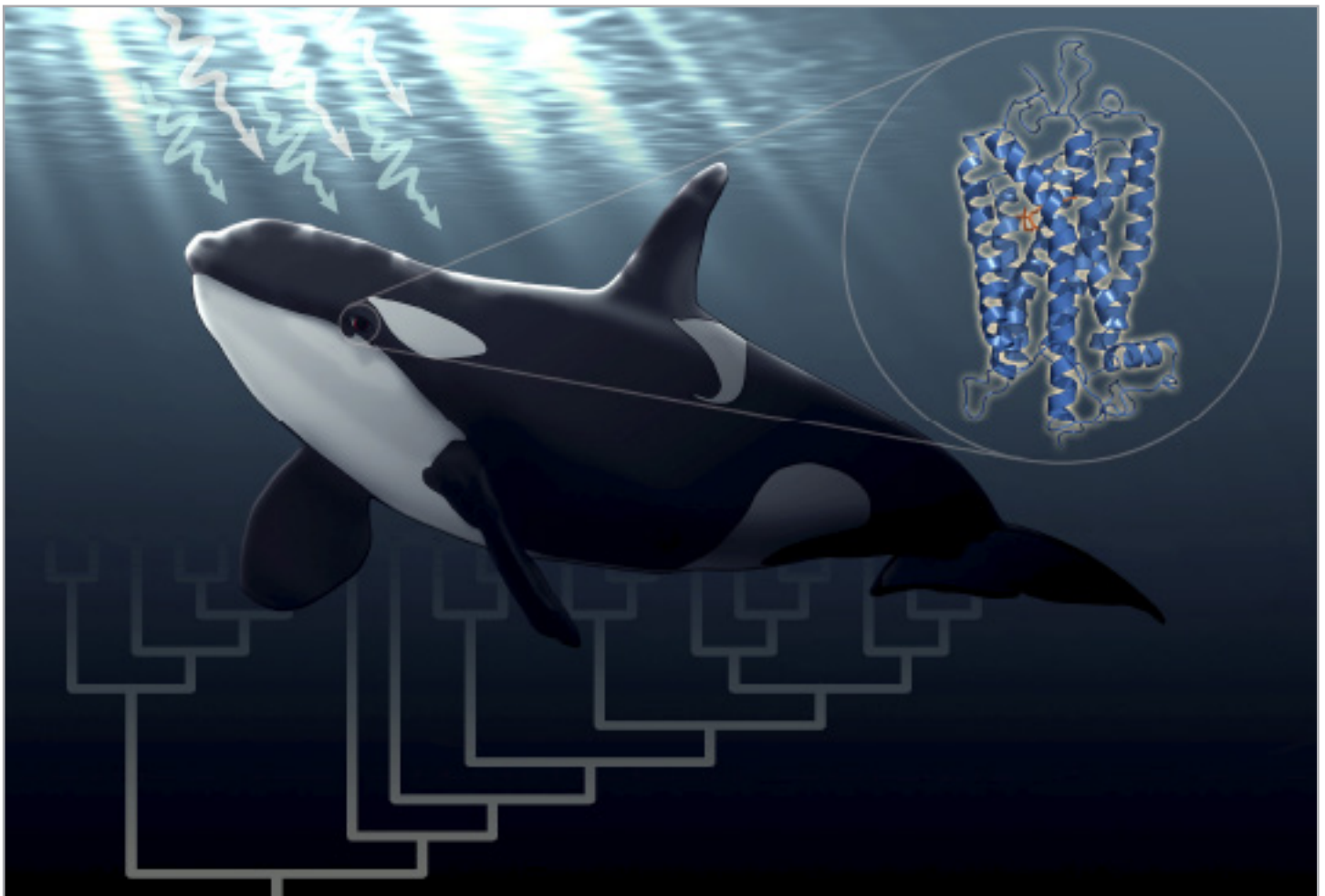
A visually-pleasing and information-rich poster you can be sure viewers will remember key points from.

# Peer-Reviewed Paper

## *Adaptations in whale genes*


Yes, whale genes were once my area of expertise. This was one of the first papers I wrote as a PhD student and it captures what I personally love about research: interdisciplinary approaches that combine concepts and techniques from different fields (bioinformatics and protein biochemistry in this case). I'll take the time to learn anything, no matter how complicated, to answer a question I'm interested in. For example, I started my PhD with zero wet lab experience, but was conducting tissue culture and protein expression experiments within 6 months.

**Even so, my favourite part of science is taking the whole process, all the data and statistics, and writing it up into a cohesive story that advances knowledge in my field.**





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**MOLECULAR BIOLOGY AND EVOLUTION**

Volume 33, Issue 2  
February 2016






**Article Contents**

- Abstract
- Introduction
- Results
- Discussion
- Materials and Methods
- Acknowledgments

## Spectral Tuning of Killer Whale (*Orcinus orca*) Rhodopsin: Evidence for Positive Selection and Functional Adaptation in a Cetacean Visual Pigment


 Sarah Z. Dungan, Alexander Kosyakov, Belinda S.W. Chang  [Author Notes](#)

*Molecular Biology and Evolution*, Volume 33, Issue 2, February 2016, Pages 323–336,  
<https://doi.org/10.1093/molbev/msv217>  
**Published:** 20 October 2015

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**Abstract**

Cetaceans have undergone a remarkable evolutionary transition that was accompanied by many sensory adaptations, including modification of the visual system for underwater environments. Recent sequencing of cetacean genomes has made it possible to begin exploring the molecular basis of these adaptations. To this end, we use a combination of experimental and computational methods to determine the spectral tuning of killer whale rhodopsin. We find that killer whale rhodopsin has a peak absorbance of 490 nm, which is significantly shorter wavelength than that of other cetacean rhodopsins. This finding is consistent with the hypothesis that killer whales have adapted to a blue-shifted underwater environment. Our results provide the first experimental evidence for the spectral tuning of killer whale rhodopsin and suggest that killer whales have adapted to a blue-shifted underwater environment.

 View Metrics

*Result*

A strong scientific publication record with nearly 400 citations and an h-index of 13 over the last 10 years.

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## Shedding light on the evolution of whale vision

by University of Toronto



A model of the killer whale rhodopsin protein illustrating its evolution in response to light. Eyes are the window between an animal and its environment, and if your environment has changed as much as a whale's has over the last 50 million years, they tell an intriguing story about your evolutionary history. As marine mammals that descended from terrestrial ancestors, whales and dolphins have many adaptations for aquatic living, including underwater vision, but we still know very little about how these adaptations evolved at the genetic level.

Researchers from the Department of Ecology and Evolutionary Biology at the University of Toronto used a combination of statistical and experimental methods to determine how the gene coding for the visual protein known as rhodopsin has evolved differently in whales and dolphins relative to terrestrial mammals. By using killer whale rhodopsin as an experimental model, their results show that not only is the rhodopsin gene under natural selection pressure in whales, but also that naturally selected mutations in the gene confer greater sensitivity towards blue-shifted underwater light. This makes it one of the first whale evolution studies to directly link selection patterns with a measurable change in function.

Their findings were published ahead of print as an Advance Access publication on October 20, 2015 in the science journal, *Molecular Biology and Evolution*, and presented at the recent biennial meeting of the Society for Marine Mammalogy in San Francisco on December 17, 2015. Funding was provided by the Natural Sciences and Engineering Research Council of Canada (NSERC).

Sarah Dungan, PhD candidate and lead author of the paper elaborates: "Rhodopsin is a light-sensitive protein in the rod cells of your eyes that allows you to see even in dark conditions. Whales are particularly reliant on rhodopsin because light fades very quickly with depth underwater. But the majority of light in the ocean is also blue, so if you're a deep diver like a sperm whale, having rhodopsin more sensitive in the blue part of the spectrum allows your eyes to make the most use of the scarce light."

**Relevant PhysicsForums posts**

- Reaction to COVID-19 Vaccine (or what to be prepared for) 11 HOURS AGO
- Australia Possibly Heading For 95% Vaccination 8 HOURS AGO
- Covid Delta variant 9 HOURS AGO
- 2021 Nobel Prize in Physiology or Medicine 10 OCT 04, 2021
- Are the COVID Vaccines Unusually Infective? 10 OCT 04, 2021
- Spike protein stability, effects etc 10 OCT 04, 2021

## Writing the same information for a different audience

Peer-reviewed papers target other experts in the field, but I wanted some experience writing for other kinds of audiences too. As such, I took the initiative to also write press releases for my published papers.

Scientific press releases get read by both other scientists and non-experts so they need to **balance interest from both audiences**. I successfully pitched the press release for this particular paper to Phys.org.

(I also digitally painted the illustration!)

 Email  
[szdungan@gmail.com](mailto:szdungan@gmail.com)

 Website  
<https://szdungan.com>

 LinkedIn  
[https://www.linkedin.com/  
in/szdungan/](https://www.linkedin.com/in/szdungan/)

## Contact & Parting Thoughts

For me, the biggest and most rewarding challenge of technical writing is in balancing the needs of target audiences with differing levels of expertise, often within the same content.

I believe that my writing skills combined with my background as a scientist put me in a unique position to navigate this balance. For most of the content I create, I occupy an empathy space in between the specialized expert and the fully naive user. As a result, it's a little easier for me to pivot between the two.

*Have you ever written (or read!) content that had to appeal to more than one target audience with differing levels of expertise?*

***What do you think allows a writer to successfully meet this challenge?***



