MIT BE
BIOLOGICAL ENGINEERING

Communication Lab

20.109
Communication Workshop 2:
Titles and Abstracts
(plus some writing basics)

Dr. Prerna Bhargava and Dr. Sean Clarke
BE Communication Lab Instructors

Titles + Abstracts:
Why do they matter?

Attract your audience: first judgment

Influence whether someone will read or cite

Indexing – Will readers even find your paper?

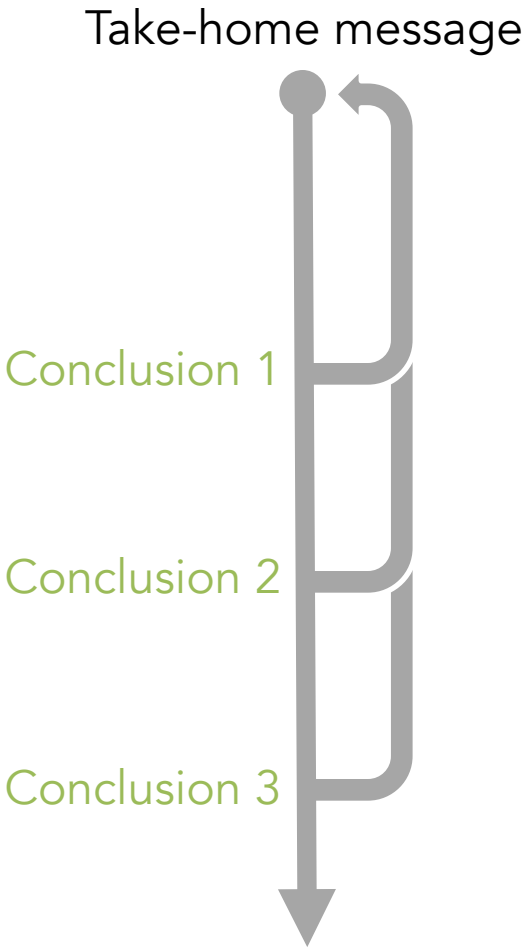
Titles + Abstracts:
Who is the audience?

- People in your field
- Editors, reviewers
- Researchers outside your field
- Students
- Reporters
- Patients
- Anyone looking for information

Titles + Abstracts:

When do you write them?

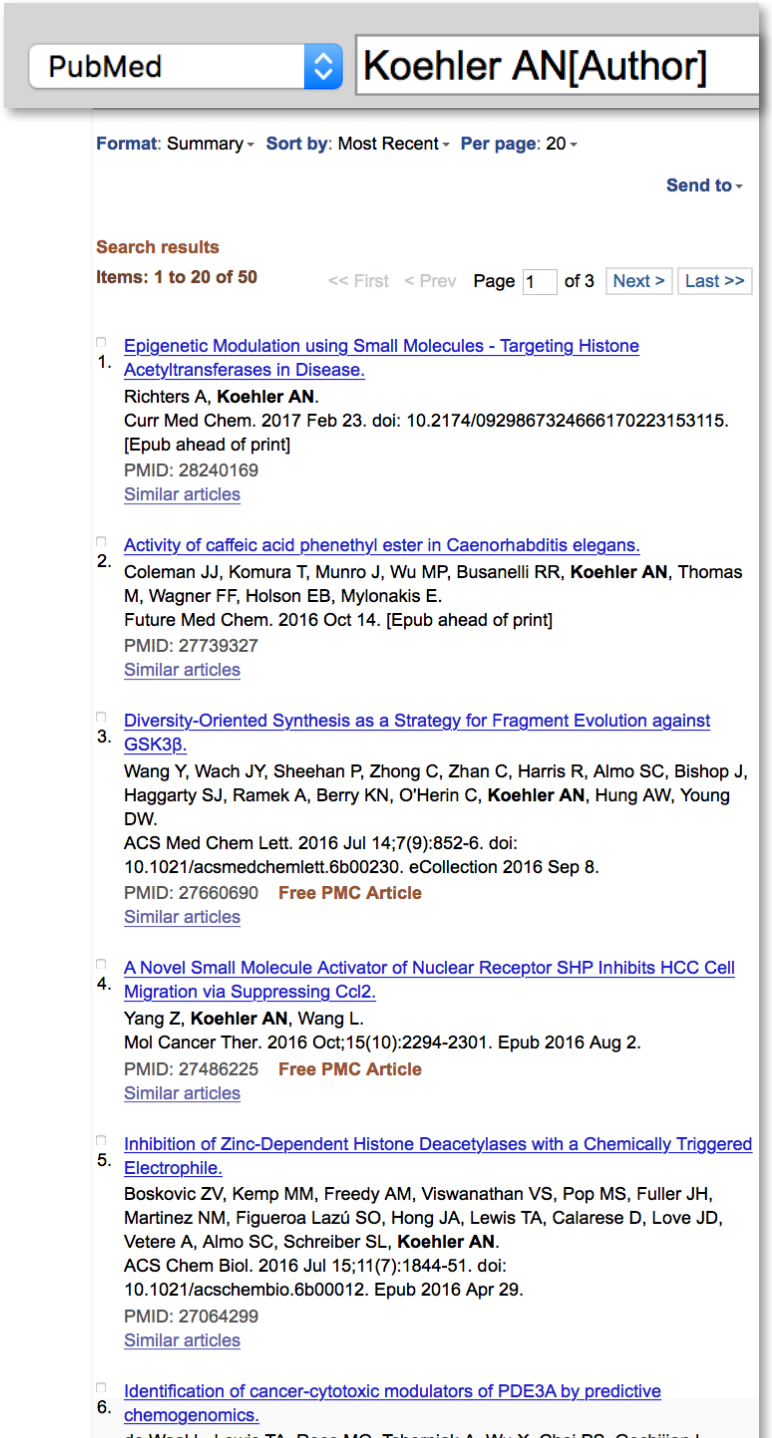
Your title and abstract convey your central hypothesis and take-home message.



Titles

Think about the last lit search you did.

1. Why did you pick the papers you picked to read?
2. What stood out to you?



Titles answer for your audience: *What did you find? So what?*

Inulin modulates conspecific antagonism towards vancomycin-resistant *B. subtilis* strain BF819 in the human gut microbiome

vs.

A human gut commensal exhibits targeted antagonism towards an antibiotic-resistant clinical counterpart

Simplify your title by identifying key terms

KEY NOUNS | KEY VERBS

Novel methods for early prediction of undesirable interference by microbial inhabitants of the human gut with metabolism of the cardiac drug digoxin give rise to strategies for alleviating drug inactivation

NEW AND IMPROVED TITLE:

"Predicting and alleviating drug interference by human gut microbiome"

LESS INFORMATIVE IF TOO SIMPLIFIED:

"Novel methods for prediction of drug interference"

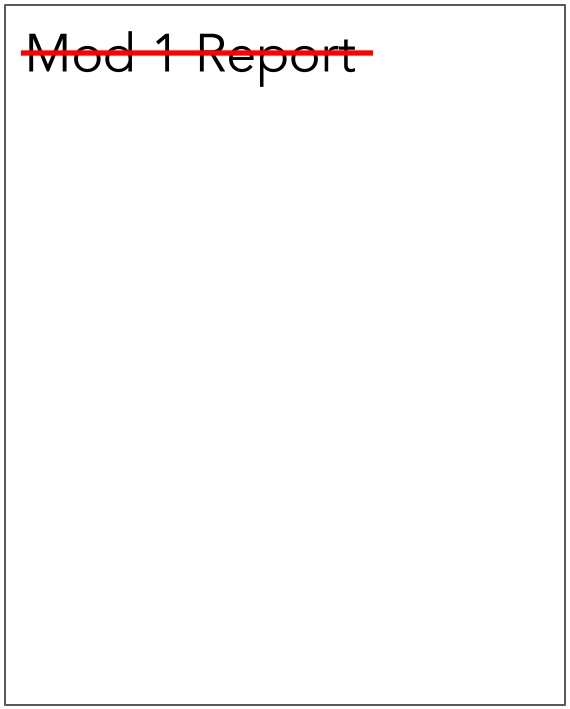
How could we edit this title?

Surveying somatic mutations in P53, EGFR, BRCA1, and HRAS for impact on MCF7 tumors with heterogeneous cell composition.

Substitute jargon to attract a broader audience

Surveying the impact of breast cancer oncogenes on tumor heterogeneity

What will your titles be?



Untitled (1968)
Mark Rothko
Phillips Collection
Washington, DC

Abstracts

Unscramble this real abstract

ARTICLE

doi:10.1038/nature13824

Clonal dynamics of native haematopoiesis

Jianlong Sun[1,2,3], Azucena Ramos[1], Brad Chapman[4], Jonathan B. Johnnidis[5], Linda Le[1], Yu-Jui Ho[6], Allon Klein[7], Oliver Hofmann[4] & Fernando D. Camargo[1,2,3]

Assemble the abstract

1. It is currently thought that life-long blood cell production is driven by the action of a small number of multipotent haematopoietic stem cells.

2. Evidence supporting this view has been largely acquired through the use of functional assays involving transplantation.

3. However, whether these mechanisms also govern native non-transplant haematopoiesis is entirely unclear.

4. Here we have established a novel experimental model in mice where cells can be uniquely and genetically labelled *in situ* to address this question.

5. Using this approach, we have performed longitudinal analyses of clonal dynamics in adult mice that reveal unprecedented features of native haematopoiesis.

6. In contrast to what occurs following transplantation, steady-state blood production is maintained by the successive recruitment of thousands of clones, each with a minimal contribution to mature progeny.

7. Our results demonstrate that a large number of long-lived progenitors, rather than classically defined haematopoietic stem cells, are the main drivers of steady-state haematopoiesis during most of adulthood.

8. Our results also have implications for understanding the cellular origin of haematopoietic disease.

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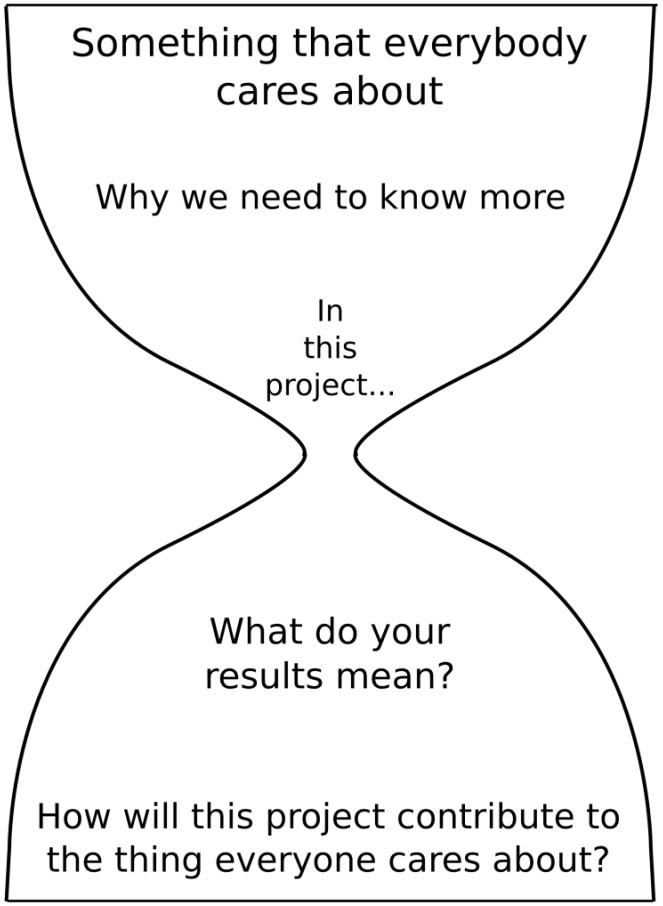
Abstract

It is currently thought that life-long blood cell production is driven by the action of a small number of multipotent haematopoietic stem cells. Evidence supporting this view has been largely acquired through the use of functional assays involving transplantation. However, whether these mechanisms also govern native non-transplant haematopoiesis is entirely unclear. Here we have established a novel experimental model in mice where cells can be uniquely and genetically labelled in situ to address this question. Using this approach, we have performed longitudinal analyses of clonal dynamics in adult mice that reveal unprecedented features of native haematopoiesis. In contrast to what occurs following transplantation, steady-state blood production is maintained by the successive recruitment of thousands of clones, each with a minimal contribution to mature progeny. Our results demonstrate that a large number of long-lived progenitors, rather than classically defined haematopoietic stem cells, are the main drivers of steady-state haematopoiesis during most of adulthood. Our results also have implications for understanding the cellular origin of haematopoietic disease.

An effective abstract is an hourglass-shaped message.



General background

Specific background

Knowledge gap, Unknown

HERE WE SHOW...

Results

Implication

Significance

See how the hourglass structure applies

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General background

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HERE WE SHOW…

See how the hourglass structure applies

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Results

Our results demonstrate that a large number of long-lived progenitors, rather than classically defined haematopoietic stem cells, are the main drivers of steady-state haematopoiesis during most of adulthood.

Implication

Our results also have implications for understanding the cellular origin of haematopoietic disease.

Significance

Signal words help guide the reader

Question + Experiment	Results	Answer/ Conclusion	Implication
To determine whether…, we…	We found…	We conclude that…	These results suggest that…
We asked whether…	Our results show…	Thus,…	These results may play a role in…
To answer this question, we…	Here we report…	These results indicate that…	X can be used to…
X was studied by…			

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general background

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specific background

knowledge gap

here we show...

results, including the methodological approach and the interpretation of the results

implication of results (they even say "implications"!)

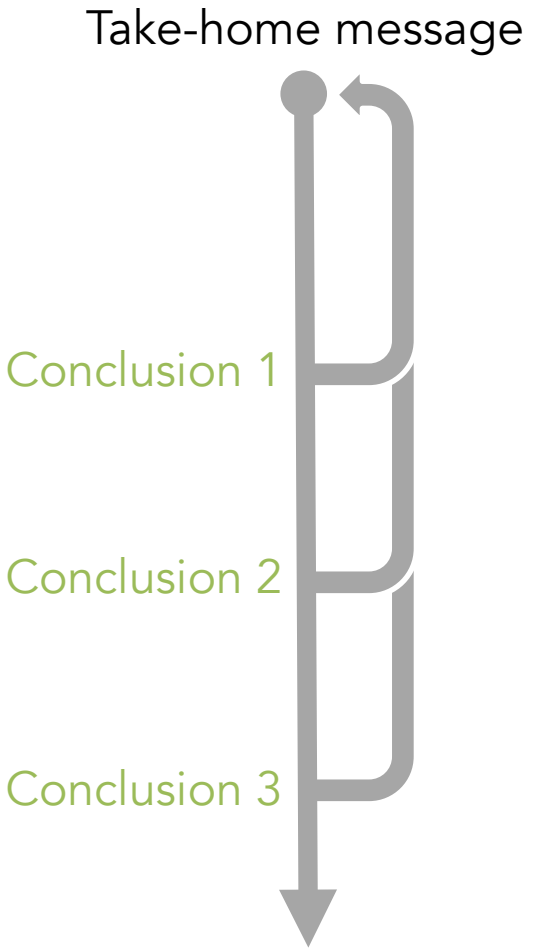
See more in the BECL CommKit

Your "Here we show" sentence relates directly to your take-home message

Examples from the same Module:

Here we show the functionality of the CometChip Assay by testing the CometChip assay's cell loading capabilities and quantifying the amount of DNA damage resulting from oxidation.

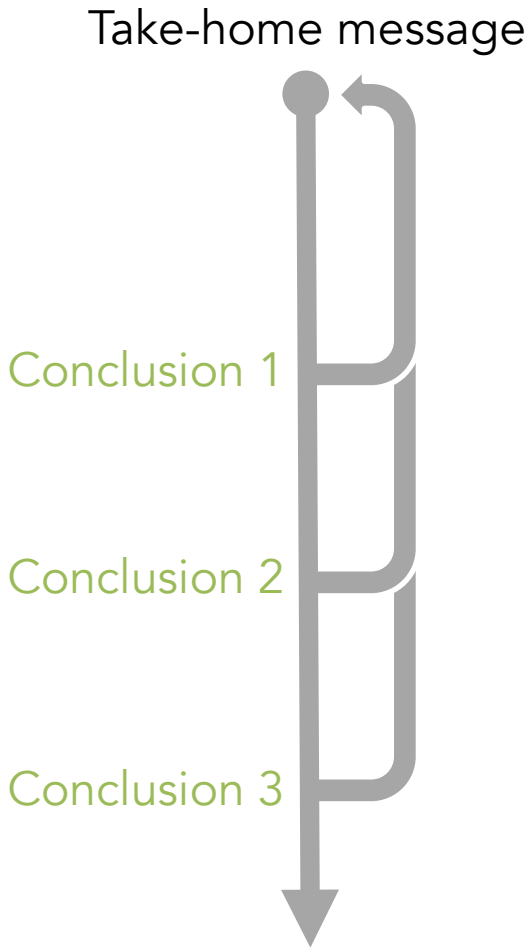
This study examines the impacts of H_2O_2 and MMS, two DNA-damaging agents, on mouse embryonic fibroblast strains that are wild-type or mutant for enzymes in the base excision repair pathway.



Abstracts contain the key results that support your take-home message

The data suggest that cells with functional BER are able to proceed with DNA repair, introducing DNA single-stranded breaks as repair intermediates, and moreover that BER is necessary but not sufficient for complete DNA double-stranded break repair.

We found that MMS (a base methylating agent) and H_2O_2 (a base oxidizing agent) caused DNA damage that was detectable by the CometChip assay. We also found that knocking out the enzymes that remove these damaged bases (Aag and Ogg, respectively) in the BER pathway did not affect detected DNA damage. If Aag was added back or the MMS incubation time was increased, however, more damage was revealed in the knockout.



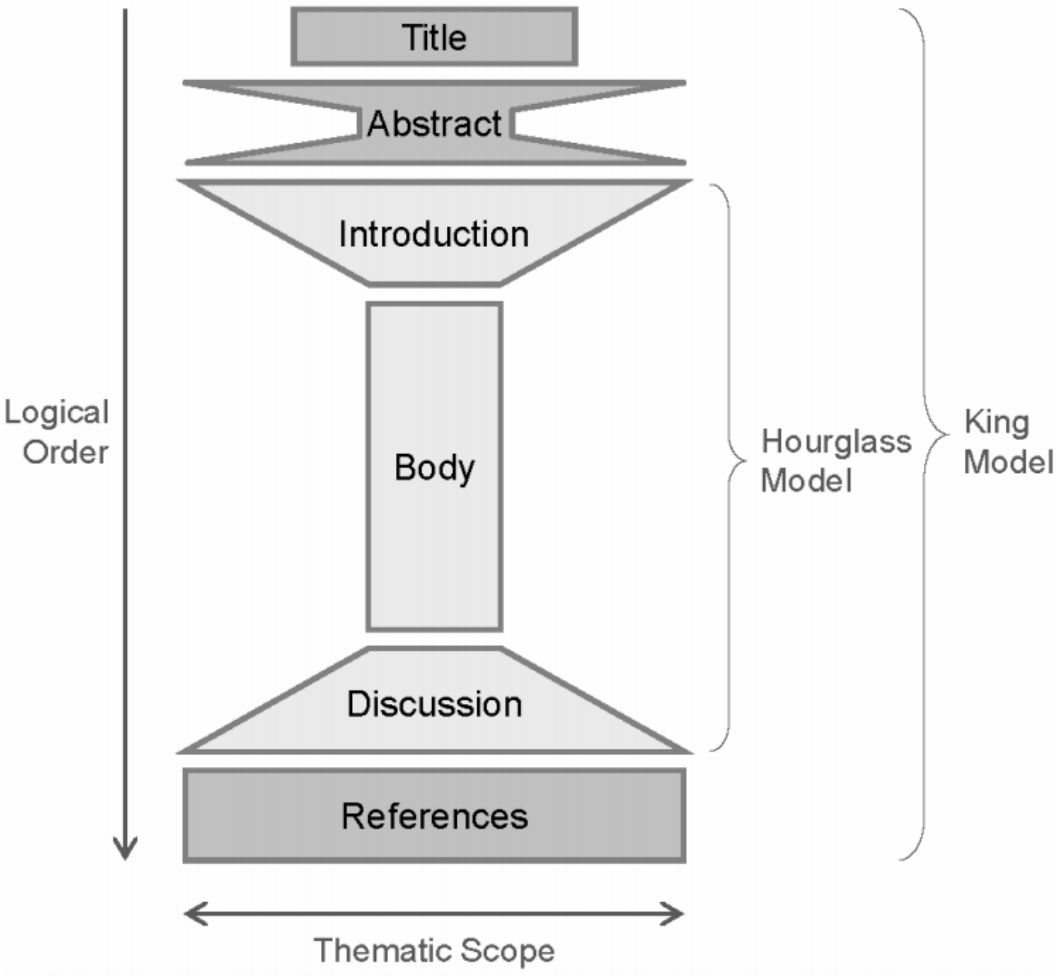
Include a brief description of key methods you used, if it aligns with your message

The rate and extent to which the different cell types respond to the chemical treatments will be determined, in addition to their capacity to maintain genomic stability. In order to determine the percentage of damaged DNA, the DNA was embedded in a gel agar and subjected to electrophoresis at high pH to allow the damaged DNA to segregate from the nucleus. The intensity of DNA that migrated away from the nucleus into what looks like a comet tail corresponded to the amount of damaged DNA in that particular cell and the extent to which the BER pathway repaired the damage.

VS.

To detect DNA single-stranded and double-stranded breaks, the CometChip assay and immunofluorescent staining were used, respectively.

Successful scientific writing is fractal



http://dbis.rwth-aachen.de/~derntl/papers

Abstracts are a preview of the shape of a full paper

General background	Something everyone in your audience cares about.	**Introduction**: beginning
Specific background	Zoom in from General Background to the thing you did.	**Introduction**: middle
Knowledge gap, Unknown	Question that will be answered by your research. Problem, phenomenon that is not understood.	**Introduction**: end
HERE WE SHOW	Conclusion, answer to the Unknown	**Introduction**: end **Results**: end **Discussion**: beginning
Results	Brief summary of approach, high-level results. Common pitfall = too much methods vs. findings.	**Introduction** (high level) **Results** (high level) **Methods**
Implication, Significance	*So what?* What do your results mean for the thing everyone cares about?	**Discussion**

Verb tense changes with section

Present Tense | Past Tense

Abstract

It is currently thought that life-long blood cell production is driven by the action of a small number of multipotent haematopoietic stem cells. Evidence supporting this view has been largely acquired through the use of functional assays involving transplantation. However, whether these mechanisms also govern native non-transplant haematopoiesis is entirely unclear. Here we have established a novel experimental model in mice where cells can be uniquely and genetically labelled in situ to address this question. Using this approach, we have performed longitudinal analyses of clonal dynamics in adult mice that reveal unprecedented features of native haematopoiesis. In contrast to what occurs following transplantation, steady-state blood production is maintained by the successive recruitment of thousands of clones, each with a minimal contribution to mature progeny. Our results demonstrate that a large number of long-lived progenitors, rather than classically defined haematopoietic stem cells, are the main drivers of steady-state haematopoiesis during most of adulthood. Our results also have implications for understanding the cellular origin of haematopoietic disease.

Quick Writing Improvements

Quick tips to improve your writing

- Word choices
- Sentence structure
- Transition phrases to convey logic

Activity:

Choose the right word for the context.

Word Choice:

- The response was blocked by phentolamine but was not *affected* by propanolol.
- The digoxin *concentration* was increased from 0.5 to 2.5 ng/ml.
- At frequent *intervals* we measured pH, P_{O_2} and P_{CO_2} in arterial blood, and during each *period* of study we measured pulmonary blood flow two or three times.
- 75% nitrous oxide *is* a subanesthetic concentration in the dog.

Word Choice: Simplify.

efficacious	effective
utilize	use
elucidate	explain
proximal	close

Word Choice: Be quantitative.

development rate was fastest at the higher temperature

development rate at 30°C was 10% faster than the development rate at 20°C

Sentence Structure:

Make the topic the subject.

The patient showed no change in symptoms.

The patient's symptoms did not change.

Transition statements provide a logical relationship between sentences.

As a result,…
Given this observation,…
According to this theory,…
In order to accomplish…

Avoid novelty claims.

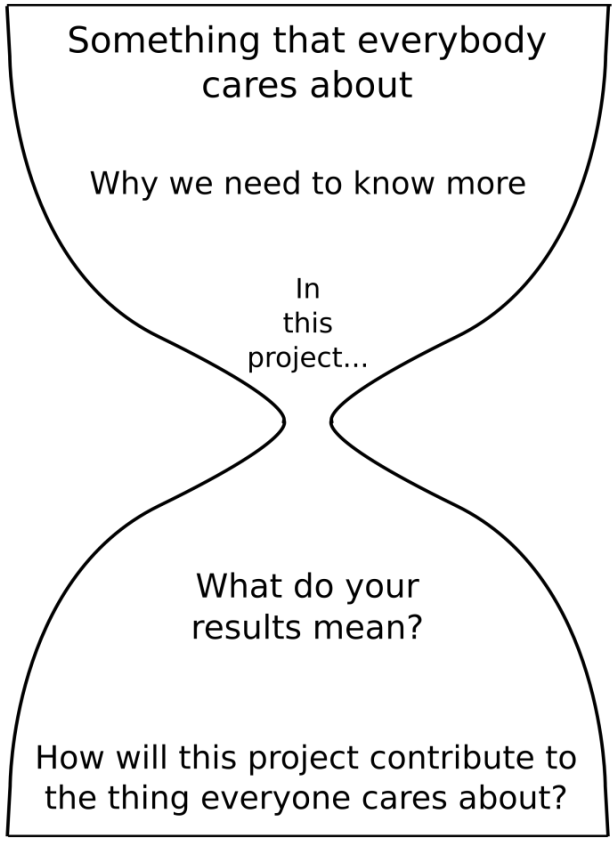
How do you know you're the first?

A surprising result, *unanticipated*, *against common dogma*, but **not** *unprecedented*

Appropriately qualified, there are certain "firsts" you do know…

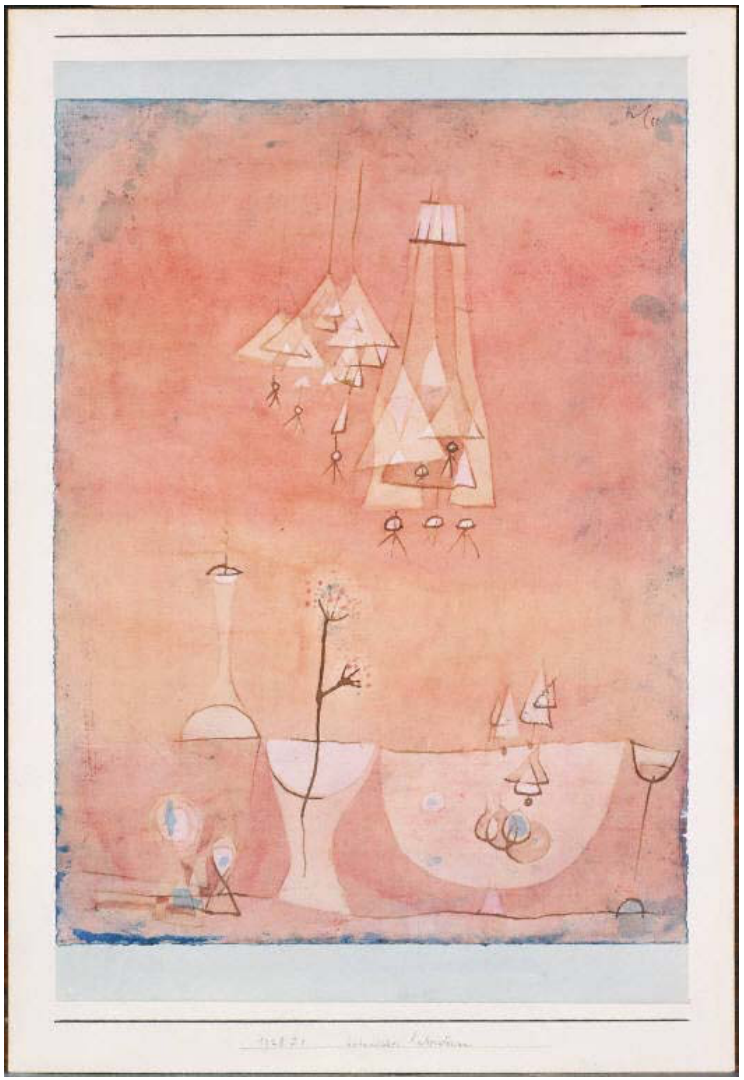
When drafting your abstracts and titles, consider these questions.

1. What is the problem?
2. Where is the gap?
3. What are you doing?
4. What is the implication?



Take-homes for Titles and Abstracts:

- Highlight your take home message: identify your research question & what your contribution is.
- Focus on findings, not methods.
- Be succinct.
- Be quantitative.



Botanical Laboratory (1928)
Paul Klee

Back to lab!

Unscramble this abstract

Evidence supporting this view has been largely acquired through the use of functional assays involving transplantation.

Using this approach, we have performed longitudinal analyses of clonal dynamics in adult mice that reveal unprecedented features of native haematopoiesis.

Our results demonstrate that a large number of long-lived progenitors, rather than classically defined haematopoietic stem cells, are the main drivers of steady-state haematopoiesis during most of adulthood.

It is currently thought that life-long blood cell production is driven by the action of a small number of multipotent haematopoietic stem cells.

Our results also have implications for understanding the cellular origin of haematopoietic disease.

Here we have established a novel experimental model in mice where cells can be uniquely and genetically labelled in situ to address this question.

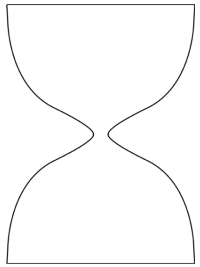
However, whether these mechanisms also govern native non-transplant haematopoiesis is entirely unclear.

In contrast to what occurs following transplantation, steady-state blood production is maintained by the successive recruitment of thousands of clones, each with a minimal contribution to mature progeny.

Choose the right word for the context.

- The response was blocked by phentolamine but was not *(affected, effected)* by propanolol.
- The digoxin *(amount, concentration, content, level)* was increased from 0.5 to 2.5 ng/ml.
- At frequent *(intervals, periods)* we measured pH, P_{O_2} and P_{CO_2} in arterial blood, and during each *(interval, period)* of study we measured pulmonary blood flow two or three times.
- Seventy-five percent nitrous oxide *(represents, is)* a subanesthetic concentration in the dog.

Here are the components of an effective abstract



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HERE WE SHOW	Conclusion, answer to the Unknown
Results	Brief summary of approach + very high-level results. Common pitfall = too much of Methods/Results
Implication, Significance	So what? What do your results mean for the thing everyone cares about? Next steps?