

Word Count (1500)

From the following list choose one (HER2, PALB2, NF1, PIK3CA, EZH2, ERK2)

Using the publicly available websites. I.e. human protein atlas (proteintlas.org) explore the role of this gene(s) in cancer. This can be in a specific cancer type, or multiple cancer types. Based on these explorations, and knowledge gained through further research of the subject area, generate a new hypothesis we would like to test.

*For example, you discover the gene you are interested in (gene X) is mutated in a high percentage of ovarian cancers. You also discover that gene x expression has a strong correlation with expression of a gene (gene y) that plays a key role in colon cancer. Further research reveals that gene y is localised at the mitochondria and plays a role in metabolism. Based on these data, you may hypothesise that mutation of gene x causes alterations in mitochondria/metabolism that leads to ovarian cancer progression.*

Title

Background: Data from the literature that provides the rationale for the study-include the cancer type(s) you will explore and the rationale for the study (gaps in knowledge). Figures are encouraged to explain complex pathways. (total ~800 words)

Preliminary data: Choose key pieces of data identified in the exploratory stage (plots or images). Present these as preliminary data. We suggest generating 2-3 figures of these data. Each figure should illustrate one key finding, with a maximum of 3 panels (images or graphs) per figure to support that finding. The figures should have clear legends that explain all elements. Write a short section describing how these data were arrived at and the key findings (results). (~200 words).

Hypothesis: The new hypothesis you arrived at from these preliminary data.

Project outline: We would like you choose one on omic approach to test this hypothesis. Describe the approach and how you will set up an experiment, or a series of experiments, using this approach. Think about the model you will use (in vitro or in vivo), the samples required and how the data will be analyzed (~450 words).

References (max 25. Not counted in word count)

The focus is to generate hypothesis from exploration of publicly available datasets and use of omics technologies to test that hypothesis. However, the background should provide good rationale for this study and, as with all scientific reports/grants papers, there should be flow through the document and a good “story” presented.