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| **PROTOCOL TEMPLATE** |

LOGO

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| **PROJECT ID** |  |
| **Title:** |  |
| **Version:** | **01** |
| **Author(s)**  **(+ initials)** |  |
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| --- | --- | --- | --- |
| **Revision / History** | | **Review** | |
| **Version** | **Change description** | **Date** | **Initials** |
| 01 | First issue |  |  |
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This template aims to guide through the production of a clear protocol. Text in red should be removed or replaced by appropriate content. Please select together with your supervisor the content blocks required for your project and remove the other, not applicable ones.

**Writing style:**

Use the active voice as much as possible; avoid to use “I” or “we”. Use concise and clear style to guide the reader through a step-by-step process.

**Format:**

The document from section 1. – 6. should be 5 pages maximum. The first page should list clearly all the authors of the protocol. Please use minimum font size of 11.

**Logbook:**

Do not forget to indicate the contribution of each author into your logbook for future discussion with the project supervisor. (not in this document)

**START OF PAGE LIMIT: 1/5**

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| 1. INTRODUCTION |

Give here a brief introduction of the technique and context in which you are using it.

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| 2. EQUIPEMENT / MATERIAL / SOFTWARE / DATA / SAMPLES (select what is applicable) |

Detail here specific instrumentation / material / software / data or biomedical samples you obtained or used to perform the experiments.

*Here are some examples…*

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| **Name** | **Description** | **Supplier / Reference** |
| Leica 3001 Fluorescence microscope | Microscope equipped for fluorescence microscopy | Leica Ltd., Tours, France |
| Lung tissue samples | Lung tissue samples from patients with severe COVID19 infection and healthy controls. Samples were obtained within a clinical trial, permission of METC granted (permission number 2022-8299) | MUMC, Department of pulmonology |
| Cytoscape (version 9.2) | Software for creation and analysis of networks. | <https://cytoscape.org/>  Shannon et al. 2013 |
| GEO-E-32998 | Transcriptomics dataset comparing SARS-CoV2 infected lung epithelial cells with healthy control, originally published by Doe et al. 2021 and available on GEO database. | Doe et al. 2021  GEO-E-32998 |
| MES buffer solution | PH buffered MES (2-(N-morpholino)ethanesulfonic acid) solution. | BASF, Ludwigsburg, Germany |

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| 3. HEALTH AND SAFETY (if applicable) |

We will be working entirely with computers thus this section is not applicable

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| 4. SPECIFIC RECOMMENDATIONS / WARNING (if applicable) |

We are using GitHub, so we have to take caution with working on our code together. If we work individually, we have push our code not together otherwise the GitHub will not accept multiple edits at once and some of the code will be lost.

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| 5. PROCEDURE TO FOLLOW |

These are the procedure to follow to get results

1. Download the lung cancer data from GEO database​ to perform the analysis of the data
2. Install and require libraries in R, the libraries we will be using are DESeq2, ggplot2, dplyr, pheatmap, clusterProfiler, org.HS.eg.db and GEOquery.
3. Load the count matrix, it has the data from step 1
4. Load metadata, this can be required from the R library GEOquery
5. Create a DESeq2 dataset in R to create a statistical model
6. Perform Quality control
7. Get results and sort by pValue
8. Filter significant genes with adjusted p-value < 0.05
9. Visualize results such as volcano plot, heatmap, MA plot
10. Functional enrichment analysis using GO, KEGG

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| 6. DATA ANALYSIS AND STATISTICS (if applicable) |

Give here a brief overview of how to analyse and present the obtained data. Name the software (e.g. Excel, R, or SPSS – also in section 2.) and statistical methods (e.g. students t-test, Fisher’s test) you used for data analysis.

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| 7. LITERATURE |

Indicate any literature if needed, or reference to other documents needed to understand / complement this protocol. That includes scientific papers, websites, databases or books.

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| 8. APPENDIX (if required) |

Add here any materials or information that are needed to understand/reproduce the protocol, but are too extensive to add to the main text.