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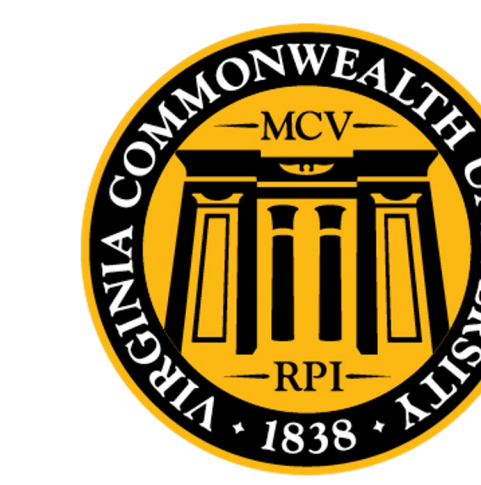
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Exploiting the SARS-CoV-2 Spike Protein Components to Guide Molecular Level Entry of a BAG-1 Inhibitor in the Treatment of Breast and Lung Cancers

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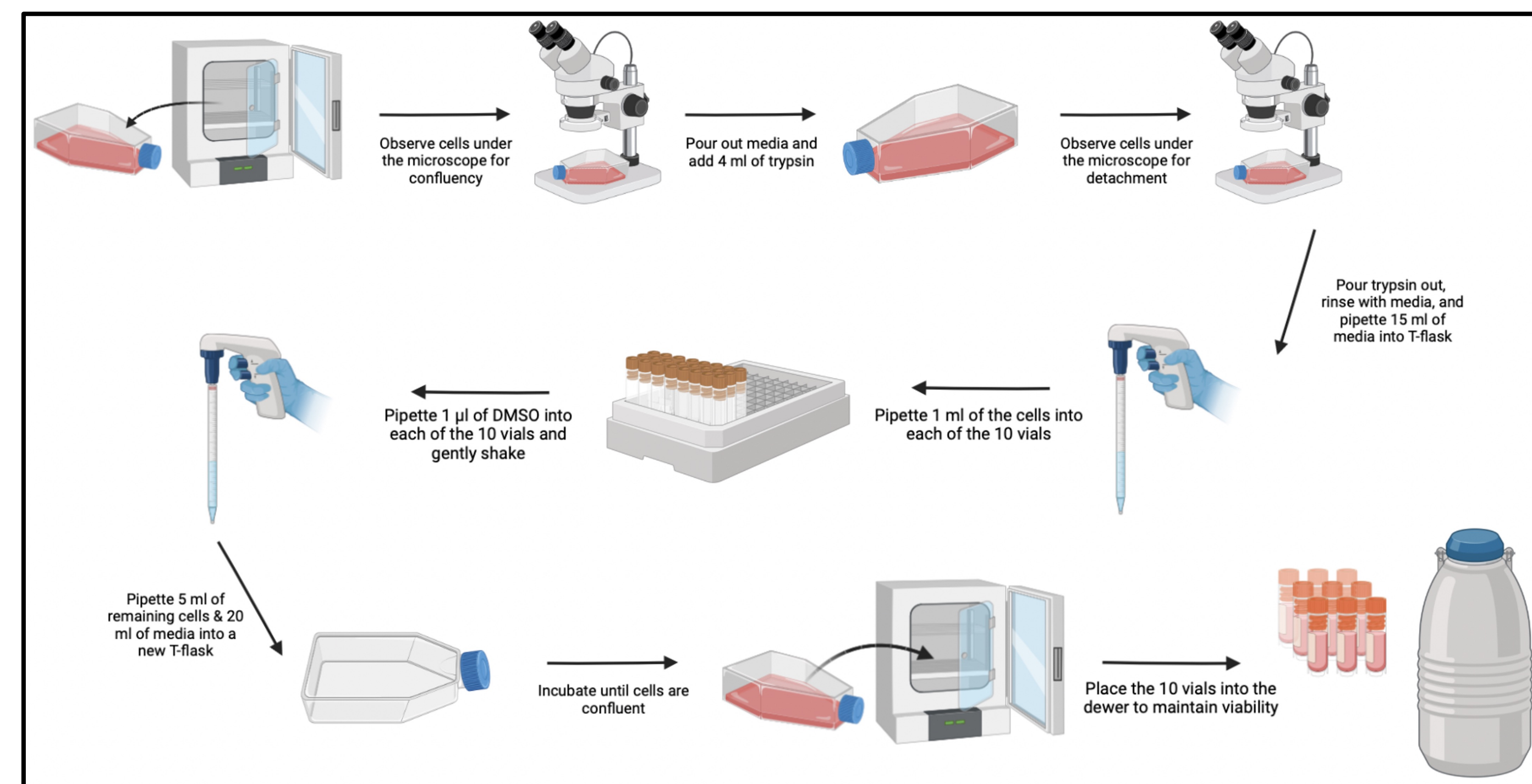
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Abstract

Chemoresistance of lung cancer cells is the primary reason as to why limitations occur with cancer treatments. A protein, known as BAG-1, is responsible for many cellular activities including cellular stress response, cell growth, and apoptosis (regulated cell death). When overexpressed, the protein has been linked to the anti-apoptotic behavior of cancer cells. BAG-1 can combine to heat shock proteins (HSPs), a family of helical molecular chaperones that are known to aid in the maturation of proteins, refolding, and degradation. This response plays a crucial role in the study of chemoresistance in cancer patients due to its detrimental nature. Prior, this combination was combated by using a synthesized poly-arginine linked peptide inhibitor alongside cell penetrating peptides (CPPs) through targeted binding domains. However, it has been found that the Spike protein of SARS-CoV-2 uses several small subdomains to efficiently bind to human epithelial cells at the nanomolar level. **This study aims to focus on the binding complex of the BAG-1 and Spike proteins to form an anti-apoptotic inhibitor that can result in a potential specific binding mechanism for drug delivery of lung cancer treatments.**

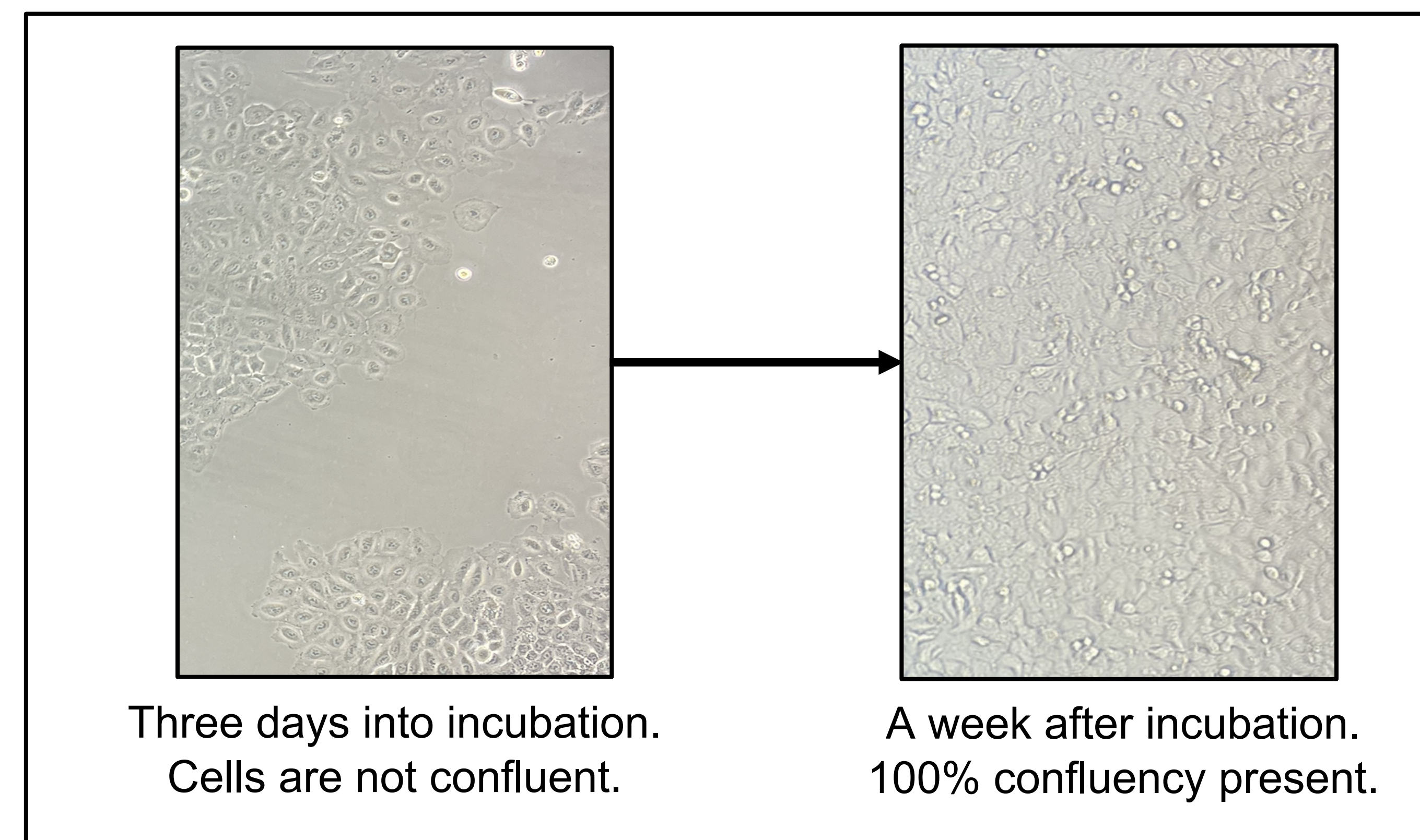
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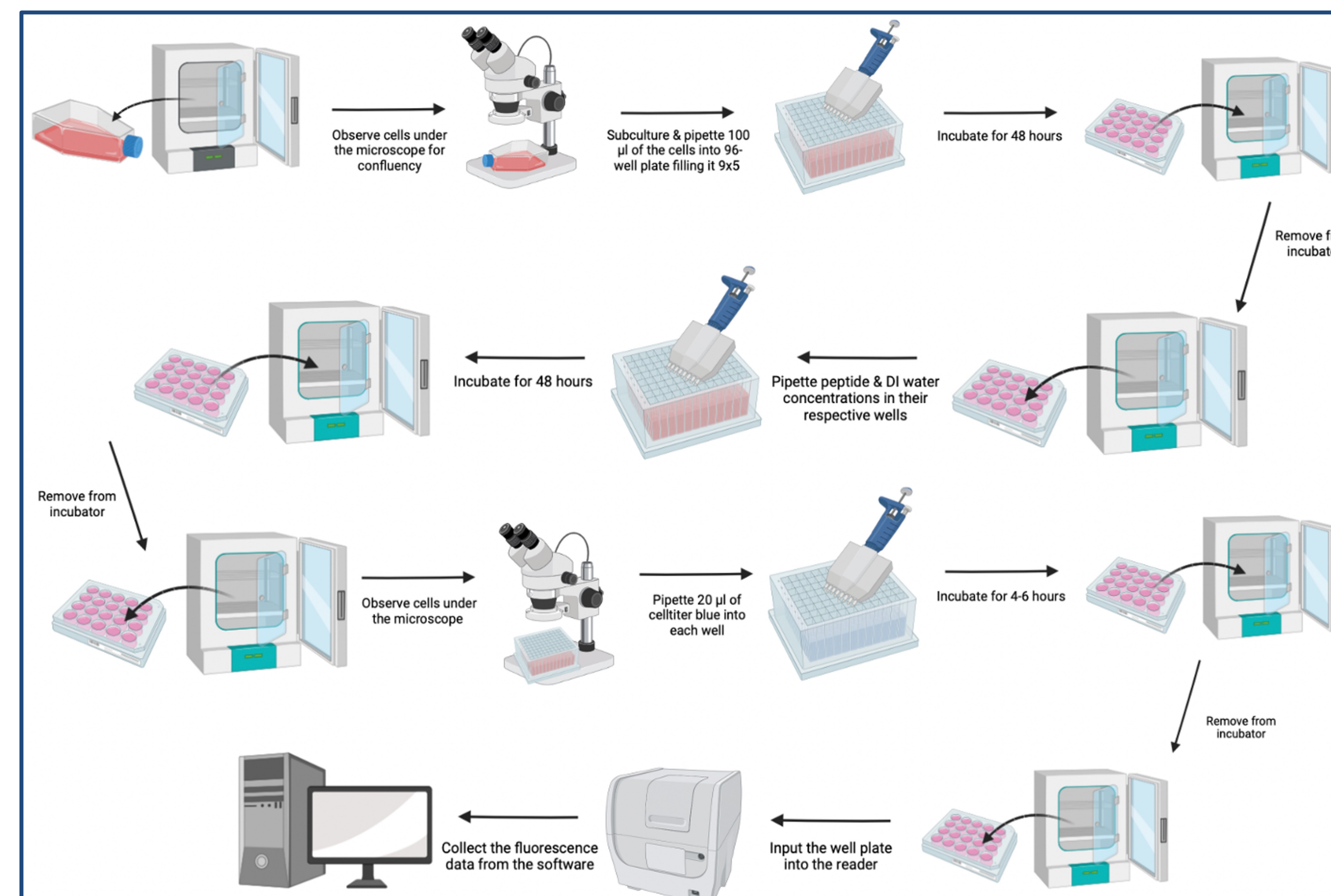
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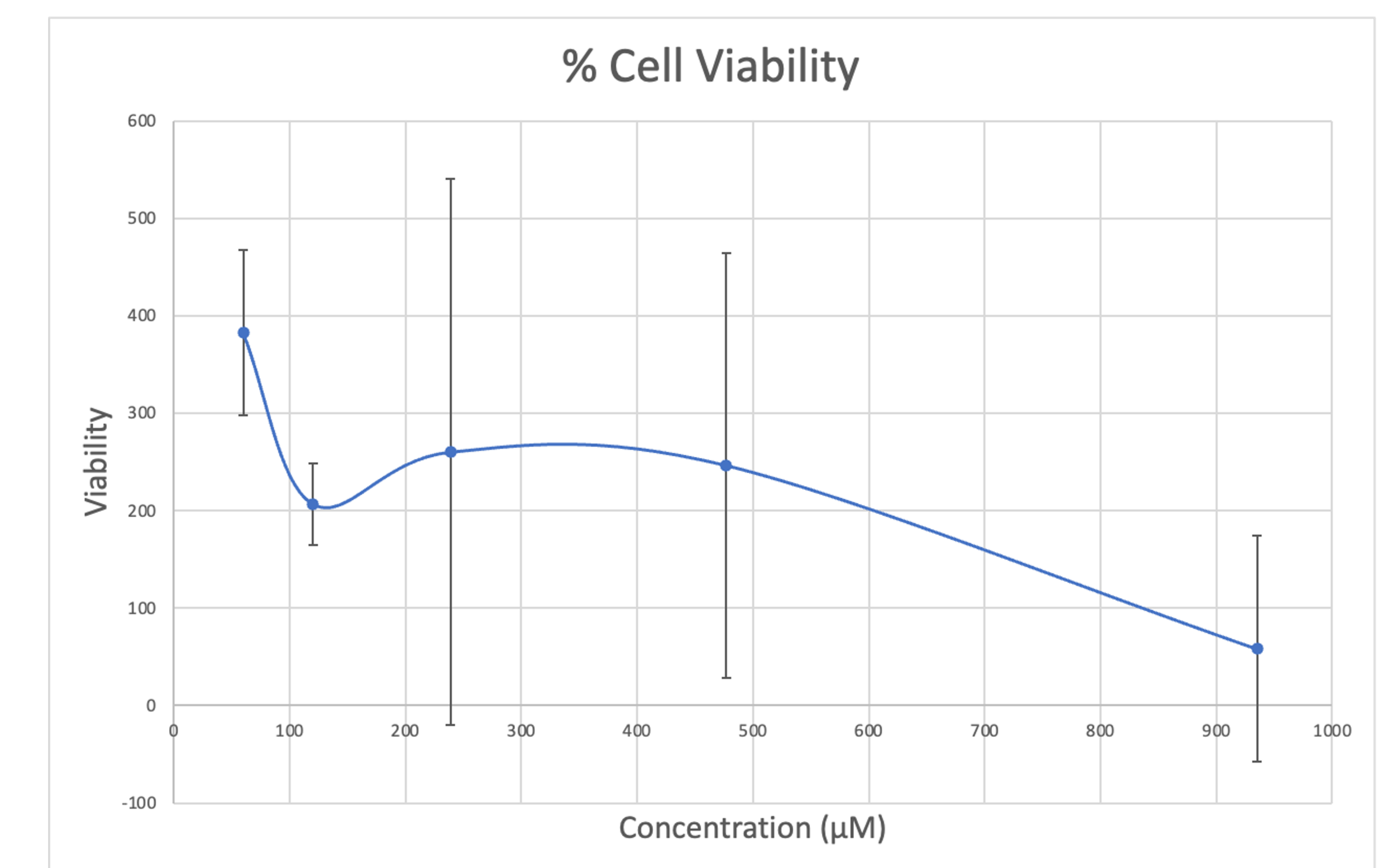
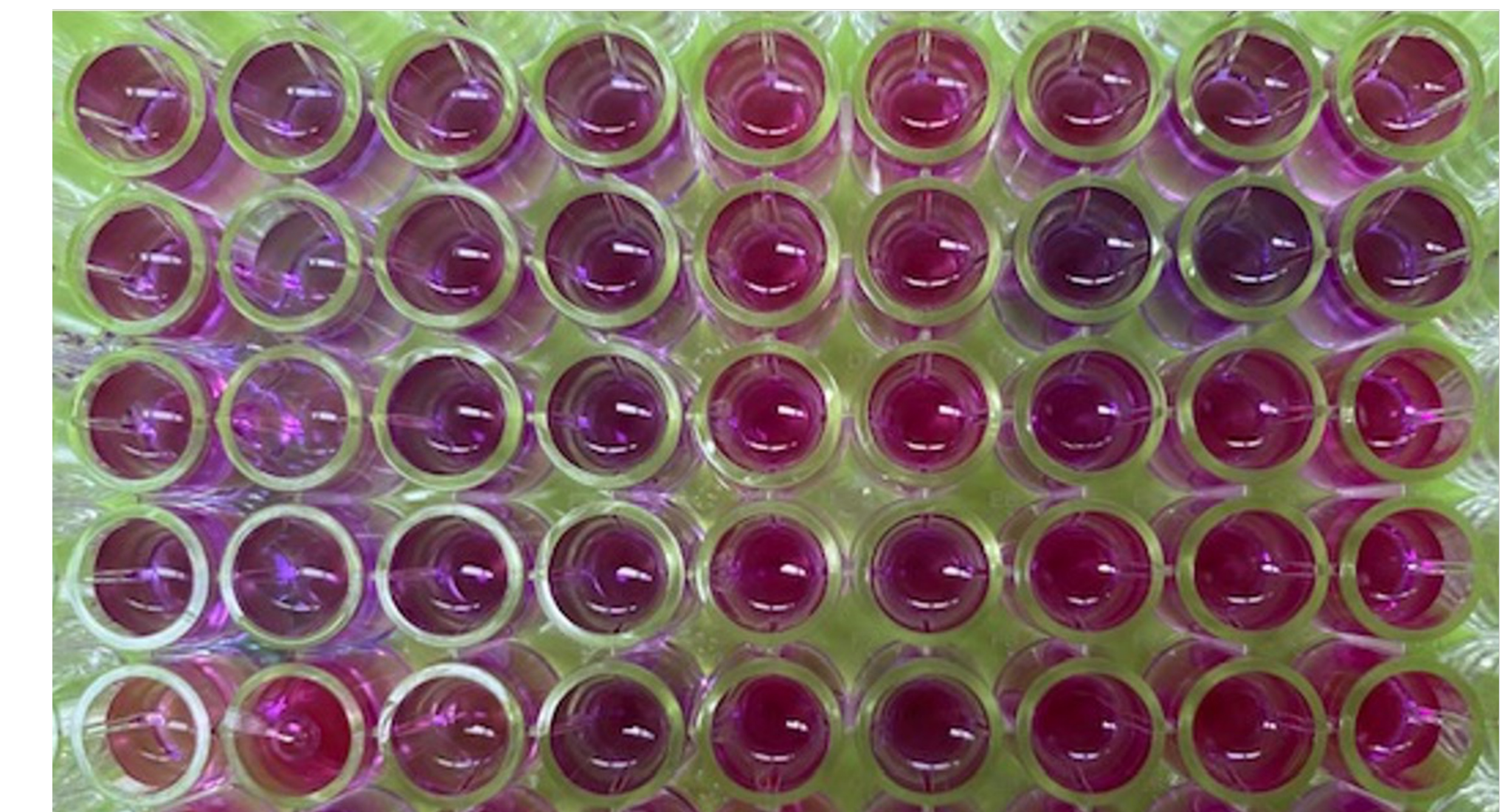
Cell Growth



Peptide Toxicity Study



Cell Viability



Conclusion & Future Direction

- Water does not cause starvation to the cells due to dilution
- 10% ethanol makes a good control for the study
- This delivery method proves to be a viable option in the delivery of cancer therapeutics
- Future Direction: Examine the use of the Spike protein subdomain as peptide penetrators by conducting another toxicity study

Acknowledgements

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