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Targeted Protein Delivery Using Modified Anthrax Toxin Protective Antigen

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Abstract

Background: It would be highly desired to develop effective strategies for trans locating tailored binding proteins to the cytosol since they might target fat and hydrophobic protein-protein interfaces, which would expand the amount of the druggable proteome. Two levels of specifcity would be gained, one for the cell type and the other for the cytosolic

protein payload make up anthrax toxin. By combining a chosen ankyrin repeat protein with PA, it is possible to engineer PA to abolish binding to its own receptor and instead bind to a desired receptor, leading to uptake in different cell types.

Results:
are both constrained by prepore-to-pore conversion of redirected PA that already takes place at the cell surface. We proposed that the deficiency of a stabilising interaction with the wild-type PA receptor is the cause. Now, PA has been redesigned to include the CMG2 anthrax receptor binding domain followed by a DARPin that binds to the desired receptor. This construct may be supplied at considerably higher concentrations without causing toxicity, undergoes prepore-to-pore conversion only in late endosomes, and is thus stable. As a result, it delivers substantially larger

Conclusion: We think that this reengineered system represents a significant advancement in the quest for effective protein delivery to the cytosol in specifc cells.

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Discussion

Results

Conclusions

Declaration of competing interest

References

Jang KS, Kim YH (2018) Rapid and robust MALDI-TOF MS techniques for microbial identification: a brief overview of their diverse applications. Microbiology 56:209-216.

Kim E, Kim J, Choi I, Lee J, Yeo WS, et al. (2020) Organic matrix-free imaging BMB reports 53:349.

3. Wang Y, Han Y, Hu W, Fu D, Wang G (2020) - Journal of separation science 43:360-371.

4. Ishii K, Zhou M, Uchiyama S (2018) dynamic protein complex. Biochim Biophys Acta Gen Subj 1862:275-286.

5. Takeo E, Sasano R, Shimma S, Bamba T, Fukusaki E, et al. (2017) Solid-phase analytical derivatization for gas-chromatography–mass-spectrometry-Journal of bioscience and bioengineering 124:700-706.

6. Micalizzi G, Vento F, Alibrando F, Donnarumma D, Dugo P, et al. (2021) Cannabis Sativa L.: A comprehensive review on the analytical methodologies

1637: 461864.

Recent advances in chemical derivatization-based chromatography-mass spectrometry methods for analysis of aldehyde Se pu Chinese Journal of Chromatography 39:845-854.

8.

Questions: A Multi-Omics Study of the Stomach Content of the Oldest Human Ice Mummy, the 5300-Year-Old Iceman or Oetzi. In Proteomic Profiling: 1-12.

9. Kuwata K, Itou K, Kotani M, Ohmura T, Naito Y, et al. (2020) enables matrix-
Rapid Communications in Mass Spectrometry 34:8720-8729.