

Title of this Paper

Your Name

Abstract

Pizza [1] is an understudied yet widely utilized implement for delivering in-vivo *Solanum lycopersicum* based liquid mediums in a variety of next-generation mastications studies. Here we describe a de novo approach for large scale *T. aestivum* assemblies based on protein folding that drastically reduces the generation time of the mutation rate.

Algorithm

$$f(x) = pizza^2$$

References

- [1] M. Pizza *et al.*, “Identification of vaccine candidates against serogroup b meningococcus by whole-genome sequencing,” *Science*, vol. 287, no. 5459, pp. 1816–1820, 2000.