

## Designing peptides on a quantum computer

Hans Melo<sup>1</sup>, Vikram K. Mulligan<sup>2</sup>

<sup>1</sup>Menten Biotechnology Labs, Inc. Toronto, Canada.

<sup>2</sup>Systems Biology, Center for Computational Biology, Flatiron Institute. New York, USA.  
hans@menten.ai

We investigated the use of quantum hardware as a potential alternative for solving conformational search problems in protein design. We developed an algorithm, the qPacker, to frame the side-chain rotamer search as a constrained binary optimization problem and solve it on two types of quantum devices: quantum annealers (e.g. D-Wave), and gate-based quantum computers (e.g. Rigetti). The qPacker algorithm was successful in finding low energy solutions for side-chain conformational optimization problems of varying sizes, and in many cases yielding results superior to Rosetta's Monte Carlo/simulated annealing methods. These promising results foreshadow an exciting new route for emerging quantum computing technologies in synthetic biology and biochemistry with a wide range of applications in the pharmaceutical and chemical industries.

- [1] Gordon, DB; Mayo, SL (September 15, 1999). "Branch-and-terminate: a combinatorial optimization algorithm for protein design". *Structure*. **7** (9): 1089–98
- [2] Desmet J, de Maeyer M, Hazes B, Lasters I. (1992). The dead-end elimination theorem and its use in protein side-chain positioning. *Nature*, **356**, 539-542.
- [3] Voigt, CA; Gordon, DB; Mayo, SL (June 9, 2000). "Trading accuracy for speed: A quantitative comparison of search algorithms in protein sequence design". *Journal of Molecular Biology*. **299** (3): 789–803.
- [4] Leaver-Fay, A; Tyka, M; Lewis SM; et al. (Jan 12, 2011). "ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules." *Methods in Enzymology*. **487**:545-74.