

# Reviews

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## 1 Review of a review

### Resource-efficient quantum algorithm for protein folding

This is a review of [this](#) blog. Actually I did not understand the real paper it was referring to. That is why I read this review. What I understood that I have to go through two more topics to understand this paper. I have to understand Variational Quantum Eigensolver (VQE) algorithm, and a modified version of VQE to sample only the parts of the data relevant to the problem, a tool called Conditional Value-at-Risk (CVaR) VQE. I understood how they related this article to Levinthal's Paradox, but I did not understand how they imagined the structure of a protein as a three-dimensional tetrahedral lattice.

## 2 Review of a simple paper

### Potential of quantum computing for drug discovery

In this world of papers full of jargons and equations, finally I read a paper peacefully. [It](#) was well written. In a simple language it expressed a lot. This paper connected CADD with QC. Well I found the term VQE in this paper as well which means I MUST read this topic out. They explained two ways of using QC in CADD here. If we have proper information on the 3d structure of the target, we can introduce **protein folding**. But if we do not know the 3d structure properly, we are gonna use ligand based methods, mostly machine learning which is a big NO NO for us. But I remembered what Rayhan said about QC-BIO. We will do something with chemistry and make it look like bioinformatics. That is the case of this paper. I felt like they mostly worked with pure chemistry, and introduced it as bioinformatics, which was nice. Ultimately it feels like all these converges to that one old thing, **protein folding**.