Abstract Submitted
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A Novel Approach to Computational Protein Folding[1] MOLLY BALL, BRITTANY SHANNON, CHRISTOPHER FASANO, Monmouth College — Protein function is controlled by the shape of the folded protein, so computing the shape of a folded protein is a critical part of understanding how proteins work and how they might be engineered to function in particular ways. We present preliminary results from a novel way of computing protein structure. We take the position that this problem should be treated quantum mechanically and we present applications of techniques from low energy nuclear physics (VMC and GFMC) to this problem. We discuss potential strengths and weaknesses of this approach given our early experiences in computing simple structures

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