1163-68-341 **Tamar Schlick*** (`schlick@nyu.edu`), Department of Chemistry, 100 Washington Square, Silver Building, New York University, New York, NY 10003. *Structure-Altering Mutations of the SARS-CoV-2 Frame Shifting RNA Element.*

Due to the high sequence conservation of the SARS-CoV-2 viral genome, its close evolutionary relationship to other viruses, and the rise of gene editing and RNA-based vaccines, studies focused on the RNA genome form a complement to work focusing on the viral proteins. Here we apply our graph-theory-based framework for representing RNA secondary structures "RAG" (RNA-As Graphs) to destroy key structural features of the frame-shifting element of the SARS-CoV-2 virus, one of three highly conserved regions of coronaviruses, potentially inhibiting protein synthesis. Specifically, using RAG machinery of genetic algorithms for inverse folding adapted for pseudoknots, we computationally predict minimal mutations that destroy a stem and/or the pseudoknot of the frame-shifting RNA element. Such transformations potentially dismantle the virus against translation of the polyproteins that start the viral replication cycle. These findings not only advance our computational design of RNAs containing pseudoknots; they pinpoint to key residues of the virus as targets for anti-viral drugs and gene editing approaches. (Received September 03, 2020)