**Peptide inhibitors that disrupt viral-viral protein interactions in HIV-1: literature-based review**

Kevin Xia\(^1\), Madara Hetti Arachchilage \(^{1,2}\), Helen Piontkivska \(^{1,3}\)

\(^1\) Department of Biological Sciences, Kent OH 44242

\(^2\) mhetti@kent.edu; \(^3\) opiontki@kent.edu

Protein-protein interactions play a key role during each stage of the viral life cycle. Thus, inhibiting viral protein-protein interactions with the peptides derived from the binding interfaces is a promising approach for potential multi-epitope based treatments. However, molecular mechanisms underlying these protein interactions are not yet fully understood. This study is focused on a comprehensive literature survey to identify known peptide inhibitors derived from the HIV-1 viral proteins, which disrupt viral-viral protein interactions. We also discuss the limitations of these studies in identifying the most promising candidates. The candidate domains/regions identified in this survey will be used in the future bioinformatics analyses that examine patterns of coevolution between binding partners, specifically, in the attempt to differentiate between direct and indirect interactors (in other words, physical and functional interactions) using a coevolutionary approach (Hetti Arachchilage and Piontkivska 2016).