AlkB was first observed in *Escherichia coli* over three decades ago, but it wasn't until 20 years later that its function as a DNA repair enzyme was discovered. Since then, similar domains have been observed in the replicase polyproteins of a select few plant viruses. However, the exact function of the AlkB domain remains unclear. Previous studies have failed to ascertain the function or ancestry of the viral AlkB domains largely due to the dissimilarity of the viral AlkB protein sequences. Here we propose a project to build a phylogenetic tree based on the predicted folding patterns of these viral AlkB domains. By comparing the AlkB domain to other related viral sequences and similar bacterial, plant, and fungal AlkBs we hope to develop an evolutionary scenario based on structural changes that have arisen in viral AlkB since its recent integration into members of the viral families Alphaflexiviridae, Betaflexiviridae, Closteroviridae, Secoviridae, and Potyviridae. The results are expected to improve our understanding of the origin and elucidate potential functions for viral AlkB domains.