Biological systems enact several pathways to maintain genomic stability and mitigate mutations that can lead to harmful diseases such as cancer and neurodegeneration. One highly conserved repair pathway is mismatch repair (MMR), which functions to detect, remove, and replace nucleotide base mismatches and insertion/deletion mispairs generated during DNA replication. UvrD (helicase II) is an essential protein in the prokaryotic MMR pathway that functions to unwind double-stranded DNA (dsDNA) and translocate along single stranded DNA (ssDNA) with 3' to 5' directionality. Although the mechanism of *Escherichia coli (E. coli)* UvrD in the prokaryotic MMR pathways is well studied, further research is necessary to understand analogous functionality in eukaryotic organisms. Certain prokaryotic organisms bypass the methyl-directed and MutH-dependent pathway characteristic of *E. coli* MMR and are predicted to create a mechanistic bridge between MMR in *E. coli* and eukaryotes. Here, we investigate thermostable proteins from such prokaryotic organisms to better understand the role of helicases in eukaryotic MMR and, thus, aid in the understanding of MMR deficiencies in humans. In this work, *Thermus aquaticus (Taq)* UvrD will be transformed, expressed, isolated, and purified via systems of autoinduction, ammonium sulfate precipitation, His-tag affinity, chitin column purification, and SDS-PAGE. The helicase activity of *Thermoanaerobacter tengcongensis (Tte)* UvrD will be analyzed and quantified through native gel, FRET and ATPase assays. We predict that the extent of helicase activity of *Tte*-UvrD is consistent with that of *E. coli*-UvrD within their respective MMR pathways. More specifically, we propose that the unwinding velocity and ATPase activity of *Tte*-UvrD is comparable to the unwinding velocity and ATPase activity of *E. coli*-UvrD at their corresponding optimal temperatures (65˚C *Tte*; 37˚C *E. coli*). Performing this study on UvrD from the thermophilic *Tte* will provide more context for the highly conserved process of DNA mismatch repair and the understanding of the proposed hybrid model.