Organisms have mechanisms in place, such as mismatch repair (MMR), to repair the erroneous insertion and deletion of bases that arise during DNA replication. Helicases are enzymes that break hydrogen bonds between double-stranded DNA, and, in MMR, between mismatched bases. Our original research focused on *Thermus aquaticus* (*Taq*) UvrD, a homologue of a human helicase involved in MMR pathways. Elucidating how *Taq* UvrD binds to DNA, what factors affect its enzymatic activity, and which direction it unwinds DNA will better inform how elements of the MMR pathway work together to correct genetic mistakes. Expression and purification techniques using column chromatography were attempted, yet unsuccessful. Instead, commercially available *Thermoanaerobacter tengcongensis* (*Tte*) UvrD was obtained. Characterizing helicases from other thermophilic organisms such as *Tte* may provide additional benefits in understanding its role in MMR and therefore the application to eukaryotic mismatch repair. FRET assays were run on dsDNA with a 3' overhang and dsDNA without an overhang. It was determined that the DNA with the 3' overhang showed increased emission from the donor molecule because it was no longer being accepted by its corollary acceptor in FRET analysis. Additionally, characterization experiments, such as ATPase assays, were performed to determine the enzyme kinetics of *Tte* UvrD. The maximum velocity was determined to be 70.59 uM/s and the Michaelis constant was 194.2 mM with a turnover rate of 0.0007807 s^{-1}. This knowledge may provide insight into MMR's complicated mechanisms and has the potential to be clinically applied in cancer research, genetic research, and other fields.