# Investigating the Interaction Between Human DHX15 Helicase and Viral G-Patch Domain Within the Virions of Mason-Pfizer Monkey Virus Using UV Crosslinking and Immunoprecipitation

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The DHX15 helicase is a member of the DEAH/RHA helicase family. It is known to take part in several critical biochemical pathways including splicing of pre-mRNA or ribosome biogenesis. A subset of this helicase family is known to be regulated by a group of proteins which contain a conserved glycine-rich motif called G-patch domain (GPD). Moreover, the GPD has been proposed as an interaction intermediary between the helicase and the GPD-containing protein, aiding in the recruitment. Interestingly, this almost exclusively eukaryotic motif was also detected in the genome of several members of the *Betaretroviridae* family, including Mason-Pfizer monkey virus (M-PMV). M-PMV is a simple retrovirus used often as a model to study the life cycle of retroviruses and the GPD coding sequence is localized at the 3’ end of the *pro* gene, just upstream of the site of the second ribosomal shift. The GPD is a part of viral protease; however, it has been observed that in some cases it could be part of the M-PMV reverse transcriptase (RT). Taken together, we aimed to investigate whether the RT (through the GPD) interacts with the human DHX15, with viral genomic RNA being the site of the potential interaction. We used the crosslinking and immunoprecipitation coupled with sequencing (CLIP-seq) approach. Both DHX15 and GPD were immunoprecipitated independently from mature M-PMV virions and the RNA bound to these proteins was isolated, purified and sequenced. We postulated a hypothesis that if the two proteins with RNA-binding capabilities do interact with each other we would observe an overlap of detected binding sites. Indeed, our data suggest that these overlaps are present and thus provide support for the potential interaction between the human DHX15 and RT of the M-PMV in mature virions.