Identification of novel peptides are very important to reveal the cause of different diseases, and the field of Proteogenomics play an important role in this regard. In this way novel peptides are identified by searching MS/MS spectra against customized protein sequence databases. These databases are contained both the predicted novel protein sequences and sequence variants and are generated using genomic and transcriptomic sequence information. In this project the RNA seq data came from Darby et al’ s published work on repetitive elements. Where they identified some novel transcripts from 10238 different genes in the human OFC. Still now there is no evidence that the proteins containing the novel RE-containing exons are actually produced in humans. The overall goal of this capstone project was to determine if any of these putative RE-exons are translated to produce protein in human cells using information from various protein databases. In order to determine whether any of the novel transcript isoforms are translated or not, we used PGA, an R/Bioconductor package that enables an automatic process for constructing customized proteomic databases based upon RNA-Seq data and search peptides using MS/MS data from publicly available proteomic database. In this study we used publicly available proteomic database PRIDE. The main success of this study is to after searching a total of 88 human brain cortex samples 33 different peptides were found in 26 samples. We found 16 isomers. We have discovered that protein isoforms containing repetitive elements are potentially translated in the human orbitofrontal cortex .Therefore we can say that PGA which works based on Proteogenomic approach is a useful tool to identify novel peptides in RNA seq data.