The workflow in the Epipe method [8] which is designed to identify functional differences between sequence variants as they are produced by alternative splicing, SNPs, or somatic mutations. The isoforms are first aligned, then analyzed by a large number of feature predictors, and finally differential features are extracted and presented and mapped onto protein structural information if available in PDB.
An example output from Epide for variants of the receptor for stem-cell growth factor (mast-cell growth factor) KIT_Human, which has tyrosine protein kinase activity. Binding of ligands leads to the autophosphorylation of KIT and its association with substrates such as phosphatidylinositol 3-kinase (PI3K). The prediction shows that several single amino-acid changes can lead to a complete shift in the prediction of the membrane protein topology using the TMHMM method [36].