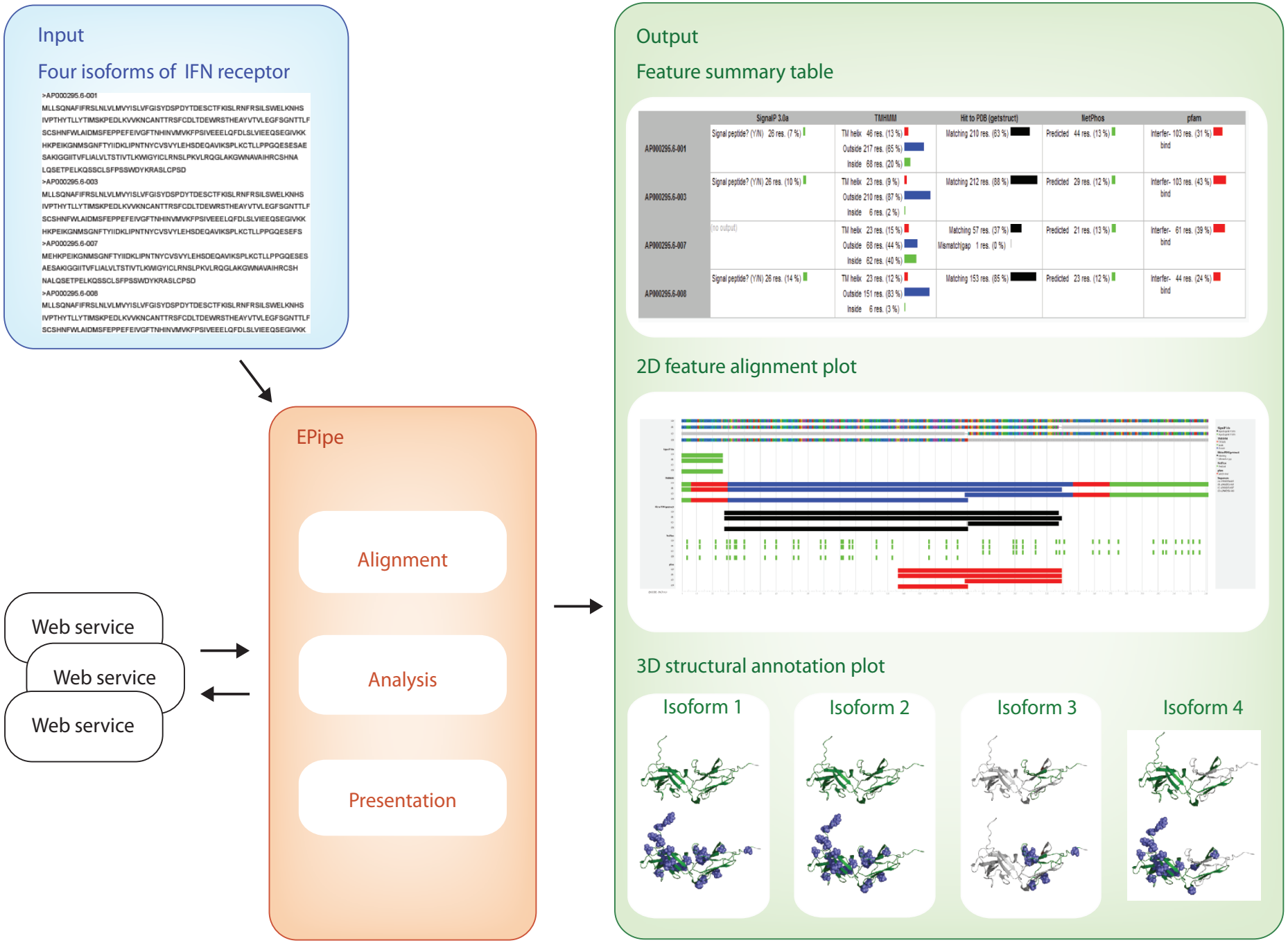
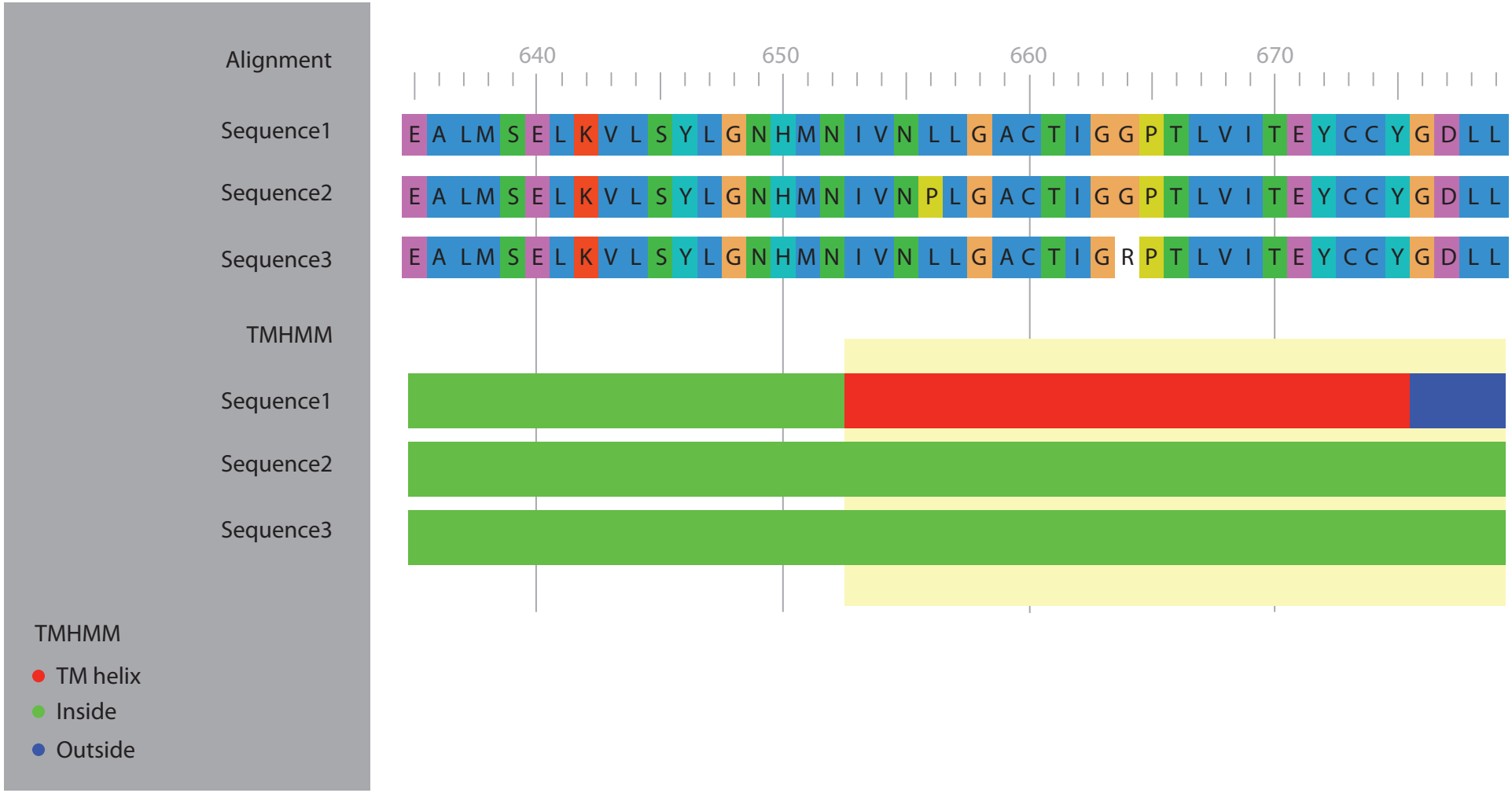


The workflow in the Epipe method [8] which is designed to identify functional differences between sequence variants as they are produced by alternative splicing, SNPs, or somatic mutations. The isoforms are first aligned, then analyzed by a large number of feature predictors, and finally differential features are extracted and presented and mapped onto protein structural information if available in PDB.

Sequence1	Reference KIT_HUMAN	976 res.
Sequence2	L656P KIT_HUMAN	976 res.
Sequence3	G664R KIT_HUMAN	976 res.



An example output from Epipe 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].