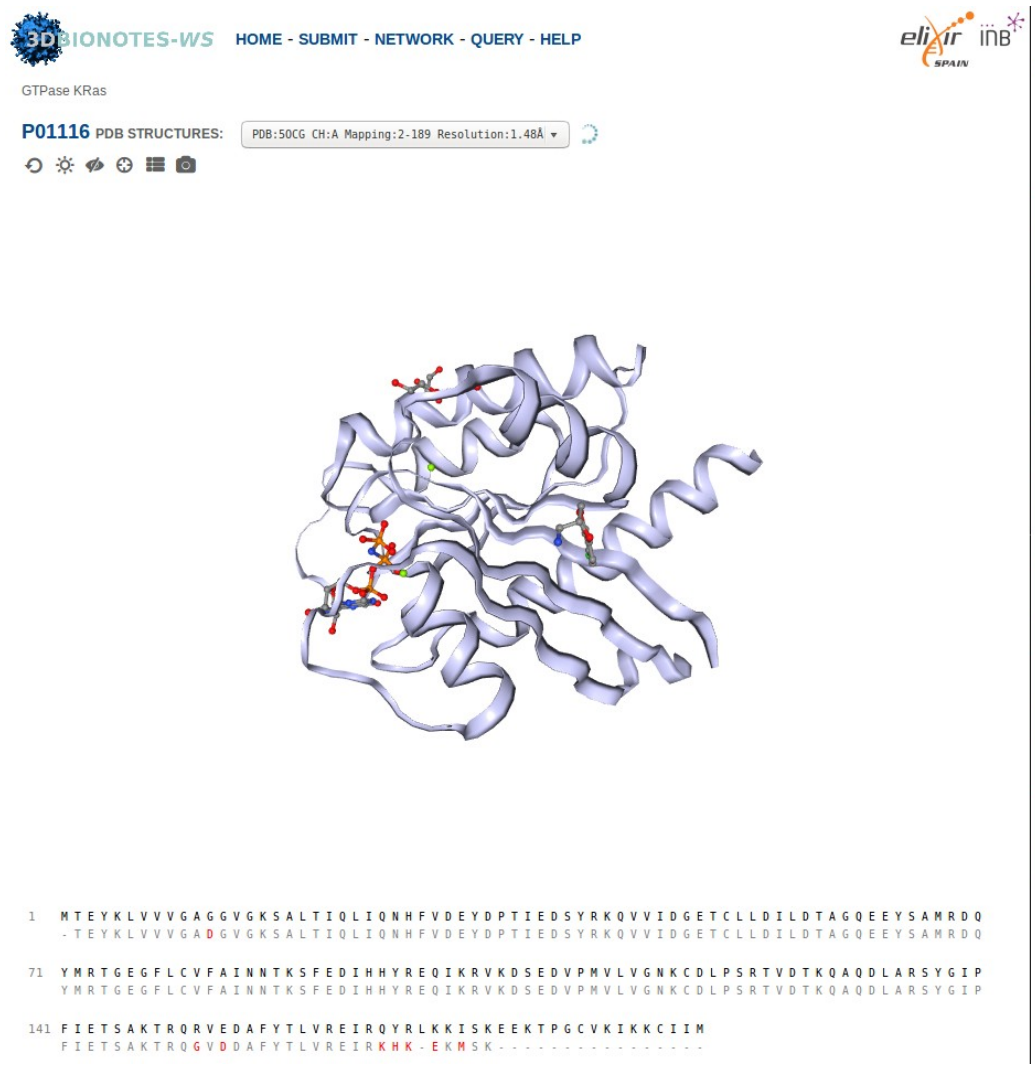
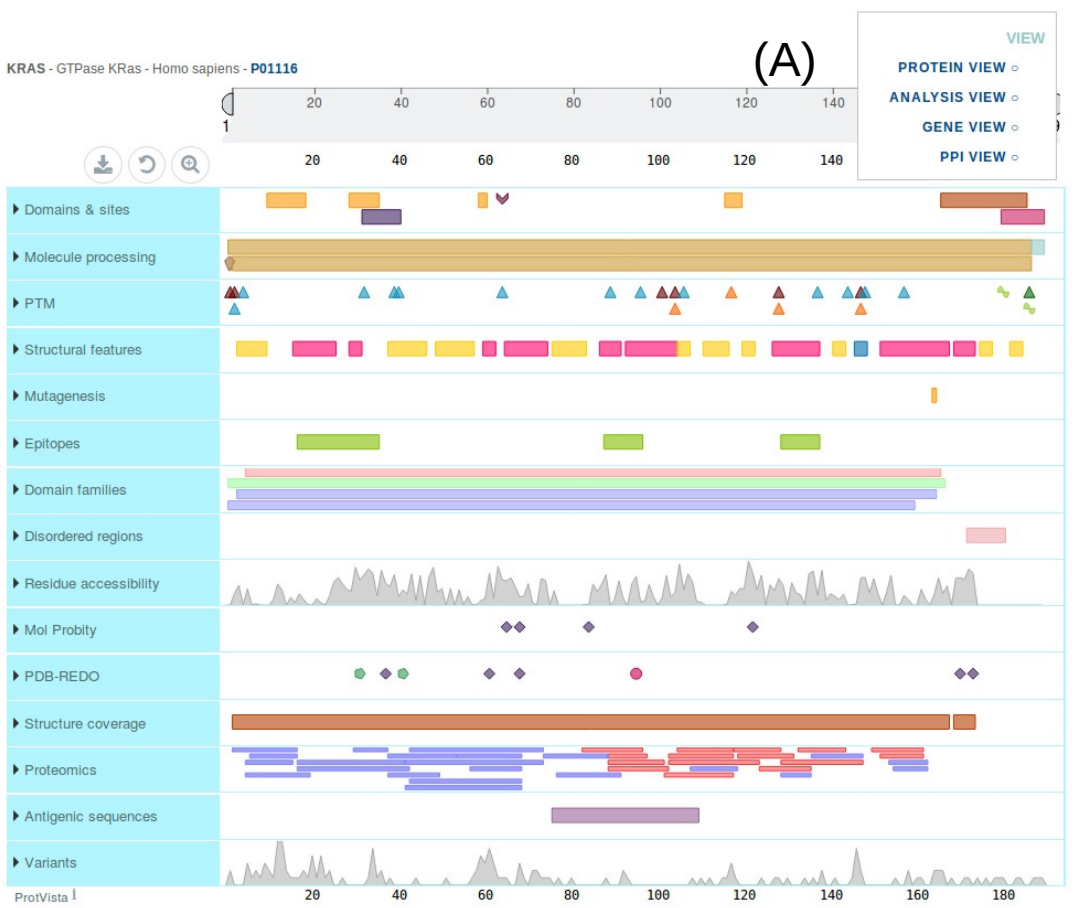
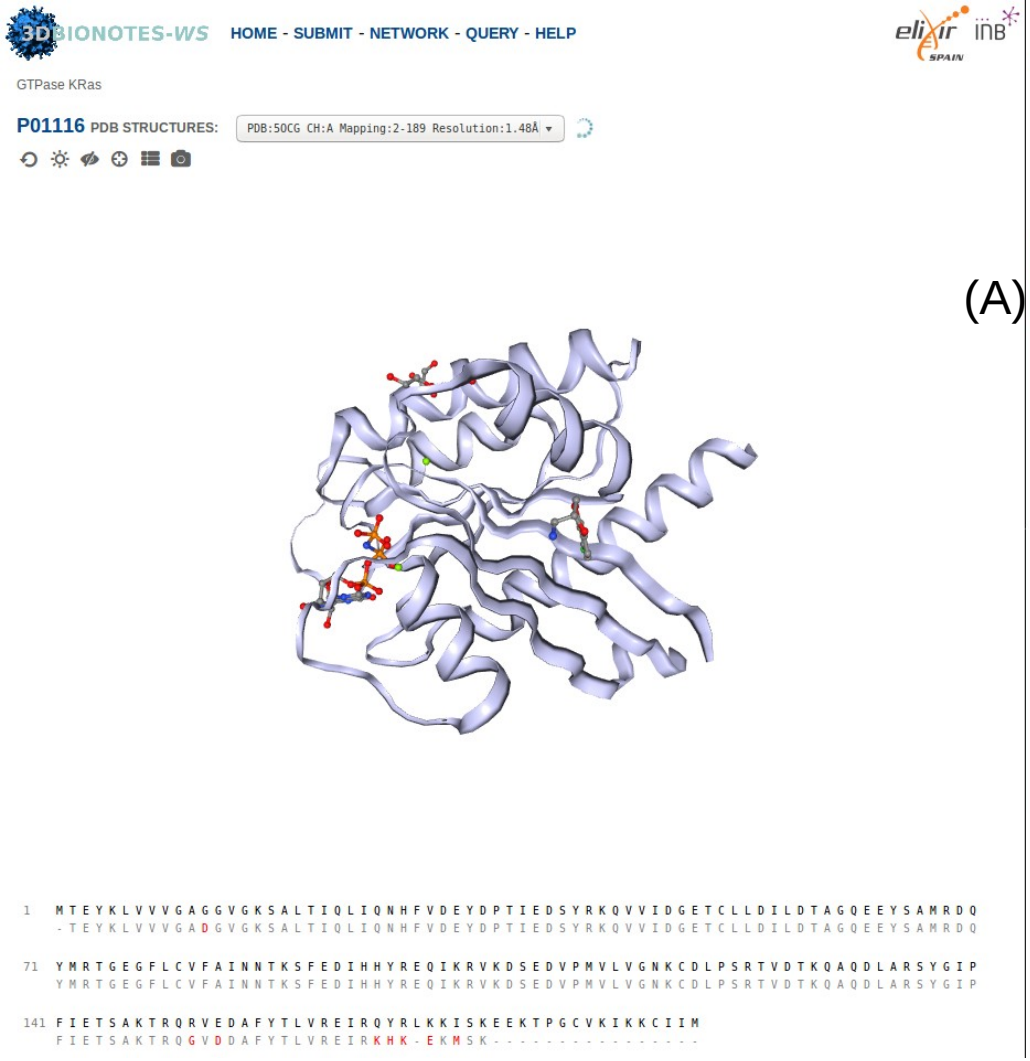
In this example we will show how to use the analysis panel to find cooccurrence between genomic variants and other biochemical features. Go to “QUERY” (A) and request the information for KRAS protein, UniProt accession P01116 (B)

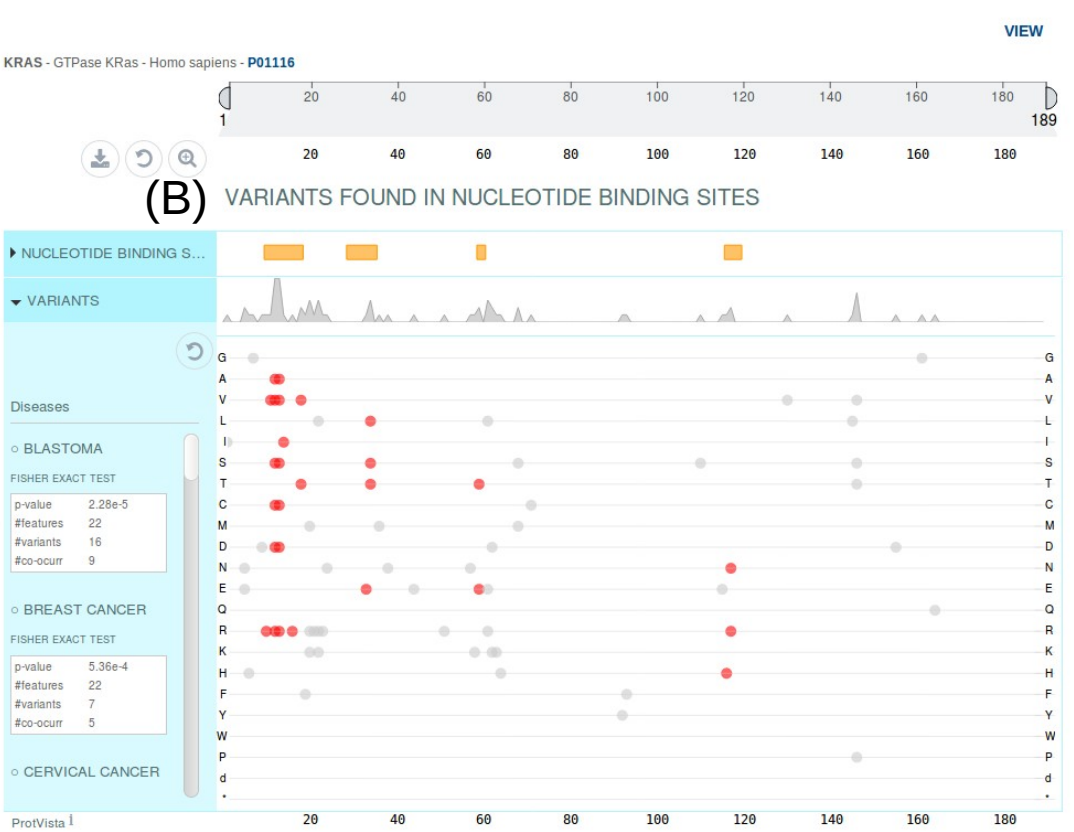




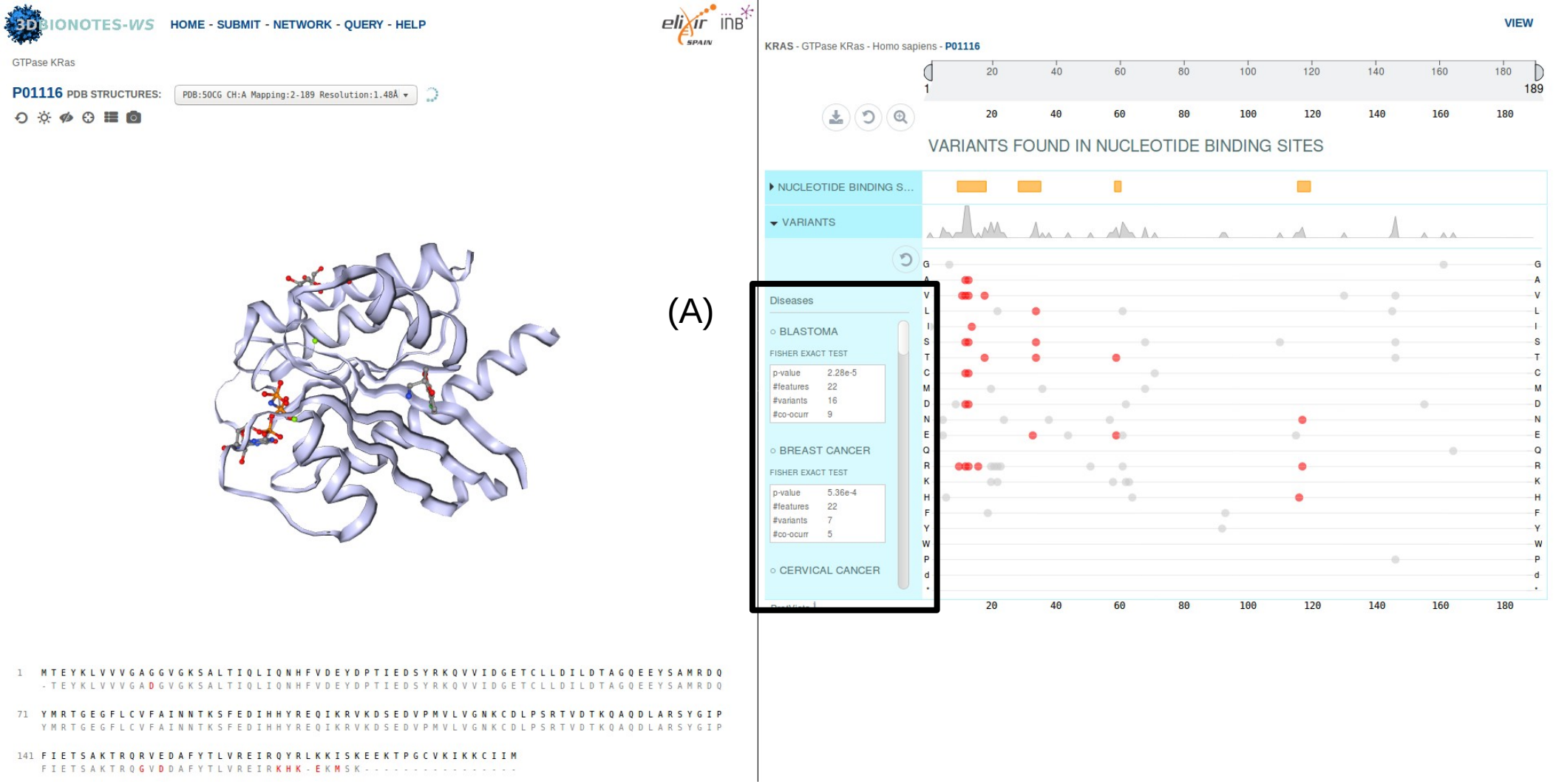
Go to the “VIEW” menu and select the “ANALYSIS VIEW” (A)



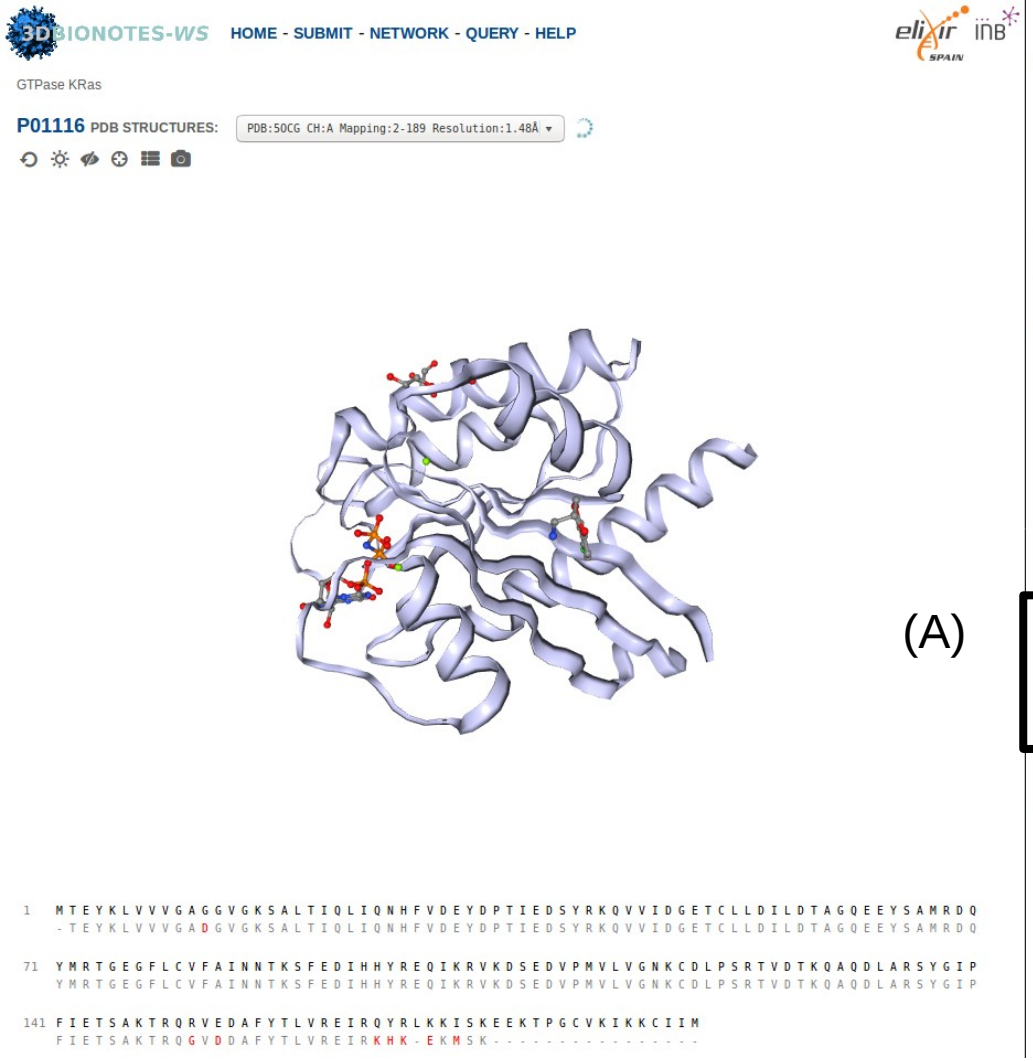
(A)



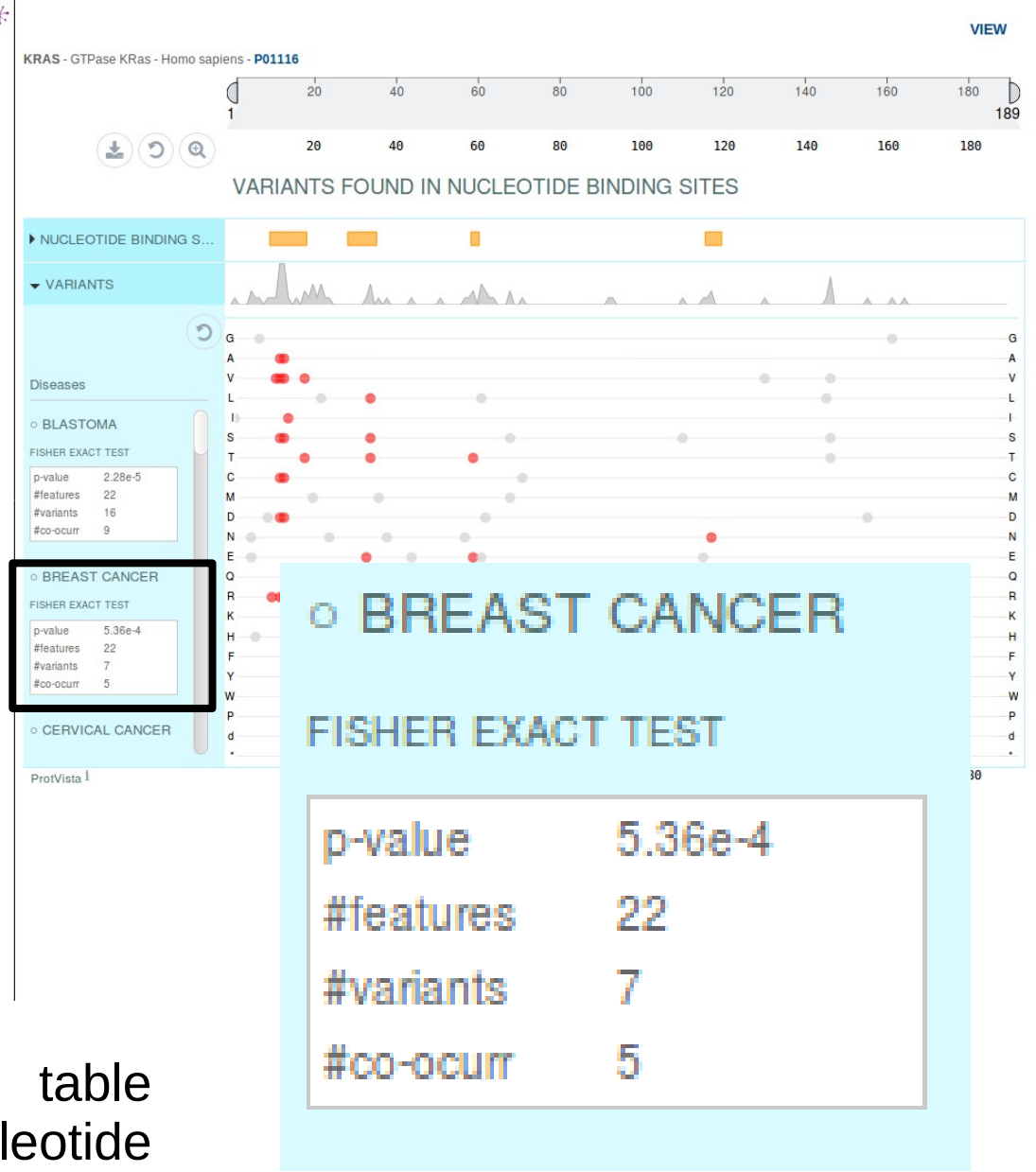
Expand the genomic variant viewer clicking on the “VARIANTS” track (A). This panel display all variants associated to diseases that statistically cooccur, in this example, in the “NUCLEOTIDE BINDING SITE” (B) of KRAS. The color code indicates whether the variant is located in the NBS (red color) or affecting other residues (gray color)



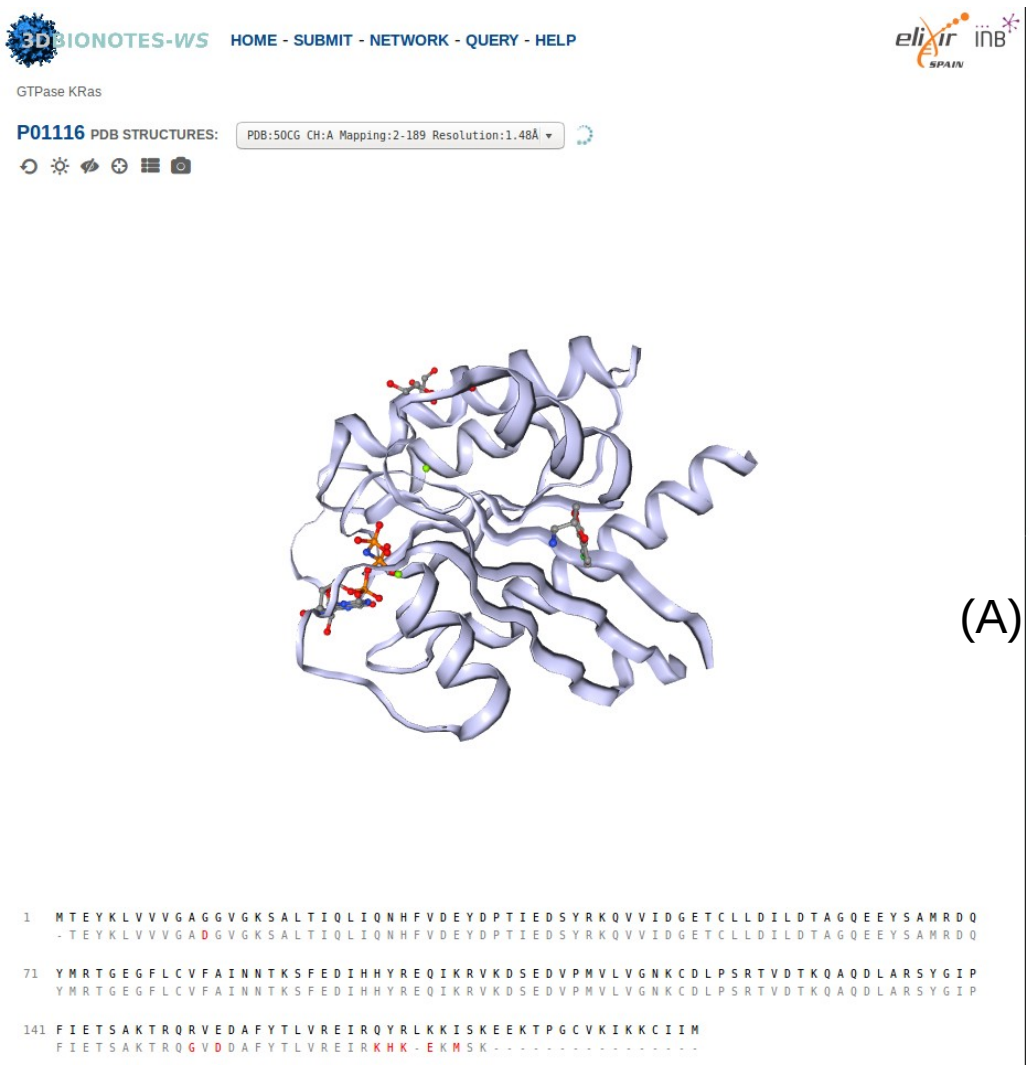
The “Diseases” panel (A) contains the statistical information for the diseases found during the analysis.



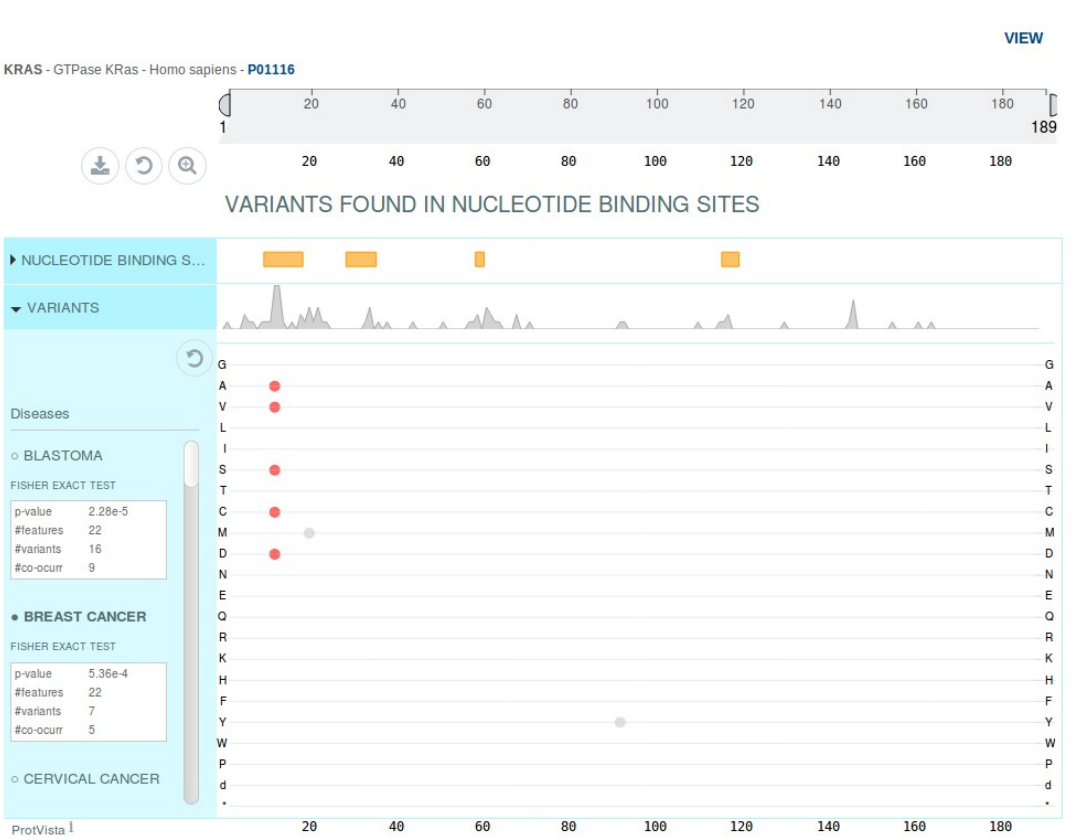
(A)



For example, “BREAST CANCER” table (A) displays that the number of Nucleotide Binding Site (NBS) residues is 22 (#features 22), the total number of variants is 7 (#variants 7) and 5 of the variants are located on NBS residues. The p-value associated to Fisher's exact test is 5.36e-4



(A)



When clicking on a disease name, in this example “BREAST CANCER” (A), only the variants associated to such disease will be displayed. The color code indicates whether the variant is located in the NBS (red color) or affecting other residues (gray color)