

# 3DBIONOTES-WS



@ **Biocomputing Unit - INB - ELIXIR**  
(A)

HOME

SUBMIT

NETWORK

QUERY

API

HELP

ABOUT US

Search by **EMDB** code, **PDB** ID or **Uniprot** accession

P01116

(B)

UPLOAD YOUR ANNOTATIONS

Browse... No file selected.

Submit

Example (HRAS)

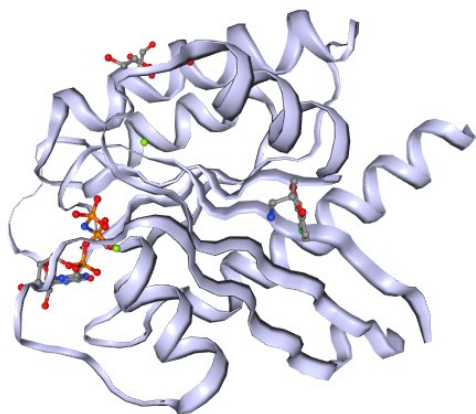
Example (Human APC/C-Cdh1-Emi1)

3DBIONOTES web-server was developed and is maintained at the [Biocomputing Unit - CNB](#) by Joan Segura Mora. Citing the web-server ?

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)

GTPase KRas

P01116 PDB STRUCTURES: PDB:50CG CH:A Mapping:2-189 Resolution:1.48Å



```

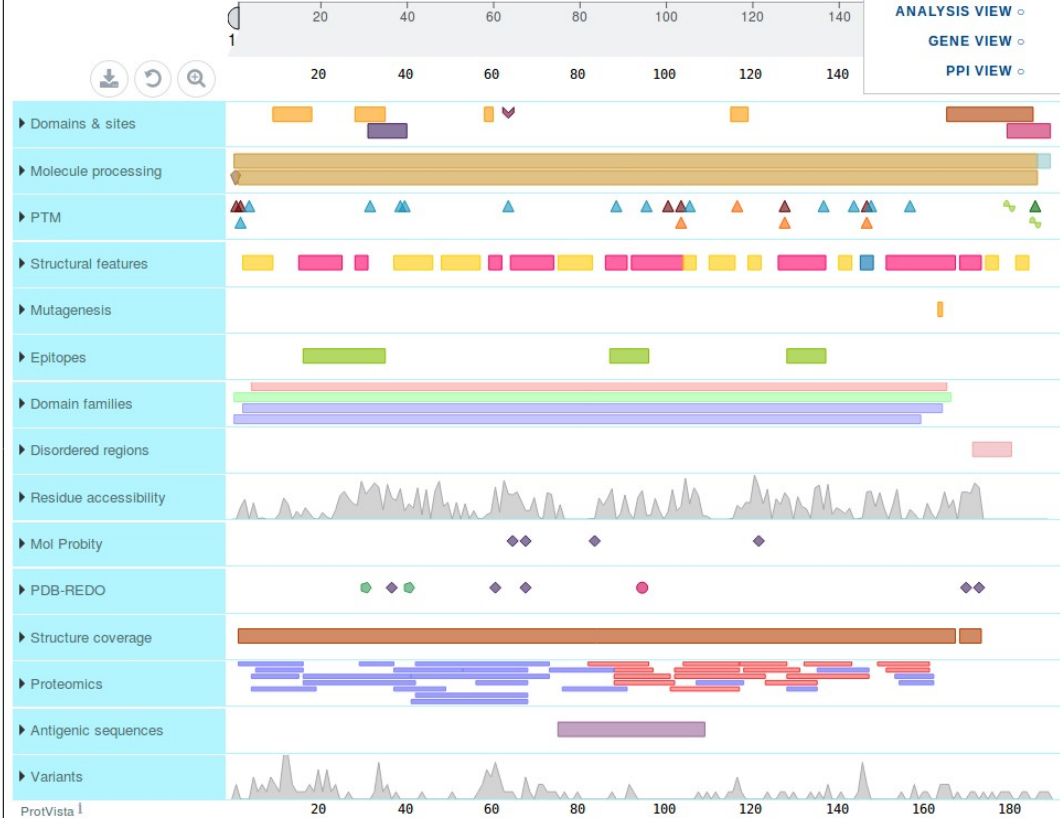
1  MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDO
  -TEYKLVVVGADGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDO
71  YMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSEDVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIP
  YMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSEDVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIP
141 FIETSAKTRQRVEDAFYTLVREIRQYRLKKISKEEKTGPKVKKKCIIM
    FIETSAKTRQGVDDAFYTLVREIRKHK-EKMSK-----
    
```

KRAS - GTPase KRas - Homo sapiens - P01116

(A)

VIEW

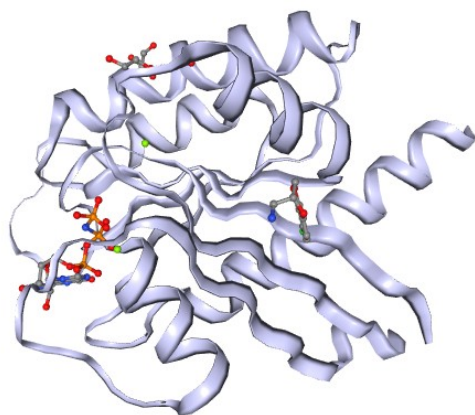
- PROTEIN VIEW
- ANALYSIS VIEW
- GENE VIEW
- PPI VIEW



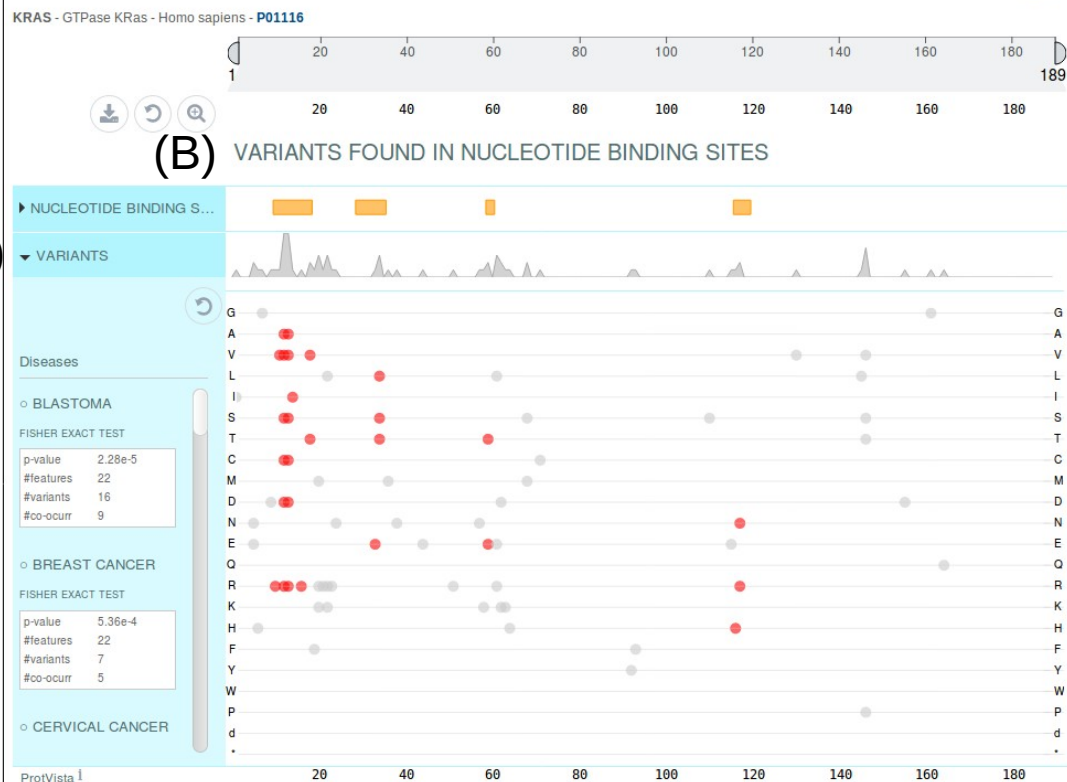
Go to the “VIEW” menu and select the “ANALYSIS VIEW” (A)

GTPase KRas

P01116 PDB STRUCTURES: PDB:50CG CH:A Mapping:2-189 Resolution:1.48Å



(A)



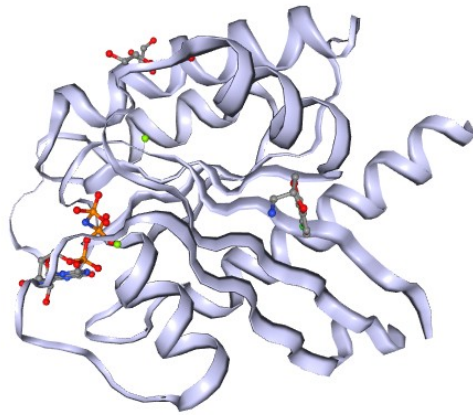
```

1  MTEYKLVVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDQ
   -TEYKLVVVVGA DGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDQ
71  YMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSSEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIP
   YMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSSEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIP
141 FIETSAKTRQVEDAFYTLVREIRQYRLKHKISKEEKTPGCVKIKKCIIM
    FIETSAKTRQGVDDAFYTLVREIRKHK - EKMSK-----
    
```

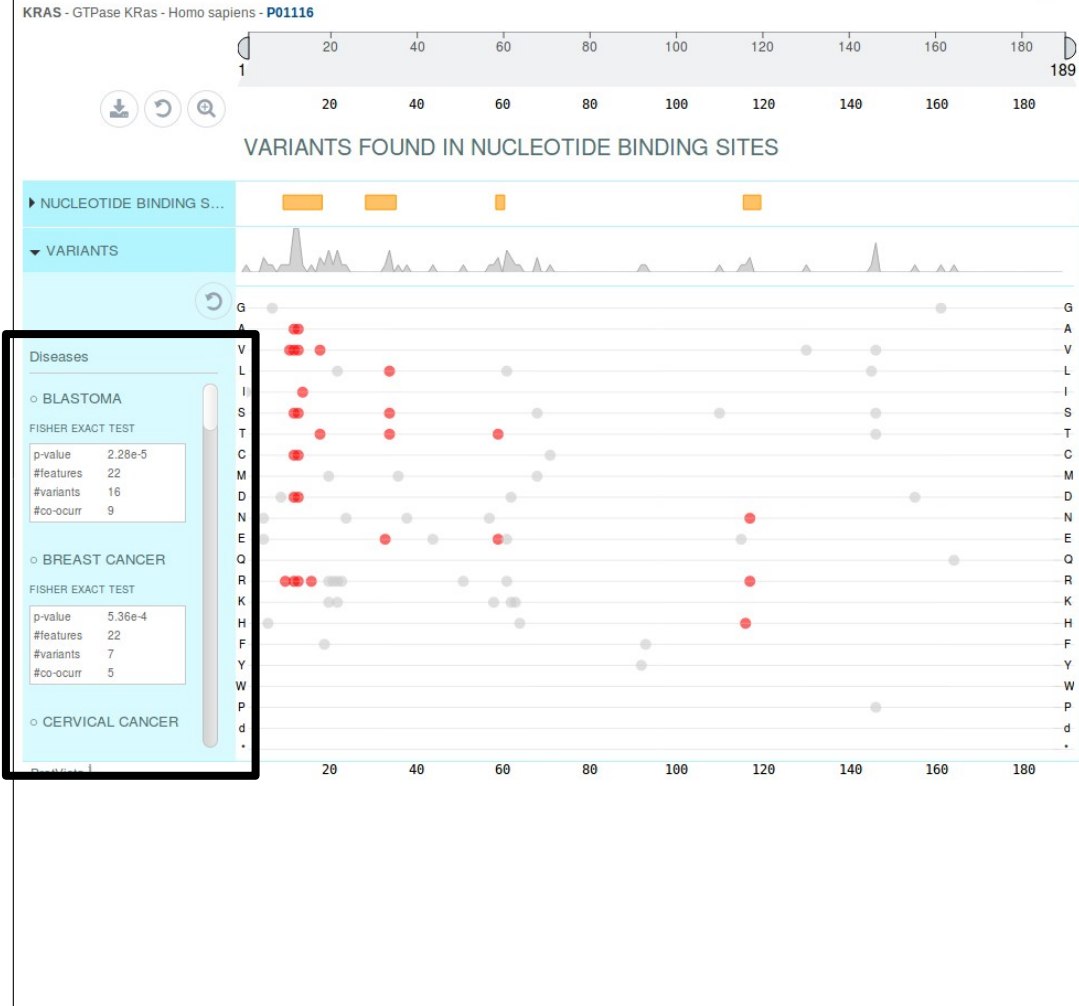
Expand the genomic variant viewer clicking on the “VARIANTS” track (A). This panel display all variants associated to diseases that statistically cooccur, in this example, in the “NUCLEOTIDE BINDING SITE” (B) of KRAS. The color code indicates whether the variant is located in the NBS (red color) or affecting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

GTPase KRas

P01116 PDB STRUCTURES: PDB:50CG CH:A Mapping:2-189 Resolution:1.48Å



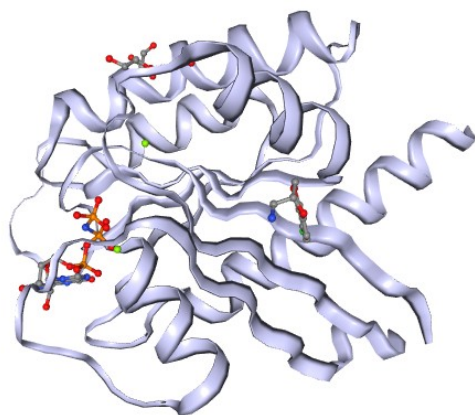
(A)



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

GTPase KRas

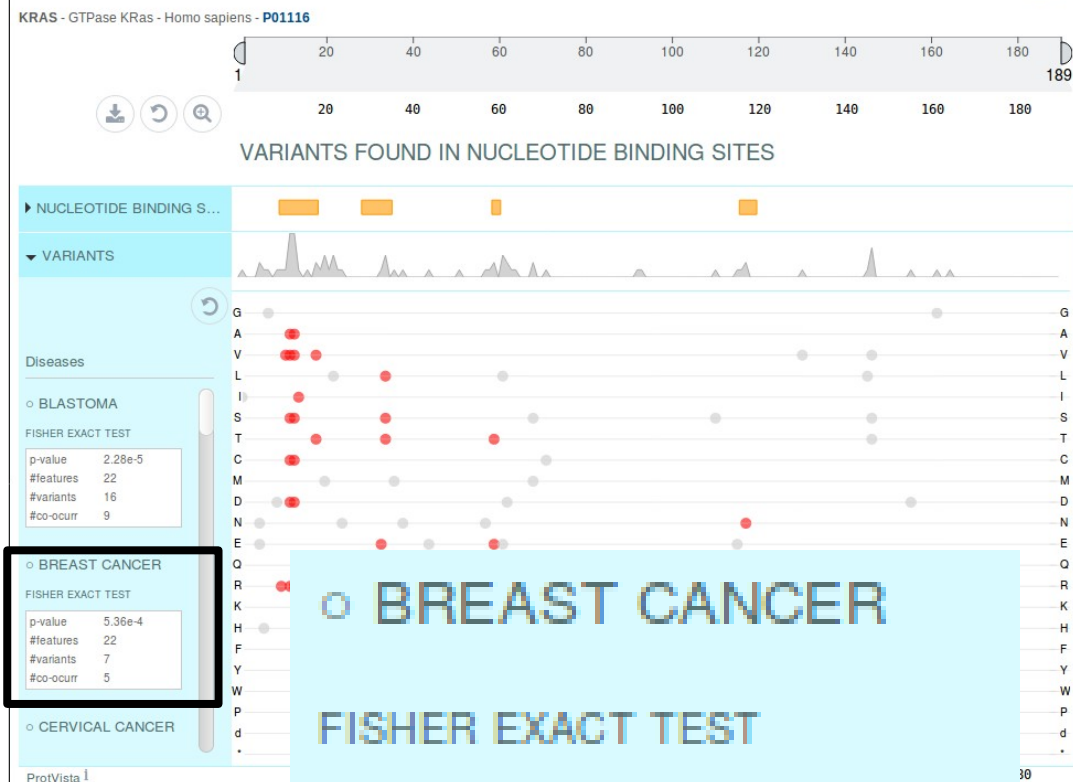
P01116 PDB STRUCTURES: PDB:50CG CH:A Mapping:2-189 Resolution:1.48Å



(A)

```

1  MTEYKLVVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDQ
   -TEYKLVVVVGA DGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDQ
71  YMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSSEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIP
   YMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSSEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIP
141 FIETSAKTRQVEDAFYTLVREIRQYRLKKISKKEEKTGCVKIKKCIIM
    FIETSAKTRQGVDDAFYTLVREIRKHK - EKMSK-----
    
```



BREAST CANCER

FISHER EXACT TEST

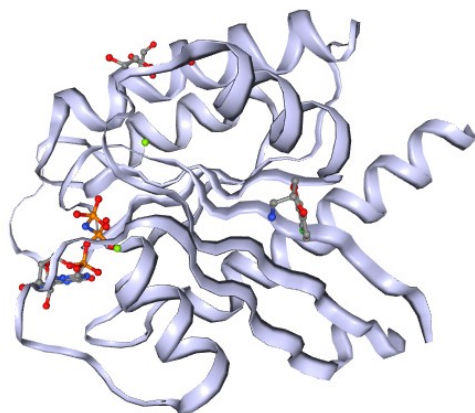
p-value	5.36e-4
#features	22
#variants	7
#co-occur	5

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



GTPase KRas

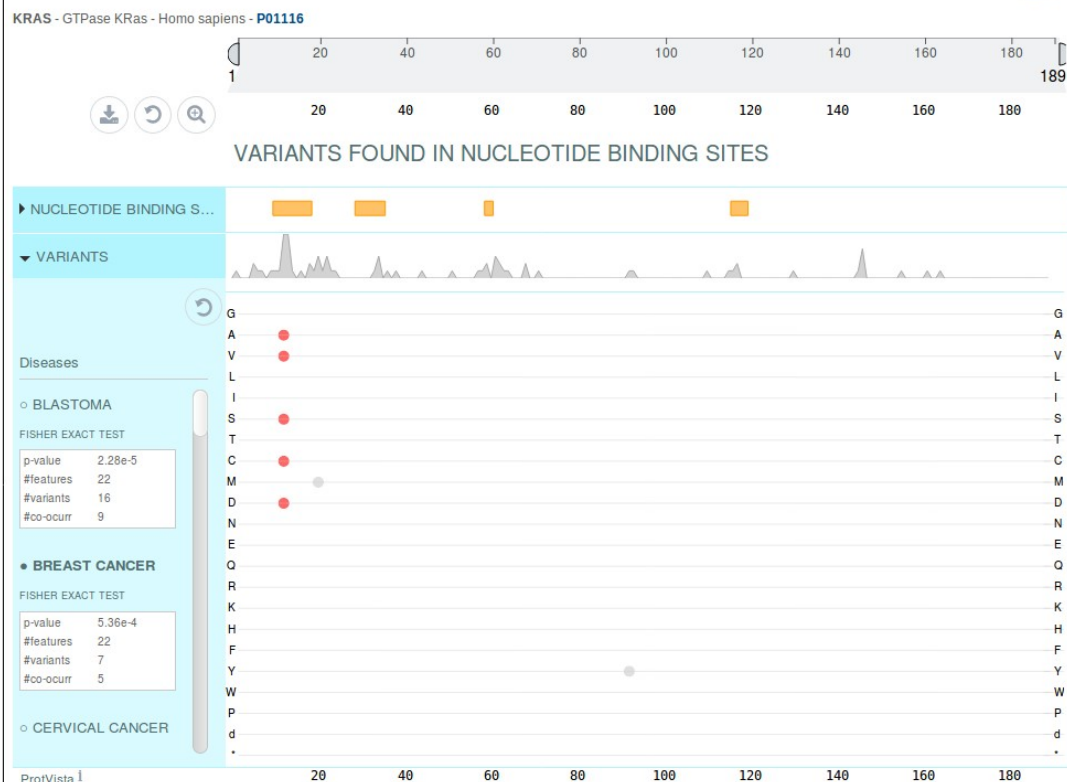
P01116 PDB STRUCTURES: PDB:50CG CH:A Mapping:2-189 Resolution:1.48Å



(A)

```

1  MTEYKLVVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDQ
   -TEYKLVVVVGA DGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDQ
71  YMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSSEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIP
   YMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSSEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIP
141 FIETSAKTRQVEDAFYTLVREIRQYRLKKISKEEKTPEGCVKIKKCIIM
    FIETSAKTRQGV DDAFYTLVREIRKHK EKMSK.....
    
```



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)