

## MANUAL:

After the initial register and login process, the system offers the following options:

- Search mutations by amino acid:  
Along the top menu you can find the following amino acids: Cys (Cysteine), Val (Valine), Arg (Arginine), Ser (Serine), Phe (Phenylalanine), Tyr (Tyrosine), Gly (Glycine), His (Histidine), Leu (Leucine), Gln (Glutamine), Ala (Alanine), Thr (Threonine) and Trp (Tryptophan).

Mousing over one of these, you can see a drop-down list with the point mutations that can be found for the specific amino acid along the whole length of the sequence, as well as the amino acid that replaces it on each instance.

For newfound mutations that are inserted to the system through the external database, there is a special drop-down list called "LATEST MUTATIONS"

When the user selects a mutation from any of these lists, he will see a prompt referring to structural changes in the NOTCH 3 protein ("the protein structure changes", or "the protein structure does not change", depending on each case). By clicking the OK button, the system displays the full (altered) NOTCH3 sequence containing the selected mutation.

- Search mutations by position in the NOTCH3 protein sequence:  
The user also has access to another menu with position numbers. When the user chooses a number, he is informed about the amount and the type of mutations that can be found on the respective position in the sequence.

All processes that we developed for static data are also executed dynamically for any additional mutation data that are received from the secondary database and are inserted to the main database, so the system can be updated accordingly.

Finally, the system implements the RCSB PDB(protein data bank) website to provide users with access to detailed information and images regarding the NOTCH3 protein. For a 3D view we direct you to

<https://www.rcsb.org/pdb/ngl/ngl.do?pdbid=4ZLP&bionumber=1#viewerPanel> .