**“eDiVa” overview**

1. ”eDiVa” (exome Disease Variants database) supports the data from exome sequencing with the integrated data covering gene annotations from NCBI, Ensembl and UCSC, known variants in the population (dbSNP, 1000 Genomes, EVS), pathway and protein-protein interaction information (e.g. KEGG and BioGRID) as well as other OMICs information and disease specific knowledge (e.g. OMIM).
2. Contains two main data sections:
   1. Data from eXomeCRG pipeline
   2. Public Omics Data
3. The main data for this project comes from the existing Exome Sequencing Pipeline (eXomeCRG) for investigated cases. For each disease we have multiple cases, one case can contain more than one sample and each sample contains thousands of SNPs and INDELs. Shortly, we will extend the capabilities to store CNVs as well.
4. Public Omics Data sources are given below.

