**GESPA Datasets**

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GESPA uses a variety of publicly available datasets in order to classify nsSNPs and provide various annotations to users. The names and links to these datasets are provided below.

1. UniProt Human polymorphisms and disease mutations (humsavar). <http://www.uniprot.org/docs/humsavar>
2. NCBI Entrez Gene. <http://www.ncbi.nlm.nih.gov/gene>
3. NCBI Entrez Protein. <http://www.ncbi.nlm.nih.gov/protein>
4. NCBI Clinvar. <http://www.ncbi.nlm.nih.gov/clinvar/>
5. NCBI HomoloGene. [www.ncbi.nlm.nih.gov/homologene](http://www.ncbi.nlm.nih.gov/homologene)
6. NCBI dbSNP. [www.ncbi.nlm.nih.gov/SNP/](http://www.ncbi.nlm.nih.gov/SNP/)
7. UCSC Blat. <http://genome.ucsc.edu/cgi-bin/hgBlat?command=start>
8. UCSC Genome Browser. <http://genome.ucsc.edu/cgi-bin/hgGateway>
9. Kyoto University Bioinformatics Center (KUBC) ClustalW. <http://www.genome.jp/tools/clustalw/>