## ClinVar: improvements to accessing data

Nucleic Acids Research 48, D835-D844 DOI: 10.1093/nar/gkz972

**Citation Report** 

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11	SNPnexus: a web server for functional annotation of human genome sequence variation (2020) Tj ETQq1 1 0.78 Genomic Landscape and Mutational Spectrum of ADAMTS Family Genes in Mendelian Disorders Based on Gene Evidence Review for Variant Interpretation. Biomolecules, 2020, 10, 449. The Human Gene Mutation Database (HGMD®): optimizing its use in a clinical diagnostic or research	4.0	4
11 12	SNPnexus: a web server for functional annotation of human genome sequence variation (2020) Tj ETQq1 1 0.78 Genomic Landscape and Mutational Spectrum of ADAMTS Family Genes in Mendelian Disorders Based on Gene Evidence Review for Variant Interpretation. Biomolecules, 2020, 10, 449.   The Human Gene Mutation Database (HGMD®): optimizing its use in a clinical diagnostic or research setting. Human Genetics, 2020, 139, 1197-1207.   In-silico analysis to identify the role of MEN1 missense mutations in breast cancer. Journal of	4.0	4
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11 12 13 14	SNPnexus: a web server for functional annotation of human genome sequence variation (2020) Tj ETQq1 1 0.78 Genomic Landscape and Mutational Spectrum of ADAMTS Family Genes in Mendelian Disorders Based on Gene Evidence Review for Variant Interpretation. Biomolecules, 2020, 10, 449.   The Human Gene Mutation Database (HGMD®): optimizing its use in a clinical diagnostic or research setting. Human Genetics, 2020, 139, 1197-1207.   In-silico analysis to identify the role of MEN1 missense mutations in breast cancer. Journal of Theoretical and Computational Chemistry, 2020, 19, 2041002.   EpigenCentral: Portal for DNA methylation data analysis and classification in rare diseases. Human Mutation, 2020, 41, 1722-1733.	4.0 3.8 1.8 2.5	4 353 3 15
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