

# Variant ANNotation workER



**VANNER is a software suite for variant annotation. The information about variants to be annotated include deleteriousness scores, allele frequencies, and functional consequences.**

## **Features in functional consequence annotation:**

- 1) Automatically checks the sequence of REF, so you will never use the wrong build without noticing.
- 2) Corrects reference sequence errors.
- 3) Chooses the most biologically relevant 5' or 3' representation for indel variants and modifies POS,REF,ALT.
- 4) Annotates against the predominant transcripts whenever such information is available.
- 5) Writes HGVS representations.
- 6) Supports multi-nucleotide polymorphisms (MNP).
- 7) Annotates variants of known significance such as those in ClinVar.
- 8) Annotates missense of the same amino acid as a ClinVar variant but with a different substitution.
- 9) Uses the dbNSFP to annotate splice-altering variants
- 10) Uses the ENSEMBL's Regulatory Build to annotate regulatory regions.
- 11) Uses the TargetScan version 7.1 to annotate microRNA binding sites.
- 12) Labels loss-of-function variants.
- 13) Labels nonsense-mediated decay variants.
- 14) Labels variants that affect translational efficiency.
- 15) Supports structural variations.

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