MANE: Matching Annotation from NCBI and EMBL-EBI

NCBI

A representative set of protein-coding transcripts, identically matched between RefSeq and Ensembl and provided to facilitate clinical variant reporting and foster communication and data exchange among the scientific community.

ncbi.nlm.nih.gov/refseq/MANE

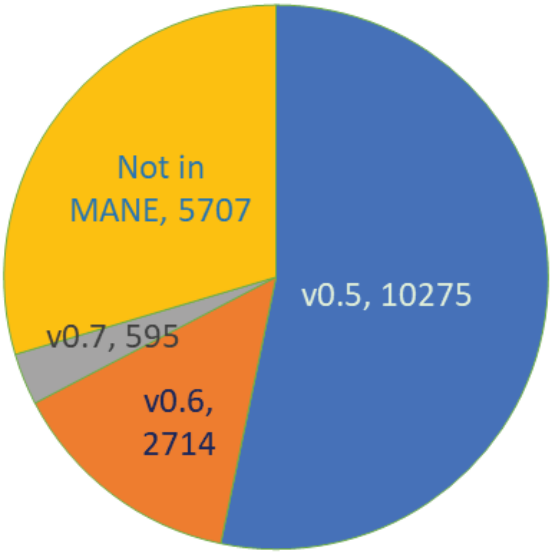
What is MANE?

Matched Annotation from NCBI and EMBL-EBI (MANE) is a collaboration between the National Center for Biotechnology Information (NCBI) and the European Molecular Biology Laboratories-European Bioinformatics Institute (EMBL-EBI). MANE aims to identify a core set of representative transcripts for human protein-coding genes and revise their sequences and genome annotation to be 100% identical between RefSeq and Ensembl.

What does MANE contain?

Each protein-coding gene will have a single "MANE Select" transcript that is well-supported by experimental data and represents the biology of the gene. The latest dataset, MANE Select v0.7, includes 70% of human protein-coding genes. Future datasets will include more genes and additional transcripts for complex genes.

Progress of MANE Select Dataset



Salient features of MANE Select

- Includes only curated transcripts from the RefSeq and the Ensembl-GENCODE annotation sets.
- Transcripts match the GRCh38 human reference genome assembly.
- It is expected to be a stable set; we will only make changes for compelling reasons

Need more detailed description?

See the full document here
ncbi.nlm.nih.gov/refseq/MANE/

Accessing MANE data

- Bulk download at https://ftp.ncbi.nlm.nih.gov/refseq/MANE/
- NCBI Entrez search in **Nucleotide** and **Protein** database: try "MANE_select[keyword]"
- RefSeq annotation files available via FTP: GFF3 and GTF include a "MANE Select" tag attribute in the rows associated with the mRNA, CDS and exon features.
- 'Genes, MANE project (release v0.7)' track in NCBI's Genome Data Viewer (GDV) or Variation Viewer browsers.
- Track hub: ftp://ftp.ncbi.nlm.nih.gov/refseq/MANE/trackhub/hub.txt.
- The MANE Select v0.6 dataset is also available as a native track in the UCSC Genome Browser

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