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.

**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.

**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.

**Accessing MANE data**
- 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.
- The MANE Select v0.6 dataset is also available as a native track in the UCSC Genome Browser.

**Progress of MANE**
- Not in MANE, 5707 (v0.5, 10275)
- v0.6, 2714
- v0.7, 595

**Excited to share thoughts and comments? Write to us**

@ncbi
ncbi.nlm
Info@ncbi.nlm.nih.gov
MANE-help@ncbi.nlm.nih.gov
linkedin.com/company/ncbinlm

**Stay in touch!**

---

**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.

**See the full document here**