

Publication

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Only a small proportion of the mouse genome is transcribed into mature messenger RNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a physical collection of clones. Here we report the manual annotation of 60,770 full-length mouse complementary DNA sequences. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4,258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the transcriptome. 41% of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2,431 sense-antisense pairs. The

present work, completely supported by physical clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics.

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