

LncExpDB: Expression database of human long non-coding RNAs

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Recently, the researchers from the Beijing Institute of Genomics of the Chinese Academy of Sciences have constructed an expression database of human long non-coding RNAs (lncRNAs), LncExpDB. This study was published in the journal *Nucleic Acids Research*.

The [human genome](#) transcribes a large number of lncRNAs, which are

extensively involved in a variety of essential biological processes and human diseases. While hundreds of thousands of human lncRNAs have been identified primarily attributable to the rapid development of high-throughput sequencing technology, only a small subset of them have been functionally characterized.

As RNA-seq data provides the most direct evidence for identifying their potential functions across various biological conditions, it is desirable to have a dedicated expression database that comprehensively integrates expression profiles and systematically characterizes expression features of human lncRNAs.

To this end, LncExpDB, an expression database of human lncRNAs, was developed.

Based on comprehensive integration and stringent curation, LncExpDB currently houses expression profiles of 101,293 high-quality human lncRNA genes derived from 1,977 samples of 337 biological conditions across nine biological contexts, i.e., normal tissue/cell line, cancer tissue/cell line, subcellular localization, exosome, cell differentiation, preimplantation embryo, organ development, circadian rhythm and virus infection.

LncExpDB estimates lncRNA genes' expression reliability and capacities, identifies 25,191 featured genes, and further obtains 28,443,865 lncRNA-mRNA interactions.

Moreover, LncExpDB is equipped with user-friendly web interfaces, which enables interactive visualization of expression profiles across various conditions and easy exploration of featured lncRNAs and their interacting partners in specific contexts.

This [database](#) features comprehensive integration and curation of

lncRNA [expression profiles](#) and thus will serve as a fundamental resource for functional studies on human lncRNAs.

More information: Zhao Li et al. LncExpDB: an expression database of human long non-coding RNAs, *Nucleic Acids Research* (2020). [DOI: 10.1093/nar/gkaa850](#)

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