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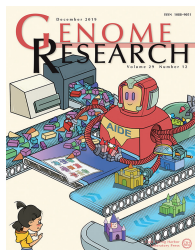
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The *C. elegans* 3' UTRome v2 resource for studying mRNA cleavage and polyadenylation, 3'-UTR biology, and miRNA targeting 2104^{OA}

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^{OA}Open Access paper



Cover In this issue, a robust statistical method, annotation-assisted isoform discovery (AIDE), is presented to facilitate transcriptome analyses. AIDE (represented by the robot) assembles short RNA-seq reads (colored building blocks) into full-length mRNA isoforms (castles). For this task, AIDE is the first bioinformatics tool that uses statistical testing (the magnifier, representing the *p*-value) to examine the assembled isoforms to control false discoveries (the castles that do not pass the test are discarded), thus allowing users to discover novel isoforms with high confidence. (Cover artwork by Zhongke Magic Color Enterprise, www.zhongkehuancai.com/en/, with conceptual input from Wei Vivian Li, Shan Li, Hubing Shi, and Jingyi Jessica Li. [For details, see Li et al., pp. 2056–2072.]