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Analysis of Alternative Splicing Mediated by the PASA Software

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Alternative splicing (AS) of mRNA transcripts provides a mechanism by which a single gene can express transcripts that encode proteins with altered functions, and physiological properties. The mechanism of AS is not completely understood but does appear to involve regulatory motifs in the transcript sequence coupled with regulatory proteins that together influence the pattern of splicing. The identification of alternatively spliced genes most often involves examining expressed transcript sequences in the form of expressed sequence tags (ESTs) or, more recently, full-length cDNAs (FL-cDNAs). Variations in mRNA processing including those derived from AS are evident from pairwise comparisons of individual fully processed transcript sequences derived from the same gene, or from examining alignments of the mRNA sequences to their cognate DNA sequence. The PASA (Program to Assemble Spliced Alignments) software includes a set of tools to leverage ESTs and FL-cDNA sequences for eukaryotic gene structure annotation and for studying AS. PASA executes a series of steps to reconstruct transcript isoforms from transcript alignments and then to identify all splicing variations evidenced by differences in gene structures between individual isoforms. Although PASA was originally developed as a genome annotation tool, the above functions of the software provide a standard framework for analyzing AS for any eukaryote provided a complete genome sequence and database of expressed transcript sequences.