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Author Daniel Andersson		
Title (English) Finding novel full length genes using EST data		
Title (Swedish)		
Abstract <p>A method using data from expressed sequence tags in gene predictions was evaluated by comparing Unveil, which had previously been modified, with Genscan and GeneID. The data set was the complete human genome. Tests were also performed to optimize the method and to check whether the programs discovered different genes. The method increased the accuracy of Unveil greatly. However, the modified Unveil is not as good as the other programs.</p>		
Keywords <p>EST, gene prediction, Unveil, evaluation, human genome</p>		
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