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Gene discovery by stringent annotation

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In the March *Nature Genetics*, Gopal *et al.* describe a two-step approach to identify novel genes by combining stringent annotation with broad gene-prediction techniques (*Nature Genetics* 2001, 27:337-340). The first step involves identification of potential exons using the GENSCAN gene-finding program. In the second step, predicted genes are compared with all available gene and protein sequences, including expressed sequence tags (ESTs) from other organisms, at the protein level (in all six translation frames). The authors combined sequence comparisons with comparative protein structure modeling to confirm their results. Gopal *et al.* applied this method to analysis of the *Drosophilagenome* to validate the technique. Filtering of over 19,000 plausible *Drosophila* genes (of which 12,124 matched the original 13,601 annotated genes) led to the identification of 1,042 putative novel genes, which had not previously been annotated but had strong supporting evidence as real gene candidates. These prediction results should serve as a basis for future experimental confirmation.

References

1. *Nature Genetics*, [<http://genetics.nature.com>]
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