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GASPing for genes

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In the Genome Annotation Assessment Project (GASP), 12 groups tested their ability to identify genes in 3 million base pairs of *Drosophila* DNA. The results are reported in eight papers in the April issue of *Genome Research*. The majority of the groups correctly identified over 95% of the coding nucleotides. Less successful were predictions of intron/exon boundaries, which were correct for just over 40% of the genes, and predictions of promoter locations, which suffered from a high rate of false positives.

References

1. Genome Research Homepage, [<http://www.genome.org/>]