GENOME RESEARCH

Drosophila Genome Annotation Assessment Project

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The Challenge of Annotating a Complete Genome: The Genome Annotation Assessment Project (GASP)

Reese, M.G., G. Hartzell, N.L. Harris, U. Ohler, J.F. Abril and S.E. Lewis. 2000. *Genome Res.* **10**:483–501.

COLOR	PROGRAM NAME	TYPE OF ANNOTATION	AUTHOR
	TRF (Tandem Repeat Finder)	Repeat Finder	Benson 1999
	Cufrepeo	Repeat Finder	Field 2000
	sh1	Gene Expert Annotation (cDNA based)	Ashburner et al. 1999b
	sh3	Gene Expert Annotation (comprehensive)	Ashburner et al. 1999b
	GRAIL	Gene Finder	Uberbacher and Mural 1991
	GeneMark.hmm	Gene Finder	Besemer and Borodovsky 1999
	GeneID	Gene Finder	Guigó et al. 1992
	FGenes (CGG1–CGG3)	Gene Finder	Solovyev et al. 1995
	NNMGene	Gene Finder	Krogh 1997
	MAGPIEexon	Gene Finder	Gaasterland and Sensen 1996
	MAGPIE (cDNA)	cDNA Alignment	Gaasterland and Sensen 1996
	Genie, **GenleEST**, **GenleESTHOM**	Gene Finder	Reese et al. 1997
	GeneWise	Homology Gene Annotation	Birney and Durbin 1997
	BLOCKS+	Homology Gene Annotation	Henikoff et al. 1999b
	MAGPIEPromoter	Promoter prediction	Gaasterland et al. 2000
	MCPromoter2.0	Promoter prediction	Ohler et al. 1999
	GenlePromoter	Promoter prediction	Reese et al. 1999
	CoreInspector	Promoter prediction	Scherf et al. 2000

No ↔5 — **Fourier Analysis** is a DNA sequence periodicity measure.
20.0% — 65.0% — **G+C Content** for the Adh region ranges from 24.5 to 64.5%.

Further details on the GASP project including the annotations can be found at `http://www.fruitfly.org/GASP1`
The plot with the Adh region annotation has been obtained using the program **gff2ps** (Abril and Guigó, 2000).
The most recent version of **gff2ps** is freely available at `http://www1.imim.es/~jabril/GFFTOOLS/GFF2PS.html`