



## GST Features

Created: April 23, 2008; Updated: June 15, 2010.

### What exactly does GST allow me to do?

The Genome Workbench (Gbench) SNP Tools (GST) are utilities completely integrated into the Gbench program that allow you to view and analyze SNP data using Gbench applications. Using GST you will be able to:

- Show significant SNPs in a Genome-Wide Association Study
- List SNPs in a given region
- Filter SNPs based on the bitfield properties described in [the dbSNP bitfield .pdf](#)
- The Gbench program itself provides many additional tools:

Database Searches (Nucleotide, Entrez Gene, Entrez Genome)

Annotation Comparison View

FASTA Text View

Feature Table View

Graphical (Alignment) View

Sequence Text View

You can find detailed information about Gbench tools and how to use them at the [Genome Workbench Help site](#). (04/23/08)

### Isn't the same information and functionality you claim for GST available elsewhere on the NCBI website?

#### What makes GST so special?

Other NCBI web services will show you publicly available data. GST can show you both public and private data. You can use GST to check your private data against publicly available data to better understand your research. (04/23/08)

### Can I use Genome Workbench to annotate SNP data for candidate genes?

At this time, users of Genome Workbench (Gbench) cannot edit annotations such as SNPs within the application. Gbench will, however, allow users to import and load annotations using GFF, Feature table, or other supported formats so that they can see custom features/SNPs displayed.

Here are references for a few of the file formats:

[GFF](#)

[Feature-table:](#)

[DDBJ/EMBL Feature Table Definitions](#)

[Sequin Feature Table definitions](#)

We are always looking for ways to improve Gbench, so if you can outline a specific use case for your needs, we can take it into consideration for future Gbench development.

**(08/19/08)**