

Project Analysis

Gene Navigation

Gene navigation allows you to view the expression profile from selected genes in your project. This is the default analysis method for projects. There are three ways that genes may be selected.

1. Search by Name

Enter a gene name or part of a gene name in the text box and search for genes in the selected project.

2. Search by Accession or UniGene ID

Use an Accession number from Genbank or UniGene cluster ID to filter probes that share the same ID. Multiple Accession numbers may be used to search by separating each with a space or two colons.

3. Search by Chromosome

Searches for and displays genes found on the selected chromosome.

The screenshot shows the 'Project Analysis: Golub' interface with three search sections. Each section is numbered 1, 2, and 3 respectively. Section 1, 'Search by Name', has a search box with a yellow highlight, 'Option: Match All Words', 'Mask (SEM/Mean): 0%', 'Statistics: No Statistics', and 'Show: 20'. Section 2, 'Search by Accession or UniGene ID', has an empty search box, 'Sort: Sort by expression', 'Mask (SEM/Mean): 0%', 'Statistics: No Statistics', and 'Show: 20'. Section 3, 'Search by Chromosome', has 'Chromosome: YX', 'Sort: Sort by expression', 'Mask (SEM/Mean): 0%', 'Statistics: No Statistics', and 'Show: 20'. The top right of the interface shows '(login: beth) > Analysis > Projects' and navigation links: '[Gene Navigation | Gene Function | Pattern Navigation | Cluster | Export]'. A '[Question / Comment]' link is at the bottom right.