

# Custom Genomes (Genomes not in IGB)

IGB supports many species and genome versions, not just the species shown on the start screen. To check whether a genome is available in IGB, click the **Current Sequence** tab and use the **Species** and **Genome Version** menus to look for your genome of interest.

However, if your genome is not available, you can still use IGB. Here's how:

## How to open a custom genome

1. Select **File > Open Genome from File...** (or click the DNA icon in the **Toolbar**.)
2. Select a sequence file to use as the reference genome (fasta or 2bit format).
3. Enter **Optional** details:
  - a. Enter Genus name
  - b. Enter the Species name
  - c. Enter the Variety as appropriate (strain/cultivar/accession)
  - d. Choose the Month of the genome release date
  - e. Enter the Year in YYYY format.
4. Click **OK** and wait for the genome to load.
5. Open data files as usual. And to view sequence, zoom in and click **Load Sequence**.

**Open Genome from File**

Reference Sequence \* Enter URL or choose a local file Browse...

Genome Details (all fields are optional)

Genus (optional) Enter genus

Species (optional) Enter species

Variety (optional) Enter strain/cultivar/accession

Genome release date (optional) Month Enter year

\* Required field  
If you choose to include the optional details, IGB will display the details in the species and genome menus.

OK Cancel

1. Choose reference sequence (2bit is best; fasta is fine.)

2. Enter genome details (optional)

**Open Genome from File**

Reference Sequence \* nome\_sequences\Folder\E\_coli\_Jan\_2012\E\_coli\_Jan\_2012.2bit Browse...

Genome Details (all fields are optional)

Genus (optional) escherichia

Species (optional) coli

Variety (optional) k12-MG1655

Genome release date (optional) January 2012

\* Required field  
If you choose to include the optional details, IGB will display the details in the species and genome menus.

OK Cancel