

# Other Options

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## Introduction

Select **File > Preferences > Other Options** to configure the following:

- Coordinates track number format
- Sequence base colors
- ORF analyzer
- Edge matching
- Gene model translations
- Track resizing
- IGB exit and data set loading behaviors

### Preferences Other options

The screenshot shows the 'Preferences Other options' dialog box. It has a title bar with standard window controls and a tabbed interface. The 'Other Options' tab is active. The 'Coordinates' section has a 'Number format' dropdown set to 'COMMA'. The 'Residue Colors' section shows color swatches for A (green), T (blue), G (yellow), C (orange), and Other (grey). The 'ORF Analyzer (Sliced View tab)' section has 'Stop Codon' (red), 'Dynamic ORF' (green), and 'Background' (grey). The 'Edge Match' section has a 'Color' dropdown set to white and a checked 'Show Edge Matching' checkbox. The 'Codon Display' section has radio buttons for 'Hide', 'One Letter' (selected), and 'Three Letter'. The 'Track Resize Behavior' section has radio buttons for 'Adjust All Tracks' and 'Adjust Adjacent Tracks' (selected). At the bottom, there are four checkboxes: 'Ask before exit' (checked), 'Confirm before loading large data set' (checked), 'Confirm before delete' (checked), and 'Display Errors on Status Bar' (unchecked). A 'Reset preference to defaults' button is located at the very bottom.

## Coordinates

These are options for changing number appearance. **FULL** shows the number with no thousands separators and the unit 'kb'. **COMMA** shows the numbers with commas at every  $10^3$  (U.S. style) and with no unit designations. This is the default. **ABBREV** will show the numbers as abbreviated as is reasonable, with unit designations. For example, when zoomed out, numbers appear as 10M, 20M etc. Changes made here to **Number Format** take effect immediately.

## Residue Colors

IGB displays letters representing DNA bases (residues) when zoomed-in. Residues are shown in alignment tracks, sequence tracks, and in underneath the coordinate axis.

By default, IGB uses cool colors for A and T residues and warmer colors for G and C residues. **Other** refers to residues that are either 'N', 'X' or '-' (missing) and can be set to a bright color if you are looking for deletions in short read sequences; otherwise you may wish to leave it as the neutral gray.

Click a color swatch to change base colors.

## ORF (Open Reading Frame) Analyzer

These preferences affect colors used to indicate stop codons, the ORFs and the background of the ORF tracks that are shown in the **Sliced View** tab.

## Edge Match

Edge matching highlights features that have identical boundaries. Edge matching becomes active when you click items in the display.

Click the swatch to change the edge match color. The selected color applies all annotation tracks.



Choose a color that has good contrast between foreground and background colors

## Codon Display

The **Codon Display** is activated when the sequence of a gene model is loaded and the user zooms in close enough to see the sequence. The codon translation appears within the gene model. User can set the amino acids to appear in one letter format (default), three letter format or be hidden. The colors is based on the chosen foreground color for the track.



Codon display is active only for tracks loaded from 14-column BED detail files.

## Track Resize Behavior

**Track Resize Behavior** is how IGB adjusts other tracks when a specific track height is changed. **Adjust All Tracks** means that as a single track is increased in height, all other tracks are reduced by a commensurate amount. **Adjust Adjacent Tracks** (default) means that all added or subtracted height is removed/added to the bordering track, leaving the rest of the display unaffected.

## Data loading and exit behaviors

### Confirmations

IGB warns you when you are about to exit the program and before you delete a file or files. Each of these warnings has the option to not be shown again. To turn off these warnings or reset your previous choice, check (or uncheck) these options.

## Reset all preferences to defaults

Click **Reset preferences to defaults** to reset all the preferences to the IGB defaults. This is sometimes useful if you need to troubleshoot IGB.



**Be careful**, as this action will reset ALL preferences and will also cause IGB to forget the location you were last viewing.