

## OSIRIS Release Notes Version 2.15.1

OSIRIS Version 2.15.1 is a bug fix version

### Bug Fixes:

- Fixed bugs introduced in 2.15 where low to medium height peaks could be classified as pull-up and not be given an allele call.
- Fixed a bug present in 2.15 and earlier versions that in situations where a large peak was close to a pull-up position, it might interfere with pull-up pattern identification. In very rare circumstances that could result in a pull-up peak being called as an allele.
- Fixed a bug present in 2.15 and earlier versions that could infrequently result in a partial pull-up peak whose RFU value was either below, or corrected to be below the allele calling threshold would retain an allele call, requiring additional editing.

### Improvements:

- Improved the robustness of the pull-up algorithm by taking into consideration additional pull-down and pull-up peak width information.

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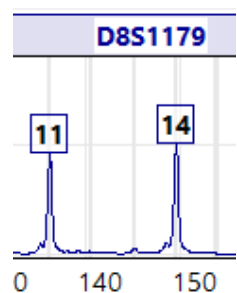
### Improvements in OSIRIS Version 2.15

Version 2.15 includes substantial improvements over previous versions

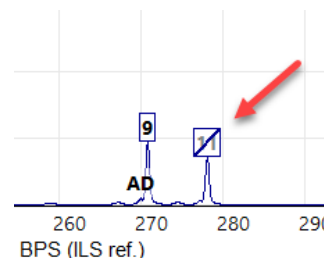
### New Features

#### New Graph display options

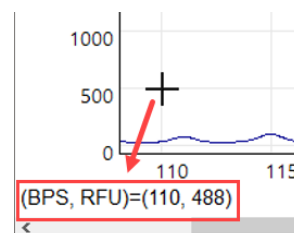
- **Allele locus bars** – at the top of each plot the locus bar containing the locus label indicates the extent of the locus ladder alleles.
- **Allele bins** – Allows the user to display or hide allele bins. The bins indicate the ladder allele position and allele bin width. Bin width is set in the “Max. Residual For Allele” on the Sample Limits tab of the Lab Settings.



- **Deleted allele labels** – Display or hide the labels of deleted alleles. The labels of deleted alleles (alleles “disabled” during editing) display with a strikethrough.



- **Cursor coordinate display** – The cursor coordinates (BP/Time and RFU) are displayed in the lower left corner of the Graph and Preview Graph.



- **Sample rows in Table view** – The selected row in the table is highlighted with black top and bottom borders to help visually identify cells in wide rows.

10, 12	12, 12	X, X	17, OL17.3, 18	13, 13	8, 8
11, 12	9, 14	X, X	OL16.3, 17	14, 15	8, 8
12, 13	10, 12	X, X	16, 19	11, 14	8, 11

- **Default Graph window display** - The Graph window has been improved to default zoomed in to the peaks in the plot, showing less blank data to the right and showing less of the primer peaks to the left. Print settings allow this as well.

### Added a new Preview Graph toolbar

Added a toolbar like that found in the Graph view window to the Table view Preview Graph allowing simple access to display changes that otherwise required stepping through menus, which makes the Preview graph significantly more usable. This includes the ability to change or display multiple channels, change the raw vs. analyzed data, change the artifact label display, display deleted alleles, and more.

### **Improved Pull-Up identification algorithm**

Implemented an improved pull-up algorithm that better handles cases in which negative and positive pull-up are both present (due to linear and non-linear pull-up). In some of those cases the previous algorithm could result in an allele peak being called as a pull-up. An option allows users to choose to apply the improved algorithm either to all pull-up cases, or only to mixed positive and negative pull-up, with the previous algorithm (versions 2.8-2.14) applied to positive-only pull-up. The new algorithm handles both and provides better results with mixed positive and negative pull-up. See details below.\*

### **Added “Errors” and “Details” tabs to the New Analysis window**

Added a new pane to the New Analysis window with “Errors” and “Details” tabs. The Errors tab opens automatically and lists any errors identified that could have caused an analysis to fail, such as selecting a kit with the wrong number of channels or missing ILS or ladder peaks. The Details tab displays the analysis run information formerly displayed by clicking the “Details button”. Details information regarding run failures will be found at the bottom of the details associated with the analysis.

### **Added a search box to the Lab Settings window Sample Limits tab**

Added a search box to the Sample Limits tab that will highlight the settings rows that have matching text to allow users to quickly locate the desired row.

### **Folder Icon to find Operating Procedures**

A folder icon at the top right of the Lab Settings window will open the folder where user-created custom Operating Procedures are stored, making it simple to find their location. This is helpful when needing to share an Operating Procedure.

### **Updated OSIRIS 2.15 User Guide**

- **The STR analysis tutorial**

The STR analysis tutorial is updated to demonstrate some of the new display features in OSIRIS 2.15.

- **Fragment analysis tutorial**

The STR analysis tutorial is updated to include both a section on determining the number of data channels in an .fsa/.hid file for fragment analysis and a list of the predefined internal standard markers (ILS) in OSIRIS 2.15.

## **Bug Fixes**

- Fixed a bug that prevented the Mac version from displaying bold and italic font in the Table view to indicate an edited cell that still needed review.
- Fixed a bug where if the number of users to “Review editing” was set to zero, the first column of the Table window that shows checks (✓) and “X” would not show “X”, only checks.
- Fixed a bug which caused the “Primary Pull-Up Threshold: Computed” setting to not be used, rather the minimum height specified was used. If the specified threshold was very high or very low, it could have impacted identification of pull-up. Currently, unless specified by the user, the default minimum height for a primary pull-up is the channel analysis RFU.
- Fixed several bugs in the pull-up algorithm that in rare cases could lead to pull-up peaks not being identified or an allele being identified as a pull-up.

## **\*Details regarding the new pull-up algorithm**

Pull-up algorithm – new features:

1. The standard pull-up pattern analysis algorithm in versions prior to 2.15 treated channels with pull-up peaks all positive and channels with mixed positive and negative pull-up the same. However, given the model for pull-up height as a function of primary peak height as a linear plus quadratic, if the signs for the two terms are opposite each other, it is possible for a taller primary peak to give rise to a shorter pull-up peak. That is, pull-up height is not a monotonically increasing function of primary height. This situation could give rise to mixed positive and negative pull-up, and the default algorithm could give poor results, possibly resulting in miscalling pure pull-up on peaks that are valid alleles. Version 2.15 incorporates a non-linear algorithm that is used on all channels with mixed positive and negative pull-up, with the result that, on such channels, the pull-up pattern is more accurately analyzed and so are allele calls.
2. Version 2.15 incorporates a new user-specified preset that directs Osiris to use the non-linear algorithm in (a) on any channel that has all positive peaks. Even under this directive, Osiris will still only apply the non-linear algorithm to channels with all positive pull-up, but with at least 5 primary pull-up/pull-up pairs. In general, using this option improves the accuracy of the analysis of the pull-up pattern, but does not miscall valid alleles.