

Effortless 1D analysis

The complete all-inclusive 1D package



“Our UViband delivers powerful and accurate analysis. We value its fast, consistent analysis and its effortless approach. It includes functions particularly useful for quantification of gels, blots, dot blots, microtitre plates plus colony counting.”

> First in lane

UViband software is designed for powerful and accurate analysis of 1D gels to produce molecular weight and quantitative data. In addition to that it also includes methods for analysis of gels, blots, dot blots, slot blots, arrays, microplates plus colony counting.

In designing UViband packages we have taken a realistic, professional, friendly approach and included features that are of genuine benefit to the user.

UViband is the most automated 1D software where saving an analysis as a template and then recalling it and applying it to a new image are possible.

Analysis in the UViband package is performed in stages, step by step. At each analysis stage the user has the facility to check and (if necessary) edit the results of automatic analysis processes.

> Designed to be used

Pick up many imaging software packages and you start to wonder if the designers have ever performed an image analysis themselves. From the start the UViband was designed with the user in mind. This means menus that make sense, buttons that are easy to understand and operate, and a wide range of automatic settings covering virtually every imaginable general molecular biology macro-imaging application.

Moreover, if you prefer a more hands-on approach you will love the manual controls.

The UViband has the ability to grow with the user and has a feature list long enough to satisfy the most demanding lab user. In research laboratories, where premium accuracy, consistency, ease of use and automation are required, UViband comes into its own.

> Powerful

UViband analysis software includes the option of reliable, fully automatic background subtraction with ‘rolling ball’ method for band quantification. It also offers optional methods for correction of gel distortions during molecular weight calculations such as smiling correction and molecular weight calibration across several channels.

> Versatile

In addition to the incredibly broad range of analysis functions available in this software there are also functions to facilitate data presentation, reports and posters. The analysis can be saved as a template so the same report can be prepared from other data.

Thus, UViband facilitates data presentation for easy preparation of reports and posters using analysis tables and figures with the standard copy/paste approach. Software output can be simply copied/pasted to Microsoft Excel™ or Word™.



Razor sharp results

> Precise and accurate quantification

- **1D molecular weight & optical density**
 - Detect the lanes automatically
 - Add new standards and create your own standard library
 - Define a template for automatic analysis of multiple gels
 - View the lanes/area profile in 2D or 3D
 - Select one from several algorithms to generate dendrograms: UPGMA, Complete Linkage, Single Linkage, Wad, Neighbor Joining, ...
 - Define a calibration curve for normalisation of one or several lanes
- **1D lanes / Free form optical density**
 - Trace any area of analysis
 - Subtract image background using one of several approaches: automatic rolling ball, local baseline, complete baseline, local valley to valley, complete valley to valley...
- **Array optical density module**
 - Auto-trace an array / microarray grid tool for spot detection
 - Define outer and inner spot diameter prior to analysis
 - Rotate the grid vertically or horizontally
 - Calculate concentration automatically using your standard
 - Define a calibration curve for normalisation
- **Colony counting**
 - Control detection sensitivity with a simple control slider bar
 - Filter your data to include or exclude detected colonies automatically
 - Characterise the colony (volume, area, perimeter, gravity, compactness, eccentricity...)
- **Calculates concentration automatically using your standard**

