

## Agilent Protein Confirmation Solution Confident identity confirmation

# **Confident identity confirmation for recombinant proteins**





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When generating recombinant proteins for critical research, you need to be sure you have created the correct proteins. Agilent's Protein Confirmation Solution is a powerful, LC/MS-based solution for confirmation of protein identities. It offers significant advantages over gels and quadrupole- or ion trap-based MS solutions.

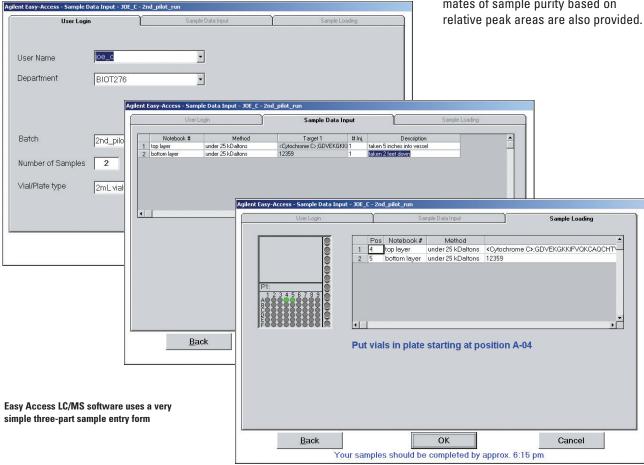
#### Easy, walk-up operation

Agilent's Protein Confirmation
Solution was designed for multiple
users who are experts in proteins,
but are not necessarily mass spectrometry specialists. It uses the
proven Agilent Easy Access LC/MS
software to reduce operational
complexity. The Easy Access software

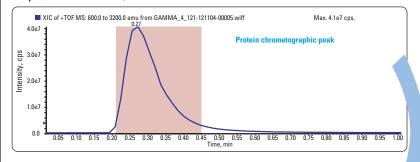
provides appropriate, customized analysis choices for each user. You simply log in and enter some brief sample information. Load your samples in the positions specified by the software and walk away. Complete, detailed confirmation reports are automatically generated for each sample and e-mailed to your office.

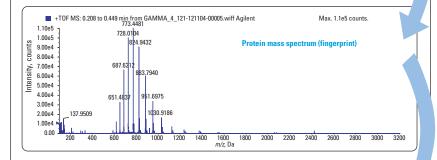
## Confirmation report gives you complete information

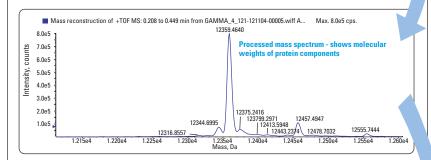
The protein confirmation report provides salient answers for the protein chemist, and enough detailed data to please the most discerning mass spectrometrist. The report confirms the molecular weight of the expected protein and lists the molecular weights and intensities of unanticipated proteins. Useful estimates of sample purity based on relative peak areas are also provided

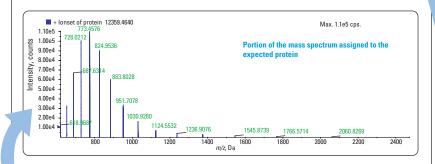


## Protein: blaster Sample Name: gamma\_4\_12 Method Name: D:\TOF\_Data\damethods\PROTEINS.ANM Data File Name: d:\data\Projects\marie\_c\Data\GAMMA\_4\_121-121104-00005.wiff Acg Time: November 12 2004, 05:39:19 AM









Target Mass Average (Da)	Measured Mass Average (Da)	Measured Mass Apex (Da)	Area	+/- ( <b>D</b> a)
12359.0593	12359.4640	12359.0000	6504804.82	0.4047

Measured Mass Average (Da)	Measured Mass Apex (Da)	Area	+/- (Da)
12359.4640	12359.0000	6504804.82	0.0000
12457.4947	12457.0000	974955.29	98.0307
12375.2416	12374.0000	877368.16	15.7776
12344.6995	12344.0000	719417.33	-14.7645
12413.5948	12413.0000	272783.83	54.1308
12555.7444	12555.0000	246575.16	196.2804
12399.2971	12399.0000	209024.19	39.8331
12443.2374	12442.0000	177753.21	83.7734
12478.7032	12479.0000	170691.53	119.2392
12316.8557	12316.0000	125552.91	-42.6083

### A superior approach to protein confirmation

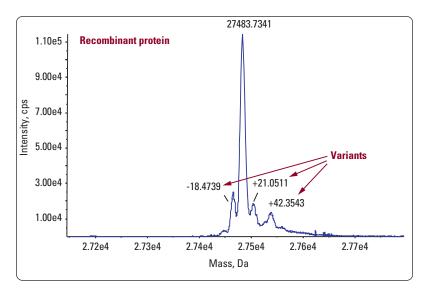
The Agilent Protein Confirmation Solution offers significant advantages relative to other approaches to protein identity confirmation.

The Protein Confirmation Solution is far more accurate than traditional gels. It is also dramatically faster, producing results in minutes instead of hours. Even with two-dimensional gels, variants are only identifiable if they affect the protein's isoelectric point. The outstanding resolving power of the Protein Confirmation Solution's LC/MSD TOF time-of-flight mass spectrometer can readily identify variants attributable to post-translational modifications or point mutations (see page 4).

Compared to quadrupole MS- or ion trap MS-based solutions, the Agilent **Protein Confirmation Solution offers** greater sensitivity, resolving power, and ease of use. When analyzing intact proteins, an ion trap requires knowledgeable, interactive adjustment to avoid space charging that hurts sensitivity and causes mass-assignment shifts. The LC/MSD TOF does not suffer from space charging and the Protein Confirmation Solution is automated for maximum throughput and ease of use. The LC/MSD TOF is superior to both ion trap and quadrupole instruments when it comes to resolving minor protein variants.

#### **Reveal variants**

With resolving power of up to 10,000, the LC/MSD TOF can readily resolve small mass differences attributable to post-translational modifications or point mutations. Its wide in-scan dynamic range ensures that you find both major and minor sample components. And with fast scanning, you can detect multiple sample components even when the proteins are not well resolved chromatographically.



Outstanding resolving power reveals small mass differences attributable to post-translational modifications or point mutations

#### Everything you need—in one solution

The Agilent Protein Confirmation Solution includes everything you need for accurate mass analysis:

- 1100 Series binary pump
- 1100 Series well-plate autosampler with cooler
- 1100 Series thermostatted column compartment
- Poroshell 300SB-C18 column, 1 x 75 mm, 5 μm
- LC/MSD TOF
- PC and printer
- TOF software for complete system control
- TOF Protein Confirmation software
- Easy Access LC/MS software

#### **Global support**

The Agilent Protein Confirmation Solution was designed for ruggedness and ease of use. But when you need help, support is never far away. Agilent's worldwide service and support organization offers a full range of service options, from application support to customizable service agreements. All Agilent service engineers are specially trained and certified—so you receive only the best, most efficient support available.

#### For more information

For more information about the Agilent Protein Confirmation Solution, call toll free:

#### 1-800-227-9770 (U.S. and Canada)

In other countries, please call your local Agilent Technologies life science and chemical analysis sales office or authorized Agilent Technologies distributor.

You can also visit our site on the World Wide Web at:

#### www.agilent.com/chem

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