

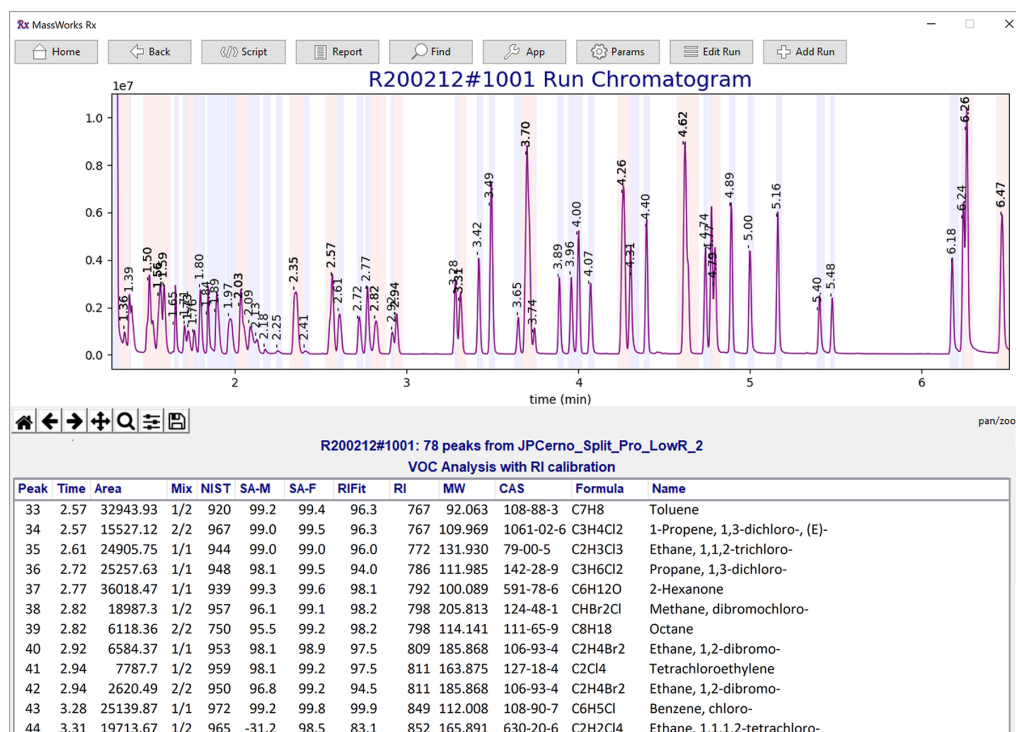
Fully Automated and Highly Confident GC/MS Compound ID

GC/ID is a fully automated data processing software that provides dramatic improvements for GC/MS qualitative analysis. By incorporating Cerno's proven TrueCal™ calibration technology for accurate mass formula ID along with conventional NIST library search, a significant improvement in compound ID certainty is achieved on single quad GC/MS systems. GC/ID also provides, for the first time, an entirely automated method of quantitatively utilizing the NIST retention index values to provide yet a third orthogonal metric for compound ID. V1.1 further improves the powerful new approach used to identify and deconvolve mixtures and the background of co-eluting peaks to minimize the mis-identification of compounds in complex samples.

These features can save the analyst hundreds of hours

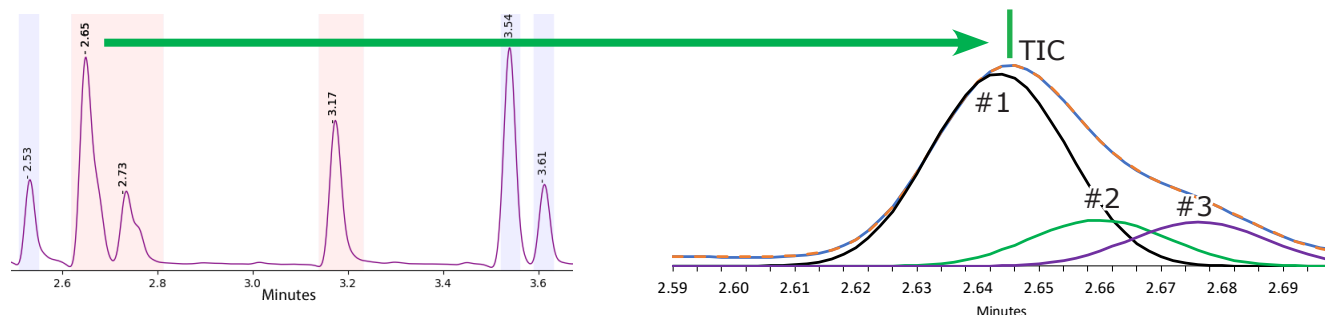
per year while increasing compound ID confidence and minimizing the number of "unidentified" peaks due to interferences, unresolved peaks, or just ambiguous library search results. GC/ID can automatically process an entire sequence of GC/MS runs from most vendor instruments including the popular Agilent GC/MSD. It also provides an easy-to-use review mode to audit results and generate reports in either PDF or spreadsheet formats.

Formula ID is a feature normally only available on high resolution instruments. Combined with library search and retention index values, these three metrics can be "blended" into an overall match quality or used independently providing dramatic improvements and valuable time savings in GC/MS compound ID.



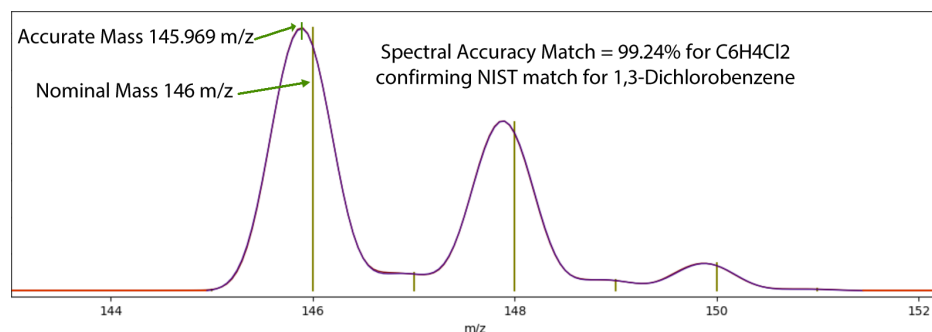
GC/ID processes an entire run in a few minutes and calculates the NIST match value (NIST) for each peak, verifies the compound formula ID by accurate mass/spectral accuracy (SA-M) as well as fragmentation (SA-F) and then calculates the peak's retention index (RI Fit). **These additional metrics can dramatically improve compound identification confidence.**

GC/ID automatically identifies "mixture" peaks and not only indicates the number of unresolved compounds, but also generates the "pure" MS



The peak at 2.65 min actually contains 3 co-eluting peaks which GC/ID deconvolves as shown.

GC/ID confirms each NIST library match by validating the formula using accurate mass/spectral accuracy



The profile spectral overlay of the calculated "True" MS (Blue) and the calibrated (Red) MS are identical to within 99.24% spectral accuracy confirming the NIST compound formula for more confident compound ID. This is a feature previously only available in high resolution MS.

Retention index (RI Fit) provides a powerful quantitative metric to readily ID the right compound, even when the library search values are close or ambiguous

The "NIST" match results (Red) cannot ID the correct compound (Ethylene, 1,2-dichloro-, Z) and neither can the formula ID from spectral accuracy (SA). "RI Fit" (Blue) easily distinguishes the correct hit and the (NIST+SA+RI Fit) blended "Match" value (Green) clearly identifies the correct compound.

HIT	Match	NIST	SA	RI Fit	Formula	Name
1	95.44%	911	99.35%	96.29%	C ₂ H ₂ Cl ₂	Ethylene, 1,2-dichloro-, (Z)-
2	86.88%	915	99.35%	52.71%	C ₂ H ₂ Cl ₂	Ethylene, 1,2-dichloro-, (E)-
3	73.78%	851	99.35%	15.71%	C ₂ H ₂ Cl ₂	Ethene, 1,1-dichloro-
4	71.80%	718	49.47%	-1.00%	C ₄ H ₄ Cl ₂ O ₂	Dihydro-4,5-dichloro-2(3H)furanon
5	70.10%	759	99.35%	15.71%	C ₂ H ₂ Cl ₂	Ethene, 1,1-dichloro-

GC/ID is the first major breakthrough in GC/MS in decades

GC/MS library search has been a powerful tool for the ID of organic compounds for decades. However, besides continued creation of additional spectral libraries, hardware improvements in terms of sensitivity and ease of use, no significant progress

has been made to assist the analyst in determining the correct match from a long list of possible hits without the tedious and time-consuming manual review or even re-analysis. Contact us today for a demo or to learn how GC/ID can make your lab more productive.