

What is ZipChip?

ZipChip is a front-end separation device that couples to your mass spectrometer. It joins capillary electrophoresis and electrospray ionization into a plug-and-play chip. There is minimal sample preparation and tiny injection volumes, so there is not much assistance needed by a scientist.

Can the ZipChip be used to analyze small and large molecules?

The beauty of the ZipChip is that you can perform large molecule (e.g., mAb's) analysis in the morning and transition to small molecule (e.g., amino acids) analysis in the afternoon. It's that fuss-free! There is no need to change mobile phases or columns to accommodate a new project.

Can I use ZipChip to perform Native Charge Variant separations of my mAb?

Yes! ZipChip performs native charge variant separations by capillary-zone electrophoresis mass spectrometry (CZE-MS). Not only can you [separate the charge variants](#) (basic lysine 2K and 1K, 0K monomer, and acidic/deamidated species), the selectivity of the mass spectrometer allows you to determine the accurate mass of each species by deconvoluting the charge envelop of each peak.

What is sample prep like?

ZipChip is extremely sample matrix tolerant. Most formulation buffers – even those containing salts or detergent – are compatible with ZipChip analysis. In many cases, we simply dilute and shoot.

Can I use ZipChip for the quantitation of small molecules?

Absolutely. ZipChip can perform formal [quantitation of amino acids](#) without any derivatization. Many users routinely use ZipChip for quantitation of amino acids and metabolites in samples such as cell culture media, plasma extracts, or other matrices. For instance, [in a study of cell culture media](#), we demonstrated the accurate absolute quantitation of amino acids with five orders of dynamic range.

What about carryover with ZipChip?

Because there is no stationary phase with the ZipChip, sample carryover is significantly reduced, and the overall carryover observed is minuscule. How minuscule, you ask? We have conducted [two separate experiments](#) to assess the carryover of both peptides and the NIST antibody standard. The average carryover for the peptides was 0.04%, and that for intact antibody (NIST) was only 0.004%.



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Email us at zipchip@908devices.com



Can the ZipChip interface to any mass spec?

Almost - the ZipChip currently interfaces to Thermo (Orbitrap Exactive and Q Exactive Series, Fusion Lumos Tribrid, Exploris 480, Eclipse Tribrid LTQ, Orbitrap Elite Series, TSQ2 Series Triple Quads), Sciex (TripleTOF 6600+, 6600, 5600 Triple Quad/QTrap 6500+, 6500, 5500+, 5500, 4500) and Bruker (timsTOF/timsTOF Pro, maXis QTOF, impact QTOF, compact QTOF) mass specs. If you don't see your mass spec listed, [reach out to us](#).

How does the ZipChip interface and control the MS acquisitions?

The ZipChip is a plug-and-play device, so just remove the ESI source and attach the ZipChip! No alignment or adjustments are required. The ZipChip will start your mass spec at the right time, just like a chromatography station would do. The data acquisition is performed by your existing mass spec software, so data processing is simple.

Can I see a ZipChip live?

We are always on the road at industry trade shows, so be sure to check out our [event log for details](#). We also host Bio & Brews events throughout the country, which allow you to meet up with some of our ZipChip team in the wild. Also, never hesitate to reach out if you want a dedicated webinar. We would be happy to remotely walk you through a ZipChip demo from our lab.



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