**The power of ion mobility-mass spectrometry for structural characterisation and the study of conformational dynamics**

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**Abstract**

Mass spectrometry (MS) is a vital tool for molecular characterisation, and the allied technique of ion mobility (IM) is enhancing many areas of (bio)chemical analysis. Strong synergy arises between these two techniques because of their ability to ascertain complementary information about gas-phase ions. IM separates ions (from small molecules up to megadalton protein complexes) based on their differential mobility through a buffer gas. IM-MS can thus act as a tool to separate complex mixtures, resolve ions that may be indistinguishable by MS alone, or to determine structural information *(e.g.* rotationally averaged cross sectional area), complementary to more traditional structural approaches. Finally, IM-MS can be used to gain insights into the conformational dynamics of a system, offering a unique means of characterising flexibility and folding mechanisms. This Review critically describes how IM-MS has been used to enhance various areas of chemical and biophysical analysis.

Ion mobility spectrometry (IMS) is an analytical technique that separates gas-phase ions based on their size and shape, analogous to electrophoresis in the condensed phase. The technique has long been used for the detection of illegal or dangerous substances *e.g.* explosives at border crossings, and to garner evidence for the illegal use of chemical agents.[1](#_ENREF_1) Mass spectrometry (MS) is also used in the analysis of gas-phase ions, permitting determination of their mass-to-charge (*m*/*z*) ratios. Therefore, the two techniques can be used to ascertain complementary information about analytes. The coupling of the two strategies, though first described in 1962,[2](#_ENREF_2) has only recently become relatively commonplace, primarily due to commercialisation of the necessary instrumentation. The last ten or so years has seen an explosion in research using ion mobility-mass spectrometry (IM-MS), as demonstrated by a rapid increase in the annual number of peer-reviewed publications (Figure 1), where the benefits of combining both analytical strategies have been exploited.

**Instrumentation for ion mobility spectrometry**

Primarily, three IMS techniques are employed in IM-MS: drift time ion mobility spectrometry (DTIMS), travelling wave ion mobility spectrometry (TWIMS) and field asymmetric ion mobility spectrometry (FAIMS) (Figure 2, Table 1); these are described in detail below.

*Drift time ion mobility spectrometry (DTIMS)*

DTIMS is the oldest and conceptually simplest form of ion mobility (Figure 2a). Ions are introduced into a drift tube. The application of a static uniform electric field (5-100 V) then propels these ions in the direction of the applied field. The tube is filled with a drift gas, typically helium. The time taken for an ion to drift through the tube is related to its rotationally averaged cross sectional area, *i.e.* the area covered by a particle, or more simply its collision cross section (CCS), Ω. Compact structures travel faster than more elongated (extended) ions due to fewer interactions with the gas. The recorded drift time of an ion allows calculation of its Ω, according to the Mason-Schamp equation[3](#_ENREF_3):



where *K0* is the reduced mobility (measured mobility at standard temperature and pressure), *z* is the charge state of the ion, *e* is the elementary charge, *N* is the number density of the drift gas, *µ* is the reduced mass of the ion-neutral pair, *kB* is the Boltzmann constant and *T* is the gas temperature. The proportional relationship between Ω and *K0* is only true at or below the “low field limit”, where the ratio between electric field strength and buffer gas density is small *i.e.* ≤2 Townsend (2 x 10-17 V•cm2).[4](#_ENREF_4) Determination of the CCS (which gives an indication of an ion’s size and shape) provides structural information that is characteristic for each compound, and can be compared to data acquired using other structural techniques such as X-ray crystallography and Nuclear Magnetic Resonance (NMR) spectroscopy. The level and quality of structural information obtainable using IMS compared to traditional techniques will be discussed below. DTIMS is advantageous due to its relatively high resolving power (*R* >100 Ω /Δ Ω) compared to other IM devices, meaning that an ion with Ω of 1000 Å2 can theoretically beseparated from an ion with Ω +/- 10 Å2. However, DTIMS can suffer from low duty cycle *i.e.* percentage of ions detected relative to those generated by the ionisation source, on devices where the ions are pulsed into the drift cell, or where entry/exit of ions into the drift cell occurs through extremely small apertures. However, limitations in duty cycle have been overcome in newer generation DTIMS instruments by incorporation of some form of ion-trapping funnel prior to the drift cell, which can accumulate ions whilst a previous pulse is being mobility separated.[5](#_ENREF_5), [6](#_ENREF_6)

*Travelling wave ion mobility spectrometry (TWIMS)*

A TWIMS device comprises a series of ring electrodes called a stacked ring ion guide (SRIG), to which a travelling voltage wave is applied.[7](#_ENREF_7) Radio-frequency (RF) voltages of opposite phases are applied to adjacent electrodes (Figure 2b). These voltages radially confine the ions, whilst application of a transient direct current (DC) voltage to each electrode in succession from one end of the device to the other propels the ions axially. The DC voltage pulse applied to each electrode in turn creates the ‘travelling wave’ upon which ions ‘surf’ and traverse the mobility cell. By altering the speed and magnitude of the travelling voltage wave, mobility separation of ions can be achieved. Higher mobility ions are ‘carried’ by the wave, whilst ions of lower mobility ‘roll over’ the wave, thus taking longer to move through the mobility cell. Complex mixture separation can be achieved by sending several travelling waves through the device in quick succession. The TWIMS device is operated below the low field limit and, following calibration, determination of CCS is therefore possible.[8-11](#_ENREF_8) Calibration of the drift time through the TWIMS cell under defined conditions (gas type/pressure, travelling wave speed/height *etc.*) is necessary as the direct relationship between Ω and *K0* is no longer applicable due to the constantly changing electric field. Optimal drift time calibration requires measurement of analytes of similar physical and chemical features with known CCS, to ensure that conditions are suitable for both calibrant and analyte. Although relatively simple to perform, the requirement for calibration does increase analysis time. The ability to employ TWIMS with and without CCS calibration means that the technique has found application as both a separation device and a structural tool.

*Field asymmetric ion mobility spectrometry (FAIMS)*

FAIMS devices are constructed of two electrodes, across which an electric field is established (Figure 2c).[12](#_ENREF_12) Ions are introduced into the device perpendicular to the electric field and collinearly to the drift gas. Two voltages are used to achieve separation: the dispersion voltage (DV) and the compensation voltage (CV). The DV is an alternating asymmetric waveform, where the value of the positive voltage is greater than that of the negative. However, the negative voltage is applied for a longer time, resulting in an equal voltage•time product for each part of the waveform (Figure 2c). This waveform exploits the fact that under high electric field conditions (>5000 Vs-1), as generated by the positive voltage period, the mobility of ions can be different to that under the low electric field conditions (<200 Vs-1) provided by the negative voltage period. This electric field-dependent mobility means that ions drift radially as they traverse the electrodes (Figure 2c). Ultimately, dispersion of the ions in this manner would lead to contact with the electrodes and neutralisation. Therefore, to refocus ions through the electrodes, a CV is applied. For a given CV, only ions of specific mobility will be repelled from the electrodes, whilst other ions will continue along their path and be neutralised. Manipulation of the CV can therefore be used to selectively permit ions of interest through the electrodes whilst removing ions of differing mobility. The FAIMS device thus operates as a mobility filter and typically finds application as an orthogonal separation technique to liquid chromatography (LC), separating ions based on different physico-chemical properties, prior to MS analysis, enabling increased selectivity and peak capacity.[13](#_ENREF_13) The major limitation of FAIMS is that CCS cannot be determined, as its operating electric field strength causes it to exceed the low field limit (Table 1); this prohibits the correlation of drift time with structural features as the mobility of an analyte is not directly related to its structure, explaining why FAIMS devices are primarily used to filter out unwanted interferences and/or to separate analytes of interest. Although the resolving power of FAIMS separation is traditionally poor (*R* < 20), the preferential inclusion of light gases in which the ions are more mobile (*i.e.* He and/or H2) as opposed to N2 in the carrier gas, has been demonstrated to significantly increase resolution, with resolving powers of up to 500 being reported.[14-16](#_ENREF_14)

Like FAIMS, the differential mobility analyser (DMA) is a spatial mobility device rather than a time-based separation device *i.e.* DTIMS or TWIMS. However, unlike FAIMS, DMAs do not invoke alternating high and low electric fields to induce analyte separation, instead using the combined force of a high flow rate sheath gas and a superimposed electric field applied perpendicular to the gas flow in order to filter ions.[17](#_ENREF_17), [18](#_ENREF_18) DMA instruments have historically been used in the area of aerosol science for the analysis of particles in excess of ~ 10 nm and have not achieved the same popularity as FAIMS devices.[17](#_ENREF_17), [19](#_ENREF_19) Newer generation DMA instrumentation with higher resolving power (*R* > 50) may yet encourage growth in this area.[20](#_ENREF_20)

While the IMS devices discussed will all separate ions based on differences in their mobility through a buffer gas, only the time-based mobility devices (DTIMS, TWIMS) can be used to determine information about cross-sectional area, either with or without the requirement for drift time calibration if there is a requirement to define CCS in Å2. In contrast, FAIMS (and DMA) devices function preferentially as filtration devices, much like quadrupoles can be used in MS analysis. However, whether the utility of IMS separation is for analyte filtration and/or differentiation, or more targeted structural analysis, the key strength comes in combining this analytical feature with mass spectrometry, due to the complementary information garnered. Examples of how IMS devices can be used either to improve the MS-based analysis of complex mixtures, or in the case of DTIMS/TWIMS, facilitate enhanced structural analysis and the study of conformational dynamics are described below.

**Enhancing the MS analysis of mixtures with IMS**

The coupling of IMS to MS can significantly improve experimental analysis as defined by a range of criteria often used to benchmark such methods: selectivity, speed and limit of detection. The improvement gained for each is considered below.

*Selectivity*

The complementary mode of separation introduced by the coupling of any type of IMS device to MS analyses can concomitantly lead to improved selectivity, which facilitates an enhanced ability to analyse mixtures. Creese and Cooper exploited the separation capability of FAIMS to resolve isomeric glycopeptides, differing only by the site of glycosylation.[21](#_ENREF_21) The isomers co-eluted using LC, making glycosite localisation extremely difficult. As these species were of the same *m/z* value they were co-isolated prior to MS/MS analysis, thus generating a chimeric product ion mass spectrum composed of fragments from both isomers. Incorporating FAIMS allowed separation of these glycopeptides based on their different mobilities, and thus selective acquisition of MS/MS data for each of the isomers, enabling definitive characterisation. Many similar experiments have been conducted to resolve and characterise complex mixtures of small molecules.[22](#_ENREF_22) Analytes may also have similar mobilities and thus drift time, meaning that they co-migrate during IMS, although this can be overcome by altering the applied voltages (timing or amplitude), changing the drift gas or adding volatile (often chiral) dopants, such as 2-butanol.[23](#_ENREF_23), [24](#_ENREF_24) Detailed studies have shown that the change in selectivity induced by such dopants is obtained through differential formation of ion–molecule clusters.[25](#_ENREF_25), [26](#_ENREF_26) Addition of shift reagents, as utilised in NMR spectroscopy, is another strategy that can improve the separation of ions of similar mobility in their native forms.[27-29](#_ENREF_27) Selective complex formation of only one of the compounds with the shift reagent changes their mobility and facilitates separation. One particularly effective use of this approach was reported by Howdle *et al.*, who used a pharmaceutical excipient, polyethylene glycol (PEG), already present in the sample as the shift reagent.[27](#_ENREF_27) Inclusion of PEG changed the mobility of the target drug, lamivudine, so that it occupied an interference-free region of the spectrum and could be analysed in isolation.

The separation capabilities of IMS have also demonstrated particular utility in MS analyses where chromatographic separation either has not or cannot be employed, providing a crucial additional analytical dimension. For example, MS imaging experiments, where analytes are ionised directly from a complex matrix such as a tissue section, are notably enhanced by incorporation of IMS. Stauber and co-workers used TWIMS in a matrix-assisted laser desorption/ionisation (MALDI)-MS imaging experiment facilitating separation of ions of the same *m/z* value (*i.e.* isobaric).[30](#_ENREF_30),[31](#_ENREF_31) While analysis of these ions in the absence of IMS produced a composite image of both species, meaning that distinct localisation could not be ascertained, incorporation of IMS enabled acquisition of separate spatial distributions for each individual compound. A similar study recorded the spatial distribution of the cytotoxic agent vinblastine following administration to rats. Although this analysis initially suffered from matrix interference at the same *m*/*z* value as the target compound, the additional selectivity afforded by TWIMS enabled vinblastine distribution to be accurately determined.[32](#_ENREF_32)

Another area where the additional separation provided by IMS has proven beneficial is non-targeted discovery proteomics. Shliaha and co-workers analysed a tryptic digest of an *E. coli* whole cell lysate and demonstrated a ~60% increase in the number of identifications at both the peptide and protein levels using LC-TWIMS-MS compared to LC-MS alone.[33](#_ENREF_33) A similar study comparing the same analytical strategies reported an even greater increase in the number of identifications, with both peptide and protein assignments rising due to the complementary separation mechanism and additional peak capacity afforded by the TWIMS device.[34](#_ENREF_34)

*Speed*

In many areas of (bio)chemistry and medical science, high-throughput sample analysis is critical. IMS is a technology that can expedite analysis, and thus is likely to play an increasing role in numerous fields where rapid analysis is required, *e.g.* drug screening. IMS typically works on the millisecond timescale, faster than chromatography (typically on the scale of seconds), and could potentially be used to increase the speed of analysis whilst retaining the necessary separation. For example, Parson and co-workers separated isomeric glucuronide metabolites of propranolol over 15 times faster using FAIMS than had been achieved using high-performance liquid chromatography (HPLC).[35](#_ENREF_35) Many other examples exist of IMS being employed to improve the rate of pharmaceutical discovery and/or screening by obviating (or significantly reducing) the need for chromatographic separation prior to MS. For example, application of TWIMS significantly increased the rate at which biological samples could be screened for the presence of natural products as potential lead therapeutics.[36](#_ENREF_36) TWIMS has also been used in metabonomics to provide additional online separation, facilitating a reduction in the upstream LC method duration and thus improving throughput.[37](#_ENREF_37)

*Limit of detection*

The limit of detection by MS is much lower than most other analytical techniques, with LC-MS shown to routinely detect low attomole amounts of analyte even in complex mixtures.[38](#_ENREF_38), [39](#_ENREF_39) The addition of IMS to the analytical workflow can further lower limits of detection by removing background interference. The group of Thibault demonstrated a greater than 10-fold improvement in the detection limits of peptides in complex mixtures when FAIMS was incorporated into their LC-MS platform.[40](#_ENREF_40) The improved limits of detection and increased power of separation doubled the number of peptide[40](#_ENREF_40) and phosphopeptide[41](#_ENREF_41) identifications from unpurified cellular extracts. Likewise, Ibrahim and co-workers used a set of model isomeric modified peptides to demonstrate that DTIMS can overcome the necessity to fragment peptides for discovering the site of covalent modification, using instead the mobility of each isomer for characterisation.[42](#_ENREF_42) By incorporating DTIMS for ions of known behaviour, determined using authentic standards, these researchers circumvented the need for tandem MS and reported an order of magnitude improvement in detection limits.

The qualitative and quantitative analysis of therapeutics in complex biological matrices can also be improved using IMS; for example, TWIMS facilitated the detection of peptide drugs by enabling the identification of low abundance metabolites following the removal of background chemical ‘noise’ in a complex mixture.[43](#_ENREF_43) Furthermore, FAIMS has been used to remove a matrix component in plasma that prevented a LC-MS assay for the drug dianicline from passing good laboratory practice acceptance criteria.[44](#_ENREF_44) The additional separation provided by incorporation of FAIMS significantly decreased the limit of detection, thus making the analytical approach more effective for assaying the drug. The same technology was employed by Guddat and co-workers, who developed methodologies for the detection of performance enhancing steroids and their metabolites in urine samples taken from athletes, reducing the detection limits in some cases to sub-picogram per mL (pgmL-1) quantities.[45](#_ENREF_45) Improvements in detectability opens up the future possibility of identifying a wide range of substances in biological fluids at significantly lower levels (and for longer periods post-dosage), with important implications for monitoring healthcare and the screening of drugs of abuse.

**IM for enhanced structural analysis of (bio)molecules**

While all modes of ion mobility spectrometry will separate analytes based on their conformation, application of DTIMS or TWIMS can further be used to determine CCS. Unlike other biophysical techniques used to characterise analyte structure, IM-MS can be used to ascertain structural information using only small amounts of sample (nanogram quantities). Moreover, as the ions of interest can be selectively isolated from complex samples, material of much lower purity can be used than is typically needed to structurally characterise compounds using X-ray crystallography or NMR spectroscopy (Table 2).[46](#_ENREF_46) Furthermore, by using IM-MS to determine changes in mobility and thus conformation and CCS, properties like conformational dynamics,[47-52](#_ENREF_47) folding and unfolding intermediates,[52-54](#_ENREF_52) ligand-induced conformational changes,[55](#_ENREF_55), [56](#_ENREF_56) aggregation intermediates[57](#_ENREF_57), [58](#_ENREF_58) and quaternary structures (topology) can be determined.[59](#_ENREF_59)-[60](#_ENREF_60)

*Determination of ion collision cross sections*

Analyte structure is determined from experimentally derived rotationally averaged temperature-dependent CCS values, which reflect the conformation and shape adopted by the ions in the gas phase under defined experimental conditions.[61](#_ENREF_61) Experimental CCS can be compared with theoretical CCS values generated by molecular dynamic (MD) simulations, often using X-ray and NMR structures as input for the calculations.[62-65](#_ENREF_62) Computational algorithms have been developed for this purpose, although choosing the right algorithm is extremely important for correct interpretation of the experimental IM-MS data. When dealing with large proteins and protein complexes, the complexity brought about by the range of molecular shapes and dimensions that arise pose serious limitations to the applicability of such algorithms, either due to their inability to deal with particular kinds of intra- and intermolecular interactions, or to the extremely demanding computational costs.

The most commonly employed models used to calculate CCS are projection approximation (PA),[66](#_ENREF_66) exact hard sphere scattering (EHSS) [67](#_ENREF_67) and the trajectory method (TM),[68](#_ENREF_68) all of which determine the CCS using helium as the buffer gas. The PA method is relatively computationally inexpensive, calculating CCS as an average of geometric projection areas of all the possible orientations of the molecule. However, it does not take into account long-range interactions or many of the features arising due to scattering between the ions and the drift gas. Due to its inability to factor for multiple collisions, this method usually underestimates CCS for ions > 2 kDa and is therefore primarily used for predicting CCS of small molecules. The EHSS method takes account of the scattering and the collisions with the drift gas but ignores long-range interactions between gas and ions. In contrast, the TM is generally considered more reliable, particularly for large biomolecules, as it takes into account long-range interactions between the drift gas and the analyte ion, as well as collision effects.[69](#_ENREF_69) However, a major limitation of the TM is the time required to perform calculations, particularly for very large molecules; for such analytes, the EHSS method is therefore often a good compromise.

Recently, the projection superposition approximation (PSA) method was introduced by Bleiholder and co-workers.[70-73](#_ENREF_70) Like PA, this algorithm computes molecular shapes as a projection approximation, but with an extra feature of superposition of atomic potentials and inclusion of a shape factor. This approach is of particular value considering that long-range, attractive van der Waals interactions between ions and buffer gas are proportional to the analyte's molecular weight and the atom density, and are therefore a function of the molecular shape. An algorithm that is capable of taking into account these size and shape effects, concomitantly lowering computational demands, is therefore particularly beneficial. The PSA method was shown to outperform EHSS following tests on three sets of molecules chosen to represent different sizes and shapes, providing results in very good agreement with TM, but with a 100-1000 fold reduction in computational time.[70](#_ENREF_70)

*IM-MS as a stand-alone technique for structural studies*

Most of the detailed structural interpretation of IM-MS generated CCS values relies on the availability of total or partial structures (either crystalline or solution phase) as input for the prediction of comparative CCS values. However, independent from the availability of X-ray or NMR derived structures, gas-phase IM-MS is a powerful tool for the interrogation of dynamic systems without the perturbation brought about by solvation effects, counter-ions and the presence of other chemical species which may bind and alter analyte conformation. This offers a unique medium to explore intrinsic physico-chemical properties, and measurement of ionic mobilities (and the consequent determination of the associated CCS values) permits understanding of the conformational landscapes that different ionic species can populate. Furthermore, as detailed below, the possibility of extracting ions of interest from near-native solutions as ‘naked’ species allows one to explore the effect of sequential binding of solvent molecules on structure, thus enabling insights into the role of hydration on conformational dynamics. Partial or total unfolding of a protein is often reflected in the observation of higher charge states due to the exposure of a greater number of protonation sites, and has an immediate effect on their ionic mobilities.[74](#_ENREF_74) Similarly, ligand binding or protein post-translational modification often induce conformational changes that can be evaluated using IM-MS without necessarily having to rely on the availability of calculated CCS values (*i.e.* prior detailed structural determination), and such measurements have also been used to explore temperature-dependent conformational dynamics.[75](#_ENREF_75) Indeed, one might argue that IM-MS is a unique analytical tool for (bio)molecules unsuited to conventional approaches.

Importantly, unlike many other biophysical techniques that provide an averaged structure, IMS can be used to interrogate dynamic heterogeneity, placing IM-MS in a privileged position over both crystallography and NMR spectroscopy (Table 2). The ability to monitor dynamics allows snapshots of short-lived folding intermediates and conformational transitions to be obtained.[47](#_ENREF_47), [48](#_ENREF_48) Identification of transient conformations is becoming ever apparent as the techniques develop: recent work from Shvartsburg and colleagues has demonstrated the additional utility of different drift gases, notably hydrogen-rich gas mixtures, for enhancing the separation of dynamic protein conformers by FAIMS.[76](#_ENREF_76) The five-fold improvement in resolution achieved under these conditions enabled distinction of ~15 conformations of ubiquitin, where previously only a handful of conformers had been distinguishable. This strategy will undoubtedly prove invaluable for future investigation into protein conformation. For biopolymers like proteins and protein complexes, investigation of both conformation and dynamics furthers our understanding of the intramolecular and intermolecular interactions that control the folding and the conformational landscapes that biomolecules can adopt *in vacuo*. A comparison of the results obtained in the gas-phase with data obtained for the same system in solution can improve our understanding of the role played by solvent molecules, counter-ions and other chemical entities in driving the formation of thermodynamically stable structures (see below).

The additional dimension of separation offered by IM in IM-MS also means that the resolution of isobaric molecular species is feasible. This has enormous potential in the case of polymeric systems where subunits can generate isobaric multimeric assemblies that would not be distinguishable by virtue of their *m*/*z* value alone. As illustrated by examples below, IM-MS has been successfully used to explore oligomerisation processes of polypeptides such as -amyloid, whose aggregation is linked to the aetiology of neurodegenerative diseases.[77](#_ENREF_77), [78](#_ENREF_78)

*Small molecules (<500 Da)*

IM-MS analysis of small molecules, especially naturally occurring metabolites and molecules derived following the metabolism of exogenous compounds, is gaining rapid impetus. Metabolites are usually present in biological samples at levels far too low for structural characterisation using NMR spectroscopy. LC-MS/MS, although having a limit of detection suitable for metabolite analysis, will often not be able to discriminate between isomeric species even after multiple rounds (*n*) of fragmentation (MS*n*).[65](#_ENREF_65) This is especially true for aromatic hydroxylated metabolites. Dear and co-workers overcame this limitation by applying TWIMS-MS and MD simulations to the analysis of ondansetron and its metabolites, thereby allowing the 6-, 7- and 8-(OH) regioisomers to be discerned, even though they generated identical product ion mass spectra (Figure 3).[64](#_ENREF_64) Regioisomers of glucuronidated metabolites have also been distinguished and identified using TWIMS-MS.[79](#_ENREF_79) Determining the CCS of product ions generated by collisional dissociation, in addition to the precursor ion from which they are derived, may also be useful since MD simulations are more accurate for molecules with fewer degrees of freedom.[80](#_ENREF_80) Such studies may also allow stereochemical information to be harnessed that would otherwise be difficult to determine from the precursor ion alone. For example, Both *et al.* were able to use drift time measurements to differentiate the stereochemistry of monosaccharide product ions generated after collision-induced dissociation (CID) of glycopeptides and free di-, tri- and pentasaccharides, suggesting that IM-MSn may have significant utility for glycan sequencing.[81](#_ENREF_81) Clemmer and colleagues have also used a novel IMS-ion trap hybrid instrument to determine the ion mobility distributions (and thus conformation) of select precursor ions by monitoring for specific CID products,[82](#_ENREF_82) a strategy which could feasibly be extended to other types of product ions, such as those arising following electron transfer dissociation. IM-MS has also been shown to be capable of resolving diastereoisomers indistinguishable by HPLC, MS and NMR spectroscopy, and that were unsuitable for X-ray diffraction due to the formation of polycrystalline solids.[80](#_ENREF_80)

*Peptides*

When combined with MD simulations, IM-MS is a powerful tool to determine the secondary structure of peptides in the gas phase. In particular, studying peptide folding *in vacuo* is likely more physiologically relevant for polypeptides integral to a cell membrane, as the cell membrane interior and a vacuum both possess a low dielectric constant (ε = 1).[83](#_ENREF_83) Factors that influence the *in vacuo* formation of particular peptide secondary structure features (*i.e.* α-helices, β-sheets or globules) have been extensively studied by IMS.[84-88](#_ENREF_84) IM-MS revealed that the *N*-terminally acetylated peptide [Lys-Ala15 + H]+ has a CCS consistent with a globular structure solvating the charge, a major driving force in peptide secondary structure folding *in vacuo*.[84](#_ENREF_84), [86](#_ENREF_86) However, relocation of lysine (Lys) to the *C*-terminus (generating *N*-terminally acetylated[Ala15Lys + H]+) appears to allow short-range solvation, and induction of an α-helical structure, stable to over 400oC.[84](#_ENREF_84) Structural changes induced by the adduction of metal ions (cationisation) to peptides have also been studied by IM-MS, revealing new information with respect to the CCS of cationised versus protonated peptide ions. Also, and arguably potentially of greater interest, analogous studies have determined how conformation changes induced by metal ion adduction can influence protein–ligand interactions.[89-92](#_ENREF_89)

IM-MS has also proven extremely useful in advancing our understanding of gas-phase peptide dissociation.[93](#_ENREF_93) Studies on product ion conformations after CID of peptides have revealed that both linear and cyclic product ions are formed regardless of the energy deposited.[94](#_ENREF_94) Subsequent ring opening of the resultant macrocycles at different positions leads to scrambling of the original linear peptide sequence, complicating sequence determination by tandem MS.[95](#_ENREF_95), [96](#_ENREF_96) Furthermore, conformations adopted by gas-phase radical cationic products can now be more readily investigated with the development of a new commercial IM-MS instrument capable of performing electron-transfer dissociation (ETD).[97](#_ENREF_97)

*Large biomolecules*

Early IM-MS studies of biologically relevant polymers focused on drift time measurements of isolated small proteins (enabling CCS calculation), and were mainly used to improve understanding of the relationship between solution-phase and gas-phase conformations. Such structures had already been explored by measuring charge state distribution by electrospray ionisation (ESI)-MS[74](#_ENREF_74) as lower charge states are generally believed to be more representative of the folded, compact conformations adopted by a protein in solution. However, care should be taken in assuming that a reduced charge state always corresponds to a native structure (see below). Indeed, depending on the contribution of hydrophobic, ionic and hydrogen bond interactions, the three dimensional structure might evolve in very specific ways upon desolvation. Therefore any general relationship between low charge state and compactness is hard to define *a priori*.[74](#_ENREF_74)

*Proteins and protein complexes under native conditions*

The possibility of generating gas-phase ions from solutions of controlled ionic strength and buffered pH enables interrogation of complex systems under near physiological conditions. This is extremely valuable if structural properties are to be related to biological activity because features of the solution-phase conformation may sometimes be preserved.[98-102](#_ENREF_98) ESI of proteins and protein assemblies generates several species with different charge states. Generally, more compact structures have a reduced number of exposed protonation sites, thus limiting the maximum charge on the corresponding gas-phase ions. IM-MS analyses of ions of reduced charge states are therefore optimal, as they are more likely to represent the biologically relevant, native folded species. However, protein complexes containing a central cavity have been observed to collapse during IM-MS, yielding ions of low charge state with more compact structures, and thus smaller CCS values, than that of their native-like conformation.[103](#_ENREF_103)

A key concept in the IM-MS analysis of proteins and protein complexes from native conditions is the ability to transfer intact species from solution into the gas phase without inducing major conformational changes upon the loss of solvating molecules, as occurs during ESI.[100](#_ENREF_100) In order for a structural analysis to be meaningful, it is important to ensure that the structure being analysed resembles that of its native, functional state. Water molecules play a major role in controlling the stability of protein (and protein complex) conformations in solution, mainly by inducing hydrophobic regions to orient themselves towards the core of the structure and thus minimise contact with the aqueous solvent.[104](#_ENREF_104) It has therefore been suggested that removal of these solvent molecules might induce major conformational changes leading to non-native (‘inside-out’) structures.[69](#_ENREF_69), [105](#_ENREF_105) A significant amount of effort has been devoted to understanding the relationship between solution and gas-phase conformation both theoretically and experimentally, and much of the currently accepted theory in this area has been generated by IM-MS measurements.[106-109](#_ENREF_106)

Investigations into the role of hydration in controlling the stability and dynamics of protein conformations in the gas phase have provided significant insight into the many factors governing the folding and unfolding of gaseous protein ions.[110-115](#_ENREF_110) Of particular relevance are studies of gas-phase hydration of folded and unfolded protein ions by DTIMS-MS in which ESI-generated cytochrome c ions were allowed to react with water in the drift tube of the IM device. The arrival time distributions (ATDs) of fully desolvated ions were then compared with ATDs of ions carrying an increasing number of solvent molecules.[112](#_ENREF_112) Using this approach, Fye *et al*. demonstrated that an unfolded charge state (*z* = 7) characterised by two peaks in the fully desolvated state, shifted towards the more compact folded conformation (*i.e.* earlier arrival time) upon hydration. This pioneering study suggested that the addition of water molecules to unfolded gas-phase protein ions promotes refolding towards more compact, native-like structures. Similar studies have been reported by Rodriguez-Cruz *et al*. using (smaller) biological peptides such as gramicidin S, outlining the competition between charge solvation with water and internal ‘self-solvation’ by hydrogen bonds and their influence on gas-phase and solution-phase structures.[110](#_ENREF_110) More recently, Gao and co-workers described the effect of hydration in the competition between salt bridges and charge solvation for isolated, protonated basic amino acids (arginine and lysine), showing how hydration of the gas-phase ions balances the competition between the two types of interactions, permitting formation of otherwise disfavoured salt bridges.[115](#_ENREF_115) Such studies have advanced our understanding of the mechanisms of ESI and how this process can contribute to preserving or disrupting the original solution-phase structure.[113](#_ENREF_113)

While IM-MS determined CCS values for lower charge states are generally in good agreement with data calculated for the same species based on X-ray crystallography or NMR spectroscopy data, gas-phase CCS values are typically slightly lower than those calculated for solid-phase crystal structures.[69](#_ENREF_69) As recently reported for a collection of theoretical and experimental CCS values of proteins of different molecular weight, the discrepancy between the two sets of data tend to increase with the size of the protein.[69](#_ENREF_69) Considering the fraction of crystal volume occupied by solvent molecules, this variation can be explained by invoking a partial collapse of the gas-phase protein ions upon desolvation.[116](#_ENREF_116) DMA-MS studies have revealed a difference as large as 40% between the gas-phase CCS and the X-ray structure of the GroEL tetradecamer, suggesting substantial compaction of the native structure *in vacuo*.[117](#_ENREF_117) However, despite this noticeable difference, the authors were still able to demonstrate that the tetradecameric complex maintains its native topology upon desolvation.

Figure 4 compares CCS values measured by TWIMS for the lowest charge state of five proteins (believed to be representative of the native conformations) with values calculated from solid phase (X-ray crystallography) and solution phase (NMR spectroscopy) studies using the PA and TM theoretical methods described above.[46](#_ENREF_46) The general observation of higher TM-derived values than those calculated using PA is likely due to the fact that PA does not consider interactions of the ions with the buffer gas, meaning that for convex structures the CCS will be underestimated.[66](#_ENREF_66) The experimentally determined CCS values are lower than the TM values but higher than the PA values for all five proteins, probably because gas-phase protein ions can adopt conformations that are more compact than the ones observed in the solid state, due to partial collapse of the charged residues as a consequence of solvent removal.[69](#_ENREF_69), [118](#_ENREF_118) A detailed description of the structural evolution of a globular protein during and after ESI has been presented by Breuker and McLafferty, who described how a gaseous environment can potentially induce major structural changes.[118](#_ENREF_118) As well as the need to consider both covalent and non-covalent interactions that stabilise protein structures in solution, it appears that the time during which ions are allowed to relax in the gas phase prior to analysis is paramount in dictating whether the original conformation is preserved or a new more stable gaseous conformation arises. IM-MS-derived structural data should therefore be interpreted with the caveat that desolvation can introduce changes in the overall gas-phase ion structure and the degree of change will be dependent on both the experimental conditions and the analyte itself.

It is clear that the relationship between gas-phase and solution- and solid-phase conformations is not easily addressed, mainly because the changes which an ion undergoes upon transfer to the gas phase are largely dependent on the relative roles played by electrostatic and hydrophobic interactions in dictating the native structure. Nonetheless, IM-MS measurements of CCS of biologically interesting species, such as proteins and protein assemblies, are invaluable as they readily enable investigation of conformation dynamics and folding/unfolding equilibria that are not easily accessible by solid-phase or solution-phase strategies. IM-MS therefore plays an important role in unravelling structural features. Arecent example includes a 3D ion trap-

IM-quadrupole-time of flight (Q-ToF)-MS-based study to monitor the effect of charge reduction on the conformation of gas-phase cytochrome c ions.[119](#_ENREF_119) Protein ions of high charge state were selected to undergo proton transfer reactions in the ion trap and the resulting CCS values compared to those of the same charge states extracted from the solution by ESI. The two values were similar, suggesting that initially unfolded, highly charged species can be induced to refold to their original compact states through charge reduction. These elegant experiments, which could only be facilitated by coupling an ion trap with IM-MS, permitted researchers to follow conformational transitions and demonstrate how coulombic-induced unfolding might be reversed. Analogous experiments followed the temporal evolution of ESI generated conformations of several charge states of cytochrome c over a timescale ranging from 10 ms to 10 s, demonstrating that initially folded conformations can relax into new minima on the conformational potential energy surface by temporarily populating unfolded intermediates.[120](#_ENREF_120) A similar study on the evolution of the native and a partially unfolded state of ubiquitin using DTIMS was also recently reported by Wyttenbach and Bowers.[121](#_ENREF_121) The compact state was found to survive for up to 100 ms *in vacuo*, whereas the ‘A state’, extracted from an acidic solution expected to induce partial unfolding, showed a faster (≤ 100 ms) decay to conformational intermediates, which then further refolded to new compact species. Electron paramagnetic resonance (EPR) spectroscopy in combination with TWIMS-MS has also revealed information about the conformational dynamics and molecular recognition processes which contribute to the functioning of the NarJ chaperone protein when bound to its substrate NarG.[122](#_ENREF_122) ESI-IM-MS measurements of the unbound and bound chaperone under native solution conditions clearly demonstrated that substrate binding was dependent on recognition and selection of a single conformer.

Despite recent advances, structural investigation of membrane proteins remains particularly challenging due to the difficulty in solubilising these species in buffers compatible with ESI whilst preserving their native structure. Much work has been done to demonstrate that native protein conformations can be maintained under the relatively harsh conditions required to release hydrophobic proteins from stabilising detergent micelles during ESI, although this process needs to be carefully controlled.[123](#_ENREF_123), [124](#_ENREF_124) As an alternative to detergents as solubilising agents that may unduly influence protein structure, Leney *et al.* recently described an amphipathic polymer for solubilising two bacterial, β-barrel-functional outer membrane proteins in a detergent-free solution prior to IM-MS analysis.[125](#_ENREF_125) Once in the gas phase, the proteins were released from their complexes with the polymer by voltage-induced activation in the source and transfer regions of the mass spectrometer, and their conformational properties studied by TWIMS. Both proteins retained their native structures based on comparison with theoretically predicted CCS, highlighting the potential of IM-MS for the examination of membrane proteins. Such strategies will undoubtedly be of great importance considering the interest that these, and other, membrane proteins have garnered as therapeutic targets.

The analysis of pathways leading to the formation of non-covalent, insoluble protein aggregates, such as amyloid fibrils, which are associated *in vivo* with the onset of pathological states including Parkinson’s and Alzheimer’s disease, has been revolutionised by IM-MS.[126](#_ENREF_126) Of particular relevance are contributions by the Bowers' group, including a fundamental study characterising the mechanism of amyloid-β protein oligomerisation and generation of toxic amyloid fibrils,[77](#_ENREF_77) and investigations into the effects of spermine binding on -synuclein protein conformation leading to protein compaction, a likely precursor for -synuclein aggregation and the onset of Parkinson’s disease.[78](#_ENREF_78) Measurement of drift times (and calculation of experimental CCS values) for different protein assemblies and prediction of model structures for the amyloid-aggregates using the PA model allowed specific pathways to be defined for the observed self-assembling processes, showing the potential of IM-MS as a complementary, and yet independent, structural tool for the investigation of these challenging systems. In addition to permitting structural characterisation of the intermediate, oligomeric species in aggregate formation,[57](#_ENREF_57), [77](#_ENREF_77), [127](#_ENREF_127) these studies employed IM to deconvolute isobaric peaks in the mass spectrum, originating from combinations of different numbers and charge states of homo-oligomers that coalesce to the same *m/z* value.[128](#_ENREF_128) Analogous studies using DTIMS[129](#_ENREF_129), [130](#_ENREF_130) or TWIMS[131](#_ENREF_131) have also been used to investigate the binding mode of inhibitors (small molecules, peptide mimetics and peptides) of formation of toxic β-amyloid aggregates, providing evidence for the mechanism of action of effective therapeutic agents for the potential treatment of Alzheimer’s disease.

The field of IM-MS analysis of large protein assemblies was pioneered by Robinson and colleagues, and represents an extremely exciting area of application for this powerful technique. For example, analysis of the trp RNA binding attenuation protein (TRAP)[60](#_ENREF_60) provided compelling evidence that many features of protein assemblies, including quaternary structure, can be preserved in the absence of solvent molecules. Indeed, this was the first IM-MS study to succeed in showing that a large multimeric protein assembly (relative molecular mass of 90 kDa) could be transferred from aqueous solution to the gas phase whilst maintaining its quaternary topology.[60](#_ENREF_60) The researchers made use of TWIMS coupled to a modified ToF mass spectrometer to measure the CCS of four charge states (19+-22+) of the 11-mer complex, demonstrating that the lowest charge state exhibited the largest CCS, with a value in close agreement to that estimated for a ring structure determined by X-ray crystallography. Further details of the identity of the conformers underlying this ionic population were provided by thorough molecular dynamic simulations using the EHSS method, showing how the experimentally determined CCS for the 19+ charge state comprised the native ring structure as well as partial ring and buckled ring conformers. IM-MS studies also revealed how binding of a 53 base pair strand of RNA to the TRAP complex had a stabilising effect on the gas-phase conformation.

Another fertile research area is virus structure and assembly, with the Heck group reporting IM-MS analysis of hepatitis B virus (HBV) capsids as large as 4 MDa.[59](#_ENREF_59) These virus particles are known to form two icosahedral capsids of different sizes depending on the number of dimers: T3 with 90 or T4 with 120 dimers. TWIMS-MS analysis identified two distinct conformations for each of the virus capsids, generating CCS values that were found to be in close agreement with the radii obtained for the same structures analysed by electron microscopy.

The study of membrane-embedded molecular machines represents a significant challenge from a structural determination point of view and has been revolutionised by IM-MS in conjunction with other MS-based techniques. Other biophysical techniques have been able to analyse subunits of these large protein machineries, generating a wealth of informative data but failing to report any structural characterisation of intact complexes. The first report on the gas-phase structure of an intact adenosine triphosphatase (ATPase)/synthase machinery appeared in 2011 using an IM-MS instrument specifically modified for transmission of high mass complexes.[132](#_ENREF_132), [133](#_ENREF_133) The recorded mass spectra revealed the subunit stoichiometries for the two complexes, and IM studies of the transmembrane proteins within the complex demonstrated conformational heterogeneity of subunit I (in ICL12), but not subunit CL12 (as determined by a broader ATD of ICL12) (Figure 5). It was only by using this IM-MS-derived structural data that a mechanism of function of this proton channel could be proposed.[133](#_ENREF_133)

*Other large molecules*

Many large compounds have been studied by IMS, including deoxyribonucleic acids (DNA),[134](#_ENREF_134) macrocycles[135](#_ENREF_135) and synthetic polymers.[136](#_ENREF_136) These large molecules often retain their solution-phase structure in the gas phase for (up to) milliseconds.[137](#_ENREF_137)

The gas-phase conformations adopted by different DNA secondary structures, including hairpins, pseudoknots and cruciforms (Holliday junction) have been studied using both IM-MS and molecular dynamics (Figure 6). At lower charge density, all these secondary structures are stable over the typical millisecond timescale of IM analysis. Where both pseudoknots and hairpins can be formed, pseudoknots are found to be favoured due to the formation of extra Watson–Crick pairs between the initial secondary structure formed (usually a hairpin) and another single-stranded region. At higher charge density these structures become elongated as Watson–Crick pairs are broken. Interestingly, the cruciform that was extensively studied formed a B-helix in the solution phase. However, this same analyte was found to exist as both a B-helix and an A-helix when desolvated, demonstrating that IM-MS can be used as tool to study structures adopted in a solvent-free environment.136 G-quadruplex formation, of particular importance in understanding the mechanism of cellular ageing and transformation, has also been monitored by IM-MS. In solution, these structures are known to form stacked planar rings where the plane is formed from four guanosine residues stabilised by atypical Hoogsteen hydrogen bonds and cations between the planes.140 These structures are retained upon vaporisation as confirmed by IM-MS. Analysis of tandem repeats of the telomeric region, where G-quadruplexes are often observed, allowed distinction and determination of G-quadruplex isomers.141 Using IM-MS, the intermediates in the assembly of these G-quadruplexes could be characterised and it was only by using such a strategy that it could be demonstrated that the final kinetically stable tetramers form an equilibrium state of DNA monomers, dimers and trimers, upon addition of ammonium cations.[138](#_ENREF_138)

Polymer chemistry is also beginning to utilise IM-MS as a structure elucidation tool, with polar homopolymers often exhibiting sharper ATDs than proteins.[136](#_ENREF_136) Early experiments were performed on thermally stable PEG ions coordinating a single alkali metal cation.[139](#_ENREF_139), [140](#_ENREF_140) For Li+ and Na+, PEG appeared to coil around the cation, forming a similar structure to a classical crown ether to solvate charge. However, precise structures differed depending on the size of the PEG oligomers and the number of oxygen atoms that were capable of coordinating to the metal cation; while Li+ and Na+ coordinated with 7 and 8 oxygen atoms respectively, Cs+ coordinated with 10-11 oxygen atoms, exhibiting a different conformation.[140](#_ENREF_140) Investigations into other polymeric systems have also indicated that, like polypeptides, they become more extended as charge is increased due to coulombic repulsion.[136](#_ENREF_136), [141](#_ENREF_141) Recently, structures of intermediates and mechanisms of gas-phase thermal polymerisation of styrene have been analysed using IM-MS, highlighting the possible application of this technology to directly monitor gas-phase reactions and polymerisation chemistry.[142](#_ENREF_142)

Synthetic molecules including metal-ring host-guest complexes, rotaxanes, catenanes, macrocyclic porphyrin-like systems and synthetic baskets like resorcinarenes represent an exciting branch of chemistry due to their potential applications in biosensing, drug delivery, catalysis, and material engineering. In many cases, the interaction between host and guest is controlled by fine structural differences, such as *cis-trans* isomerism. In-depth characterisation is therefore challenging, especially when classical biophysical methodologies are not applicable. The coupling of IM to MS offers a unique strategy to address the structural features of these systems with evident advantages over other techniques, combining the possibility of resolving different chemical entities by virtue of their *m*/*z* values before measuring their gas-phase conformations, without the need for highly pure, concentrated sample solutions and offering high speed of analysis. Recent studies have highlighted the importance of IM-MS to resolve very similar structures: *cis-trans* cyclometallated cages[143](#_ENREF_143) and rigid coordination-based rectangular, triangular and prismatic platinum-complexes[144](#_ENREF_144) were separated using DTIMS-MS; regio- and stereo-isomeric pairs of multi-ruthenated porphyrins[145](#_ENREF_145) and entire libraries of supramolecular assemblies using TWIMS.[146](#_ENREF_146) In many instances, prediction of candidate structures by molecular modelling was also used to help corroborate these results.

**Conclusions and future perspectives**

The broad-ranging utility of IM-MS instrumentation by scientists in academia, process chemistry, pharmaceutical science and biotechnology is spurring rapid developments in instrument design and utilisation, with next-generation instrumentation demonstrating improvements in versatility, resolution and limits of detection compared with earlier models.[147](#_ENREF_147), [148](#_ENREF_148) Continuous advances in both ion optics[149](#_ENREF_149) and the mobility devices themselves,[150-153](#_ENREF_150) which improve ion transmission and instrument resolving power, are significantly improving IMS capability, enabling studies of larger analytes at submicromolar concentrations. For example, the inclusion of high pressure electrodynamic ion funnels (originally developed by Smith and colleagues)[154](#_ENREF_154) either side of the drift cell has significantly improved IMS resolution without negatively influencing sensitivity, due to the ability to perform mobility separation at higher pressures.[149](#_ENREF_149) The more recent development of a cyclical ion drift tube with ion trapping capabilities to enhance ion current, has further improved the resolving power of ion mobility separation (*R* > 1000), although the sensitivity of such measurements is currently poor.[153](#_ENREF_153) Further developments in ion transmission will undoubtedly lead to improved performance. Future commercial availability of different combinations of hybrid IM and MS instrumentation with improved specifications and greater versatility can only enhance the already broad utility of this powerful analytical strategy.

Traditionally, MS, which operates on the microsecond timescale, has been combined with chromatographic separation (either liquid or gas) operating in the region of seconds to minutes, for the analysis of mixtures. IM separation typically operates on the millisecond timescale, and consequently can be nested between chromatographic separation and MS analysis. Thus, the benefits of IMS for improved analysis of mixtures can be leveraged without detriment to the already established complementarity of chromatography and MS. We anticipate that in the future, (GC/LC)-IM-MS will become standard for optimal analytical capability in many situations. However, significant improvements in IM resolution will be required for it to ‘outperform’ recent developments in ultra-high performance LC, and its benefits for high-throughput analyte separation lie in its capability of separating ions by different physico-chemical properties.

A great strength of IM-MS is the ability to characterise and compare dynamic changes in analyte structure, which has previously been extremely difficult for most biological samples. At present IM-MS studies often require ‘validation’ by other strategies, in part due to natural scepticism towards ‘new’ (or rather unfamiliar) techniques. However, the field is now approaching sufficient maturity that it should be possible for IM-MS generated structural information, acquired under carefully controlled conditions, to stand alone on its own merits. Indeed, structures inferred by X-ray crystallography, should ideally be used to complement, rather than purely validate the gas-phase conformational information generated by IM-MS. IMS is limited in that it is not capable of providing detailed atomic-level structural information. However, this is counterbalanced by its utility in studying conformational dynamics of rapidly evolving systems.

Like mass spectrometry before it, we believe that IM-MS is rapidly becoming an invaluable tool for wide-ranging chemical analysis, with different modes of IMS employed depending on specific experimental requirements *i.e.* discrimination of compounds in mixtures *versus* CCS value determination. That IM can be used both for analyte separation and structural investigation of a wide range of sample types makes it an extremely powerful addition to the analytical ‘toolbox’ of all chemists and biochemists.

**Table 1 Comparison of the three main types of IMS: drift tube ion mobility separation (DTIMS), travelling wave ion mobility spectrometry (TWIMS) and field asymmetric ion mobility spectrometry (FAIMS).** CCS: collisional cross-section; CV: compensation voltage; FWHM: full width at half maximum

|  |  |  |  |
| --- | --- | --- | --- |
|  | **DTIMS** | **TWIMS** | **FAIMS** |
| **Advantages** | Rotationally averaged collisional cross section (CCS; Ω) *i.e.* ‘shape’ can be measured (Å2) | Rotationally averaged CCS can be determined |  |
| Can be used to separate species of very similar mobility *i.e.* has high resolving power (>100 as defined by Ω/ΔΩ measured at full width at half maximum (FWHM))[155](#_ENREF_155) |  | High resolving power (≤~100 as defined by Ω/ΔΩ at FWHM)[14](#_ENREF_14) |
|  |  | Relatively straightforward to transfer the ion mobility device between different mass spectrometers |
|  | Can be used to mobility separate product ions generated either by collision-induced dissociation or electron-transfer dissociation |  |
| **Disadvantages** |  | CCS determination requires calibration of the drift time through the TWIMS cell, ideally using a calibrant of similar physical and chemical properties | CCS cannot be determined |
|  | Relatively low resolving power (≤ ~45 as defined by Ω/ΔΩ at FWHM) [150](#_ENREF_150) |  |
| The geometric configuration of current commercial DTIMS-MS instruments means that it can only be used to separate analytes immediately post-ionisation |  | The geometric configuration of a FAIMS-MS instrument means that it can only be used to separate analytes immediately post-ionisation |
| Gating-type instruments are susceptible to ion losses when transferred from atmospheric pressure during ionisation to the reduced pressure required for analysis | Ion heating can occur as ions are injected into the TWIMS cell which may affect gas-phase conformation. Unless carefully controlled, the process of measurement may therefore perturb analyte structure | The percentage of ions detected relative to those generated following ionisation (*i.e.* the duty cycle) is relatively low when operated under conditions where the compensation voltage (CV) is ramped (CV scanning mode), reducing sensitivity |

**Table 2** **Some advantages and disadvantages of commonly applied analytical techniques for determining structural information about analytes**[156](#_ENREF_156), [157](#_ENREF_157)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **IM-MS** | **MS*n a*** | **NMR spectroscopy** | **X-ray crystallography** | **Circular dichroism** |
| **Phase of analyte during analysis** | Gas | Gas | Liquid(/Solid) | Solid | Liquid (Gas/solid) |
| **Advantages** | Very sensitive | Very sensitive | Non-destructive | Non-destructive | Non-destructive |
| Can analyse mixtures of products | Can analyse mixtures of products |  |  |  |
|  |  | Can be very rapid when analysing smaller molecules (<500 Da) | Can directly determine structural information at the atomic level | Can measure exchanging structures (>pico seconds) |
| Fairly rapid for simple structures, with the most time-consuming parts being molecular dynamics (MD) simulations | Fairly rapid, aided by mass spectra search engines and spectral databases |  |  | Rapid direct diagnostic test for certain structural features *e.g.* relative helicity |
| Under carefully controlled ionisation and acquisition conditions, can be used to determine structure from native conditions |  | As most biologically relevant compounds are found in aqueous media, the ability to perform solution-state NMR means that structure can be analysed under native-like conditions. |  | Can determined native structural features |
| Can determine stoichiometry of complexes | Can determine stoichiometry of complexes | May allow stereochemical information, bond angles and distances to be elucidated | May allow stereochemical information, bond lengths and angles to be elucidated | Allows determination of stereochemistry |
| Measures 3-D structure in dynamic motion | Products of electron-mediated dissociation can be used to infer 3D-structure | Conventional solution state NMR spectroscopy can measure 3D structure in dynamic motion |  |  |
| **Disadvantages** | Analyte must be able to be ionised | Analyte must be able to be ionised | Difficult to analyse mixtures of products. Samples often have to be purified and concentrated, which may affect the structure of biological samples | Requires purified and crystallised material. May be time-consuming or impossible to generate crystals | Cannot be used for mixtures. Requires relatively concentrated (~0.5 mgmL-1) purified samples |
|  | Relies on MD simulations to indirectly determine precise structural information from CCS values. MD simulations become more challenging as molecules become larger | Difficult to ascertain detailed 3D structure information directly from mass spectra | Analysis of spectra becomes difficult for larger molecules |  | Gives no specific structural information at the atomic level |
|  | Destructive | Destructive |  | Analyte may be damaged by the X-rays |  |

a MS*n* refers to multi-stage MS/MS experiments designed to record product ion spectra where *n* is the number of stages of mass analysis[158](#_ENREF_158)

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**Figure 1 Number of peer-reviewed papers published annually (to end of 2013) combining ion mobility and mass spectrometry**. Data generated using Web of Science, SCI-expanded between 1985 and 2013, search terms – “ion mobility” and “mass spectrometry”. The years that various commercial ion mobility devices were made available is indicated. UltraFAIMS (Owlstone) and SelexION (ABSciex) are variants of the FAIMS device described below.



**Figure 2** **Schematic diagrams of the major types of IM device.** Small ions are in red, large ions are in blue. **a)** Drift time ion mobility spectrometry (DTIMS) for direct calculation of an ion’s collision cross section (Ω; CCS) by means of the Mason-Schamp equation. Separation is achieved by passing the ions through a drift gas along the axis of an applied electric field. The flight of a small ion (red) is retarded to a lesser degree than a large ion (blue) due to fewer interactions with the gas. The time taken to traverse the device *i.e.* the drift time, is correspondingly shorter. **b)** Travelling wave ion mobility spectrometry (TWIMS) used for both CCS calculation (after calibration of the drift time with ions of similar Ω and charge state), and differential separation of ions in a complex mixture. Application of a travelling voltage wave to a series of electrically connected ring electrodes (stacked ring ion guide; SRIG) pushes ions through the device. Separation is achieved since, for a given wave speed and magnitude, higher mobility ions (red) will be carried forward by the wave, whilst lower mobility species (blue) will roll over the wave, thus taking longer to exit the device. **c)** Field asymmetric ion mobility spectrometry (FAIMS) used primarily for differential separation of ions in a complex mixture. Introduction of ions into an alternating asymmetric electric field (E) causes them to drift towards to two electrodes at different rates. Time at positive voltage (t1) is shorter than the time at negative voltage (t2), although an equal voltage•time product for each part of the waveform is maintained. Application of a DC voltage, termed the compensation voltage (CV), repels the ions and refocuses their flight through the device. Different analytes require different CVs to prevent collision with the electrodes. In this case, the analyte with the smaller CCS (red) drifts quickly towards the electrode and requires a high CV to refocus it through the device. The analyte with the larger CCS (blue) is less affected by the RF voltage and travels towards the electrode more slowly, and thus requires a lower CV to correct its trajectory.



**Figure 3** **Arrival time distributions (ATDs) as determined by travelling wave ion mobility spectrometry, and structures of the parent drug ondansetron (1) and its isomeric metabolites GR90315 (8-hydroxy), GR63418 (7-hydroxy) and GR60661 (6-hydroxy) (2-4, respectively).** Metabolite **2** can clearly be discriminated from metabolites **3** and **4** by their respective ATDs following ion mobility separation, discrimination which would be impossible by mass spectrometry alone. ATD for **4** is differentiated from ATD for **3** by means of a dashed line. The experimentally determined collision cross section values are reported in Å2. *Reproduced with permission from* [*64*](#_ENREF_64)*. Copyright 2010, John Wiley & Sons Ltd.*

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**Figure 4 Comparison of experimentally estimated collision cross sections (Å2) (CCS) of five protein standards.** CCS values calculated using either the projection approximation (PA) or the trajectory method (TM) from available X-ray and NMR structures of the same proteins are plotted for each of the proteins together with the CCS as determined by travelling wave ion mobility-mass spectrometry. The crystallographic structures obtained from the Pdb files in the RSCD Protein Data Bank ([www.rcsb.org/pdb](http://www.rcsb.org/pdb)) are depicted. Chicken lysozyme c PDB IDs: 1DPX (X-ray), 1GXX (NMR); human lysozyme c PDB IDs: 2NWD (X-ray); 1IY3 (NMR); sperm whale myoglobin PDB IDs: 1VXG (X-ray), 1MYF (NMR); equine myoglobin PDB ID: 1WLA (X-ray); equine cytochrome c PDB IDs: 1HRC (X-ray); 1LC1 (NMR). *Figure adapted with permission from* [*46*](#_ENREF_46)*. Copyright 2008, John Wiley & Sons Ltd.*

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**Figure 5** **Conformational heterogeneity and dissociation of subunit I from ICL12 implies a mechanism for closing the H+ channel.** Arrival time distributions (ATDs) for ICL12 (**a**) and CL12 (**b**) complexes (drift time measures in milliseconds (ms)). The broader ATDs observed for selected charge states of the intact ICL12 complex are indicative of multiple conformations of the subunit I. (**c**) Coarse-grained and atomic model of complex ICL12 based on ion mobility spatial restraints. The flexible subunit I is shown in grey, with the nucleotide binding region highlighted in orange. (**d**) Proposed mechanism for the closure of the proton channel upon lateral movements of the subunit I (view from the top). Mass spectrometry identifies loss of the subunit I under low [ATP] and low [H+] concentrations; the gap left between subunit L and the rest of the complex can then be filled with membrane lipids. *Adapted with permission from* [*133*](#_ENREF_133)*. Copyright 2011, American Association for the Advancement of Science.*

Figure 6.tif

**Figure 6 Polynucleotide structures as determined using a combination of molecular dynamic simulations and experimentally determined arrival time distributions.** Depicted (top) are the arrival time distributions (ATDs) and structures as predicted using molecular dynamics (MD), together with the polynucleotide sequence(s) and expected conformations (bottom). **a)** 5’-TGCGATACTCATCGCA-3’ adopts a hairpin secondary structure where the nucleotide backbone ‘loops’ back to form a series of Watson-Crick pairs. **b)** 5’-GCGATTTCTGACCGCTTTTTTGTCAG-3’ could adopt one of two potential conformations, forming either a hairpin structure, or a pseudoknot where two loops are formed and held in place by Watson-Crick pairs to the adjacent nucleotide sequence. MD and ion mobility-mass spectrometry (IM-MS) measurements both indicate the presence of a single structure corresponding to the pseudoknot. **c)** The DNA strands CF1 (5’-CCGGCCGGATACGCGCGCG-3’) and CF2 (5’-CGCGCGCGATACCGGCCGG-3’) together form two IM resolvable structures, that MD shows are cruciform secondary structures adopting both A and B helical conformations.*Adapted with permission from* [*134*](#_ENREF_134)*. Copyright 2009, American Chemical Society.*

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