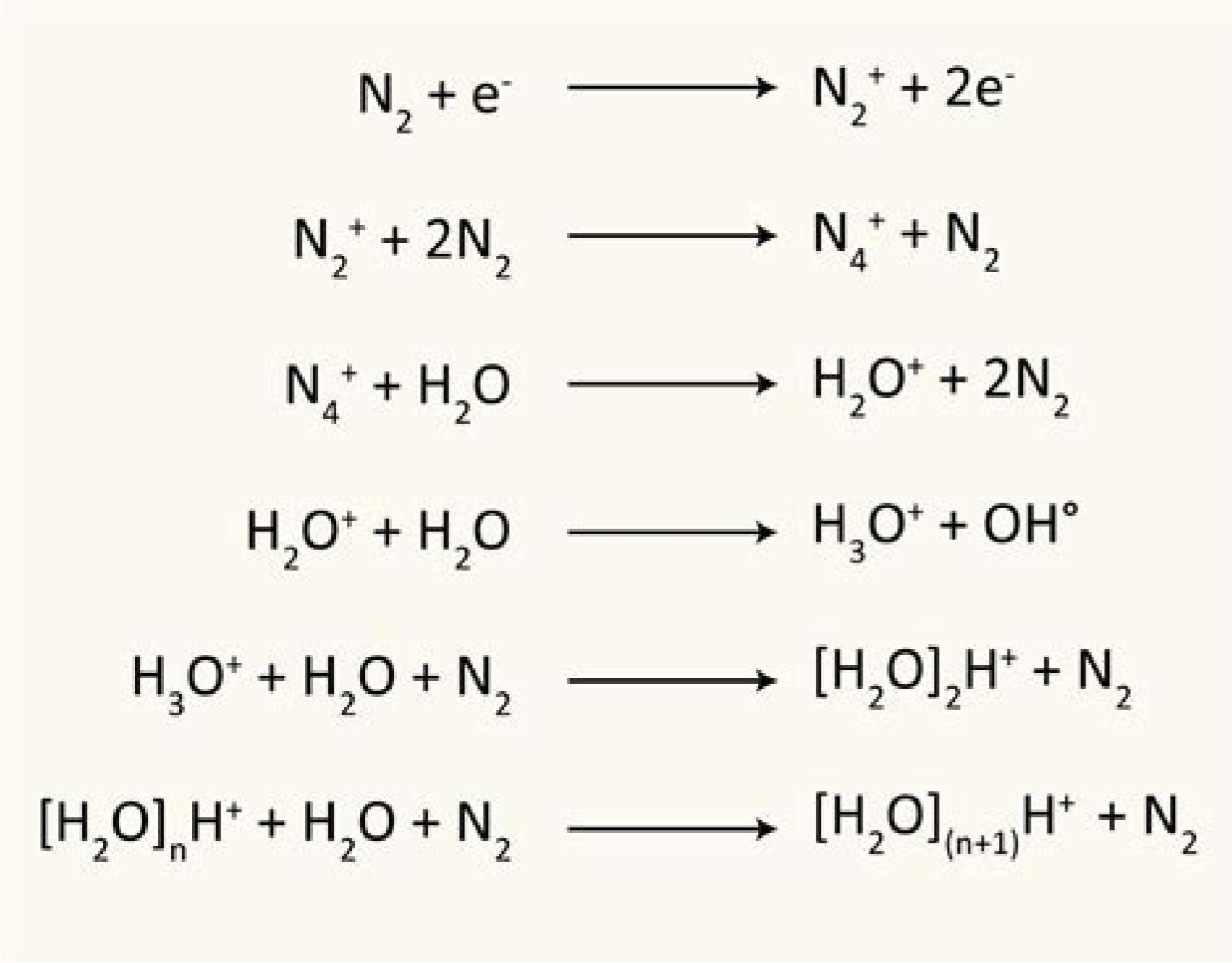
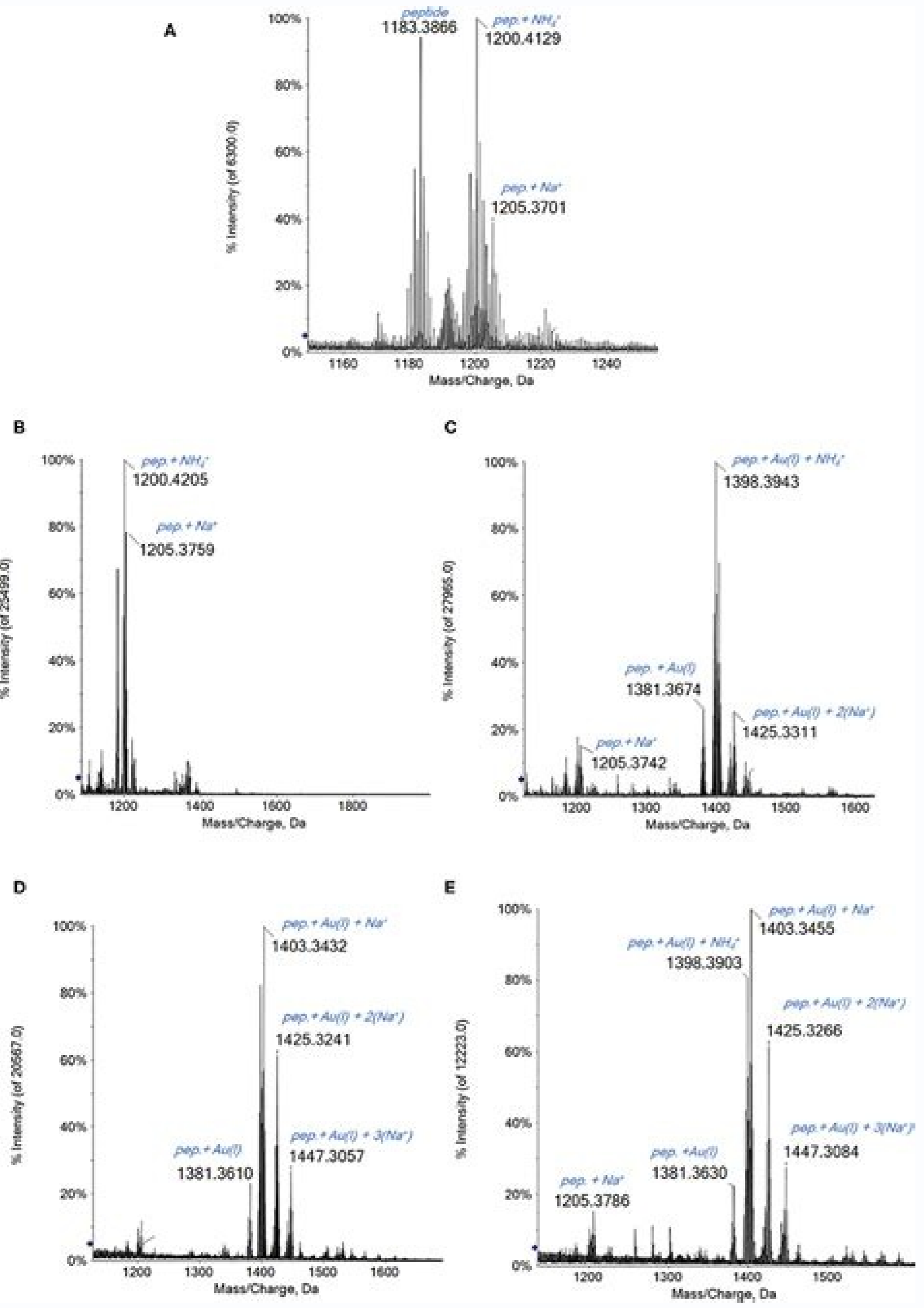
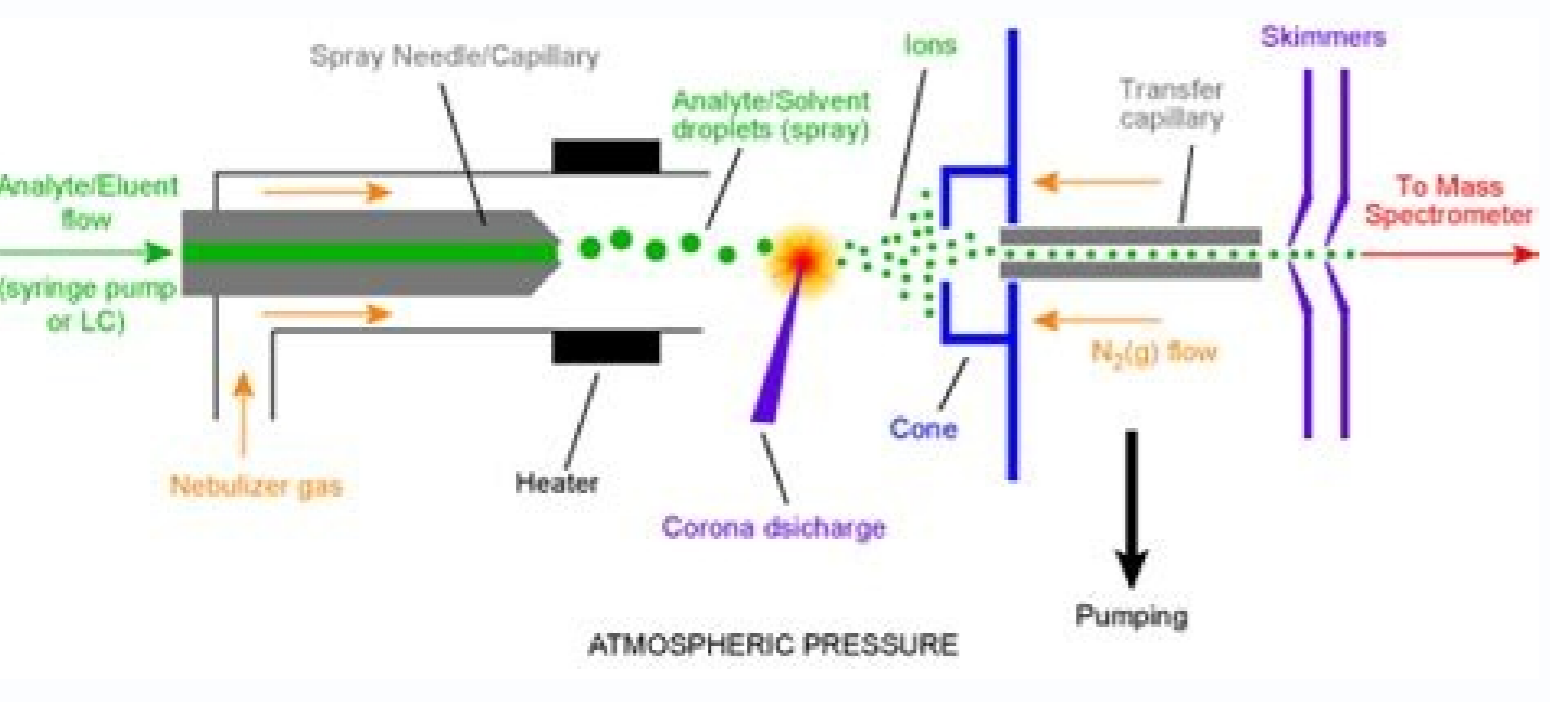
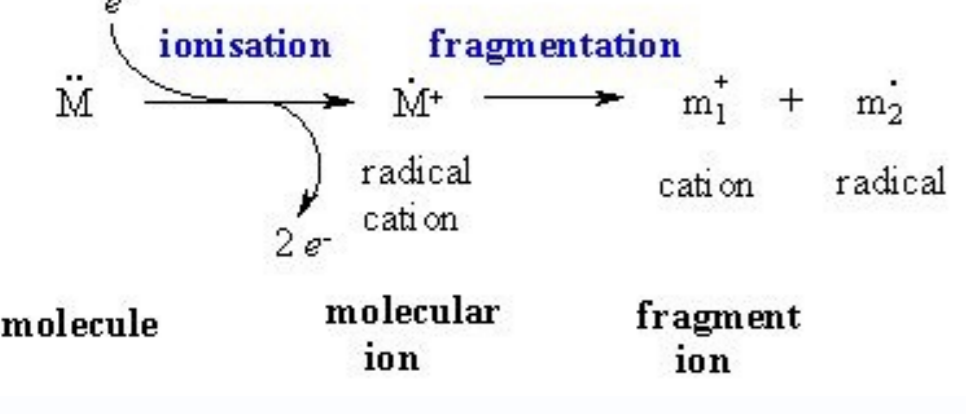


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This calculator allows to identify some adduct ions from ESI-MS (electrospray) mass spectrometry measurements or other soft ionization techniques like CI-MS or FI-MS or FD-MS or APCI-MS or MALDI-TOF. Actually this task should be done by every good LC-MS software automatically, directly integrated, no questions asked. You may check out IntelliXtract or esi - a R package for annotation of LC/ESI-MS Mass Signals using xcms. The successful detection of adduct ions requires either pure mass spectra or a deconvolution and peak detection or peak picking step prior adduct assignment. This template is based on an table from: Huang N.; Siegel M.M.I.; Kruppa G.H.; Laukien F.H.; J Am Soc Mass Spectrom 1999, 10, 1166-1173; Automation of a Fourier transform ion cyclotron resonance mass spectrometer for acquisition, analysis, and e-mailing of high-resolution exact-mass electrospray ionization mass spectral data [DOI]. Another important source also including contaminations (solvents, plasticisers, repeating units, solvent clusters) is hidden in the supplement section of Interferences and contaminants encountered in modern mass spectrometry (Bernd O. Keller, Jie Sui, Alex B. Young and Randy M. Whittall, ANALYTICA CHIMICA ACTA, 627 (1): 71-81) [DOI] Download the EXCEL table here as [XLS]. Please check the values carefully, some of the table ion names were lost during translation, for high mass accuracy the mass of the electron must be included (thanks to Jason and Matt) [DOI]. If you are interested in molecular formula determination or determination of elemental compositions and subsequent isomer structure annotation you may find the Seven Golden Rules helpful. After removal of adducts you can enter your results into the Seven Golden Rules software and find highly probable elemental compositions. These elemental compositions can be matched against molecular compound databases to get a first hint of a possible isomer structure. The Seven Golden Rules can be used for low resolution and high resolution mass spectral data. For quick calculation of formula masses use the Molecular Weight Calculator. Example: 1) Find Adduct: Taxol, C47H51NO14, M=853.33089 Enter 853.33089 in green box read M+22.9, m/z=876.320108 2) Reverse: take 12 Tesla-FT-MS result out of MS m/z=876.330 suspect M+Na adduct, read M=853.340782, enter this value into formula finder with 2 ppm mass accuracy (CHNSOP enabled) get some thousand results, compare isotopic pattern, get happy. Table 1. Monoisotopic exact masses of molecular ion adducts often observed in ESI mass spectra (Download 2020 XLS for corrections) Your M here: Your M+X or M-X 853.33089 876.32 Ion name Ion mass Charge Mult Mass Result: Reverse: 1. Positive ion mode M+3H M/3 + 1.007276 3+ 0.33 1.007276 285.450906 291.099391 M+2H+Na M/3 + 8.334590 3+ 0.33 8.334590 292.778220 283.772077 M+H+2Na M/3 + 15.7661904 3+ 0.33 15.766190 300.209820 276.340476 M+3Na M/3 + 22.989218 3+ 0.33 22.989218 307.432848 269.117449 M+2H M/2 + 1.007276 2+ 0.50 1.007276 427.672721 437.152724 M+H+NH4 M/2 + 9.520550 2+ 0.50 9.520550 436.185995 428.639450 M+H+Na M/2 + 11.998247 2+ 0.50 11.998247 438.663892 426.161753 M+H+K M/2 + 19.985217 2+ 0.50 19.985217 446.650662 418.174783 M+ACN+2H M/2 + 21.520550 2+ 0.50 21.520550 448.185995 416.639450 M+2Na M/2 + 22.989218 2+ 0.50 22.989218 449.654663 415.170782 M+2ACN+2H M/2 + 42.033823 2+ 0.50 42.033823 468.699268 396.126177 M+3ACN+2H M/2 + 62.547097 2+ 0.50 62.547097 489.212542 375.612903 M+H M + 1.007276 1+ 1.00 1.007276 854.338166 875.312724 M+NH4 M + 18.033823 1+ 1.00 18.033823 871.364713 858.286177 M+Na M + 22.989218 1+ 1.00 22.989218 876.320108 853.330782 M+CH3OH+H M + 33.033489 1+ 1.00 33.033489 886.364379 843.286511 M+K M + 38.963158 1+ 1.00 38.963158 892.294048 837.356842 M+ACN+H M + 42.033823 1+ 1.00 42.033823 895.364713 834.286177 M+2Na-H M + 44.971160 1+ 1.00 44.971160 898.302050 831.348840 M+IsoProp+H M + 61.06534 1+ 1.00 61.065340 914.396230 815.254660 M+ACN+Na M + 64.015765 1+ 1.00 64.015765 917.346655 812.304235 M+2K-H M + 76.919040 1+ 1.00 76.919040 930.249930 799.400960 M+DMSO+H M + 79.02122 1+ 1.00 79.021220 932.352110 797.298780 M+2ACN+H M + 83.060370 1+ 1.00 83.060370 936.391260 793.259630 M+IsoProp+Na+H M + 84.05511 1+ 1.00 84.055110 937.386000 792.264890 2M+H 2M + 1.007276 1+ 2.00 1.007276 1707.669056 1751.632724 2M+NH4 2M + 18.033823 1+ 2.00 18.033823 1724.695603 1734.606177 2M+Na 2M + 22.989218 1+ 2.00 22.989218 1729.650998 1729.650782 2M+K 2M + 38.963158 1+ 2.00 38.963158 1745.624938 1713.676842 2M+ACN+H 2M + 42.033823 1+ 2.00 42.033823 1748.695603 1710.606177 2M+ACN+Na 2M + 64.015765 1+ 2.00 64.015765 1770.677545 1688.624235 2. Negative ion mode M-3H M/3 - 1.007276 3- 0.33 -1.007276 283.436354 293.113943 M-2H M/2 - 1.007276 2- 0.50 -1.007276 425.658169 439.167276 M-H2O-H M- 19.01839 1- 1.00 -19.01839 834.312500 895.338390 M-H M- 1.007276 1- 1.00 -1.007276 852.323614 877.327276 M+Na-2H M + 20.974666 1- 1.00 20.974666 874.305556 855.345334 M+Cl M + 34.969402 1- 1.00 34.969402 886.300292 841.350598 M+K-2H M + 36.948606 1- 1.00 36.948606 890.279496 839.371394 M+FA-H M + 44.998201 1- 1.00 44.998201 898.329091 831.321799 M+Hac-H M + 59.013851 1- 1.00 59.013851 912.344741 817.306149 M+Br M + 78.918885 1- 1.00 78.918885 932.249775 797.401115 M+TFA-H M + 112.985586 1- 1.00 112.985586 966.316476 763.334414 2M-H 2M - 1.007276 1- 2.00 -1.007276 1705.654504 1753.647276 2M+FA-H 2M + 44.998201 1- 2.00 44.998201 1751.659981 1707.641799 2M+Hac-H 2M + 59.013851 1- 2.00 59.013851 1765.675631 1693.626149 3M-H 3M - 1.007276 1- 3.00 -1.007276 2560.999946 2627.952724 Corrected values (C. Amstler et al., "Review of Particle Physics" Physics Letters B667, 1 (2008)) m(1H) = 1.00727646677 u = mass of proton; charge +1 m(1H+e-) = 1.00782504 u = mass of electron; charge -1 m(e-) = 0.00054858026 u = new determination of electrons mass The ultimate source of accurate masses and isotope values are IUPAC and CAWIA (Commission on Atomic Weights and Isotopic Abundances) for a list of the latest corrected values please see Pure Appl. Chem., Vol. 75, No. 6, pp. 683-800, 2003 the recommended values A(r) should be included into accurate mass calculators including corrections for positive and negative charges depending on ionization type (odd or even electron). [PDF] - ATOMIC WEIGHTS OF THE ELEMENTS: REVIEW 2000 (IUPAC Technical Report) Access through your institutionVolume 985, Issues 1-2, 24 January 2003, Pages 531-539 02|01732-6Get rights and contentView full text This work serves as a follow-up to Part I of experiments designed to determine the underlying principles in the formation of pseudomolecular, or adduct, ions during electrospray ionization. Aromatic acids were studied by flow injection analysis in the negative ionization mode of electrospray ionization mass spectrometry. Part I dealt with common acidic anti-inflammatory pharmaceuticals, such as ibuprofen and related analogues. Part II deals with functionally less complex molecules, namely benzoic acid (BA) and substituted benzoic acids. Halide-substituted molecules are investigated to deduce the effect of electron-withdrawing substituents (bromo-, chloro-, and fluoro-) and ring position (ortho-, meta- and para-) on the response of a traditional deprotonated molecular ion ([M-H]-) and a sodium-bridged dimer ion ([2M-2 H+Na]-). Amino-substituted benzoic acids are also analyzed in order to study the effect of an additional ionizable group on the molecule, and para-tert-butyl-BA is analyzed to study the effect of increased hydrophobicity, as they relate to the formation of pseudomolecular ions. This study shows that solution character (octanol-water partition coefficient (or log P) and pKa) of the model compounds controls the relative efficiency of formation of [M-H]- and [2M-2H+Na]- ions. However the relative gas phase character (gas phase basicity and proton affinity) also has a significant effect on the formation of the sodium-bridged dimer ion. For the halide-substituted species, placement of the electron-withdrawing atom at the meta-position gives the greatest enhancement in sensitivity. Observations also show that as the structural complexity of the model compound increases, predictions relating analyte acidity to sodium-bridged dimer ion formation give way to a stronger dependence between log P values and ionization efficiency. Supporting this hypothesis is the nearly ten-fold enhancement in signal for tert-butyl BA relative to BA, due to the greater hydrophobicity, and consequently, increased surface activity in an electrosprayed droplet of the analyte molecule. Hydrophilic interaction liquid chromatography (HILIC)/ electrospray ionisation-mass spectrometry (ESI-MS) has gained interest for the analysis of polar analytes in bioanalytical applications in recent years. However, ESI-MS is prone to adduct formation of analytes. In contrast to reversed phase chromatography, small inorganic ions have retention in HILIC, i.e. analytes and inorganic ions may co-elute, which could influence the adduct formation. In the present paper, it was demonstrated that the co-elution of sodium ions or potassium ions and analytes in HILIC/ESI-MS affect the adduct formation and that different concentrations of sodium ions in biological samples could have an impact on the quantitative response of the respective adducts as well as the quantitative response of the protonated adduct. The co-elution also lead to cluster formation of analytes and sodium formate or potassium formate, causing extremely complicated spectra. In analytical applications using HILIC/ESI-MS where internal standards are rarely used or not properly matched, great care needs to be taken to ensure minimal variation of inorganic ion concentration between samples. Moreover, the use of alkali metal ion adducts as quantitative target ions in relative quantitative applications should be made with caution if proper internal standards are not used. Keywords: Adduct formation; Cluster formation; Hydrophilic interaction liquid chromatography; Mass spectrometry; Metabolomics; Screening.

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