



1 **A multi-instrumental approach for calibrating two real-time**
2 **mass spectrometers using high performance liquid**
3 **chromatography and positive matrix factorization**

4 Melinda K. Schueneman¹, Douglas A. Day¹, Dongwook Kim¹, Pedro Campuzano-Jost¹, Seonsik
5 Yun¹, Marla P. DeVault¹, Anna C. Ziola¹, Paul J. Ziemann¹, and Jose L. Jimenez¹

6 ¹Department of Chemistry and Cooperative Institute for Research in Environmental Sciences, University of
7 Colorado, Boulder, CO 80309, USA

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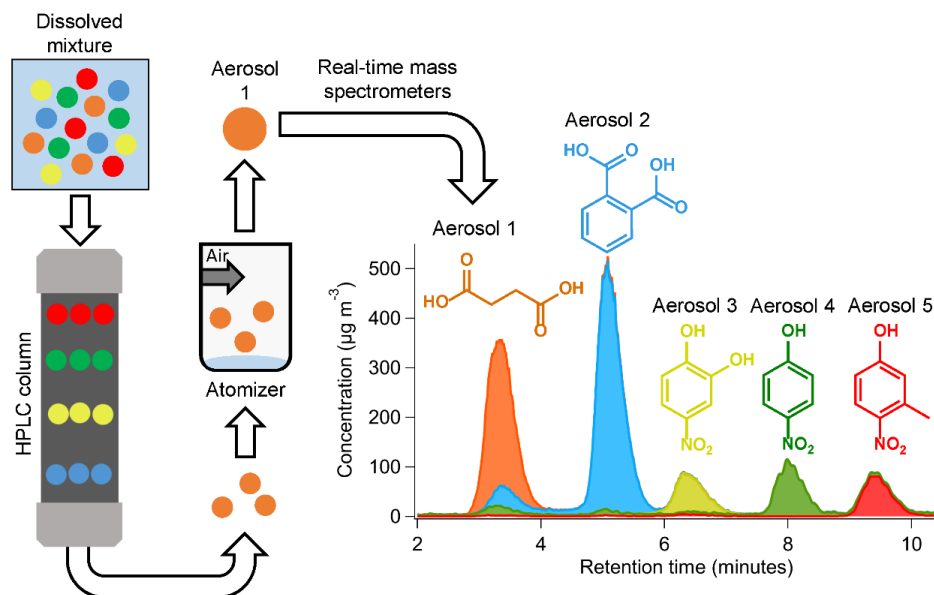
9 Corresponding Author: Jose Jimenez, jose.jimenez@colorado.edu

10

11 **Abstract.** Obtaining quantitative information from real-time soft-ionization aerosol instruments such as an
12 Extractive Electrospray time-of-flight Mass Spectrometer (EESI) can be challenging, due to many individual species
13 having different, and often hard to predict, sensitivities. Directly calibrating is time-consuming and relevant
14 standards are often hard to obtain. In addition, the molecular identities of many of the sampled species may be
15 ambiguous. Bulk OA sensitivities are sometimes used to estimate molecular sensitivities, but different types of OA
16 can have bulk sensitivities that vary by a factor of ~10. A system to separate the compounds present in complex
17 samples can enable their direct calibration. Here, high performance liquid chromatography (HPLC) followed by
18 aerosol formation via atomization was combined with online, 1 Hz measurements to calibrate the EESI and a High
19 Resolution Aerosol Mass Spectrometer (AMS) for compounds present in a secondary organic aerosol (SOA)
20 mixture. Pure compounds were used to test the method and characterize its uncertainties. Pure compound calibration
21 factors were consistent within $\pm 20\%$ for direct atomization vs. HPLC separation, which is far superior to the orders
22 of magnitude sensitivity differences that are possible with EESI. For species that were not well separated by
23 chromatography, Positive Matrix Factorization (PMF) based on AMS spectra was used to test its ability to separate
24 overlapping species. In two test cases, further separation was achieved using PMF, but derived sensitivities from
25 direct and HPLC calibrations varied by up to a factor of 2.



26 TOC figure



27



28 1 Introduction

29 Atmospheric aerosols are a complex, and often poorly understood, component of Earth's atmosphere. Aerosols have
30 significant effects on both human and ecosystem health, and are significant contributors to anthropogenic climate
31 forcing (Dockery et al., 1996; Lighty et al., 2000; Lohmann et al., 2004; IPCC, 2013). Organic aerosol (OA) is a
32 substantial component of global aerosol levels (Kanakidou et al., 2005; Zhang et al., 2007; Jimenez et al., 2009).
33 Since the early 2000s an important instrument for measuring OA concentrations in real-time has been the Aerosol
34 Mass Spectrometer (AMS) (Jayne et al., 2000; Canagaratna et al., 2007) and its high-resolution version (HR-AMS)
35 (DeCarlo et al., 2006). Soft-ionization aerosol mass spectrometers, such as the Extractive Electrospray Time-of-
36 Flight Mass Spectrometer (EESI-ToF-MS, EESI hereinafter), have more recently become important tools for
37 obtaining more detailed OA speciation (Lopez-Hilfiker et al., 2014, 2019; Eichler et al., 2015).

38 EESI can detect individual molecular ions (referred to henceforth as either molecular ions or individual
39 species, even if they may comprise several isomers) from the particle-phase with 1 s time resolution (Lopez-Hilfiker
40 et al., 2019; Pagonis et al., 2021). EESI has been used to measure aerosols in urban areas (Qi et al., 2019, 2020;
41 Stefanelli et al., 2019; Kumar et al., 2022), in biomass burning (Qi et al., 2019; Pagonis et al., 2021), in cooking
42 emissions (Qi et al., 2019; Brown et al., 2021), and for chamber studies of secondary OA (SOA) formation (Liu et
43 al., 2019; Pospisilova et al., 2020). Many studies have illustrated the low detection limits, limited fragmentation, and
44 other capabilities of the EESI; e.g. Lopez-Hilfiker et al. (2019) and Pagonis et al. (2021).

45 However, obtaining quantitative information for individual species from EESI measurements of complex
46 mixtures of unknown species can be challenging, due to each species having different, and often hard to predict,
47 sensitivities (Law et al., 2010; Lopez-Hilfiker et al., 2019; Brown et al., 2021; Wang et al., 2021). In addition, EESI
48 measures molecular ions, but can in some cases cause fragmentation, such as due to loss of HNO₃ from nitrates (Liu
49 et al., 2019). For an SOA mixture from a single precursor, the bulk sensitivity compared to SOA formed from a
50 different precursor has been shown to vary by a factor of 15 or more (Lopez-Hilfiker et al., 2019). Different studies
51 also show that the bulk sensitivity for OA formed from different emission sources (e.g. cooking, biomass burning)
52 can vary by a factor of ~10 (Qi et al., 2019; Stefanelli et al., 2019; Brown et al., 2021). For pure organic standards,
53 the sensitivity can vary by a factor of 30 or more (Lopez-Hilfiker et al., 2019). Instead of directly measuring
54 compound sensitivity, some groups use machine-learning (Liigand et al., 2020) or thermodynamic modeling (Krueve
55 et al., 2014) to approximate instrument response factors for individual species. Other studies use bulk calibration
56 factors for complex mixtures as an approximation for quantification (Tong et al., 2022).

57 Sensitivities can vary due to differences in analyte solubility (Law et al., 2010), EESI working fluid
58 composition, sample composition, and different instrument conditions and settings, including polarity and changes
59 in inlet pressure (Lopez-Hilfiker et al., 2019; Pagonis et al., 2021). Calibrating the EESI for individual species can
60 be a challenging task, especially when standards are unavailable for most atmospheric oxidation products. In
61 addition, OA from chamber experiments or field studies often contains unidentified molecular ions, or those whose
62 species identity is ambiguous.

63 Several calibration methods have been applied to EESI. For example, direct calibrations were performed
64 for many organic standards in Lopez-Hilfiker et al. (2019), for 4-nitrocatechol (EESI(-)) and levoglucosan (EESI+)



65 in Pagonis et al. (2021) to track sensitivity during each aircraft flight, and levoglucosan for regular sensitivity
66 tracking during an indoor cooking study (and several other compounds less frequently and bracketing the campaign)
67 in Brown et al. (2021). During research field studies, often only one or two species are calibrated frequently, and
68 the rest are quantified using relative response factors measured less frequently (Qi et al., 2019; Brown et al., 2021;
69 Pagonis et al., 2021).

70 A recent paper combined measurements from the Vocus Proton-Transfer Mass Spectrometer (Vocus),
71 AMS, and EESI to measure speciated response factors without the need for standards. In that study, SOA was
72 generated using an Oxidation Flow Reactor (OFR). Following SOA formation, the Vocus measured the gas phase
73 species, and the AMS and EESI measured the bulk and speciated particulate phase, respectively. EESI response
74 factors were obtained through comparison to decreasing gas-phase mixing ratios measured by the Vocus as they
75 condensed to the particle-phase (Wang et al., 2021).

76 Another method for obtaining calibration information is Positive Matrix Factorization (PMF). PMF is a
77 type of factor analysis that allows approximately apportioning aerosol mass measured with online mass spectrometer
78 and other instruments to atmospheric sources or level of oxidation (Zhang et al., 2005; Lanz et al., 2007; Ulbrich et
79 al., 2009). To our knowledge, PMF has not been used with AMS data alone to obtain mass spectra and time series
80 for individual molecular components. Separation with PMF alone would be difficult for ambient or chamber
81 experiment data, in part, since most compounds likely co-vary in time and thus would not be statistically resolvable
82 (Craven et al., 2012). Direct calibrations have been conducted to generate high-resolution AMS mass spectra for
83 individual species (Ulbrich et al., 2019). A combination of AMS and PMF has been used to obtain quantitative
84 information for EESI bulk measurements or PMF factors (Qi et al., 2019, 2020; Kumar et al., 2022). PMF has also
85 been used on a combined data set consisting of both EESI and AMS data (Tong et al., 2022).

86 To our knowledge, PMF has not been applied previously to AMS and EESI chromatographically-separated
87 data. Running PMF on chromatographic data may be able to generate species-specific mass spectra for compounds
88 that cannot be obtained directly. PMF has been applied in the past to GC-MS data (Zhang et al., 2014, 2016; Gao et
89 al., 2018), but not to High Performance Liquid Chromatography (HPLC) data, which is better suited for oxidized
90 SOA species than GC, to our knowledge. AMS detection following HPLC separation has been conducted previously
91 (Farmer et al., 2010) to explore AMS spectra of the separate compounds, but not for quantification. HPLC has not
92 been previously combined with EESI or PMF, to our knowledge.

93 Here, for the first time, we demonstrate a method combining High Performance Liquid Chromatography
94 (HPLC), atomization, and detection by EESI, AMS, and Scanning Mobility Particle Sizer (SMPS). The method was
95 validated by separating a mixture of standards, and then applied to chamber SOA. The analyte peak measured with
96 each instrument was integrated, and calibration factors for separated species were calculated for the EESI. The AMS
97 response factor (CF_x^A , or $RIE \cdot CE$, the product of the relative ionization efficiency and collection efficiency) and the
98 atomic oxygen to carbon (O:C) ratio for different analytes were quantified. EESI calibration factors (CF_x^E) for
99 individual compounds were determined and compared to literature values. In cases where full peak separation via
100 HPLC alone was not achieved, PMF was run on the EESI and AMS mass spectral matrices to obtain further
101 compound separation.



102 2 Methods

103 2.1 Chamber experiments and filter mass collection

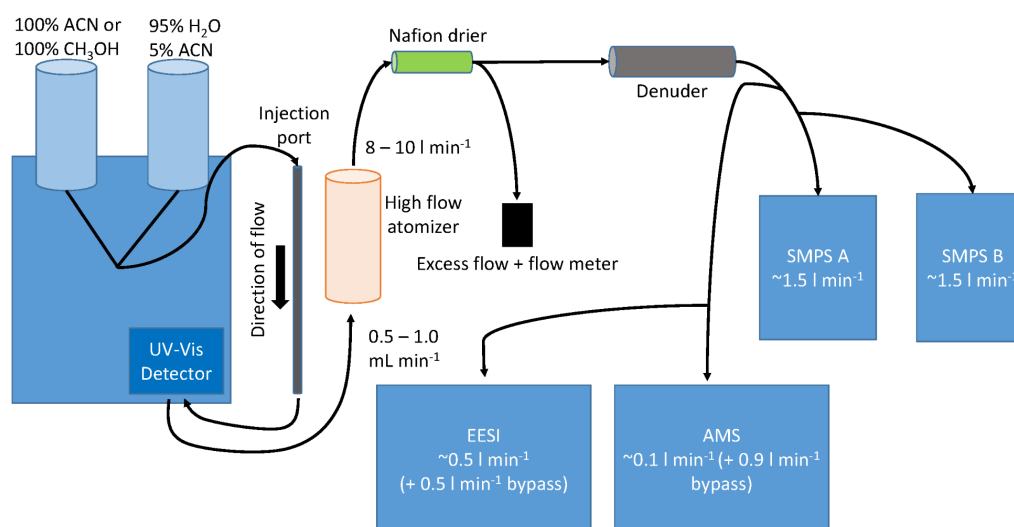
104 SOA was generated using the procedure of DeVault et. al. (2022). Briefly, chamber experiments were conducted in
105 a 6.9 (± 0.5) m³ teflon chamber (Bakker-Arkema and Ziemann, 2021). The temperature (23°C) and atmospheric
106 pressure (0.83 atm) were constant. Ammonium sulfate seed was added to a humidified chamber (RH=55%),
107 followed by β -pinene, which was evaporated from a heated glass bulb. In the dark, N₂O₅ was added as the NO₃
108 source, from the sublimation of cryogenically-trapped solid N₂O₅. The experiment was modeled after Claflin et. al.
109 (2018).

110 Following SOA formation, a 0.45 μ m Millipore Fluoropore PTFE filter was used to collect SOA. The
111 filter+aerosol was weighed after aerosol collection. The filter+aerosol was exposed to minimal ambient air, and was
112 always handled with artificial lighting turned off and outdoor blinds drawn. After weighing, each filter was extracted
113 in 2 mL of HPLC grade ethyl acetate (EtAc) twice. The 4 mL aerosol extract/EtAc mixture was dried using pure N₂.
114 Once the EtAc was evaporated, the leftover material was dissolved in HPLC grade acetonitrile (ACN) and stored in
115 a freezer at -23°C (DeVault et al., 2022). The extract used here was the same as DeVault et. al. (2022), and was one
116 year old at the time of analysis. That study showed that the SOA is composed entirely of acetal dimers, which are
117 exceptionally stable, so the SOA is unlikely to have changed over this period.

118 2.2 High Performance Liquid Chromatography (HPLC)

119 HPLC separation was performed using a Shimadzu Prominence HPLC, coupled to a Zorbax Eclipse XDB-C18
120 column (250 \times 4.6 mm with 5 μ m particle size). A Nexera X2 SPDM30A UV/vis photodiode array detector was
121 used to generate absorbance chromatograms. The column stationary phase was designed for reverse mode, where
122 smaller, more polar species had shorter elution times. Separated species were measured first at $\lambda=210$ and $\lambda=254$ nm
123 using an UV-Vis diode array detector with a reference wavelength of 300 nm. Separated chemical components then
124 flowed into a high-flow Collision atomizer, forming droplets and then aerosols consisting solely of the SOA
125 compounds after evaporating the HPLC solvent in a Nafion drier. The aerosols were then measured by a suite of
126 instruments, shown in Fig. 1, and pictured in Fig. S1. Tubing delay times are also included in Table S1.

127



128
129 **Figure 1. HPLC schematic. Left, HPLC containing a column and a UV-Vis detector. Following separation, the column**
130 **effluent was sent to an atomizer, dried, and the aerosol was detected by each of the instruments shown.**
131

132 A maximum volume of 50 μL ACN/aerosol mixture was injected into the column at once. At the beginning of each
133 day, the HPLC solvent lines (HPLC grade acetonitrile and HPLC grade water) were flushed to remove any air
134 bubbles that may affect elution. Following this, a clean cycle was run by injecting 50 μL HPLC grade ACN into the
135 reverse-phase column. This ensured previous HPLC run species did not contaminate new runs. The first run of the
136 day, post cleaning cycle, was a 4-nitrocatechol/4-nitrophenol mixture (dissolved in ACN). These species were well
137 characterized by the particle-phase instruments and have measurable absorbances at the recorded UV wavelengths.

138 For each experiment, the mobile phase consisted either of an ACN/water mixture or an ACN/CH₃OH/water
139 mixture. The mixture varied in relative concentrations of each solvent over the course of each HPLC run. Most
140 experiments were started at 95% water/5% ACN (solvent mixture A). The mobile phase became less polar over
141 time. For some systems, solvent B (pure acetonitrile) replaced solvent system A as time went on. For other systems,
142 solvent C (pure methanol) was used. Each standard and/or SOA system was run under different conditions,
143 depending on the separability of different components.

144 For the standard solution run, a mixture of solvent A and solvent B was used. Using a flow of 1.0 mL min⁻¹,
145 solvent B was increased from 0% to 35% in 1 minute, then 35%-40% for 5 minutes, followed by 40%-50% for 3
146 minutes, and 50%-100% for 2 minutes, this is also shown in Fig. S2a. For the β -pinene SOA extract, the flow rate
147 was set to 0.5 mL min⁻¹, and a mobile phase gradient started at 20% solvent C for 2 minutes, then increased at a rate
148 of 6% min⁻¹ up to solvent C of 50%, followed by an increase of 3% min⁻¹ to a concentration of 80% solvent C, then
149 0.75% min⁻¹ until 95% solvent C, held at 95% C for 20 minutes and increased by 1.7% min⁻¹ to 100%, following 10
150 minutes at 100% solvent B, shown in Fig. S2b (DeVault et al., 2022).



151 2.3 Standards for HPLC measurements

152 Two standard solutions of atmospherically relevant species were made for this study. Standard solution 1 contained
153 0.4% (by mass) 3-methyl-4-nitrophenol, 0.2% phthalic acid, 0.5% 4-nitrophenol, 0.6% succinic acid, and 0.1% 4-
154 nitrocatechol, dissolved in HPLC grade acetonitrile. Solution 2 contained 8 species: 0.3% phthalic acid (by mass),
155 0.3% L-malic acid, 0.1% succinic acid, 0.3% citric acid, 0.3% levoglucosan, and 0.2% 4-nitrocatechol in HPLC
156 grade acetonitrile. Source information and calculated saturation mass concentrations for all species are shown in
157 Table S2.

158 Each species was chosen for its relevance in biomass, urban, or manufacturing processes. 3-methyl-4-
159 nitrophenol, 4-nitrophenol, 4-nitrocatechol and levoglucosan are cyclic C₆ carbon species found in biomass burning.
160 Succinic acid, malic acid, and phthalic acid are non-cyclic acids of secondary origin found in urban atmospheres.
161 Citric acid is found in food and/or medicine. A critical property of these compounds is that they absorb in the UV-
162 Vis, whereas most SOA does not. Nitrates and aromatics have strong absorbance and carboxylic acids have a very
163 weak absorbance.

164 2.4 Aerosol Generation and Sampling System

165 The HPLC was coupled to particle phase measurements by using a high-flow Collison atomizer. First, a teflon line
166 was attached to the waste port of the HPLC. The flow from the HPLC was 0.5-1 mL min⁻¹, all of which was sent to
167 the atomizer. The atomizer operated by first introducing pressurized compressed air (~20 psi) into a small chamber
168 (473 ml jar). Perpendicular, sample flow at a rate of 0.5 or 1 mL min⁻¹ intersected the pressurized air. This led to the
169 generation of particles of a consistent size distribution, and provided a total flow ranging from 8 to 10 l min⁻¹.
170 Instrument specific flows were measured daily.

171 Following atomization, ~10 l min⁻¹ of aerosol/solvent flow was sent through a Nafion dryer before being
172 sent through an activated carbon denuder. This denuder is in a stainless steel, ~1 inch diameter and 8 inch length
173 tube, composed of activated carbon honeycomb cross-sections. Flow was then sent into each particle instrument.
174 Solvent was efficiently removed (>99.0%, Pagonis et. al. (2021)) using the carbon denuder. Acetonitrile (a solvent
175 used in the HPLC system) was monitored using the EESI. If acetonitrile started to increase, the EESI denuder was
176 regenerated.

177 Residence times in different parts of the system were estimated to enable synchronizing the aerosol
178 instrument observations with the measured UV-Vis absorbances. Calculations shown in Table S1 suggest that a
179 delay of at least 41 seconds should be observed between the UV-Vis measurement and detection with the aerosol
180 instruments, which is consistent with the measured delay. Retention times for EESI, AMS, and SMPS may differ
181 from each other by 1-2 seconds, depending on the residence times in the tubing. In addition, bypass flows (shown in
182 Fig. 1) were added to the EESI and AMS to reduce residence times in the tubing and thus particle losses or
183 evaporation. These delay differences were handled by shifting instrument data by the delay times.

184 2.5 Description of particle measurements



185 2.5.1 Extractive Electrospray Time-of-Flight Mass Spectrometry (EESI)

186 The EESI uses a soft ionization technique that detects particle-phase analytes based on their solubility and proton
187 affinity/adduct formation stability (Lopez-Hilfiker et al., 2019). Briefly, particle/gas sample flow was sent into the
188 EESI source at $\sim 0.5\text{-}1\text{ l min}^{-1}$, where gases are removed using a charcoal denuder ($>99\%$ removal efficiency for
189 acetic acid, when regenerated daily) (Tennison, 1998; Pagonis et al., 2021). The aerosol inlet for the instrument used
190 in this study was pressure controlled (Pagonis et al., 2021), and was run at 766 mbar. While designed for aircraft
191 applications, the pressure-controlled inlet provides better spray and signal stability as it shields the spray from small
192 pressure perturbations from changes in upstream inlet flow conditions such as switching between different sampling
193 modes and plumbing pathways. The working fluid consisted of a mixture of 25% milli-Q water and 75% (by
194 volume) HPLC grade methanol. The EESI was run in two polarity modes. The positive polarity mode (henceforth
195 “EESI+”) contained 200 ppm of sodium iodide (NaI) (Pagonis et al., 2021). This working fluid generally forms
196 Analyte- Na^+ adducts. The negative polarity mode (EESI-) was doped with 0.1% (by volume) formic acid (Chen et
197 al., 2006; Gallimore and Kalberer, 2013; Pagonis et al., 2021). Species with a lower proton affinity than formate
198 donate a proton and become negatively charged. This ionization mode is generally sensitive to acidic species that
199 can readily donate a proton and become anionic.

200 For both polarities, a fused silica capillary (TSP Standard FS tubing, 50 μm ID, 363 μm OD) was used to
201 transport working fluid solution from a pressurized (250-300 mbar above ambient) fluid bottle. Typical resolution at
202 m/z 150 was 4000, and mass spectra were saved every second.

203 The mass concentration of a species ($\mu\text{g m}^{-3}$) can be quantified from its EESI signal (I_x ion counts s^{-1}) as
204 (Lopez-Hilfiker et al., 2019):

$$205 \quad \text{Mass}_x = I_x \left(\frac{MW_x}{RF_x} \right) \cdot \frac{1}{F} \quad (1)$$

206 MW_x is the molecular weight of species x , F is the flow rate (in L min^{-1}), and RF_x is the combined response factor
207 representing fundamental parameters which can be found in Lopez-Hilfiker et. al. (2019). Here, we define a new
208 variable, calibration factor (CF_x^E , in $\mu\text{g m}^{-3} \text{ counts}^{-1} \text{ s}$), such that

$$209 \quad \text{Mass}_x = I_x \cdot CF_x^E \quad (2)$$

210 Generally, CF_x^E is directly determined by calibrations with standards, when possible. Here, CF_x^E was determined by
211 direct calibrations using either commercially available standards or HPLC-separated analytes. Calibration factors are
212 reported as absolute values (in units of $\text{counts s}^{-1} \mu\text{g}^{-1} \text{ m}^3$) and also relative to 4-nitrocatechol for EESI- and
213 levoglucosan for EESI+ (unitless).

214 2.5.2 High Resolution Aerosol Mass Spectrometer (HR-AMS)

215 A high-resolution time-of-flight aerosol mass spectrometer (hereinafter AMS) (DeCarlo et al., 2006; Canagaratna et
216 al., 2007) was used to obtain 1 Hz chemical composition for organic aerosol (OA) and nitrate aerosol (pNO_3). The



217 AMS was run with an inlet flow of 0.1 l min^{-1} , and a bypass flow of $\sim 1.3 \text{ l min}^{-1}$. The AMS was run exclusively in
218 “fast mode” (Kimmel et al., 2011; Nault et al., 2018), and size distributions were not recorded. AMS backgrounds
219 were measured for 6 seconds every 52 seconds. Additional backgrounds, in part to test for solvent influence from
220 the HPLC, were taken during the times where no peaks were eluting, and generally remained $< 2 \mu\text{g m}^{-3}$. The latter
221 were conducted by flowing the sampler air through a particle filter. AMS data was analyzed in the ToF-AMS
222 analysis software (PIKA version = 1.25F, Squirrel = 1.65F) (DeCarlo et al., 2006; Sueper, 2023) within Igor Pro 8
223 (Wavemetrics, Lake Oswego, OR). The AMS OA relative ionization efficiency (RIE) and collection efficiency (CE)
224 were assumed to be 1.4 (OA_{default} , (Canagaratna et al., 2007) and 1, respectively. The AMS NO_3 RIE*CE (NO_3 ,
225 $_{\text{default}}$) was assumed to be 1.1 (Canagaratna et al., 2007). Data herein is reported in $\mu\text{g m}^{-3}$, using Boulder pressure
226 ($P=830 \text{ mbar}$) and average lab temperatures ($\sim 20^\circ\text{C}$).

227 Here, the quantification of different particle-phase species that have been separated by HPLC (and thus are
228 mostly in single component particles) is assessed for the AMS. This is a function of $RIE_X * CE_X$ (a.k.a. “response
229 factor”, or CF_X^A) for a species X. Direct AMS calibration has been reported for many OA species (Slowik et al.,
230 2004; Dzepina et al., 2007; Jimenez et al., 2016; Xu et al., 2018; Nault et al., 2023). An RIE of 1.4 is typically
231 applied to ambient aerosols (Canagaratna et al., 2007), which has been shown to perform well in most outdoor
232 intercomparisons (Jimenez et al., 2016; Guo et al., 2021). Laboratory measurements typically require specific
233 calibrations, as RIE can be higher for some compounds and mixtures (Jimenez et al., 2016; Xu et al., 2018; Nault et
234 al., 2023). CE can vary considerably, from $CE=0.15$ to a $CE=1$ (Docherty et al., 2013).

235 The material densities of the known standards were determined by running the AMS in PToF mode and
236 calculating the density as d_{val}/d_m (d_{va} is the aerodynamic vacuum diameter, and d_m is the SMPS measured mobility
237 diameter (DeCarlo et al., 2004)). Calculated densities are shown in table S2. For the unknown species present in the
238 SOA, densities were estimated using the atomic ratio of oxygen plus nitrogen to carbon (O+N:C) and H:C, as
239 demonstrated in Day et. al. (Day et al., 2022), which builds upon the method of Kuwata et. al. (Kuwata et al., 2012)
240 which did not account for nitrate content. The O:C ratio attributed to the non-nitrate OA was calculated per
241 Canagaratna et. al. (2015). The organic nitrate contribution was quantified per Day et. al. (2022). All nitrate here
242 was assumed to be from organic nitrate functional groups, as the aerosol studied here likely contain little inorganic
243 nitrate. For the density calculation, the total nitrate was multiplied by the ratio of the molecular weights of $\text{NO}_2:\text{NO}_3$
244 ($46/62$) and converted into a molar concentration using the molecular weight of NO_2 (46 g mol^{-1}). Only the NO_2
245 functionality was included for the density calculation, since the nitrate oxygen bonded to the carbon is expected to
246 typically be included as part of the standard AMS OA O:C estimation (Farmer et al., 2010). Carbon was also
247 converted into a molar concentration using the molecular weight (12 g mol^{-1}). That organic nitrogen to organic
248 carbon ratio was added to the standard AMS OA O:C ratio to obtain the organic nitrate-corrected O+N:C ratio.

249 For isolated peaks that contained organic nitrate, the organic nitrate (NO_3) concentration was added to the
250 AMS OA to get the total measured AMS mass. The SMPS mass was then compared to the AMS mass calculated
251 with the default CF_X^A , and the correct CF_X^A was determined with Eq. 3 (further details in Sect. 2.7).

$$252 \quad CF_X^A = \frac{OA_{\text{default}} + NO_{3,\text{default}}}{SMPS \text{ mass}} \quad (3)$$



253 For HPLC peaks composed of multiple species (like in the β -pinene SOA sample), the average CF_x^A was calculated
254 by adding the average NO_3 contribution ($\sim 5\%$) to the measured AMS OA contribution (Fig. S3). This CF_x^A was then
255 applied to the AMS PMF organic chromatographic time series, in order to determine CF_x^E . For species not
256 containing any nitrate, the $\text{NO}_{3, \text{default}}$ was set to 0.

257 We note that some recent work has suggested that the sensitivity of organic nitrate functional groups may
258 be lower than for ammonium nitrate (for which the nitrate is calibrated by default in AMS data processing). Thus, a
259 correction of $\sim 62/46$ may be more appropriate here for computing nitrate functional group mass concentrations
260 (Takeuchi et al., 2021). However, due to the small nitrate contribution overall, such a correction is not applied.

261 2.5.3 Scanning Mobility Particle Sizer (SMPS)

262 Two SMPSs were run with a 20 second offset during HPLC experiments (consisting of all TSI, Inc components) in
263 order to improve the time resolution of the total particle volume measurement. For both SMPSs, a 3081 differential
264 mobility analyzer (DMA) was run with a 3080 Electrostatic Classifier. Each was coupled with either a 3776
265 condensation particle counter (CPC) (referred to as SMPS A) or a 3775 CPC (SMPS B). Both systems were run in
266 the CPC “high flow” mode. Sample flow rates were nominally set to 1.5 l min^{-1} , but the actual (measured flow) was
267 1.43 and 1.49 l min^{-1} for the 3776 and 3775, respectively. DMA sheath flows were set to 6.0 l min^{-1} . Data were
268 compared to that acquired in a reference mode, with a sample flow of 0.3 l min^{-1} , a sheath flow of 3.0 l min^{-1} , and
269 120 s scans. Testing was done to ensure that number and volume distributions and integrated concentrations
270 matched between the reference and fast scanning modes, shown in Fig. S4 and discussed in depth in Sect. S3. The
271 SMPSs were also run concurrently during an HPLC run to confirm that data from both instruments matched (Fig.
272 S5). Overall, the SMPSs in the reference and fast modes agreed within 10%. Flows were measured every day, and
273 delay times (from the SMPS inlet to the CPC detection, which affect sizing) were calculated when changes in
274 plumbing were made. Further details on SMPS delays can be found in Table S3.

275 2.6 Positive Matrix Factorization (PMF)

276 Positive Matrix Factorization (PMF) (Paatero and Tapper, 1994; Paatero, 1997) is a bilinear deconvolution model
277 that relies on the assumption of mass balance with components with constant spectral profiles. Briefly, time series
278 for signals at individual m/z 's are entered into a two-dimensional matrix with m rows (points in time) and n columns
279 (m/z 's) (Ulbrich et al., 2009; Kumar et al., 2022). PMF works to minimize the squared weighted residuals between
280 the measured and reconstructed matrices, producing multiple potential solutions that could explain different
281 chemical or physical sources in a given data set, along with the total residual of each solution.

282 The model is solved using PMF2 (Paatero, 2007) and the multilinear engine, developed by Paatero et. al.
283 (1999), run from the PMF Evaluation tool (“PET”) software v3.08 in Igor Pro v8 (Wavemetrics, Lake Oswego, OR).
284 Choosing the best PMF solution always has a subjective component, as it is usually impossible to know the
285 “correct” number of factors that completely capture a complex data-set (Ulbrich et al., 2009). Several methods can
286 be used to assess the validity of a given solution. First, the Q-value (Q), which is the total sum of the error-weighted
287 square residuals for a data set, is used. Q_{exp} is the expected value of Q if all residuals are due to random errors with



288 the estimated precision at each point. If the individual data points in a solution are fit so that the residuals are
289 consistent with random noise, then $Q/Q_{\text{exp}} \sim 1$. Note that this also requires accurate estimation of the precision
290 (random error) in the entire data matrix. In some situations, PMF cannot explain a data set within an acceptable
291 error. In these situations, $Q/Q_{\text{exp}} \gg 1$. All solutions here have $Q/Q_{\text{exp}} \leq 1$.

292 The second criteria for picking the best PMF solution is by exploring the time series and mass spectra for a
293 given solution for different approximate rotations (FPEAK values) (Lee et al., 1999; Lanz et al., 2007; Ulbrich et al.,
294 2009). Simply, PMF rotations are non-unique solutions that are represented across multiple factors. In a real-world
295 example, a source profile (for example, biomass burning OA), might split across multiple PMF factor's time series
296 and/or mass spectra, despite only being from a singular source. Factor splitting can sometimes reduce residuals, and
297 mathematically may appear as a more correct solution for a particular dataset. This is where the user must
298 thoroughly assess different solutions, specifically those with $Q/Q_{\text{exp}} \sim 1$.

299 PMF solutions chosen here are based on the above criteria and a third: the time series of the residuals. In a
300 chromatogram, the shape of the peaks are generally known. Here, 4 different instruments generate unique
301 chromatograms: UV-Vis, HRAMS, EESI, and the SMPSs. Thus, across those four instruments, the shape of the
302 chromatogram was fairly well constrained. When choosing solutions here, the shape of the chromatogram was
303 compared to the time series of the residuals. If the residuals showed significant peaks, then that was an indicator that
304 not enough factors were used to represent the complete chromatogram and all of the factors therein.

305 The $m \times n$ matrix for AMS data was generated for HR ions using the PMF export option in the PIKA data
306 analysis software. Briefly, unit mass and high resolution AMS data were first fit as described in Sect. 2.5.2. After
307 confirming that all ions of interest were well fit, the organic data was exported into an $m \times n$ matrix (both signal and
308 precision matrices). Any HR ions not associated with the following families: C_x , CH, CHO_1 , and CHO_{gl} were
309 removed, as NO_3 was not included in the PMF input, and the included families were the only measured ions with
310 substantial signal during the experiments included here. PMF was run from 1-20 factors. Rotations (FPEAKS) were
311 enabled, ranging from -1.0 to 1.0, in steps of 0.2.

312 2.7 Calculating calibration factors for species using the multi-instrumental method

313 For unknown species (or known species with an unknown AMS response factor) the following method was used to
314 obtain EESI and AMS calibration factors:

- 315 1. Calculation of composition-dependent density using the measured elemental composition or d_{va}/d_m
316 measured densities.
- 317 2. SMPS size distributions are fit with a lognormal curve, and integrated volume concentrations are obtained.
- 318 3. SMPS integrated volume time series were multiplied by the density, to produce the reference mass
319 concentration time series.
- 320 4. The high-time-resolution AMS OA and NO_3 time series are obtained for an assumed $RIE \cdot CE = 1.4$
321 (OA_{default}) and $RIE \cdot CE = 1.1$ ($NO_{3, \text{default}}$).
- 322 5. The SMPS mass concentration time series and the AMS OA+ NO_3 time series, for an individual
323 chromatographic peak, are fit with a Gaussian distribution



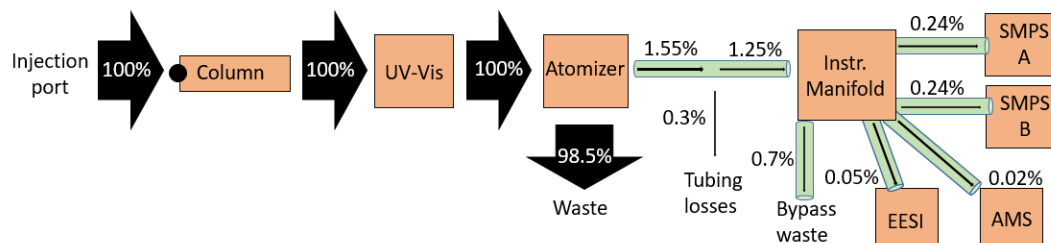
- 324 6. The AMS and SMPS Gaussian distributions are integrated ($\mu\text{g m}^{-3} \text{ s}$).
- 325 7. The CF_x^A was obtained using the ratio of the integrated SMPS to the integrated AMS time series fits (Eq.
- 326 3).
- 327 8. The time series for the EESI m/z was fit with a Gaussian and integrated along the retention time.
- 328 9. The integrated gaussian for the EESI m/z was divided by the integrated AMS (OA+NO₃, after AMS
- 329 calibration by the SMPS) or SMPS gaussians to obtain CF_x^E (counts $\text{s}^{-1} \text{ m}^3 \mu\text{g}^{-1}$).
- 330



331 3 Results

332 3.1 Mass Balance of the Analyte in the Experimental System

333 There was substantial plumbing between the injected sample and the instruments measuring the analyte, where
334 losses can occur (Fig. 1, Table S1). In order to better understand the experimental system, the mass flux was
335 calculated using the known, injected mass as well as the tubing diameters, lengths, and flow rates, as shown in Fig.
336 2.
337



338
339 **Figure 2. Mass flux across the multi-instrumental setup. Arrows are sized by the percentage of analyte mass, which is**
340 **included alongside each arrow. EESI and AMS have bypass lines (represented as the total by 0.7% bypass waste).**
341 **Percentages shown are for the actual measured mass percent. Tubing details are also included in Fig. 1.**
342

343 By injecting a known amount of sample into the HPLC column, we were able to account for all the measured mass
344 by the four instruments sampling. As shown in Fig. 2, all of the injected mass was analyzed by the UV-Vis
345 spectrometer, but only a small fraction of it was analyzed (0.55%) by the online instruments. There was substantial
346 fluid loss at the atomizer, which is thought to account for the bulk of the mass leaving the HPLC. The EESI and
347 AMS measure the least mass, due to their low flow rates (0.28 l min⁻¹ and 0.1 l min⁻¹, respectively). Of the mass that
348 exited the atomizer, ~20% was lost in the tubing (~10 m, ¼" I.D.) to the aerosol sampling manifold (represented as
349 0.3% of total in Fig. 2). Overall, the efficiency in sampling the injected mass with the online instruments was very
350 low with this system, primarily due to the atomization process. In SOA extracts that are highly concentrated, this is
351 not a major problem. However, application of this method to lower concentration samples would benefit from use of
352 a lower-flow liquid chromatography method and a more efficient atomizer.

353

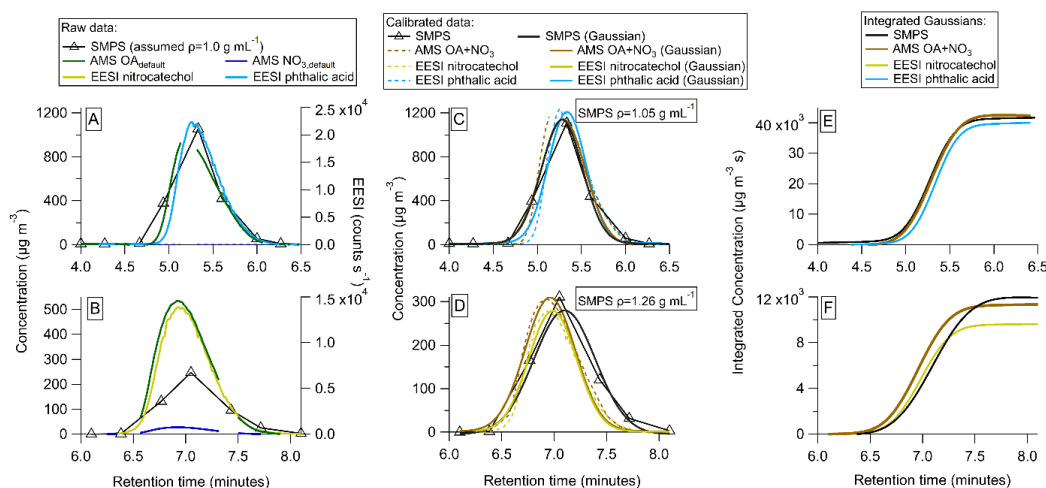
354 3.2 Application of multi-instrumental method and PMF for standard species' calibrations

355 3.2.1 Cross comparison between directly calibrated one-component chromatographic standards vs. multi- 356 instrumental method

357 In order to test the efficacy of the proposed method, two solutions were made containing one standard each (phthalic
358 acid and 4-nitrocatechol). These species were first calibrated directly in order to obtain CF_x^E and CF_x^A . Direct



359 calibration hereout refers to the standard method of generating monodisperse aerosol from a calibrant solution with a
360 Collision atomizer (TSI model 3076) drying with a Nafion dryer, size selecting at 275 nm with a 3080 electrostatic
361 classifier / 3081 DMA, removing double-charged particles with an impactor, measuring the particle concentration
362 with a 3775 CPC, and measuring with the EESI and/or AMS. Then, each solution was injected into the HPLC to
363 generate isolated chromatograms (Fig. 3).
364



365
366 **Figure 3. (A) Uncalibrated data collected during a single standard (phthalic acid) HPLC run, (B) raw data from a**
367 **nitrocatechol HPLC run, (C) calibrated phthalic acid data (using the monodisperse calibration factors), (D) calibrated**
368 **nitrocatechol data, (E) integrated Gaussian peaks from (C), and (F) integrated Gaussian peaks from (D).**

369
370 In Fig. 3a, the uncalibrated background-subtracted data is shown. Phthalic acid contains no nitrate moiety, so AMS
371 NO_3 was 0. Fig. 3b shows the raw data for 4-nitrocatechol. Due to the nitro group, AMS NO_3 is added to AMS OA
372 to obtain the total mass measured by the AMS. If the method was followed as described in Sect. 2.7, the raw data
373 would be fit with Gaussian curves and integrated, in order to produce CF_x^E and CF_x^A for each species. However, in
374 this test study, CF_x^E and CF_x^A are already known.

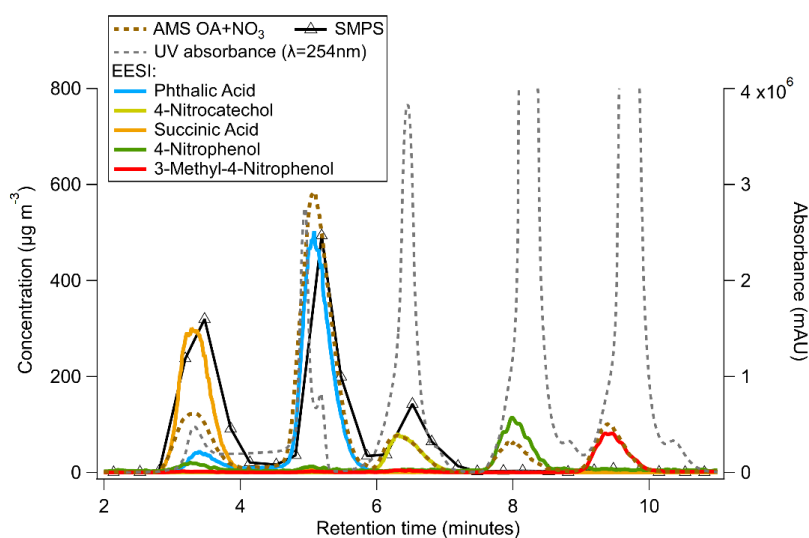
375 Figure 3c shows the directly calibrated (as opposed to the multi-instrumental approach calibrated) data for
376 phthalic acid. It is clear that the AMS, EESI, and SMPS data line up well, indicating that the multi-instrumental
377 approach produces very similar CF_x^E and CF_x^A as the direct calibrations. Fig. 3d echoes this, showing good overlap
378 across each instrument for nitrocatechol.

379 Figures 3e and 3f show the integrated, calibrated Gaussian curves. If the multi-instrumental method worked
380 as well as direct calibrations, the maximum integrated values would be expected to be the same for each instrument.
381 For phthalic acid, the instruments agree within 6%, with the EESI showing the largest deviation from the other
382 instruments. For 4-nitrocatechol, this difference is 20%, and again the EESI is the farthest from the other
383 instruments. Such discrepancies could be due to changes in EESI sensitivity, which may be driven by the different
384 solvents used for calibration (water for direct calibrations, and a mixture of acetonitrile and water for the multi-



385 instrumental method). It could also be due to the high concentrations of each solute, which may change CF_x^E
386 slightly.

387 Following method validation through comparison between direct calibrations and the multi-instrumental
388 calibration method, a mixture containing five standards (phthalic acid, 4-nitrocatechol, succinic acid, 4-nitrophenol,
389 and 3-methyl-4-nitrophenol) was run through the HPLC column (Fig. 4). Like above, each species was first
390 calibrated directly, in order to compare the direct calibration values vs. the multi-instrumental calibration method for
391 a more complex chemical system.
392



393
394 **Figure 4. Time series of UV absorbance (milli-absorbance units) and AMS, EESI, and SMPS mass concentrations for a**
395 **mixed-solution standard HPLC run.**

396
397 In Fig. 4, succinic acid was the first peak to elute from the HPLC column, from ~2.5-4 minutes. The EESI and
398 SMPS data match well, but the AMS data is lower by a factor of ~2. This is potentially driven by the phthalic
399 acid/succinic acid co-elution (as evidenced by the EESI). The CF_x^A for both species is shown in Table 1. CF_x^A differ
400 substantially, and an internal mixture of aerosols containing succinic acid and phthalic acid may result in a larger
401 AMS bias (as $CF_{Succinic\ Acid}^A$ and $CF_{Phthalic\ Acid}^A$ differ significantly) than the EESI (where we measured molecular
402 ions) or the SMPS (as the density of phthalic acid and succinic acid are similar, table S2).

403
404



405 **Table 1. Calibration factors for resolved (or mostly resolved) standard species. CF_x^E values are reported in counts $s^{-1} \mu g^{-1}$**
 406 **m^3 and the relative EESI calibration factors (CF_x^E/CF_{nitro}^E (EESI-) or CF_x^E/CF_{levo}^E (EESI+)), and the AMS calibration**
 407 **factors (CF_x^A) are unitless values.**

Species	Direct calibration CF_x^E (counts $s^{-1} \mu g^{-1} m^3$)	Multi- instr. calibration CF_x^E (counts $s^{-1} \mu g^{-1} m^3$)	Direct calibration CF_x^E/CF_{nitro}^E (EESI-) or CF_x^E/CF_{levo}^E (EESI+)	Multi- instr. calibration CF_x^E/CF_{nitro}^E (EESI-) or CF_x^E/CF_{levo}^E (EESI+)	Direct calibration CF_x^A (unitless)	Multi- instr. CF_x^A (unitless)
4-nitrocatechol (EESI-)	44.1±5	23	1	1	1.96±0.17	1.05
4-nitrocatechol (EESI+)	-	18	-	0.020	-	-
Succinic Acid (EESI-)	30±4.0	22	0.68	0.98	1.6±0.10	0.52
Succinic Acid (EESI+)	-	26	-	0.029	-	-
Phthalic Acid (EESI-)	18.1±2.8	18	0.41	0.82	0.79±0.070	1.0
Phthalic Acid (EESI+)	-	620	-	0.68	-	-
4-nitrophenol (EESI-)*	1.6±0.57	26	0.036	1.2	0.59±0.050	5.9
3-methyl-4- nitrophenol (EESI-)*	5.8±4.0	42	0.14	1.9	0.90±0.10	8.0
Levoglucosan (EESI+)	200±10	900	1	1	0.45±0.06	-

408 * The reported values here are highly uncertain due to differences in evaporation for each instrument

409

410 Phthalic acid elutes as two isomers, with the largest eluting between 4 and 6 minutes. All three instruments match
 411 well. 4-nitrocatechol was next, and showed very good agreement between the EESI and AMS, but a factor of ~2
 412 difference between the SMPS and AMS/EESI. The exact cause for this discrepancy is unknown.

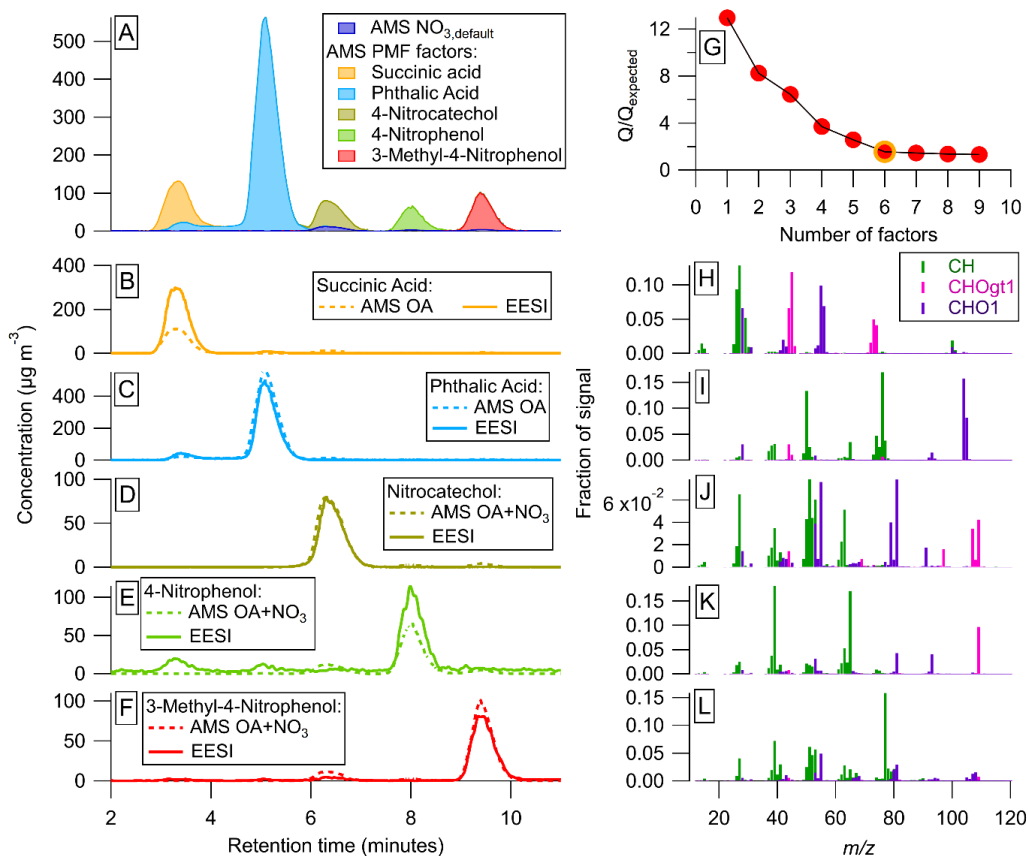
413 4-nitrophenol and 3-methyl-4-nitrophenol both match well between the EESI/AMS, but the SMPS
 414 concentration is a factor of 20 less than the other two instruments. The likely explanation is that 4-nitrophenol and 3-
 415 methyl-4-nitrophenol are volatile (table S2). Compared to succinic acid, >90% of these species evaporated from
 416 injection to detection by the EESI/AMS. The SMPS measurement is slower than the other instruments, and dilutes
 417 the incoming aerosol by a factor of 4 inside the DMA column. The AMS and EESI measurements are faster and do
 418 not dilute the incoming aerosol. Due to these differences, nearly all of the injected mass evaporated in the SMPS.



419 This suggests that volatile species (where $C^* \gg OA$) are not able to be calibrated for by this method. Evaporation
420 would also likely occur during direct calibrations, but to a lesser degree due to the higher pure-species OA
421 concentrations.

422 **3.2.2 Combined application of the multi-instrumental calibration method and PMF on two mixed standards**
423 **solutions**

424 PMF was combined with the multi-instrument calibration method to better separate succinic acid and phthalic acid,
425 which overlap in Fig. 4. The results of applying PMF to the AMS data is shown below in Fig. 5. A 6-factor solution
426 was chosen (Fig. 5g).
427



428
 429 **Figure 5. Time series for the PMF solution, (A) stacked plot of each factor and AMS NO₃, (B)-(F) PMF factor with CF_x^A**
 430 **applied to individual species, along with EESI concentrations. (G) Q/Q_{expected} vs. number of PMF factors, chosen solution**
 431 **circled in yellow. (H)-(L) mass spectra (colored by associated AMS HR family) for each AMS PMF factor.**

432
 433 Figure 5a-5f show excellent separation by PMF between the time series for each of the standards present in the
 434 mixture. This is likely due to the very different mass spectra for each species (Fig. 5h-5l) as well as the time
 435 separation achieved by the HPLC. The mass spectra for each standard was compared to the direct calibration mass
 436 spectra to confirm the PMF factors were assigned correctly (Fig. S6 and table S4). For all species, there was
 437 excellent correspondence, and the uncentered correlation coefficient (UC) between the mass spectral peaks was
 438 >0.95 .

439 Here, the CF_x^A and CF_x^E values are known for each pure standard (from direct calibrations). When applying
 440 the CF to individual species, the overall agreement between the AMS and EESI time series is comparable to that
 441 shown in Fig. 4. The AMS still underestimates succinic acid by a factor of ~ 2 compared to the EESI, even after
 442 better separation is achieved with PMF. As discussed previously, this could be due to the mixing of the two species,
 443 which might change the viscosity or phase of the sampled aerosols compared to the pure species, which in turn

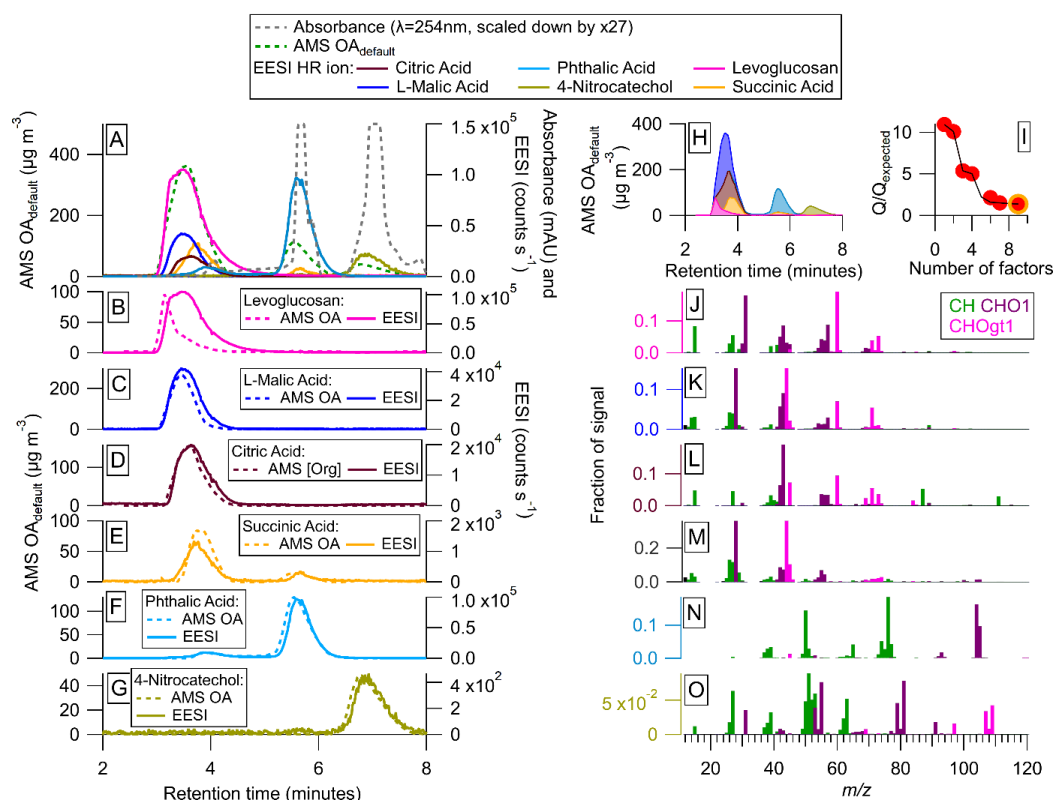


444 could fundamentally change the CF_x^A due to the change in CE. Whilst separation was achieved with PMF, PMF time
445 series are likely more accurate for systems where different species have similar CF_x^A (e.g. SOA mixtures from a
446 single precursor and oxidant).

447 The mixture studied in Fig. 4 and Fig. 5 was mostly well-separated without PMF. In order to assess the
448 ability of PMF to separate a more complex mixture, PMF was run on a different standard solution shown in Fig. 6.



449



450
 451 **Figure 6.** (A) time series of AMS total OA (assumed $CF_x^A=1.4$), EESI HR ion, and absorbance ($\max=4\times 10^6$, milli-
 452 absorbance units). (B)-(G) AMS PMF factor (assumed $CF_x^{A, default}=1.4$) and EESI HR ion for 6 calibrants. (H) Stacked
 453 PMF factor solution time-series, (G) $Q/Q_{expected}$ for AMS PMF solution, a 9-factor solution was chosen (yellow circle) with
 454 $FPEAK=0.2$, and (J)-(O) AMS family-colored mass spectra for 6 PMF factors.

455

456 Unlike the data shown in Fig. 3-5, the species run in the standard solution shown in Fig. 6 were not calibrated
 457 directly. Thus, Fig. 6 serves as a test of PMFs ability to resolve complex mixtures, rather than a comparison of the
 458 calibration methods. Figure 6a shows the uncalibrated time series/chromatogram for the standards in the mixture. In
 459 contrast to the previous mixture, this solution contains 5 co-eluting peaks: levoglucosan, L-malic acid, citric acid,
 460 succinic acid, and a small fraction of the phthalic acid and its isomer. These 5 co-eluting peaks suggest that the
 461 application of only HPLC with the separation method being used here is not sufficient for these species, likely due
 462 to how polar they are. Further separation could be achieved by either changing the HPLC method (through the use
 463 of a normal phase chromatography, which uses e.g. a silica column) or running PMF on the AMS data.

464

465 Figures 6b-6h shows PMF time series for the standards present in the mixture. In Fig. 6b, both the AMS
 466 and EESI levoglucosan peaks have different shapes. The EESI peak has a right tail, which is potentially due to the
 “sticky” (semi-volatile) nature of levoglucosan (Brown et al., 2021). The AMS peak has a sharp increase and slow



467 descent, and does not resemble a Gaussian (which is the approximate shape we expect eluting peaks to have). This is
468 likely due to an imperfect PMF separation. Despite that, when comparing the mass spectra in Fig. 6j to the direct
469 calibration mass spectra in Fig. S7, UC (table S5) is 0.93, suggesting consistency between the two mass spectra.

470 L-malic acid and citric acid also co-elute with levoglucosan. The PMF factors assigned to those species do
471 look like Gaussian curves, but the mass spectra shown in Fig. 6j-6l are somewhat similar. The assigned malic acid
472 factor has a UC of 0.89 with the directly calibrated mass spectra, but citric acid was not directly calibrated for, and it
473 is likely there is some overlap in the AMS factors between those three species. This was an especially complex
474 solution for PMF to resolve due to the very similar retention times and mass spectra between these species.

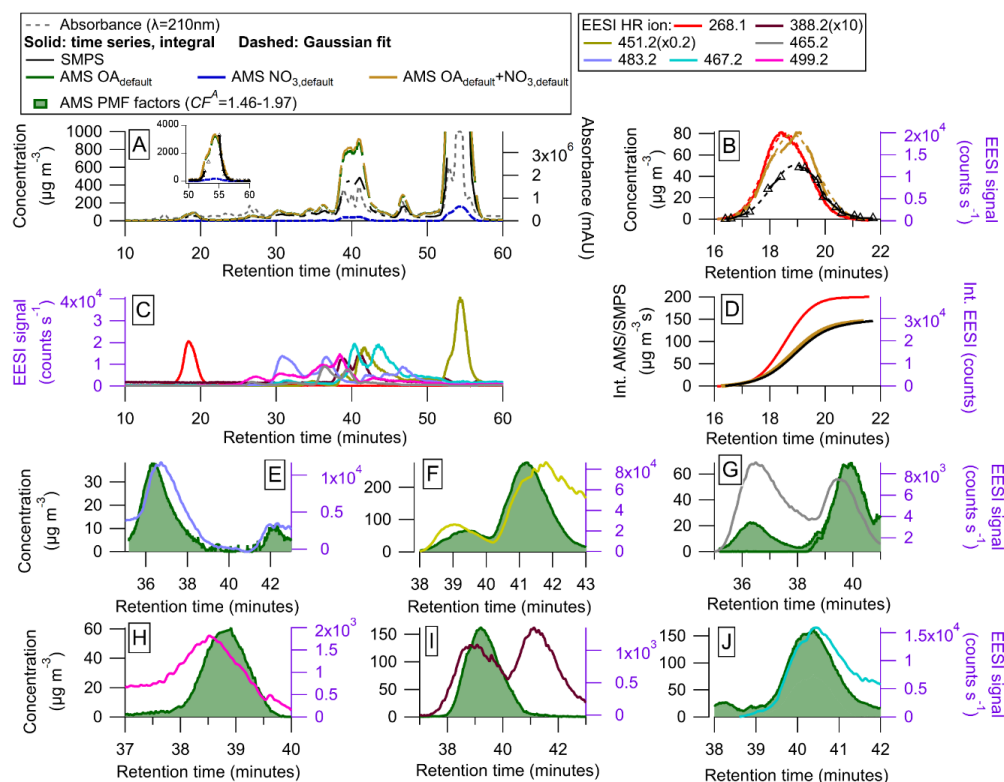
475 As in Fig. 5, succinic acid, phthalic acid, and 4-nitrocatechol (Fig. 6e-6g and Fig. 6m-6o) are easily
476 resolved when running PMF on the HPLC chromatograms. This is likely due to both the retention time differences
477 and the different AMS mass spectra for these three species. In Table 1, calibration factors are shown for
478 levoglucosan, succinic acid, phthalic acid, and 4-nitrocatechol. CF_x^A is known from the direct calibrations done in
479 Fig. 4. Only levoglucosan was cross-calibrated with a direct calibration, but the multi-instrumental calibration value
480 is highly affected by the shape of the AMS PMF factor associated with levoglucosan. Thus, the multi-instrumental
481 calibration factor for levoglucosan is likely incorrect. The PMF factor stacked time series is shown in Fig. 6h.

482 **3.3 Combined application of the multi-instrumental calibration method and PMF on β -pinene/ NO_3 SOA**

483 In order to test the applicability of the proposed method to a complex real system, SOA from β -pinene + NO_3 was
484 generated, collected on a filter, extracted, and analyzed with our multi-instrument system (per Sect. 2.1). This SOA
485 system has been studied in depth previously and many of the products have been identified (Claflin and Ziemann,
486 2018; DeVault et al., 2022). The HPLC method was that of DeVault et al. (2022). Species here are identified based
487 on comparison to the results in the aforementioned papers, and the observed EESI+ HR ions that show peaks in the
488 time series (Fig. 7). Per Claflin and Ziemann (2018), many of the known products are oligomers, formed primarily
489 from the reactions of two carbonyl nitrate monomers. For simplicity, the SOA peaks observed will be referenced by
490 their associated EESI HR ion.



491



492

493 **Figure 7. Results of an HPLC run for SOA from β -pinene + NO₃ (A) AMS, SMPS, and UV-Vis chromatograms (milli-**
 494 **absorbance units), with inset showing peak from 50-60 minutes. (B) Time series and Gaussian fits for the peak between 16**
 495 **and 20 minutes (without using PMF), (C) EESI HR ions time series (D) time integrated mass concentrations (ion signal)**
 496 **for AMS OA and NO₃, SMPS total mass, and EESI+ HR ion ($m/z=268.1$). (E)-(J) show AMS PMF factors against**
 497 **measured EESI+ HR ions. (G), (I), and (J) represent split AMS PMF factors for the measured EESI+ HR ions. The AMS**
 498 **PMF factors have a CF_x^A ranging from 1.46-1.97 as shown in Fig. S3 and Table 2. Densities are applied to the SMPS data,**
 499 **shown in Fig. S8.**

500

501 Figure 7a shows the full time-series for the β -pinene system. Many chromatographic peaks are observed by the
 502 AMS, SMPS, EESI, and UV-Vis. Many of the peaks are present in clusters and not well enough resolved to fit
 503 individual Gaussian curves to the EESI and AMS data. Claflin and Ziemann (2018) measured a similar (albeit
 504 slightly better separated) UV-Vis chromatogram (Fig. S9). Differences could potentially arise due to the age of the
 505 SOA extract used here (~ 1 year) vs. the fresh SOA extract used in that study, or other experimental factors.

506

507 Overlapping peaks are also observed in the EESI data (Fig. 7c). There are two isolated peaks, from 15-21
 508 minutes and 52-58 minutes. One peak, measured at EESI HR ion m/z 483.2 (suspected structure shown in table S6),
 was mostly resolved, and also shows up from ~ 46 -48 minutes. The raw (and fitted) data is shown in Fig. 7b for the



509 EESI ion measured at m/z 268.1 (a monomer, tricarboxyl nitrate) (Claflin and Ziemann, 2018). The integrated fits
 510 are shown in Fig. 7d.

511 Multiple peaks overlap from ~30 to ~50 minutes (based on the EESI data shown in Fig. 7c). These peaks
 512 are likely all dimers, the species identified by Claflin and Ziemann (2018) and measured by the EESI are shown in
 513 Table 5. Not every peak observed in Claflin and Ziemann (2018) was identified here, which is likely due to lack of
 514 EESI sensitivity to some species and potential decomposition of SOA products (specifically for the trimer identified
 515 in Claflin and Ziemann (2018)). In contrast, some EESI HR ions that do not correspond to peaks identified in Claflin
 516 and Ziemann (2018) were detected here, but structures for those species are unknown.

517 In Fig. 7e-7j, AMS PMF time series for the middle third of the run are shown alongside EESI HR ions. The
 518 full PMF solution can be found in Fig. S10-S12. AMS factors were matched with EESI HR ions based on the
 519 retention time and general shape of the time series. For some peaks, the retention times differ by up to 0.5 min.
 520 These peaks are assigned based on the similarity in time series between the EESI and AMS. The complexity of this
 521 solution, as well as the similarities in the products' molecular structures, likely hindered the ability of PMF to fully
 522 resolve each individual product. For the peaks that overlap the most in time, the magnitude of the individual AMS
 523 PMF factors separated during this time are comparable to each other.

524 CF_x^E and CF_x^A are given for each identified species in Table 2. Many of the identified species have CF_x^E in
 525 the same range as levoglucosan, within a factor of 3.

526

527 **Table 2. EESI HR ion, CF_x^E (counts $s^{-1} \mu g^{-1} m^3$), CF_x^E/CF_{levo}^E , CF_x^A , and associated PMF factor for the β -pinene + NO_3 SOA**
 528 **mixture. $CF_{levo}^E = 441.6$ counts $s^{-1} \mu g^{-1} m^3$. CF_x^E was calculated using the AMS PMF [Org] $\times 1.05$ (the average [NO_3]**
 529 **contribution was ~5%, Fig. S3).**

EESI ion	CF_x^E (counts $s^{-1} \mu g^{-1} m^3$)	CF_x^E/CF_{levo}^E (unitless)	CF_x^A (unitless)	AMS PMF factor(s)
268.1	270	0.61	1.46	-
388.2	10.9	0.023	1.97	9, 13
451.2 (1)	407	0.92	1.97	13
451.2 (2)	423	0.96	1.73	13
451.2 (3)	83.2	0.19	1.97*	-
465.2 (1)	670	1.5	1.97	2
465.2 (2)	170	0.38	1.97	10
467.2	139	0.31	1.73	5,8
483.2	435	0.99	1.97	14
499.2	54.2	0.12	1.97	12

530 * Incomplete SMPS data, assuming $CF_x^A=1.97$.



531

532 Some species, like the EESI HR ions measured at m/z 388.2 and m/z 499.2 have much lower EESI sensitivity than
533 the other species. These species could be fragments of a larger parent ion, or they could be species that, for whatever
534 reason, do not form a strong adduct with Na^+ . The ambiguity in the PMF factors may result in some errors in CF_x^E ,
535 but they are unlikely to fully explain the factor of ten difference in sensitivity between the most and least sensitive β -
536 pinene+ NO_3 products. In future runs with slightly better chromatographic separation a multi-variate fit of individual
537 factors vs. the SMPS may allow further constraining the quantification.

538 In this system, many of the products differ only by one or two oxygens. Some may contain a carboxylic
539 acid functional group in the place of a ketone, whilst others contain a cyclic ether, and some do not. The subtle
540 differences in structure could influence the sensitivity with the EESI, as the oxygenated moieties may change the
541 likelihood of forming a strong $[\text{M}+\text{Na}]^+$ adduct. Further, some EESI HR ions elute multiple times (e.g. m/z 451.2).
542 Claflin and Ziemann (2018) identified the structure of this ion for the third peak (Table S6). However, this ion is
543 measured twice more, from 38-43 minutes. Due to the chromatographic separation between these peaks and the third
544 peak, it is likely that the first two species are some isomeric form of the species identified in Claflin and Ziemann
545 (2018). As is shown for m/z 483.2 (Table S6), isomers can have different structures and very different CF_x^E (327.2
546 vs. 54.2 counts $\text{s}^{-1} \mu\text{g}^{-1} \text{m}^3$).

547 Despite differences in CF_x^E , CF_x^A was more consistent. For the mixed peaks (individual EESI m/z 's shown
548 in Fig. 7e-7j), CF_x^A was either 1.48 or 1.58, as shown in Fig. S3. For the three isolated peaks (m/z 268.2, m/z 451.2
549 [peak 3], and m/z 483.2 [peak 2]), the CF_x^A spanned from 1.31 to 1.75. For one of the isolated peaks, m/z 451.2 (peak
550 3), the actual CF_x^A was not calculated, due to a malfunction of the SMPS system between 54-56 minutes. Individual
551 peaks' Gaussian fits and integrated curves are shown in Fig. S13.

552 4 Conclusions

553 A multi-instrumental calibration method has been demonstrated here, that uses the chemical separation power of the
554 HPLC, combined with analytical aerosol detection of SMPS, AMS, and EESI to calibrate the mass spectrometers for
555 individual species in mixtures. When running individual standards, the multi-instrumental calibration method agreed
556 with direct calibration within 20%. As the sensitivities of EESI measured species can vary by over an order of
557 magnitude, quantification within 20% is very useful. In a mixed standard run that contained mostly resolved species,
558 the EESI and SMPS agreed within a factor of 1.5 (for non-volatile species). The AMS and EESI matched
559 moderately well, except when measuring succinic acid.

560 In situations where the HPLC column/method was unable to fully separate injected components, PMF was
561 used to methodically compare the time series and mass spectra for different species, and generate time resolved OA
562 data for the AMS. This was especially important for the AMS data, as overlapping peaks are measured as large and
563 wide "total OA" peaks for that instrument.

564 The β -pinene SOA solution was the most complex mixture studied here, primarily due to the suspected
565 presence of many isomers. The majority of the SOA peaks overlapped during the middle third of the HPLC run.
566 PMF separation conducted on the HPLC-separate AMS results produced a more complicated solution than the AMS



567 PMF done on the standards' runs. This was likely due to similarities in mass spectra and retention times for the
568 overlapping peaks. Despite that analytical challenge, when the middle third of the chromatogram was scrutinized
569 using both the AMS PMF solution and the measured EESI+ HR ions, approximate calibration factors were obtained.

570 For future studies, additional effort should be focused on tuning the HPLC performance (e.g. through
571 changing the column or mobile phase gradients) that provides higher resolution for whatever system is being
572 studied. In this demonstration project we were limited to a C₁₈ column, which is most often used for less polar
573 species. In many situations, especially when there is significant oxidation and smaller precursor gases, the resulting
574 products are likely to be more polar than can be separated by a C₁₈ column. In future experiments, columns with
575 more polar stationary phases should be considered. If HPLC separation alone could completely resolve all chemical
576 peaks, then PMF would not be needed, however in practice it is likely to help the chemical resolution of complex
577 systems.

578 These results introduce a new technique for better quantifying the instrument responses of the EESI and
579 AMS to different molecular species present in complex mixtures such as from biomass burning, urban, and/or
580 biogenic SOA.

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586 **6 Author Contributions**

587 MKS, DAD, JJJ, and PJZ designed the experiments, MKS carried them out with support from DAD, DK, SY, and
588 PCJ. ACZ, PJZ, and MPD provided the HPLC instrument support. MKS carried out all data analysis and preparation
589 of the manuscript, with contributions from all coauthors.

590 **7 Competing Interests**

591 The authors declare that they have no conflict of interest.



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