

Analytical and Bioanalytical Chemistry

Electronic Supplementary Material

Reagent-free total protein quantification of intact extracellular vesicles by attenuated total reflection Fourier transform infrared (ATR-FTIR) spectroscopy

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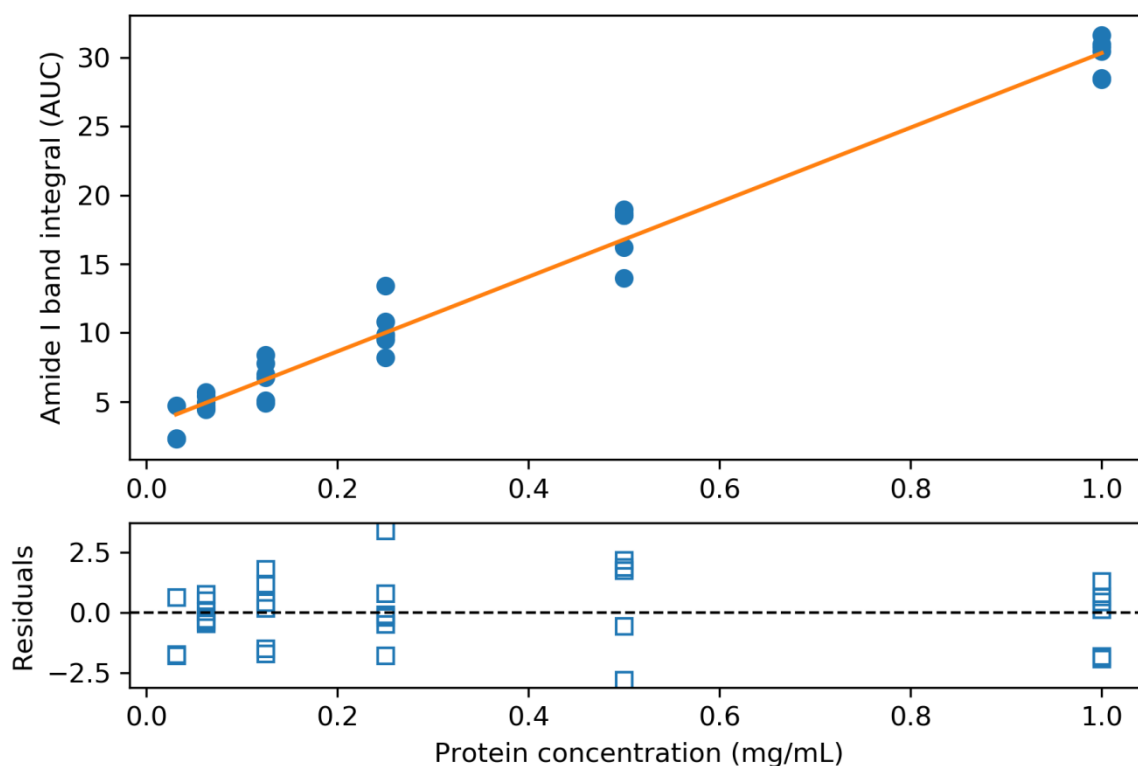


Fig. S1 Protein standard plot with the fitting residuals. The result of the F-test are listed below

Weighted residual sum of squares : $SS(w)r = 36.4696$
 Weighted sum of squares for pure error: $SS(w)e = 33.0000$
 Sum of squares due to lack of fit : $SS(w)r - SS(w)e = 3.4696$
 Mean squares due to pure error : $MS(w)e = 1.1000$
 Mean squares due to lack of fit : $MS(w)lof = 0.8674$
 Number of points in x : $n = 6$
 Number of independent measurements : $p = 6$
 F statistics : $MS(w)lof / MS(w)e = 0.7886$
 F($n-2=4$, $n(p-1)=30$) 95% percentile : 2.6896
 Fit results:
 slope: (27.1 ± 0.5) AUC/(mg/mL)
 intercept: (3.2 ± 0.2) AUC

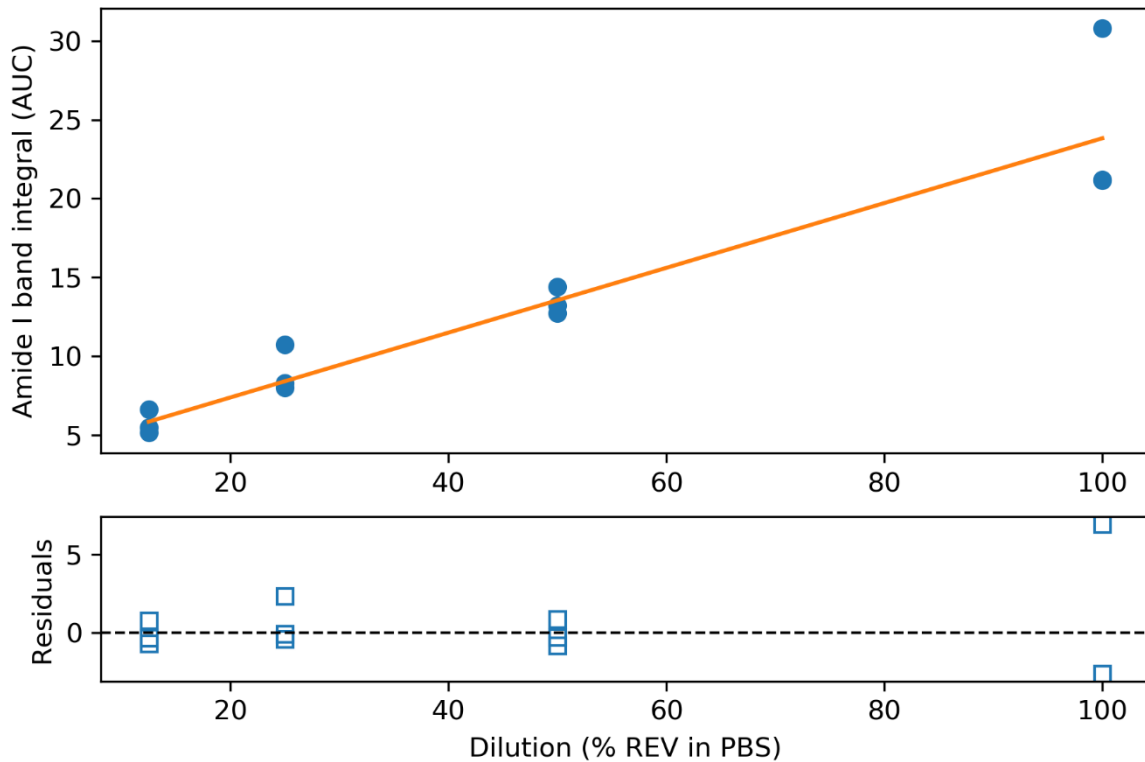


Fig. S2 Amide I AUC plot vs. red blood cell derived extracellular vesicle (REV) dilution test (presented as %REV in PBS). The result of the F-test are listed below

Weighted residual sum of squares : $SS(w)r = 12.8773$
 Weighted sum of squares for pure error: $SS(w)e = 12.0000$
 Sum of squares due to lack of fit : $SS(w)r - SS(w)e = 0.8773$
 Mean squares due to pure error : $MS(w)e = 1.5000$
 Mean squares due to lack of fit : $MS(w)lof = 0.4386$
 Number of points in x : $n = 4$
 Number of independent measurements : $p = 3$
 F statistics : $MS(w)lof / MS(w)e = 0.2924$
 F($n-2=2$, $n(p-1)=8$) 95% percentile : 4.4590
 Fit results:
 slope: (0.21 ± 0.01) AUC/(% REV in PBS)
 intercept: (3.3 ± 0.5) AUC

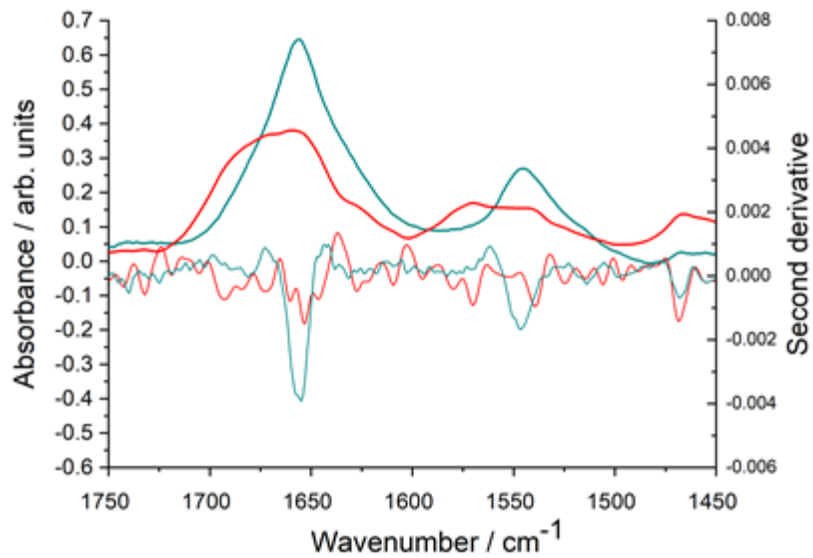


Fig. S3 Amide I and amide II spectral region of intact REV sample (green line) and after disassembling by ethanol abs. (red line). For better visualization of changes in secondary structure, the second derivative spectra are also included: while the intact REV sample contains proteins mainly with helical structure (thinner green line), after treatment with ethanol high amount of β -sheets, turns and disordered motifs of aggregated and/or denatured proteins appear (thinner red line)