## **Electronic supplementary information (ESI) to:**

# Structure of hyaluronan during acid catalyzed hydrolysis according to a kinetic study of both chain scission and disaggregation

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#### **Section A - Error Analysis**

Before comparing our  $E_a$  values to literature values we make an indication of its reliability. Since  $E_a$  was determined from the slope of a line through only 4 points, we approached this as follows. For the  $k_h$  values resulting from reducing-end analysis, we took the vertical distance from the determined data points to the fitted line in the Arrhenius plot. The largest difference in  $\ln(k_h)$  was found to be 0.04. We assumed this as a maximum error, and used it to calculate a range for the determined  $E_a$  within which, differences in  $E_a$  are insignificant. Changing the slope of the fitted line by elevating it at the beginning (at T = 70 °C) by 0.04 and lowering the end (at T = 40 °C) by 0.04 and vice versa yields a range for  $E_a$  between 94 and 100 kJ/mol for the reducing-end analysis ( $E_a = 97 \pm 3$  kJ/mol).

Based on Tømmeraas<sup>1</sup> published data points, we calculate similarly to above, that the largest difference in  $\ln(k_h)$  is 0.58, and that consequently, the  $E_a$  may range between 110 to 164 kJ/mol ( $E_a = 137 \pm 27$  kJ/mol).

For the light scattering results, we calculate similarly to above, that the largest found vertical distance of the data points to the fitted line, in units of  $\ln(k_d)$  was 0.18 resulting in an  $E_a$  range of 91 to 112 kJ/mol ( $E_a = 101 \pm 10$  kJ/mol).

#### Section B – Fitting Details Scattered Light Intensity



**Figure S1** Total scattered light intensity (*I*) vs. time measurements for 2 g/l hyaluronan being degraded at pH 1.1 and 70 °C (rhombi). Background *I* was determined by fitting a mono-exponential function + background (black line) to the  $I_{(t)}$  data points. Data from the first 3 h were excluded, so, the x axis in this figure starts at t=0 where the  $I_{(t)}$  measurement was already at t = 3h. The complete fitted function had the form:  $I = b + ae^{(-ct)}$ , in which *b* is the background with a value of 15.95 kcps (kilo counts per second)

### Reference

1. K. Tømmeraas and C. Melander, *Biomacromolecules*, 2008, 9, 1535-1540.

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