Supplementary information for

Fourier-transform infrared spectroscopy for characterization of protein chain reductions in enzymatic reactions

Ulrike Böcker[a]*, Sileshi Gizachew Wubshet[a], Diana Lindberg[a], and Nils Kristian Afseth[a]

[a]Nofima – Norwegian Institute of Food, Fisheries and Aquaculture Research, P.O. Box 210, Osloveien 1, 1431 Ås, Norway.

* Corresponding author: Ulrike Böcker

E-mail address: ulrike.bocker@nofima.no (Ulrike Böcker).

Figure S1: Score (A: salmon muscle(SF) and C: chicken muscle(CF)) and loading(B: salmon muscle(SF) and D: chicken muscle(CF)) plot from FTIR-based PCA of protein hydrolysates collected during Alcalase catalyzed protein hydrolysis. The PCA was based on an FTIR spectral region from 1800-700 cm^{-1}.
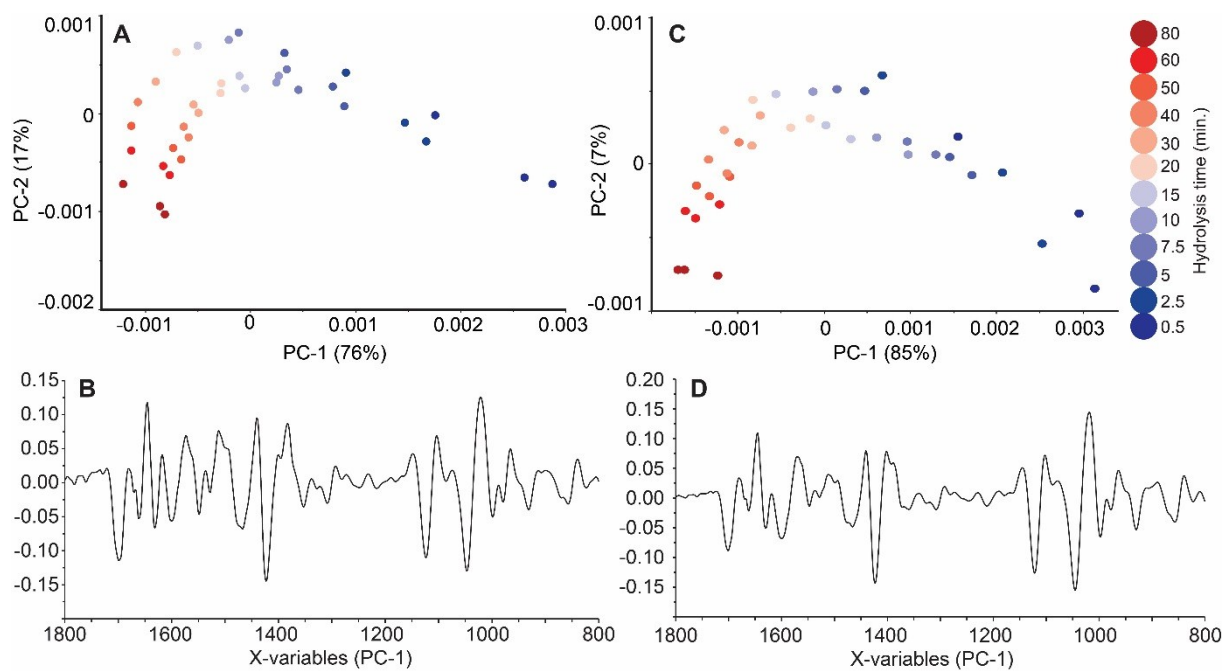
Figure S2: Score (A: salmon processing by-products(SPB) and C: mechanical chicken deboning residues (MCDR)) and loading(B: salmon processing by-products(SPB) and D: mechanical chicken deboning residues (MCDR)) plot from FTIR-based PCA of protein hydrolysates collected during Alcalase catalyzed protein hydrolysis. The PCA was based on an FTIR spectral region from 1800-700 cm^{-1}.
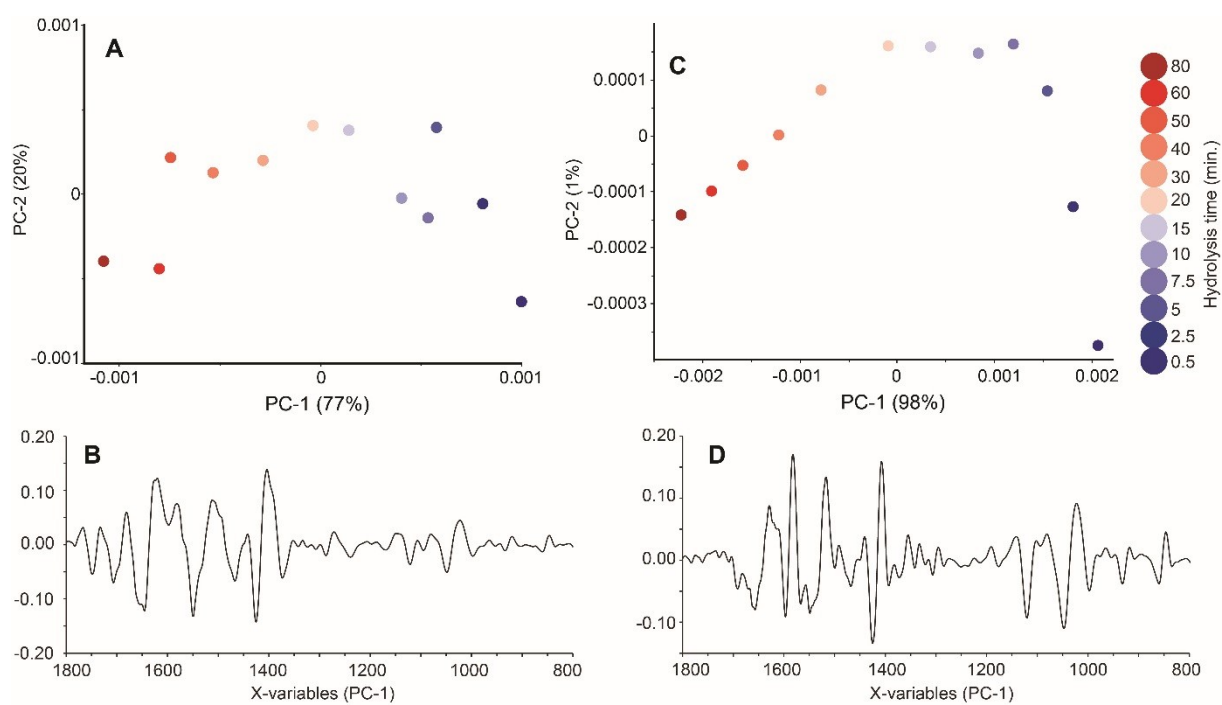
Figure S3: Exemplary EMSC-corrected absorbance spectra of hydrolysate of MCDR from 4 hydrolysis time points (0.5, 10, 40, and 80 min). Region a and b highlight bands that display ratio change with increasing hydrolysis time.