

Title:**How food protein structure can modulate the protein digestion behaviour:
Evaluation by nutritional peptidomics****Authors & affiliations:**

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Abstract: (Your abstract must use **Normal style** and must fit in this box. Your abstract should be no longer than 300 words. The box will 'expand' over 2 pages as you add text/diagrams into it.)

This study aimed to investigate the impact of protein aggregate structure on the nutritional value of proteins, and especially on the extent of digestion, the nature and amount of peptides released. Ovalbumin was chosen as a model protein source. A range of four typical aggregate structures, from linear to spherical-agglomerated, were obtained after heating under different combinations of pH and ionic strength. The non-aggregated and aggregated ovalbumins were digested using an *in vitro* digestion model that simulated gastrointestinal digestion. The extent of digestion was determined based on the disappearance of intact ovalbumin and the appearance of soluble peptides. The peptide profile of the digests was analyzed using LC-MS/MS.

The extent of hydrolysis differed according to the aggregate structure with linear aggregates being more extensively hydrolyzed than the spherical aggregates. The results suggest that the surface area to volume ratio, and probably the degree of unfolding of its constituent protein before ingestion are the major influencing criteria. Ovalbumin aggregation appeared to render a number of peptide bonds accessible to digestive proteases, whereas these bonds were not accessible in the native ovalbumin; moreover, cleavage sites appeared to be specific depending on the structure of aggregates (fig.1). Nutritional peptidomics analysis by multivariate statistical approaches made it possible to connect the aggregate structure and the profile of generated peptides. For instance, it was possible to demonstrate that bioactive peptides were significantly promoted after digestion of spherical and spherical-agglomerated aggregates.

This work highlights the existing links between food structures resulting from technological processes and their breakdown during the digestive process. Such results imply that a fine tuning of unfolding and aggregation conditions can be used for targeted structuring that can lead to an improvement of the nutritional quality of food proteins.

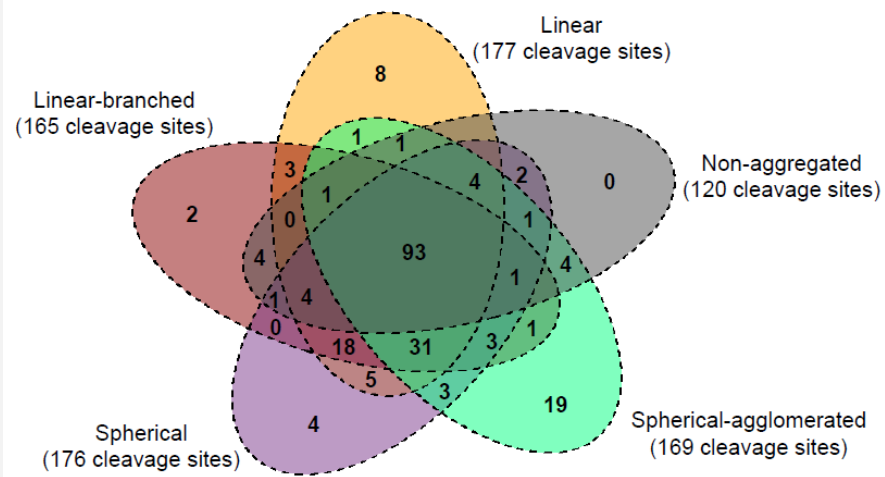


Figure 1 - Visualization of common and specific cleavage sites of the different ovalbumin aggregate structures