## Supplementary data



Figure S1. Influence of bromelain on the protein network attributes. Flour-water-systems with increasing concentrations of bromelain were analysed by CLSM followed by PNA; a) lacunarity, b) branching rate, c) protein width, d) average protein length, e) end-point rate and f) CLSM image of an entirely destroyed protein polymer structure by proteolysis (scale $215 \times 215 \mu \mathrm{~m}$, BRN $6100 \mathrm{mg} / \mathrm{kg}$ flour). Means are shown with standard error ( $\mathrm{n}=24$ ).


Figure S2. Influence of potassium bromate on the protein network attributes. Flour-water-systems with increasing concentrations of potassium bromate were analysed by CLSM followed by PNA; a) lacunarity, b) branching rate, c) protein width, d) average protein length, e) end-point rate and f) CLSM image (scale $215 \times 215 \mu \mathrm{~m}, \mathrm{KBrO} 3120$ $\mathrm{mg} / \mathrm{kg}$ flour). Means are shown with standard error ( $\mathrm{n}=24$ ).


Figure S3. Influence of rapeseed oil on the protein network attributes. Flour-water-systems with increasing concentrations of rapeseed oil were analysed by CLSM followed by PNA; a) lacunarity, b) branching rate, c) protein width, d) average protein length, e) end-point rate and f) CLSM image (scale $215 \times 215 \mu \mathrm{~m}$, ROI $50 \mathrm{~g} / 100 \mathrm{~g}$ flour). Means are shown with standard error $(\mathrm{n}=24)$.


Figure S4. Influence of shortening on the protein network attributes. Flour-water-systems with increasing concentrations of shortening were analysed by CLSM followed by PNA; a) lacunarity, b) branching rate, c) protein width, d) average protein length, e) end-point rate and f) CLSM image (scale $215 \times 215 \mu \mathrm{~m}$, SHO $50 \mathrm{~g} / 100 \mathrm{~g}$ flour). Means are shown with standard error $(\mathrm{n}=24)$.


Figure S5. Influence of a reduced hydration level on the protein network attributes. Flour-water-systems with decreasing water hydration levels were analysed by CLSM followed by PNA; a) lacunarity, b) branching rate, c) protein width, d ) average protein length, e) end-point rate and f) CLSM image (scale $215 \times 215 \mu \mathrm{~m}$, RHL $45.85 \mathrm{ml} / 100$ g flour). Means are shown with standard error ( $\mathrm{n}=24$ ).

