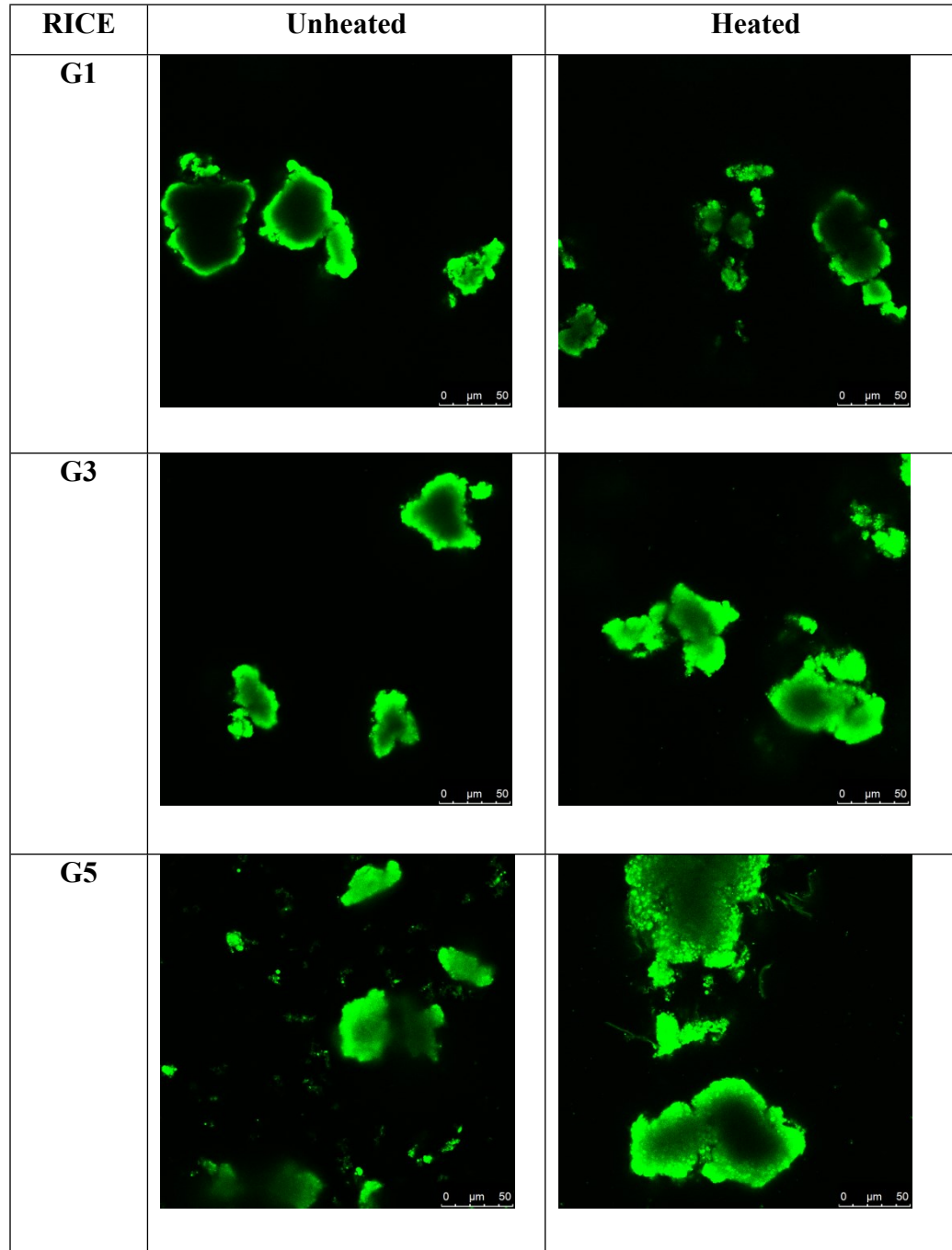
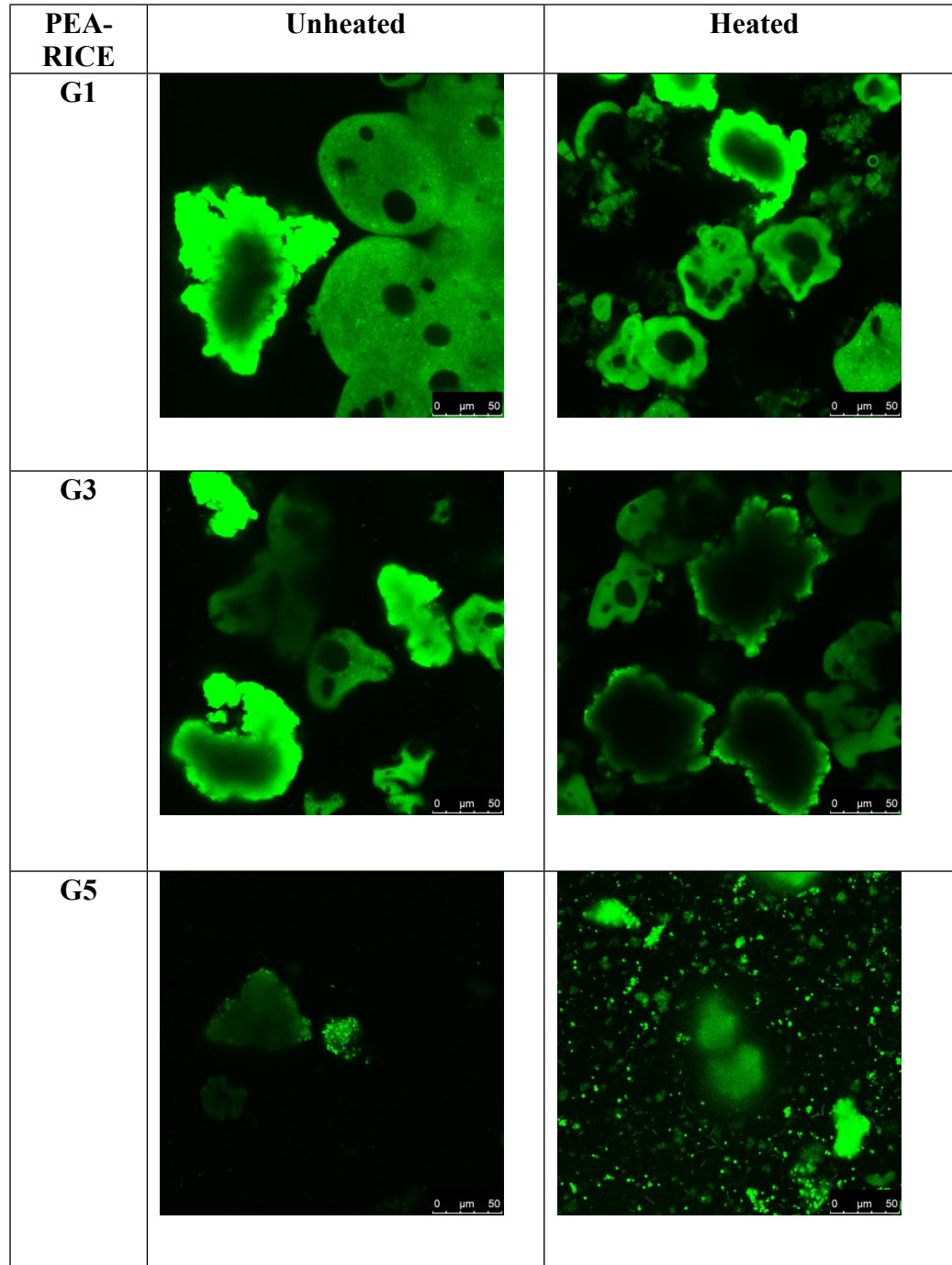


**Supplementary Figure 1.** Microstructure (confocal laser scanning microscopy, right hand side) images of digesta for Pea Protein isolate (PPI) suspensions (5% protein, w/w) dispersed at room temperature (first row) or heated at 90°C for 15 min (second row). Different gastric end point shown: G1 (10.72 min), G3 (32.1 min), G5 (53.53 min). Scale bars: 50  $\mu\text{m}$ .

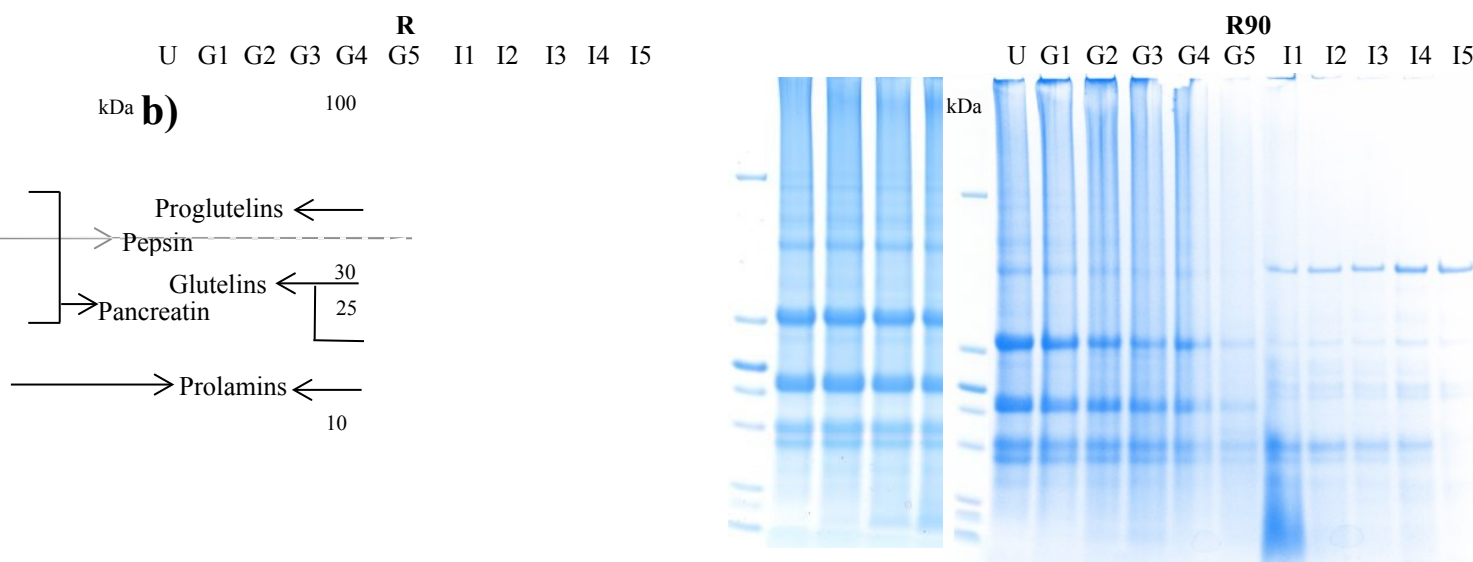
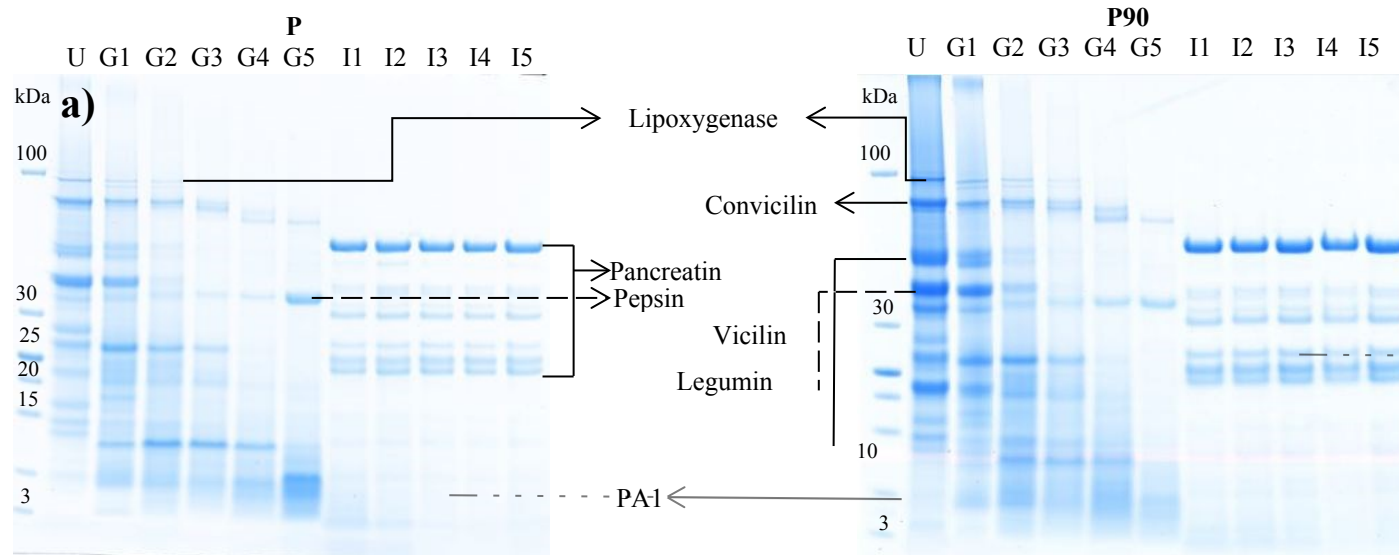


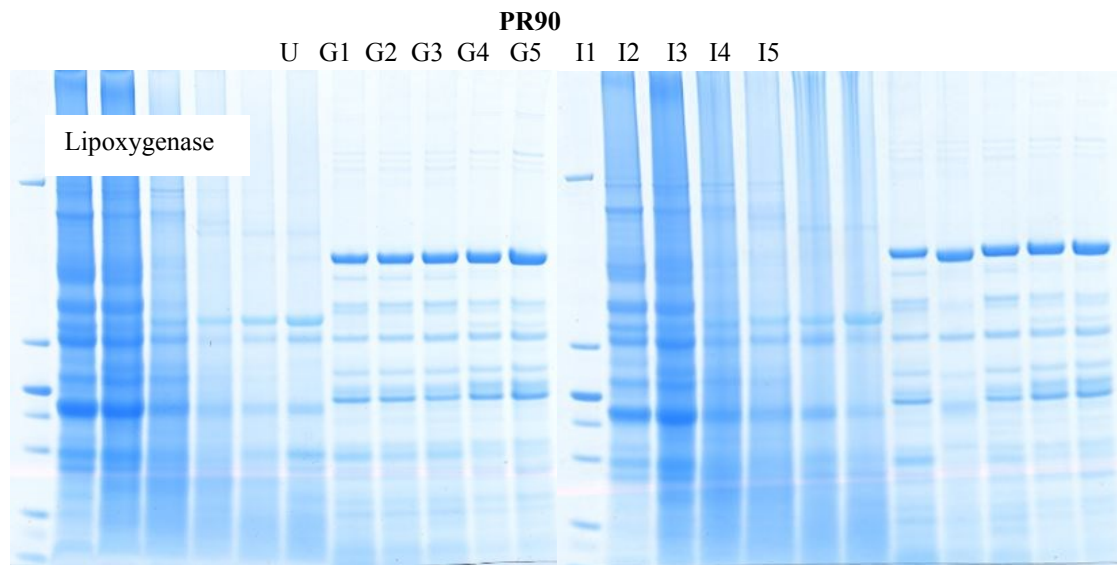
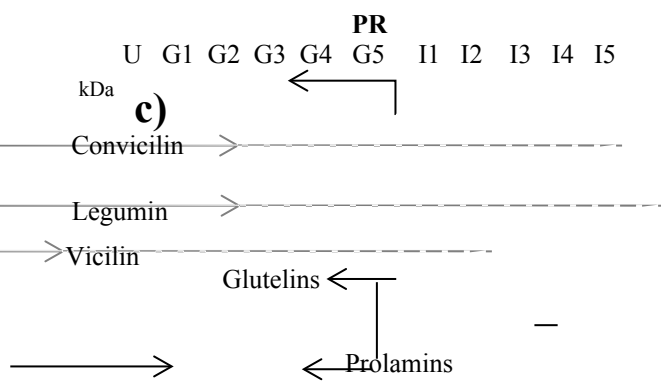
**Supplementary Figure 2.** Microstructure (confocal laser scanning microscopy, right hand side) images of digesta for Rice Protein isolate (RPI) suspensions (5% protein, w/w) dispersed at room temperature (first row) or heated at 90°C for 15 min (second row). Different gastric end point shown: G1 (10.72 min), G3 (32.1 min), G5 (53.53 min). Scale bars:50  $\mu\text{m}$ .



**Supplementary Figure 3.** Microstructure (confocal laser scanning microscopy, right hand side) images of digesta for the mixture of Pea and Rice Protein isolate suspensions (5% protein, w/w) dispersed at room temperature (first row) or heated at 90°C for 15 min (second row). Different gastric end point shown: G1 (10.72 min), G3 (32.1 min), G5 (53.53 min). Scale bars: 50  $\mu\text{m}$ .

## Comparison of heated and unheated samples by gel Electrophoresis





**Supplementary Figure 4.** Comparison of SDS PAGE profiles of protein dispersions (5%, w/w): **a)** pea room temperature (P), pea 90°C (P90). **b)** rice room temperature (R), rice 90°C (R90) and **c)** their blends pea-rice 2:1, room temperature (PR) and 90°C (PR90). U: undigested samples, Gastric points: GE1 (10.72 min), GE2 (21.45 min), GE3, (32.17 min), GE4 (42.9 min), GE5 (53.62 min). Intestinal endpoints taken after 15 min of digestion: I1 (following G1), I2 (following G2), I3 (following G3), I4 (following G4), I5 (following G5).

Statistical results obtained by applying two-way Manova on SEC-HPLC molecular weight distribution data

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Multivariate Tests<sup>a</sup>

Effect		Value	F	Hypothesis df	Error df	Sig.	Partial Eta Squared
Intercept	Wilks' Lambda	,005	8893,462 <sup>b</sup>	2,000	83,000	,000	,995
Treatment	Wilks' Lambda	,834	8,268 <sup>b</sup>	2,000	83,000	,001	,166
Source	Wilks' Lambda	,078	106,874 <sup>b</sup>	4,000	166,000	,000	,720
Timepoints	Wilks' Lambda	,004	208,111 <sup>b</sup>	12,000	166,000	,000	,938
Treatment*Source	Wilks' Lambda	,809	4,639 <sup>b</sup>	4,000	166,000	,001	,101
Treatment*Timepoints	Wilks' Lambda	,498	5,761 <sup>b</sup>	12,000	166,000	,000	,294
Source*Timepoints	Wilks' Lambda	,038	28,609 <sup>b</sup>	24,000	166,000	,000	,805
Treatment*Source*Timepoints	Wilks' Lambda	,367	4,505 <sup>b</sup>	24,000	166,000	,000	,394

a. Design: Intercept + Treatment + Source + Timepoints + Treatment \* Source + Treatment \* Timepoints + Source \* Timepoints + Treatment \* Source \* Timepoints

b. Exact statistic

c. The statistic is an upper bound on F that yields a lower bound on the significance level.

**Supplementary Table 1.** Statistical significance by effect of the factors and their interactions using Wilk's Lamda. Factor "Treatment" contains two levels (room temperature and heated), "Source" contains three (pea, rice and blend) and "Timepoints" has seven levels (undigested, G1-G5 and I1).

#### Tests of Between-Subjects Effects

Source	Dependent Variable	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	Mw_Big	5,846 <sup>a</sup>	41	,143	52,734	,000	,963

	Mw_Medium	5,359 <sup>b</sup>	41	,131	36,527	,000	,947
	Mw_Small	6,776 <sup>c</sup>	41	,165	71,682	,000	,972
Intercept	Mw_Big	4,050	1	4,050	1,498,126	,000	,947
	Mw_Medium	19,622	1	19,622	5,483,138	,000	,985
	Mw_Small	22,874	1	22,874	9,921,439	,000	,992
Treatment	Mw_Big	,045	1	,045	16,718	,000	,166
	Mw_Medium	,026	1	,026	7,366	,008	,081
	Mw_Small	,003	1	,003	1,095	,298	,013
Source	Mw_Big	1,228	2	,614	227,188	,000	,844
	Mw_Medium	,565	2	,282	78,893	,000	,653
	Mw_Small	,403	2	,201	87,350	,000	,675
Timepoints	Mw_Big	2,392	6	,399	147,454	,000	,913
	Mw_Medium	4,015	6	,669	186,985	,000	,930
	Mw_Small	4,833	6	,805	349,367	,000	,961
Treatment * Source	Mw_Big	,027	2	,014	5,017	,009	,107
	Mw_Medium	,070	2	,035	9,817	,000	,189
	Mw_Small	,010	2	,005	2,187	,119	,050
Treatment * Timepoints	Mw_Big	,103	6	,017	6,322	,000	,311
	Mw_Medium	,125	6	,021	5,806	,000	,293
	Mw_Small	,075	6	,012	5,398	,000	,278
Source * Timepoints	Mw_Big	1,842	12	,154	56,782	,000	,890
	Mw_Medium	,392	12	,033	9,128	,000	,566
	Mw_Small	1,355	12	,113	48,971	,000	,875
Treatment * Source * Timepoints	Mw_Big	,208	12	,017	6,409	,000	,478
	Mw_Medium	,167	12	,014	3,880	,000	,357
	Mw_Small	,098	12	,008	3,548	,000	,336
Error	Mw_Big	,227	84	,003			
	Mw_Medium	,301	84	,004			
	Mw_Small	,194	84	,002			

a. R Squared = ,963 (Adjusted R Squared = ,944)

b. R Squared = ,947 (Adjusted R Squared = ,921)

c. R Squared = ,972 (Adjusted R Squared = ,959)

**Supplementary Table 2.** Statistical differences in the means of response variables according to individual factors and their interactions. Response variable “Mw\_Big” corresponds for proteins and polypeptides in the range of 90-15 kDa, “Mw\_Medium” for polypeptides between 15-2 kDa and “Mw\_Small” for peptides below 2 kDa.

**Mw\_Medium**

Tukey HSD<sup>a,b</sup>

**Mw\_Big**

Tukey HSD<sup>a,b</sup>

Source	N	Subset		
		1	2	3
R	42	,04804		
PR	42		,20363	
P	42			,28621
Sig.		1,000	1,000	1,000

Means for groups in homogeneous subsets are displayed.

Based on observed means.

The error term is Mean Square(Error) = ,003.

a. Uses Harmonic Mean Sample Size = 42,000.

b. Alpha = ,05.

Source	N	Subset	
		1	2
P	42	,30059	
PR	42		,43220
R	42		,45110
Sig.		1,000	,321

Means for groups in homogeneous subsets are displayed.

Based on observed means.

The error term is Mean Square(Error) = ,004.

a. Uses Harmonic Mean Sample Size = 42,000.

b. Alpha = ,05.

**Mw\_Small**

Tukey HSD<sup>a,b</sup>

Source	N	Subset		
		1	2	3
PR	42	,36417		
P	42		,41320	
R	42			,50086
Sig.		1,000	1,000	1,000

Means for groups in homogeneous subsets are displayed.

Based on observed means.

The error term is Mean Square(Error) = ,002.

a. Uses Harmonic Mean Sample Size = 42,000.

b. Alpha = ,05.

**Supplementary Table 3.** Significant different means of the three Mw distribution groups (Mw\_Big: 90-15 kDa, Mw\_Medium: 15-2, Mw\_Small: 2 kDa >) between plant protein sources (P: Pea protein isolate, R: Rice protein isolate, PR: Blend of pea and rice) by Tukey's Post hoc homogenous subsets.

**Mw\_Big**

Tukey HSD<sup>a,b</sup>

Timepoints	N	Subset
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		1	2	3	4
G5	18	,03341			
G4	18	,05820			
G3	18	,08400			
G2	18		,14041		
I1	18		,16891		
G1	18			,35714	
U	18				,41299
Sig.		,065	,654	1,000	1,000

Means for groups in homogeneous subsets are displayed.

Based on observed means.

The error term is Mean Square(Error) = ,003.

a. Uses Harmonic Mean Sample Size = 18,000.

b. Alpha = ,05.

### Mw\_Medium

Tukey HSD<sup>a,b</sup>

Timepoints	N	Subset				
		1	2	3	4	5
I1	18	,00000				
U	18		,32684			
G1	18			,41456		
G5	18			,42859	,42859	
G4	18				,47500	
G3	18					,53782
G2	18					,57959
Sig.		1,000	1,000	,992	,244	,365

Means for groups in homogeneous subsets are displayed.

Based on observed means.

The error term is Mean Square(Error) = ,004.

a. Uses Harmonic Mean Sample Size = 18,000.

b. Alpha = ,05.

### Mw\_Small

Tukey HSD<sup>a,b</sup>

Timepoints	N	Subset
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		1	2	3	4	5	6
G1	18	,22830					
U	18	,26017	,26017				
G2	18		,28000				
G3	18			,37818			
G4	18				,46681		
G5	18					,53800	
I1	18						,83109
Sig.		,428	,877	1,000	1,000	1,000	1,000

Means for groups in homogeneous subsets are displayed.

Based on observed means.

The error term is Mean Square(Error) = ,002.

a. Uses Harmonic Mean Sample Size = 18,000.

b. Alpha = ,05.

**Supplementary Table 4.** Significant different means of the three Mw distribution groups (Mw\_Big: 90-15 kDa, Mw\_Medium: 15-2, Mw\_Small: 2 kDa >) between different gastrointestinal points “Timepoints” (U: Undigested, G1-G5: Gastric emptying 1-5, I1: Intestinal point corresponding to G1) by Tukey’s Post hoc homogenous subsets.