

Figure S1. *Rhizostoma pulmo* jellyfish products obtained by the new proposed method. Ca-C: *R. pulmo* jellyfish after treatment in calcium citrate brine (a); Ca-L: *R. pulmo* jellyfish after treatment in calcium lactate brine (b); NaCl-Alum: *R. pulmo* jellyfish obtained by salt-alum traditional method (c).

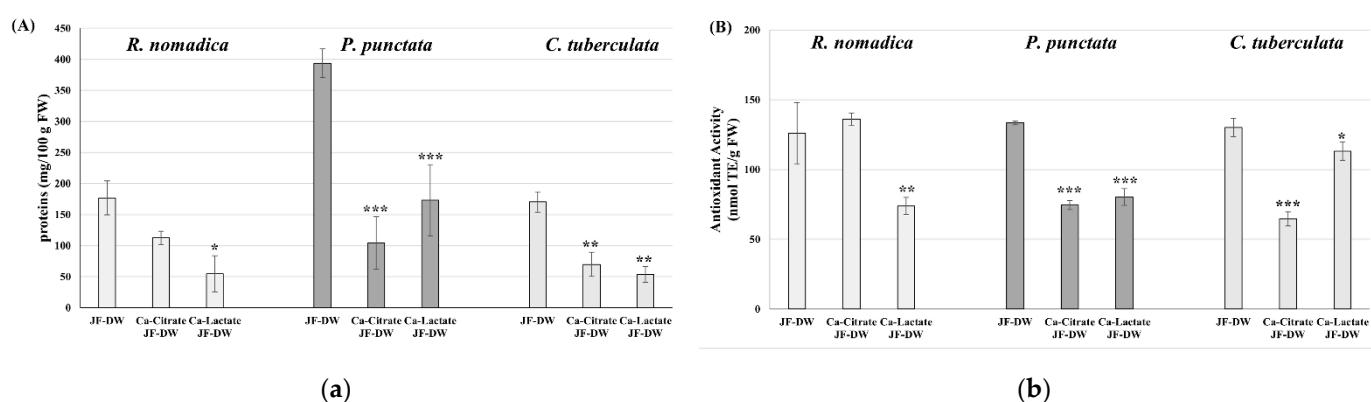


Figure S2. Proteins content (a) and Antioxidant activity (b) in *Cotylorhiza tuberculata*, *Rhopilema nomadica* and *Phyllorhiza punctata* JF-DW samples and the corresponding calcium salt treated samples (Ca-Lactate JF-DW and Ca-Citrate JF-DW). Protein contents were expressed as mg per 100 grams of fresh weight (mg/100 g FW) and antioxidant activity was expressed as nmol TE per gram of FW (nmol TE/g FW). Values are the means of three independent measurements, \pm standard deviation. ANOVA statistic test followed by Bonferroni's multiple comparison post-hoc test was used to compare each treatment with the others for each JF species.

Table S1. Microbiological analyses of JF-DW (JF transported on lab and pre-treated with drinking water) untreated and treated with brines containing different calcium salts at 5 days treatment at 4 °C (Ca-Citrate: calcium citrate; Ca-Lactate: calcium lactate). The different letters in line indicate significant differences between samples ($p < 0.05$)

Microorganisms	Medium	JF-DW					
		Untreated		Ca-Citrate		Ca-Lactate	
		Mean (CFU/g)	SD	Mean (CFU/g)	SD	Mean (CFU/g)	SD
TBC	PCA	0 (a)	0	8.75×10^1 (b)	3.54	2.90×10^2 (c)	5.66×10^1
<i>Bacillus</i> spp.	BCSA	3.00 (a)	1.05	0 (b)	0	0 (b)	0
H ₂ S-producing bacteria	IRON AGAR	0	0	0	0	0	0
Enterobacteriaceae	VRBGA	0	0	0	0	0	0
Coli-Aerogenes Bacteria	VRBA	0	0	0	0	0	0
Coagulase positive staphylococci	Baird Parker Agar	0	0	0	0	0	0
Pathogenic staphylococci	MSA	0	0	0	0	0	0
<i>Pseudomonas</i> spp.	Pseudomonas Agar	0	0	0	0	0	0
<i>Vibrio</i> spp.	TCBSA	0	0	0	0	0	0
Yeast	DRBC	0	0	0	0	0	0
Moulds		0	0	0	0	0	0
Halophilic Bacteria	R2A	0 (a)	0	1.15×10^1 (a)	2.12	6.75×10^1 (b)	3.54
	Marine Agar	0	0	0	0	0	0
	sCMA	0	0	0	0	0	0
Halophilic Yeasts	sSDA	0	0	0	0	0	0
	R2A	0	0	0	0	0	0
	Marine Agar	0	0	0	0	0	0
Halophilic Moulds	sCMA	0	0	0	0	0	0
	sSDA	0	0	0	0	0	0
	R2A	0	0	0	0	0	0
	Marine Agar	0	0	0	0	0	0

TBC: total bacterial count at 30 °C; sCMA: saline Corn Meal Agar; sSDA: saline Sabouraud Dextrose Agar

Table S2. Microbiological analyses of JF-B (JF directly pre-treated on boat) untreated and treated with brines containing different calcium salts at 5 days treatment at 4 °C (Ca-Citrate: calcium citrate; Ca-Lactate: calcium lactate). The different letters in line indicate significant differences between samples ($p < 0.05$)

Microorganisms	Medium	JF-B					
		Untreated		Ca-Citrate		Ca-Lactate	
		Mean (CFU/g)	SD	Mean (CFU/g)	SD	Mean (CFU/g)	SD
TBC	PCA	4.60×10^1 (a)	4.58	7.50(b)	2.12	6.40×10^1 (a)	1.98×10^1
<i>Bacillus</i> spp.	BCSA	2.40×10^1 (a)	5.66	0 (b)	0	1.35×10^1 (a)	2.12
H ₂ S-producing bacteria	IRON AGAR	0	0	0	0	0	0
Enterobacteriaceae	VRBGA	0 (a)	0	0 (a)	0	1.45×10^1 (b)	8.15×10^{-1}
Coli-Aerogenes Bacteria	VRBA	0	0	0	0	0	0
Coagulase positive staphylococci	Baird Parker Agar	0	0	0	0	0	0

Pathogenic staphylococci	MSA	0	0	0	0	0	0
<i>Pseudomonas</i> spp.	<i>Pseudomonas</i> Agar	3.50 (a)	5.08 x 10 ¹	0 (b)	0	0 (b)	0
<i>Vibrio</i> spp.	TCBSA	0	0	0	0	0	0
Yeast	DRBC	0	0	0	0	0	0
Moulds		0	0	0	0	0	0
Halophilic Bacteria	R2A	7.60 x 10 ¹ (a)	7.16	0 (b)	0	0 (b)	0
	Marin Agar	0	0	0	0	0	0
	sCMA	0	0	0	0	0	0
Halophilic Yeasts	sSDA	0	0	0	0	0	0
	R2A	0 (a)	0	0 (a)	0	2.75 x 10 ¹ (b)	1.06 x 10 ¹
	Marine Agar	0	0	0	0	0	0
Halophilic Moulds	sCMA	0	0	0	0	0	0
	sSDA	0	0	0	0	0	0
	R2A	0	0	0	0	0	0
	Marine Agar	0	0	0	0	0	0

TBC: total bacterial count at 30 °C; sCMA: saline Corn Meal Agar; sSDA: saline Sabouraud Dextrose Agar

Table S3. Microbiological analyses of *Rhizostoma pulmo* JF sample washed in drinking water and then treated with NaCl-alum (Salt-Alum JF-DW). This sample was obtained after 20 days at 4 °C and 2 days air drying (as described in Material and Methods section).

Microorganisms	Medium	Mean (CFU/g)	SD
TBC	PCA	5.80x 10 ¹	3.11x10 ¹
<i>Bacillus</i> spp.	BCSA	4.15x10 ¹	1.20x10 ¹
H ₂ S-producing bacteria	IRON AGAR	0	0
Enterobacteriaceae	VRBGA	0	0
<i>Coli-Aerogenes</i> Bacteria	VRBA	0	0
Coagulase positive staphylococci	Baird Parker Agar	0	0
Pathogenic staphylococci	MSA	0	0
<i>Pseudomonas</i> spp.	<i>Pseudomonas</i> Agar	0	0
<i>Vibrio</i> spp.	TCBSA	0	0
Yeast	DRBC	1.30x10 ²	1.41x10 ¹
Moulds		0	0
Halophilic Bacteria	R2A	9.88x10 ²	2.23x10 ²
	Marine Agar	4.43x10 ²	2.49x10 ²
	sCMA	2.22x10 ²	8.20x10 ¹
Halophilic Yeasts	sSDA	5.00x10 ²	4.24x10 ²
	R2A	1.16x10 ³	6.22x10 ²
	Marine Agar	9.00x10 ²	4.24x10 ²
	sCMA	0	0
Halophilic Moulds	sSDA	0	0
	R2A	0	0
	Marine Agar	0	0

TBC: total bacterial count at 30° C; sCMA: saline Corn Meal Agar; sSDA: saline Sabouraud Dextrose Agar

Table S4. Amino acid composition of *Rhizostoma pulmo* JF fresh and untreated (Untreated JF), washed in drinking water (JF-DW), and treated with calcium citrate (Ca-Citrate JF-DW) and calcium lactate (Ca-Lactate JF-DW). Data are mean \pm Standard deviation (\pm SD) of four independent analyses. AA. amino acids; Nd. Not detected.

Amino acids	Rhizostoma pulmo samples							
	Untreated JF		JF-DW		Ca-Citrate JF-DW		Ca-Lactate JF-DW	
	Percentage per dry weight (% of dw)	Percentage of total AA	Percentage per dry weight (% of dw)	Percentage of total AA	Percentage per dry weight (% of dw)	Percentage of total AA	Percentage per dry weight (% of dw)	Percentage of total AA
Amino acids	Average \pm SD	(%)						
Taurin	0.3 \pm 0.1	5.4	0.1 \pm 0.1	0.6	0.1 \pm 0.1	0.9	0.2 \pm 0.1	1.2
Methionine sulfoxide	n.d.	-	n.d.	-	n.d.	-	n.d.	-
Hydroxyproline	0.0	-	0.1 \pm 0.1	1.2	0.2 \pm 0.2	1.3	0.2 \pm 0.2	1.1
Aspartic acid + Asparagine	0.4 \pm 0.1	5.9	0.6 \pm 0.2	6.8	1.0 \pm 0.1	6.7	1.0 \pm 0.2	6.5
Threonine	0.2 \pm 0.0	3.6	0.3 \pm 0.1	3.4	0.6 \pm 0.0	4.2	0.7 \pm 0.1	4.7
Serine	0.3 \pm 0.0	5.3	0.5 \pm 0.1	5.0	0.9 \pm 0.2	6.0	0.8 \pm 0.2	5.6
Glutamic acid + Glutamine	0.6 \pm 0.1	9.9	0.9 \pm 0.3	9.4	1.7 \pm 0.1	11.1	1.6 \pm 0.1	10.4
Proline	0.2 \pm 0.2	3.0	0.5 \pm 0.3	5.5	1.1 \pm 0.2	7.2	1.1 \pm 0.1	7.4
Glycine	0.6 \pm 0.0	9.4	1.6 \pm 0.4	17.0	2.4 \pm 0.0	15.5	2.2 \pm 0.1	14.4
Alanine	0.4 \pm 0.0	7.0	0.8 \pm 0.2	8.5	1.1 \pm 0.2	7.2	1.5 \pm 0.3	9.5
Cystine (Cys-Cys)	0.0 \pm 0.0	0.5	n.d.	-	0.0 \pm 0.1	0.3	0.1 \pm 0.1	0.4
Valine	0.3 \pm 0.0	5.0	0.4 \pm 0.1	4.0	0.8 \pm 0.0	5.1	0.8 \pm 0.0	5.3
Methionine	0.0 \pm 0.0	0.8	0.1 \pm 0.1	0.6	0.2 \pm 0.0	1.3	0.2 \pm 0.0	1.3
Isoleucine	0.2 \pm 0.0	3.8	0.3 \pm 0.1	3.2	0.5 \pm 0.0	3.3	0.5 \pm 0.0	3.0
Leucine	0.3 \pm 0.0	5.8	0.4 \pm 0.1	4.5	0.7 \pm 0.0	4.6	0.7 \pm 0.0	4.4
Tyrosine	0.3 \pm 0.1	5.8	0.3 \pm 0.1	3.7	0.5 \pm 0.1	3.3	0.4 \pm 0.1	2.9
Phenylalanine	0.4 \pm 0.1	7.4	0.4 \pm 0.1	4.8	0.7 \pm 0.1	4.5	0.7 \pm 0.2	4.5
Histidine	0.2 \pm 0.0	2.9	0.3 \pm 0.1	3.5	0.4 \pm 0.0	2.9	0.5 \pm 0.1	2.9
Hydroxylsine	n.d.	-	n.d.	-	n.d.	-	n.d.	-
Lysine	0.4 \pm 0.0	7.3	0.5 \pm 0.1	5.5	0.8 \pm 0.0	5.1	0.8 \pm 0.0	5.1
Tryptophan	n.d.	-	n.d.	-	n.d.	-	n.d.	-

Arginine	0.7 ± 0.2	11.1	1.2 ± 0.4	12.7	1.5 ± 0.4	9.8	1.4 ± 0.3	9.2
Ammonia	0.1 ± 0.0	1.7	0.1 ± 0.0	1.5	0.2 ± 0.0	1.6	0.2 ± 0.0	1.5
Total (AA only)	6.0 ± 0.1	100.0	9.2 ± 2.1	100.0	15.4 ± 0.7	100.0	15.3 ± 0.8	100.0
Total (AA + ammonia)	6.1 ± 0.1		9.3 ± 2.1		15.7 ± 0.7		15.5 ± 0.8	

Table S5. Microbiological analyses of *Cotylorhiza tuberculata* JF sample washed with drinking water (JF-DW) and treated with brines containing calcium salts (Ca-Citrate: calcium citrate; Ca-Lactate: calcium lactate). The different letters in line indicate significant differences between samples ($p < 0.05$)

<i>Cotylorhiza tuberculata</i>							
Microorganisms	Medium	JF-DW		Ca-Citrate		Ca-Lactate	
		Mean (CFU/g)	SD	Mean (CFU/g)	SD	Mean (CFU/g)	SD
TBC	PCA	0	0	0	0	0	0
<i>Bacillus</i> spp.	BCSA	0	0	0	0	0	0
H ₂ S-producing bacteria	IRON AGAR	0	0	0	0	0	0
Enterobacteriaceae	VRBGA	0	0	0	0	0	0
<i>Coli-Aerogenes</i> Bacteria	VRBA	0	0	0	0	0	0
Coagulase positive staphylococci	Baird Parker Agar	0	0	0	0	0	0
<i>Pseudomonas</i> spp.	Pseudomonas Agar	0	0	0	0	0	0
Yeasts	DRBC	0	0	0	0	0	0
Moulds		0 (a)	0	0 (a)	0	3.60x10 ¹ (b)	1.69 x10 ¹
Halophilic Bacteria	R2A	0 (a)	0	2.80x 10 ¹ (b)	8.48	1.60x10 ¹ (b)	1.13 x10 ¹
	Marine Agar	0 (a)	0	1.20 x10 ¹ (a)	2.82	3.21 x10 ¹ (b)	1.56 x10 ¹
Halophilic Yeasts	sCMA	0 (a)	0	0 (a)	0	2.53 x10 ¹ (b)	1.75 x10 ¹
	sSDA	0 (a)	0	0 (a)	0	3.20x 10 ¹ (b)	1.18 x10 ¹
	R2A	0 (a)	0	0 (a)	0	1.20 x10 ¹ (b)	5.65
	Marine Agar	0	0	0	0	0	0
Halophilic Moulds	sCMA	0	0	0	0	0	0
	sSDA	0	0	0	0	0	0
	R2A	0	0	0	0	0	0
	Marine Agar	0	0	0	0	0	0

TBC: total bacterial count at 30°C; sCMA: saline Corn Meal Agar; sSDA: saline Sabouraud Dextrose Agar

Table S6. Microbiological analyses of *Rhopilema nomadica* JF sample washed with drinking water (JF-DW) and treated with brines containing calcium salts (Ca-Citrate: calcium citrate; Ca-Lactate: calcium lactate). The different letters in line indicate significant differences between samples ($p < 0.05$)

<i>Rhopilema nomadica</i>							
Microorganisms	Medium	JF-DW		Ca-Citrate		Ca-Lactate	
		Mean (CFU/g)	SD	Mean (CFU/g)	SD	Mean (CFU/g)	SD
TBC	PCA	4.20×10^1 (a)	1.27×10^1	3.60×10^1 (a)	5.74	0 (b)	0
<i>Bacillus</i> spp.	BCSA	0 (a)	0	2.40×10^1 (b)	7.48	0 (a)	0
H ₂ S-producing bacteria	IRON AGAR	0	0	0	0	0	0
Enterobacteriaceae	VRBGA	0	0	0	0	0	0
<i>Coli-Aerogenes</i> Bacteria	VRBA	0	0	0	0	0	0
Coagulase positive staphylococci	Baird Parker Agar	0	0	0	0	0	0
<i>Pseudomonas</i> spp.	Pseudomonas Agar	0	0	0	0	0	0
Yeasts	DRBC	0	0	0	0	0	0
Moulds		2.40×10^1 (a)	6.45	0 (b)	0	0 (b)	0
Halophilic Bacteria	R2A	0 (a)	0	1.02×10^2 (b)	1.48×10^1	0 (a)	0
	Marine Agar	0 (a)	0	7.80×10^1 (b)	4.24	1.60×10^1 (a)	7.85
Halophilic Yeasts	sCMA	0	0	0	0	0	0
	sSDA	0	0	0	0	0	0
	R2A	7.20×10^1 (a)	6.52	0 (b)	0	0 (b)	0
	Marine Agar	9.60×10^1 (a)	8.13	2.46×10^1 (b)	9.13	0 (c)	0
Halophilic Moulds	sCMA	0	0	0	0	0	0
	sSDA	0	0	0	0	0	0
	R2A	0	0	0	0	0	0
	Marine Agar	0	0	0	0	0	0

TBC: total bacterial count at 30 °C; sCMA: saline Corn Meal Agar; sSDA: saline Sabouraud Dextrose Agar

Table S7. Microbiological analyses of *Phyllorhiza punctata* JF sample washed with drinking water (JF-DW) and treated with brines containing calcium salts (Ca-Citrate: calcium citrate; Ca-Lactate: calcium lactate). The different letters in line indicate significant differences between samples ($p < 0.05$)

<i>Phyllorhiza punctata</i>							
Microorganisms	Medium	JF-DW		Ca-Citrate		Ca-Lactate	
		Mean (CFU/g)	SD	Mean (CFU/g)	SD	Mean (CFU/g)	SD
TBC	PCA	1.08 × 10 ² (a)	8.74	5.10 × 10 ¹ (b)	2.34	7.12 × 10 ¹ (b)	1.10 × 10 ¹
<i>Bacillus</i> spp.	BCSA	1.20 × 10 ¹ (a)	6.98	1.20 × 10 ¹ (a)	3.61	0 (b)	0
H ₂ S-producing bacteria	IRON AGAR	1.80 × 10 ¹ (a)	4.26	0 (b)	0	0 (b)	0
Enterobacteriaceae	VRBGA	0	0	0	0	0	0
<i>Coli-Aerogenes</i> Bacteria	VRBA	0	0	0	0	0	0
Coagulase positive staphylococci	Baird Parker Agar	0	0	0	0	0	0
<i>Pseudomonas</i> spp.	Pseudomonas Agar	0	0	0	0	0	0
Yeasts	DRBC	0	0	0	0	0	0
Moulds		0	0	0	0	0	0
Halophilic Bacteria	R2A	1.68 × 10 ² (a)	5.09 × 10 ¹	1.50 × 10 ¹ (b)	2.12	2.46 × 10 ² (a)	3.81 × 10 ¹
	Marine Agar	6.60 × 10 ¹ (a)	4.08	2.70 × 10 ¹ (b)	2.44	1.02 × 10 ² (c)	1.27 × 10 ¹
Halophilic Yeasts	sCMA	0 (a)	0	9.05 (b)	2.32	0 (a)	0
	sSDA	0	0	0	0	0	0
	R2A	0	0	0	0	0	0
	Marine Agar	0	0	0	0	0	0
Halophilic Moulds	sCMA	0	0	0	0	0	0
	sSDA	0 (a)	0	1.20 × 10 ¹ (b)	4.06	0 (a)	0
	R2A	0	0	0	0	0	0
	Marine Agar	0 (a)	0	1.50 × 10 ¹ (b)	2.16	0 (a)	0

TBC: total bacterial count at 30°C; sCMA: saline Corn Meal Agar; sSDA: saline Sabouraud Dextrose Agar

Table S8. Texture, salinity and pH values of *Cotylorhiza tuberculata*, *Rhopilema nomadica* and *Phyllorhiza punctata* JF samples washed with drinking water (JF-DW) and treated with brines containing calcium salts at 5 days treatment (Ca-Citrate: calcium citrate; Ca-Lactate: calcium lactate). The different letters in line indicate significant differences between samples ($p < 0.05$)

	Texture (N)			Salinity (% NaCl)			pH		
	JF-DW	Ca-Citrate	Ca- Lactate	JF-DW	Ca-Citrate	Ca- Lactate	JF-DW	Ca-Citrate	Ca- Lactate
<i>C. tuberculata</i>	-16.6 ± 4 (a)	-34.9 ± 5 (b)	-29.6 ± 8 (b)	2	1	1.2	7.9	7.1	7.2
<i>R. nomadica</i>	-63.3 ± 9 (a)	-27.2 ± 3 (b)	-30.7 ± 9 (b)	3.5	1	1	7.9	7	6
<i>P. punctata</i>	-47.2 ± 9 (a)	-24.3 ± 3 (b)	-22.7 ± 8 (b)	1.2	0.5	1	7.9	6	6.8

Table S9. Comparison of the fatty acid composition of and *Rhopilema nomadica*, *Phyllorhiza punctata* and *Cotylorhiza tuberculata* JF samples washed with drinking water (JF-DW) and treated with brines containing calcium salts at 5 days treatment (Ca-Citrate: calcium citrate; Ca-Lactate: calcium lactate). Fatty acid composition data are expressed as percentage of the total fatty acids ± SD.

	Fatty acids composition (%)								
	<i>R. nomadica</i> JF-DW			<i>P. punctata</i> JF-DW			<i>C. tuberculata</i> JF-DW		
	JF-DW	Ca-Citrate	Ca-Lactate	JF-DW	Ca-Citrate	Ca-Lactate	JF-DW	Ca-Citrate	Ca-Lactate
Saturated FA (SFA)									
Myristic acid C_{14:0}	6.6 ± 0.7	—	9.2 ± 0.2	10.5 ± 1.1	8.4 ± 0.8	7.7 ± 0.8	—	—	—
Pentadecanoic acid C_{15:0}	—	—	—	2 ± 0.4	—	—	—	—	—
Palmitic acid C_{16:0}	32.4 ± 4.0	44.2 ± 4.5	38.8 ± 0.4	28.3 ± 3.0	20.9 ± 2.0	20.1 ± 2.0	44.7 ± 4.5	43.2 ± 4.0	41.2 ± 3.3
Margaric acid C_{17:0}	2.6 ± 0.2	1.6 ± 0.2	—	1.4 ± 0.2	2.5 ± 0.2	2.3 ± 0.2	—	—	—
Stearic acid C_{18:0}	26.0 ± 3.9	37.6 ± 4.0	29.8 ± 2.8	15.2 ± 3.5	14.6 ± 1.5	14.2 ± 2.7	34.4 ± 4.0	38.8 ± 3.8	35.2 ± 3.4
Nonadecanoic acid C_{19:0}	—	—	—	—	—	—	—	13.2 ± 1.3	—
Arachidic acid C_{20:0}	2.2 ± 0.2	5.1 ± 0.5	1.4 ± 0.2	—	1.5 ± 0.2	1.2 ± 0.3	—	—	1.9 ± 0.2
Total SFA	69.8 ± 7.0	88.5 ± 8.9	79.2 ± 8.0	57.3 ± 5.7	48.0 ± 4.8	45.5 ± 4.5	79.1 ± 8.1	95.2 ± 8.2	78.3 ± 7.8
Monounsaturated FA (MUFA)									
Palmitoleic acid C_{16:1} (ω7)	—	—	—	5.0 ± 0.5	4.4 ± 0.5	4.0 ± 0.4	—	—	—
Oleic acid C_{18:1} (ω9)	3.1 ± 0.2	3.3 ± 0.4	3.7 ± 0.4	4.3 ± 0.3	4.8 ± 0.5	—	—	—	—
Isooleic acid C_{18:1} trans-10	2.3 ± 0.4	—	1.2 ± 0.1	—	—	6.7 ± 0.3	—	—	8.6 ± 0.9
Vaccenic acid C_{18:1} cis-11 (ω7)	—	—	—	1.5 ± 0.2	2.2 ± 0.2	—	—	—	—

Total MUFA	5.4 ± 0.5	3.3 ± 0.4	4.9 ± 0.5	10.8 ± 0.3	11.4 ± 0.7	10.7 ± 0.3	0	0	8.6 ± 0.9
Polyunsaturated FA (PUFA)									
Linoleic acid C_{18:2} (ω6)	2.3 ± 0.3	—	6.9 ± 0.7	4.8 ± 0.5	2.9 ± 0.3	2.8 ± 0.3	—	—	—
Isolinoleic acid C_{18:2 trans 8,11}	—	—	—	—	—	—	—	—	11.1 ± 1.1
Linolenic acid C_{18:3} (ω3)	2.7 ± 0.4	—	—	3.3 ± 0.3	4.2 ± 0.4	4.9 ± 0.5	—	—	—
Stearidonic acid C_{18:4} (ω3)	2.0 ± 0.2	—	—	3.8 ± 0.4	4.2 ± 0.4	4.0 ± 0.4	7.5 ± 0.8	—	—
Eicosadienoic acid C_{20:2} (ω6)	—	—	—	—	—	0.6 ± 0.2	—	—	—
Arachidonic acid C_{20:4} (ω6)	7.4 ± 0.7	4.6 ± 0.5	5.0 ± 0.4	3.8 ± 0.4	7.9 ± 0.5	5.5 ± 0.6	4.4 ± 0.3	2.0 ± 0.1	2.0 ± 0.2
Eicosapentaenoic acid C_{20:5} (ω3)	5.6 ± 0.6	1.5 ± 0.2	1.0 ± 0.5	8.5 ± 0.6	9.5 ± 0.8	13.2 ± 1.0	4.1 ± 0.3	1.9 ± 0.2	—
Docosapentaenoic acid C_{22:5} (ω3)	0.9 ± 0.1	—	—	0.9 ± 0.1	1.6 ± 0.1	1.8 ± 0.2	—	—	—
Docosahexaenoic acid C_{22:6} (ω3)	4.2 ± 0.4	2.1 ± 0.2	3.0 ± 0.3	6.8 ± 0.6	10.2 ± 0.2	10.9 ± 1.1	5.0 ± 0.5	0.9 ± 0.1	—
Total PUFA	25.0 ± 2.6	8.2 ± 0.8	15.9 ± 1.3	34.6 ± 3.2	40.6 ± 4.1	43.8 ± 4.4	20.9 ± 0.8	4.8 ± 0.5	13.1 ± 1.3
Σω6	9.6	4.6	11.9	8.6	10.8	9.0	4.4	2	2
Σω3	15.4	3.7	4.0	23.2	29.8	34.8	16.5	2.7	-
ω6/ω3	0.6	1.2	3.0	0.4	0.4	0.3	0.3	0.7	-
Total Lipids (%DW)	26.5	72.0	68.6	83.8	56.5	72.4	29.0	12.5	4.0