

Supplementary Materials

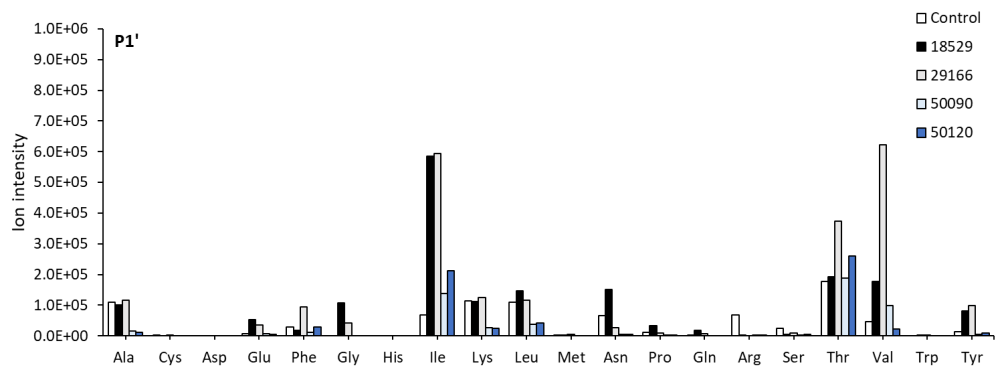
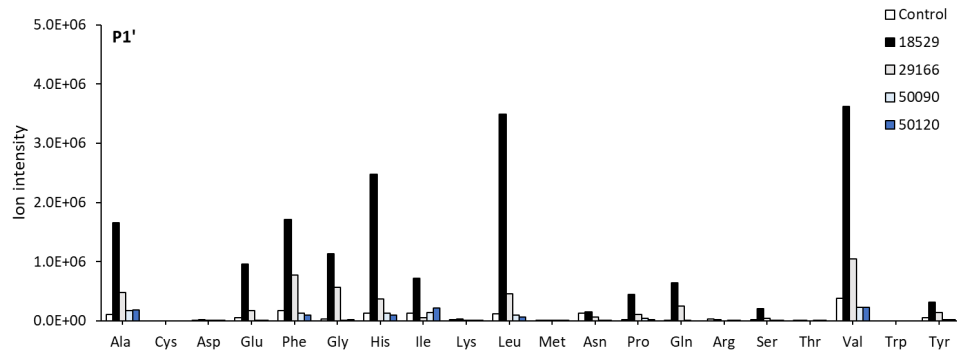
Table S1. Bacterial growth of the four studied strains

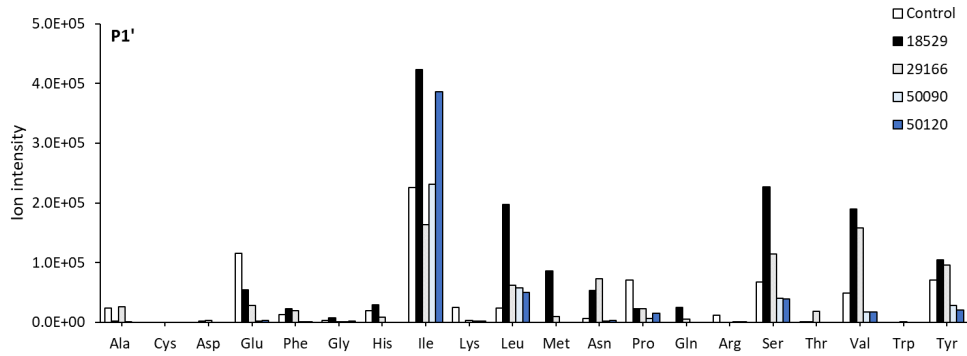
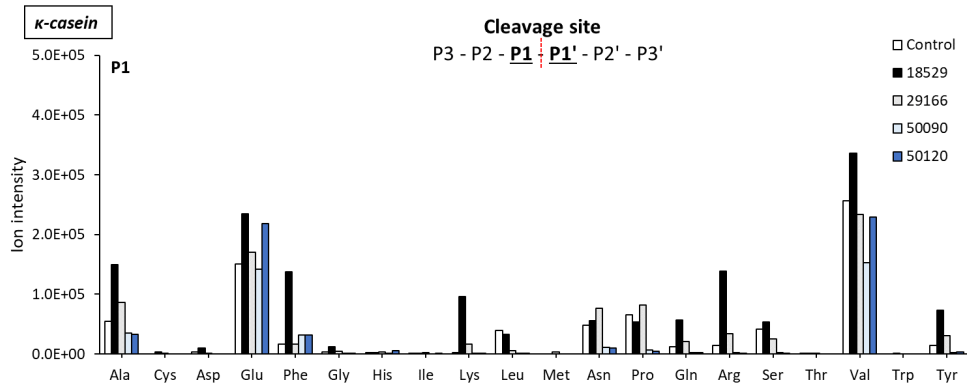
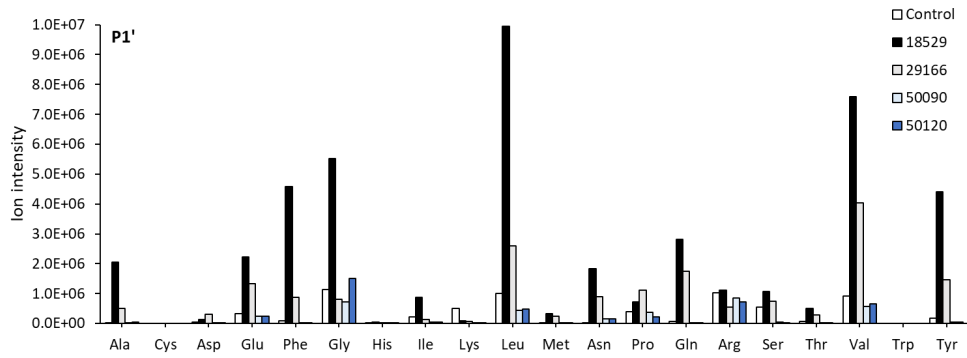
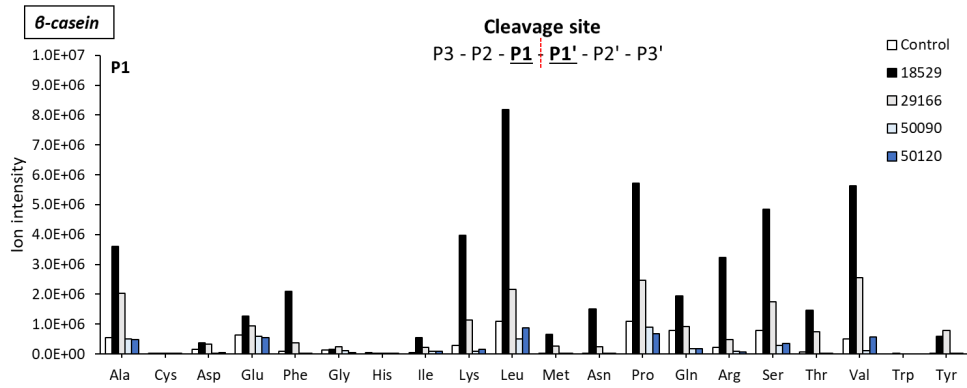
Species (Strain)	Bacterial count* [CFU/mL]
<i>Pseudomonas panacis</i> (DSM 18529)	8.0×10^9
<i>Pseudomonas weihenstephanensis</i> (DSM 29166)	8.0×10^8
<i>Pseudomonas fluorescens</i> (DSM 50090)	9.8×10^9
<i>Pseudomonas fluorescens</i> (DSM 50120)	3.2×10^9

*Bacterial growth measured in TSA (24 h, 30 °C) after initial culture in TSB (24 h, 30 °C)

Table S2. Number of identified peptides and their log transformed ion intensities formed in UHT milk during storage after inoculation with extracellular extracts from each of the four studied *Pseudomonas* strains as determined by peptidomic analyses using timsTOF Pro nanoLC-MS/MS.

Sample		Control		<i>P. panacis</i> DSM 18529		<i>P. weihenstephanensis</i> DSM 29166		<i>P. fluorescens</i> DSM 50090		<i>P. fluorescens</i> DSM 50120	
Storage Time (days)		0	45	0	45	0	45	0	45	0	45
Number of identified peptides	β -casein	159 ± 21	326 ± 13	71 ± 7	693 ± 9	129 ± 1	499 ± 4	45 ± 7	182 ± 8	74 ± 2	186 ± 8
	α s1-casein	103 ± 5	168 ± 4	64 ± 2	343 ± 2	86 ± 2	235 ± 1	38 ± 2	102 ± 4	57 ± 1	96 ± 0
	α s2-casein	50 ± 1	84 ± 4	36 ± 4	136 ± 3	54 ± 2	138 ± 5	17 ± 4	51 ± 1	38 ± 1	45 ± 0
	κ -casein	39 ± 2	93 ± 1	20 ± 4	124 ± 3	34 ± 1	119 ± 5	11 ± 2	46 ± 3	29 ± 1	43 ± 4
	β -lactoglobulin	25 ± 0	51 ± 2	15 ± 1	97 ± 2	24 ± 0	73 ± 1	9 ± 0	21 ± 3	13 ± 2	21 ± 2
Ion Intensity (Log10)	β -casein	6.02	6.52	5.66	7.36	5.87	6.95	5.43	6.25	5.66	6.32
	α s1-casein	5.64	5.86	5.47	6.95	5.50	6.36	4.88	5.71	5.27	5.69
	α s2-casein	5.45	5.63	4.91	5.95	5.68	6.06	4.55	5.43	5.61	5.50
	κ -casein	4.93	5.56	4.83	5.86	5.15	5.61	4.60	5.29	5.20	5.43
	β -lactoglobulin	5.29	5.39	5.04	6.03	5.15	5.72	4.71	5.16	4.86	5.32





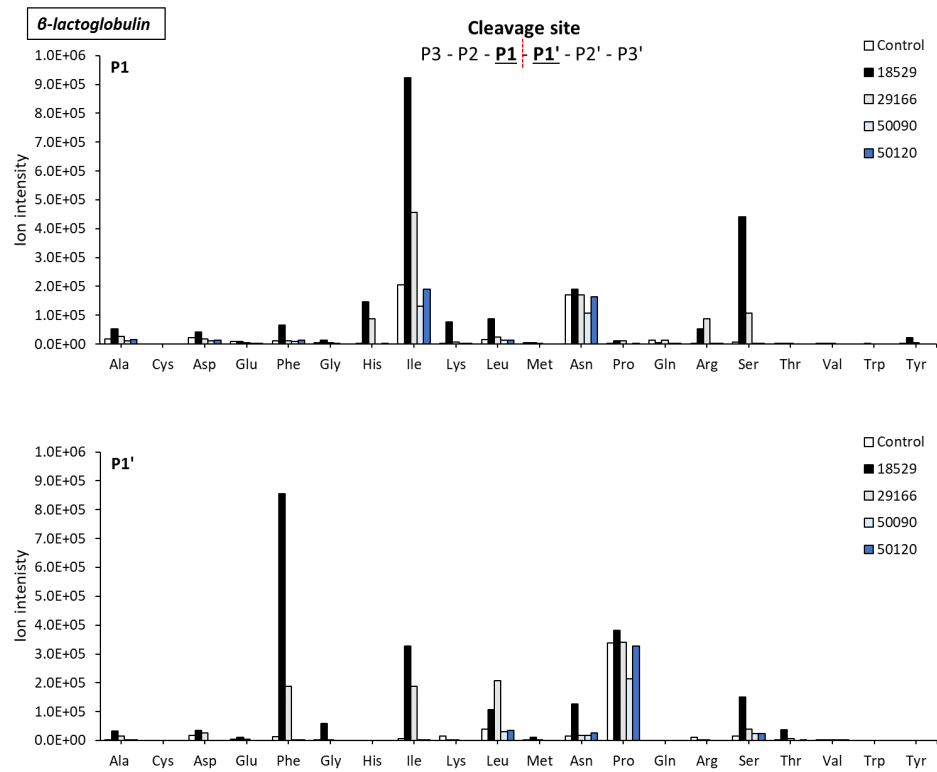


Figure S1. Total ion intensities of peptides distributed according to their P1 and P1' cleavage sites in the five individual major milk proteins per strain and control after 45 days of skimmed UHT milk storage based on extracted peptides subjected to nano timsTOF Pro LC-MS/MS peptidomics.