Comprehensive profiling of the native and modified peptidomes of raw bovine milk and processed milk products

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Supporting information

Table S1: List of targeted dynamic modifications corresponding to Amadori products (red), advanced glycation end-products (green), and oxidation/carbonylation (blue).

Modification	Mass shift [Da]	Amino acid residue
Acetylation[c]	+42.011	K
Acrolein[c]	+56.026	C, H, K
Argpyrimidine[e]	+80.026	R
Carboxyethyl[f]	+72.021	K, R
Carboxymethyl[a]	+58.005	K, R
Crotonaldehyde[c]	+70.042	C, H, K
Formylation[a]	+27.995	K
Glutamic semialdehyde[b]	-43.053	R
Glyceraldehyde-derived pyridinium[f]	+109.029	K
Glycerinyl lysine[c]	+88.016	K
Glyoxal-derived hydroimidazolium[e]	+39.995	R
Hexosylation[a] (Hex)	+162.053	K
Lactosylation[a] (Lac)	+324.106	K
Methylglyoxal-derived hydroimidazolones[e]	+54.011	R
Oxalic acid monolysinylamide[f]	+71.985	K
Oxidation[b] (Ox)	+15.995	P, C, W, Y
Pentenal[c]	+84.060	C, H, K
Pyrraline[f]	+108.021	K
Tetrahydropyrimidine[e]	+144.042	R
+14 Da Carbonylation [b]	+13.979	A, E, I, L, K, Q, V
2-Amino-3-ketobutyric acid[b] (T(Ox))	-2.016	T
2-Aminoadipic semialdehyde[b]	-1.032	K
4-Hydroxy-2-hexanal[d]	+114.068	C, H, K
4-Hydroxy-2-nonenal[d]	+156.115	C, H, K
4-Oxo-2-hexanal[d]	+112.052	C, H, K
4-Oxo-2-nonenal[d]	+154.099	C, H, K

[a-f] denote the templates in which modifications were searched together within Proteome Discoverer. Each template additionally contained oxidation of methionine and phosphorylation of serine as dynamic modifications. As PEAKS allows targeting many PTMs, all modifications were included as dynamic modifications.

Table S2: Unmodified peptides identified by both Proteome Discoverer 2.2 (Xcorr) and PEAKS Studio 10.5 (-10lgP) sorted by proteins (if present signal peptides were removed). An "x" indicates that the peptides was present in RM, UHT milk or IF, whereas a "blank" indicates that it was not detected. Methionine oxidation (M(Ox)) and phosphorylation of serine* (S(Phospho)) were considered as variable modifications.

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
Alpha-S1-casein (P02662)													
1	1	21	RPKHPIKHQGLPQEVLNENLL	none	3 (4)	820.799	38.94	3.8	57.7	x	x	x	1; 3; 5
2	1	22	RPKHPIKHQGLPQEVLNENLLR	none	4 (5)	654.878	35.38	3.5	44.8	x	x	x	1; 3; 5
3	4	19	HPIKHQGLPQEVLNEN	none	3	618.325	27.28	3.3	36.2	x	x	x	1; 7; 5
4	4	21	HPIKHQGLPQEVLNENLL	none	3 (2,4)	693.717	43.32	3.4	68.6	x	x	x	1; 3; 5
5	4	22	HPIKHQGLPQEVLNENLLR	none	3 (4)	745.749	39.00	5.0	59.4	x	x	x	1; 3; 5
6	4	23	HPIKHQGLPQEVLNENLLRF	none	3	794.773	48.95	5.0	54.4	x	x		5
7	7	16	KHQGLPQEVL	none	2	574.824	29.04	2.5	56.9	x	x	x	
8	7	23	KHQGLPQEVLNENLLRF	none	3	679.041	51.10	3.3	58.3			x	
9	8	21	HQGLPQEVLNENLL	none	2	802.425	49.46	2.9	58.9	x	x	x	1; 5
10	8	22	HQGLPQEVLNENLLR	none	3 (2)	587.320	44.19	4.7	92.6	x	x	x	1; 3; 5
11	9	17	QGLPQEVLN	none	2	499.269	35.17	1.7	43.1			x	
12	9	21	QGLPQEVLNENLL	none	2	733.897	55.28	3.4	53.5			x	5
13	9	22	QGLPQEVLNENLLR	none	2	811.948	49.07	3.4	74.6	x	x	x	5
14	9	23	QGLPQEVLNENLLRF	none	2	885.482	59.94	3.3	77.2			x	
15	10	17	GLPQEVLN	none	2	435.239	34.78	1.9	46.4	x	x	x	1
16	10	18	GLPQEVLNE	none	2	499.761	38.33	2.2	46.7			x	
17	10	20	GLPQEVLNENL	none	2	613.325	47.92	2.0	38.0	x	x	x	5; 7
18	10	21	GLPQEVLNENLL	none	2	669.867	55.75	2.8	45.7	x	x	x	1; 3; 5
19	10	22	GLPQEVLNENLLR	none	2	747.917	49.28	4.3	74.3	x	x	x	1; 3; 5; 7
20	10	23	GLPQEVLNENLLRF	none	2	821.451	60.49	4.0	75.2	x	x	x	1; 5
21	10	24	GLPQEVLNENLLRFF	none	2	894.988	70.69	3.9	55.5			x	
22	11	20	LPQEVLNENL	none	2	584.813	42.74	2.6	50.3	x	x		1
23	11	21	LPQEVLNENLL	none	2	641.357	51.48	2.2	42.9	x	x	x	1; 3; 5
24	11	22	LPQEVLNENLLR	none	2	719.407	44.47	3.8	68.1	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
25	11	23	LPQEVLNENLLRF	none	2 (3)	792.941	56.68	3.7	70.7	x	x	x	1; 3; 5; 7
26	13	22	QEVLNENLLR	none	2	614.337	37.50	2.6	48.7	x	x	x	1; 3; 5
27	13	23	QEVLNENLLRF	none	2	687.873	51.93	2.7	56.3			x	5
28	14	21	EVLNENLL	none	2	472.258	44.55	2.2	39.6			x	1
29	14	22	EVLNENLLR	none	2	550.309	36.43	2.4	50.8	x	x	x	1; 4
30	14	23	EVLNENLLRF	none	2	623.844	51.49	2.7	53.6	x	x	x	1; 5; 7
31	14	24	EVLNENLLRFF	none	2	697.379	63.20	2.8	43.5			x	
32	15	22	VLNENLLR	none	2	485.786	32.27	3.1	50.2	x	x	x	1
33	15	23	VLNENLLRF	none	2	559.321	48.86	2.8	55.9	x	x	x	1; 5
34	16	22	LNENLLR	none	2	436.252	28.15	2.6	38.8	x	x		1
35	16	23	LNENLLRF	none	2	509.787	46.08	3.2	49.0	x	x	x	1; 5
36	16	24	LNENLLRFF	none	2	583.321	58.93	2.9	51.5	x	x	x	5
37	17	23	NENLLRF	none	2	453.244	40.95	2.4	39.8	x	x	x	1; 4
38	17	24	NENLLRFF	none	2	526.779	55.49	2.9	46.7	x	x	x	1; 5
39	23	33	FFVAPFPEVFG	none	2	628.821	70.01	1.9	57.0	x	x		1; 5
40	23	34	FFVAPFPEVFGK	none	2	692.869	60.89	2.8	67.1	x	x	x	1; 3; 5
41	23	35	FFVAPFPEVFGKE	none	2	757.390	61.19	3.4	76.5	x	x		5
42	23	36	FFVAPFPEVFGKEK	none	2 (3)	821.437	55.07	3.1	73.0	x	x	x	1; 3; 5
43	23	37	FFVAPFPEVFGKEKV	none	2 (3)	870.972	57.29	3.3	75.3	x	x	x	5
44	23	39	FFVAPFPEVFGKEKVNE	none	2 (3)	992.515	55.58	3.9	85.0	x	x	x	1; 3; 5
45	23	41	FFVAPFPEVFGKEKVNELS	none	2 (3)	1092.573	58.00	3.2	84.2	x	x	x	5
46	23	42	FFVAPFPEVFGKEKVNELSK	none	4 (3)	578.813	53.57	1.8	40.2	x	x	x	5
47	24	32	FVAPFPEVF	none	2	526.775	63.22	2.4	51.6	x	x	x	1; 3; 5
48	24	33	FVAPFPEVFG	none	2	555.286	62.41	2.6	68.8	x	x	x	1; 5
49	24	34	FVAPFPEVFGK	none	2	619.334	53.66	2.5	56.7	x	x	x	1; 3; 5; 7
50	24	35	FVAPFPEVFGKE	none	2	683.854	54.21	2.7	72.1	x	x	x	5
51	24	36	FVAPFPEVFGKEK	none	2 (3)	747.903	48.16	3.0	76.5	x	x	x	1; 5
52	24	37	FVAPFPEVFGKEKV	none	2 (3)	797.437	51.04	3.5	73.2	x	x	x	1; 2; 5; 7
53	24	41	FVAPFPEVFGKEKVNELS	none	2 (3)	1019.038	52.38	3.3	73.9	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
54	25	32	VAPFPEVF	none	2	453.241	55.28	1.8	46.5	x	x	x	1; 5
55	25	33	VAPFPEVFG	none	2	481.751	54.34	2.5	61.2	x	x	x	1; 5
56	25	34	VAPFPEVFGK	none	2	545.799	45.43	1.4	50.7	x	x	x	1; 5
57	25	35	VAPFPEVFGKE	none	2	610.322	46.21	2.1	58.8	x	x	x	1; 5; 7
58	25	36	VAPFPEVFGKEK	none	2	674.368	39.75	2.0	72.9	x	x	x	2; 5
59	25	37	VAPFPEVFGKEKV	none	2 (3)	723.903	43.89	2.9	73.1	x	x	x	1; 2; 5
60	25	41	VAPFPEVFGKEKVNELS	none	2	945.505	46.15	2.5	70.8	x	x	x	
61	26	33	APFPEVFG	none	2	432.218	51.00	1.5	40.1	x	x		1; 3; 5
62	26	34	APFPEVFGK	none	2	496.265	42.16	2.7	66.3	x	x	x	1
63	26	35	APFPEVFGKE	none	2	560.786	42.90	3.2	77.3	x	x	x	1; 3; 5
64	26	36	APFPEVFGKEK	none	2 (3)	624.835	36.41	2.8	71.3	x	x	x	1; 3; 5
65	26	37	APFPEVFGKEKV	none	2 (3)	674.368	40.86	3.5	82.8	x	x	x	1; 5
66	26	39	APFPEVFGKEKVNE	none	3 (2)	530.944	38.68	3.0	68.8	x	x	x	1; 5
67	26	40	APFPEVFGKEKVNEL	none	3	568.637	46.12	2.7	47.5	x	x	x	
68	26	41	APFPEVFGKEKVNELS	none	2 (3)	895.971	43.69	2.5	80.6	x	x	x	1
69	27	34	PFPEVFGK	none	2	460.747	45.54	2.1	51.0	x	x	x	
70	27	36	PFPEVFGKEK	none	2	589.315	39.85	3.0	61.5	x	x	x	
71	27	37	PFPEVFGKEKV	none	3 (2)	426.236	47.50	2.1	40.3	x	x	x	2; 5
72	28	34	FPEVFGK	none	2	412.221	36.92	2.4	55.6	x	x	x	
73	28	36	FPEVFGKEK	none	2	540.788	31.18	2.5	53.6	x	x	x	1
74	28	37	FPEVFGKEKV	none	2	590.323	36.71	2.9	61.2	x	x	x	1; 5
75	35	58	EKVNELSKDIGSESTEDQAMEDIK	none	3 (4)	899.092	36.84	6.8	99.4	x	x	x	
76	35	58	EKVNELSKDIGSESTEDQAmEDIK	M20(Ox)	3 (4)	904.427	31.78	7.2	83.1	x	x	x	
77	35	58	EKVNELSKDIGSEsTEDQAMEDIK	S14(Phospho)	3	925.750	38.67	6.2	55.2	x	x	x	5
78	37	58	VNELSKDIGSESTEDQAMEDIK	none	3	813.379	38.03	5.6	85.0	x	x	x	5
79	37	58	VNELSKDIGSESTEDQAmEDIK	M18(Ox)	3	818.711	32.25	6.0	81.1	x	x	x	
80	37	58	VNELSKDIGSEsTEDQAMEDIK	S12(Phospho)	3	840.034	40.51	6.9	69.5	x	x	x	
81	38	53	NELSKDIGSESTEDQA	none	2	861.887	26.89	4.6	80.3	x	x	x	5
82	43	58	DIGSESTEDQAMEDIK	none	2	884.384	34.89	4.9	99.3	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
83	43	58	DIGSESTEDQAmEDIK	M12(Ox)	2	892.378	27.47	5.0	94.7	x	x		
84	43	58	DIGSEsTEDQAMEDIK	S6(Phospho)	2	924.367	38.89	4.8	74.7	x	x	x	
85	44	58	IGSESTEDQAmEDIK	M11(Ox)	2	834.865	24.02	3.4	59.9	x	x		
86	69	79	EEIVPNsVEQK	S7(Phospho)	2	676.311	26.67	2.5	39.0			x	
87	80	90	HIQKEDVPSER	none	3 (2)	669.342	13.87	4.1	54.9	x	x	x	1; 3; 4; 5
88	80	91	HIQKEDVPSERY	none	2 (3)	750.875	19.18	3.1	63.8	x	x	x	1; 3; 5
89	80	92	HIQKEDVPSERYL	none	3 (2)	538.614	27.07	3.5	74.9	x	x	x	1; 5
90	80	93	HIQKEDVPSERYLG	none	3 (2)	557.621	25.35	4.5	61.2	x	x	x	1; 3; 5
91	80	94	HIQKEDVPSERYLGY	none	3	611.975	30.72	4.5	76.5	x	x	x	1
92	80	95	HIQKEDVPSERYLGYL	none	3	649.672	40.11	3.6	51.9	x		x	
93	80	96	HIQKEDVPSERYLGYLE	none	3	692.686	38.90	3.8	54.7	x		x	
94	80	97	HIQKEDVPSERYLGYLEQ	none	3	735.371	38.91	4.1	62.9	x	x	x	1
95	80	98	HIQKEDVPSERYLGYLEQL	none	3	773.065	50.14	4.1	58.0	x	x	x	1
96	80	99	HIQKEDVPSERYLGYLEQLL	none	2 (3)	1215.638	61.48	4.0	71.3	x	x	x	5
97	80	100	HIQKEDVPSERYLGYLEQLLR	none	4 (3,5)	647.346	58.44	4.5	57.3	x	x	x	1; 3; 5
98	80	101	HIQKEDVPSERYLGYLEQLLRL	none	4 (3)	675.618	67.03	3.9	48.5	x	x	x	
99	80	102	HIQKEDVPSERYLGYLEQLLRLK	none	5 (3,4)	566.314	60.64	4.5	57.2	x	x	x	1; 3; 5
100	80	103	HIQKEDVPSERYLGYLEQLLRLKK	none	3 (4,5,6)	985.888	56.22	3.2	28.2	x	x	x	1
101	80	104	HIQKEDVPSERYLGYLEQLLRLKKY	none	5	624.547	57.25	4.0	39.7	x	x	x	
102	81	89	IQKEDVPSE	none	2	522.762	17.04	2.2	36.3	x	x	x	1; 3; 5
103	81	90	IQKEDVPSER	none	2 (3)	400.878	15.15	2.9	54.6	x	x	x	1; 3; 5
104	81	91	IQKEDVPSERY	none	2	682.345	21.29	2.7	50.6	x	x	x	5
105	81	92	IQKEDVPSERYL	none	3	492.927	29.90	3.1	50.6	x	x	x	1
106	81	93	IQKEDVPSERYLG	none	3	511.934	28.05	2.8	37.5	x	x	x	1
107	82	93	QKEDVPSERYLG	none	3 (2)	474.240	25.15	2.6	27.4	x	x		1
108	83	91	KEDVPSERY	none	2	561.773	17.22	3.1	46.1	x	x	x	1; 5
109	83	93	KEDVPSERYLG	none	2	646.827	24.93	2.8	54.4	x	x		1
110	84	91	EDVPSERY	none	2	497.727	20.58	1.4	46.9	x	x	x	
111	86	97	VPSERYLGYLEQ	none	2	727.370	40.77	2.2	47.0	x	x	x	1

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
112	86	98	VPSERYLGYLEQL	none	2	783.911	53.16	2.7	58.0	x	x		1
113	86	99	VPSERYLGYLEQLL	none	2	840.453	65.13	2.6	51.1	x	x	x	1
114	91	99	YLGYLEQLL	none	2	556.304	64.78	1.5	24.2	x	x		5
115	91	100	YLGYLEQLLR	none	2	634.355	58.27	3.3	67.7	x	x	x	
116	91	102	YLGYLEQLLRLK	none	2 (3)	754.945	60.51	3.8	68.5	x	x	x	
117	91	103	YLGYLEQLLRLKK	none	3 (4)	546.330	54.07	2.5	36.5	x	x		
118	92	100	LGYLEQLLR	none	2	552.823	51.92	3.2	55.6	x	x	x	1; 3; 5
119	92	102	LGYLEQLLRLK	none	3	449.278	55.65	3.0	56.8	x	x		
120	93	99	GYLEQLL	none	2	418.231	53.87	1.8	34.9	x	x		
121	93	100	GYLEQLLR	none	2	496.281	46.78	2.6	50.9	x	x	x	1
122	93	101	GYLEQLLRL	none	2	552.823	61.34	2.1	44.7	x	x		5
123	93	102	GYLEQLLRLK	none	2 (3)	616.871	51.98	3.4	58.7	x	x	x	5
124	94	100	YLEQLLR	none	2	467.771	39.11	2.6	39.9	x	x	x	1; 5
125	94	101	YLEQLLRL	none	2	524.312	54.57	2.5	38.1	x	x		1
126	94	102	YLEQLLRLK	none	2	588.360	44.78	2.8	49.6	x	x	x	1
127	95	101	LEQLLRL	none	2	442.782	45.15	2.3	32.2	x	x	x	1
128	95	102	LEQLLRLK	none	2	506.828	34.31	3.0	36.8	x	x	x	1
129	101	123	LKKYKVPQLEIVPNsAEERLHSM	S15(Phospho)	3 (4,5)	930.486	43.25	5.4	62.6	x	x	x	5
130	103	119	KYKVPQLEIVPNSAEER	none	3	667.365	36.59	3.4	50.4	x	x	x	3; 5
131	103	119	KYKVPQLEIVPNsAEER	S13(Phospho)	3 (2)	694.021	38.01	4.7	62.6	x	x	x	1; 3; 5
132	103	121	KYKVPQLEIVPNsAEERLH	S13(Phospho)	4	583.304	40.08	4.4	40.6	x	x	x	
133	103	122	KYKVPQLEIVPNsAEERLHS	S13(Phospho)	4 (3)	605.061	40.30	4.3	27.0	x	x	x	
134	103	123	KYKVPQLEIVPNSAEERLHSM	none	3 (4)	823.437	42.87	5.0	56.7	x	x	x	5
135	103	123	KYKVPQLEIVPNSAEERLHSm	M21(Ox)	4	621.827	38.29	4.3	42.2	x	x	x	
136	103	123	KYKVPQLEIVPNsAEERLHSM	S13(Phospho)	3 (2,4)	855.424	44.86	5.5	56.3	x	x	x	5
137	103	124	KYKVPQLEIVPNsAEERLHSMK	S13(Phospho)	4 (5)	669.844	40.83	4.4	23.3	x	x	x	3; 5
138	104	114	YKVPQLEIVPN	none	2	650.369	43.92	2.6	69.9			x	
139	104	119	YKVPQLEIVPNSAEER	none	2 (3)	936.497	40.61	4.1	78.7	x	x	x	5
140	104	119	YKVPQLEIVPNsAEER	S12(Phospho)	2 (3)	976.481	42.23	5.6	77.4	x	x	x	1; 3; 5

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141	104	122	YKVPQLEIVPNsAEERLHS	S12(Phospho)	3	763.714	43.72	4.7	48.8	x	x	x	5
142	104	123	YKVPQLEIVPNSAEERLHSM	none	3 (4)	780.740	46.08	3.8	55.8	x	x	x	5
143	104	123	YKVPQLEIVPNSAEERLHSm	M20(Ox)	3	786.071	41.64	3.7	58.3	x	x	x	3
144	104	123	YKVPQLEIVPNsAEERLHSM	S12(Phospho)	3 (2,4)	807.394	48.27	4.7	56.7	x	x	x	1; 3; 5
145	104	124	YKVPQLEIVPNsAEERLHSMK	S12(Phospho)	3 (4)	850.091	43.88	5.0	50.6	x	x	x	3; 5
146	105	114	KVPQLEIVPN	none	2	568.837	38.05	1.6	46.1			x	
147	105	119	KVPQLEIVPNSAEER	none	3	570.312	35.01	4.3	62.0	x	x	x	1
148	105	119	KVPQLEIVPNsAEER	S11(Phospho)	2 (3)	894.949	37.14	4.0	41.8	x	x	x	3; 5
149	105	121	KVPQLEIVPNsAEERLH	S11(Phospho)	3	680.350	39.51	4.3	40.3			x	
150	105	123	KVPQLEIVPNSAEERLHSM	none	3	726.384	42.75	5.2	57.1	x	x	x	5; 7
151	105	123	KVPQLEIVPNSAEERLHSm	M19(Ox)	3	731.715	37.46	4.2	59.0	x	x	x	7
152	105	123	KVPQLEIVPNsAEERLHSM	S11(Phospho)	3 (2)	753.040	45.20	5.5	50.4	x	x	x	
153	105	124	KVPQLEIVPNsAEERLHSMK	S11(Phospho)	4	597.057	40.50	2.9	24.5	x	x	x	
154	106	119	VPQLEIVPNSAEER	none	2 (3)	790.917	38.22	3.9	86.8	x	x	x	1; 3; 5
155	106	119	VPQLEIVPNsAEER	S10(Phospho)	2	830.901	40.32	4.7	67.8	x	x	x	1; 3; 5
156	106	121	VPQLEIVPNsAEERLH	S10(Phospho)	3 (2)	637.652	42.59	4.5	47.6	x	x	x	
157	106	122	VPQLEIVPNSAEERLHS	none	3	640.007	40.51	3.5	40.5	x	x	x	1; 5
158	106	122	VPQLEIVPNsAEERLHS	S10(Phospho)	2 (3)	999.488	42.66	4.7	59.0	x	x	x	
159	106	123	VPQLEIVPNSAEERLHSM	none	3 (2)	683.685	45.68	4.8	89.8	x	x	x	5
160	106	123	VPQLEIVPNSAEERLHSm	M18(Ox)	3 (2)	689.017	40.08	4.9	84.4	x	x	x	
161	106	123	VPQLEIVPNsAEERLHSM	S10(Phospho)	3 (2)	710.342	48.28	5.4	73.3	x	x	x	3; 5
162	106	124	VPQLEIVPNSAEERLHSMK	none	3	726.383	41.19	3.3	37.6	x	x	x	
163	106	124	VPQLEIVPNsAEERLHSMK	S10(Phospho)	2 (3,4)	1129.056	42.96	4.4	66.1	x	x	x	5
164	106	131	VPQLEIVPNsAEERLHSMKEGIHAQQ	S10(Phospho)	3	1007.494	43.59	4.8	34.5	x	x	x	
165	106	132	VPQLEIVPNsAEERLHSMKEGIHAQQK	S10(Phospho)	4 (5)	630.518	41.32	3.8	23.0	x	x	x	
166	108	119	QLEIVPNSAEER	none	2	692.855	31.41	2.4	62.7	x	x	x	5
167	108	119	QLEIVPNsAEER	S8(Phospho)	2	732.840	33.73	2.9	54.2	x	x	x	1; 3; 5
168	108	123	QLEIVPNSAEERLHSM	none	3	618.312	41.19	2.9	41.1	x	x	x	
169	108	123	QLEIVPNsAEERLHSM	S8(Phospho)	3 (2)	644.967	44.50	2.7	28.1	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
170	108	124	QLEIVPNsAEERLHSMK	S8(Phospho)	3	687.667	39.02	2.5	23.3	x	x	x	5
171	109	119	LEIVPNSAEER	none	2	628.827	29.74	2.7	56.5	x	x	x	1; 5
172	109	119	LEIVPNsAEER	S7(Phospho)	2	668.809	32.06	2.8	45.2	x	x	x	1; 5
173	109	123	LEIVPNsAEERLHSM	S7(Phospho)	2	902.919	43.78	3.5	57.5	x	x		
174	110	119	EIVPNSAEER	none	2	572.284	20.14	1.9	40.4	x	x	x	1; 5
175	110	119	EIVPNsAEER	S6(Phospho)	2	612.268	22.13	2.2	47.2	x	x	x	5
176	111	123	IVPNsAEERLHSM	S5(Phospho)	2	781.856	33.02	2.8	35.6	x	x	x	
177	112	123	VPNsAEERLHSM	S4(Phospho)	2	725.311	27.58	2.8	60.0	x	x	x	
178	114	123	NsAEERLHSM	S2(Phospho)	2	627.252	23.47	1.8	46.0	x	x		5
179	115	123	SAEERLHSM	none	2	530.247	17.95	1.9	58.6			x	
180	115	123	sAEERLHSM	S1(Phospho)	2	570.230	19.99	2.7	45.3			x	
181	125	144	EGIHAQQKEPMIGVNQELAY	none	3	752.377	39.50	2.9	46.1	x	x	x	5
182	125	150	EGIHAQQKEPmIGVNQELAYFYPELF	M11(Ox)	3	1023.168	63.21	2.7	22.5	x	x		
183	131	144	QKEPMIGVNQELAY	none	2	810.411	40.43	2.5	72.3			x	
184	132	144	KEPMIGVNQELAY	none	2	746.380	40.35	2.9	65.4			x	
185	145	154	FYPELFRQFY	none	2	705.348	58.74	2.2	55.3	x	x	x	5
186	166	199	YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW	none	3	1252.600	65.31	3.4	54.3	x	x	x	5
187	166	199	YVPLGTQYTDAPSFSDIPNPIGSENSEKTTmPLW	M31(Ox)	3	1257.929	62.01	4.5	52.1	x	x	x	5
188	171	199	TQYTDAPSFSDIPNPIGSENSEKTTmPLW	M26(Ox)	3	1081.500	57.92	3.5	42.8		x		
189	172	194	QYTDAPSFSDIPNPIGSENSEKT	none	2	1249.073	47.31	3.5	61.6	x	x	x	
190	172	199	QYTDAPSFSDIPNPIGSENSEKTTMPLW	none	3 (2)	1042.486	61.70	3.4	66.4	x	x	x	
191	172	199	QYTDAPSFSDIPNPIGSENSEKTTmPLW	M25(Ox)	3 (2)	1047.818	57.99	4.0	59.5	x	x	x	
192	174	197	TDAPSFSDIPNPIGSENSEKTTMP	none	2	1268.082	49.71	3.0	50.8	x	x	x	5; 7
193	174	199	TDAPSFSDIPNPIGSENSEKTTMPLW	none	2 (3)	1417.666	60.94	3.2	67.1	x	x	x	5
194	174	199	TDAPSFSDIPNPIGSENSEKTTmPLW	M23(Ox)	3 (2)	950.777	57.11	3.6	69.4	x	x	x	5
195	176	190	APSFSDIPNPIGSEN	none	2	772.865	47.97	3.0	66.6		x		
196	176	193	APSFSDIPNPIGSENSEK	none	2	944.951	43.49	4.7	78.3	x	x	x	
197	176	199	APSFSDIPNPIGSENSEKTTMPLW	none	2	1309.627	59.81	4.6	94.1	x	x	x	1; 5; 6
198	176	199	APSFSDIPNPIGSENSEKTTmPLW	M21(Ox)	2	1317.626	56.21	4.2	86.6	x	x	x	3

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
199	177	199	PSFSDIPNPIGSENSEKTTMPLW	none	2	1274.110	59.48	3.5	74.3		x		
200	177	199	PSFSDIPNPIGSENSEKTTmPLW	M20(Ox)	2	1282.107	55.39	3.2	57.2		x		
201	178	199	SFSDIPNPIGSENSEKTTMPLW	none	2	1225.582	58.20	3.8	82.7	x	x	x	
202	178	199	SFSDIPNPIGSENSEKTTmPLW	M19(Ox)	2 (3)	1233.580	53.81	3.7	76.0	x	x	x	
203	179	199	FSDIPNPIGSENSEKTTMPLW	none	2	1182.068	56.90	4.0	78.2	x	x	x	5
204	179	199	FSDIPNPIGSENSEKTTmPLW	M18(Ox)	2	1190.061	52.31	3.7	82.9		x		
205	180	193	SDIPNPIGSENSEK	none	2	743.853	29.93	2.2	53.4	x	x		5
206	180	194	SDIPNPIGSENSEKT	none	2	794.379	30.65	3.7	73.9	x	x	x	
207	180	197	SDIPNPIGSENSEKTTMP	none	2	958.950	38.11	2.3	61.5	x	x	x	1; 5; 7
208	180	197	SDIPNPIGSENSEKTTmP	M17(Ox)	2	966.946	32.71	4.4	71.7	x	x	x	1; 5; 7
209	180	198	SDIPNPIGSENSEKTTMPL	none	2	1015.493	44.62	3.2	54.4	x	x	x	
210	180	199	SDIPNPIGSENSEKTTMPLW	none	2 (3)	1108.531	53.03	4.2	99.0	x	x	x	1; 2; 5
211	180	199	SDIPNPIGSENSEKTTmPLW	M17(Ox)	2 (3)	1116.529	48.45	4.3	98.7	x	x	x	1; 2; 5
212	181	197	DIPNPIGSENSEKTTMP	none	2	915.434	39.17	2.7	52.4	x	x	x	1; 5
213	181	197	DIPNPIGSENSEKTTmP	M16(Ox)	2	923.429	33.43	3.0	50.8	x	x	x	1; 5
214	181	199	DIPNPIGSENSEKTTMPLW	none	2	1065.015	54.84	3.9	78.7	x	x	x	1; 5
215	181	199	DIPNPIGSENSEKTTmPLW	M16(Ox)	2	1073.012	50.01	3.8	88.1	x	x	x	
216	182	193	IPNPIGSENSEK	none	2	642.826	25.99	2.7	52.1		x		
217	182	197	IPNPIGSENSEKTTMP	none	2	857.920	35.69	4.5	56.0	x	x	x	1; 2; 5
218	182	197	IPNPIGSENSEKTTmP	M15(Ox)	2	865.916	29.42	4.5	55.1	x	x	x	1
219	182	199	IPNPIGSENSEKTTMPLW	none	2	1007.501	51.48	4.4	100.8	x	x	x	1; 4; 5
220	182	199	IPNPIGSENSEKTTmPLW	M15(Ox)	2	1015.499	46.94	4.9	98.0	x	x	x	1
221	182	199	IPNPIGsENSEKTTMPLW	S7(Phospho)	2	1047.486	55.91	4.6	52.4		x		
222	183	199	PNPIGSENSEKTTMPLW	none	2	950.959	60.00	2.4	66.2	x	x	x	
223	183	199	PNPIGSENSEKTTmPLW	M14(Ox)	2	958.955	56.06	3.3	65.1	x	x	x	
224	184	197	NPIGSENSEKTTMP	none	2	752.851	25.82	2.2	46.8	x		x	1; 7
225	184	197	NPIGSENSEKTTmP	M13(Ox)	2	760.848	19.12	2.3	58.0	x	x	x	5
226	184	199	NPIGSENSEKTTMPLW	none	2	902.435	45.67	3.6	87.8	x	x	x	
227	184	199	NPIGSENSEKTTmPLW	M13(Ox)	2	910.431	38.94	4.0	89.7	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
228	185	197	PIGSENSEKTTMP	none	2	695.826	23.71	3.0	56.9	x	x	x	1; 3; 5
229	185	197	PIGSENSEKTTmP	M12(Ox)	2	703.826	16.47	3.3	62.3	x	x	x	3
230	185	198	PIGSENSEKTTmPL	M12(Ox)	2	760.369	24.90	2.4	52.5		x		
231	185	199	PIGSENSEKTTMPLW	none	2	845.412	45.26	4.0	103.5	x	x	x	1; 4; 6
232	185	199	PIGSENSEKTTmPLW	M12(Ox)	2	853.410	38.98	3.7	96.8	x	x	x	
233	185	199	PIGsENSEKTTMPLW	S4(Phospho)	2	885.395	49.91	3.2	64.1		x		
234	186	197	IGSENSEKTTMP	none	2	647.302	21.38	1.8	52.1	x	x	x	
235	186	199	IGSENSEKTTMPLW	none	2	796.886	43.86	2.9	73.8	x	x	x	
236	186	199	IGSENSEKTTmPLW	M11(Ox)	2	804.884	36.41	2.8	63.7	x	x	x	
237	188	199	SENSEKTTMPLW	none	2	711.833	41.59	3.2	66.1	x	x	x	
238	188	199	SENSEKTTmPLW	M9(Ox)	2	719.829	33.19	2.8	67.6	x	x	x	
239	189	199	ENSEKTTMPLW	none	2	668.316	41.90	2.2	58.9		x	x	
240	189	199	ENSEKTTmPLW	M8(Ox)	2	676.313	33.41	2.7	49.0		x	x	
241	190	199	NSEKTTMPLW	none	2	603.793	41.04	2.6	58.7		x		
242	190	199	NSEKTTmPLW	M7(Ox)	2	611.791	32.42	2.3	56.9		x		
243	191	199	SEKTTMPLW	none	2	546.773	41.20	2.1	47.5	x	x	x	1
244	191	199	SEKTTmPLW	M6(Ox)	2	554.770	32.54	2.5	49.9	x	x	x	
245	192	199	EKTTMPLW	none	2	503.257	41.54	1.0	44.0		x		
246	193	199	KTTMPLW	none	2	438.735	40.39	1.7	40.2		x		
Alpha-S2-casein (P02663)													
247	1	20	KNTMEHVSSSEESIISQETY	none	3	767.017	35.33	4.1	36.9	x	x	x	5
248	1	20	KNTmEHVSSSEESIISQETY	M4(Ox)	3	772.349	31.91	4.2	44.4	x	x	x	
249	1	21	KNTMEHVSSSEESIISQETYK	none	3 (4)	809.715	32.13	7.3	84.3	x	x	x	5
250	1	21	KNTmEHVSSSEESIISQETYK	M4(Ox)	3 (4)	815.049	28.41	5.7	60.9	x	x	x	
251	1	21	KNTMEHVSSSEESIIsQETYK	S16(Phospho)	3	836.371	33.11	7.4	86.0	x	x	x	5
252	1	23	KNTMEHVSSSEESIISQETYKQE	none	3	895.417	32.58	3.9	50.2	x	x	x	
253	1	24	KNTMEHVSSSEESIISQETYKQEK	none	3 (4)	938.119	30.37	7.1	69.4	x	x	x	1; 3; 5
254	1	24	KNTmEHVSSSEESIISQETYKQEK	M4(Ox)	4 (3)	707.836	26.64	6.1	59.5	x	x	x	5
255	1	24	KNTMEHVSSSEESIIsQETYKQEK	S16(Phospho)	3 (4)	964.769	31.28	6.3	63.9	x	x	x	3; 5

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
256	9	21	SSEESIISQETYK	none	2	750.858	30.66	3.1	58.6	x	x	x	
257	11	21	EESIIsQETYK	S6(Phospho)	2	703.808	32.97	2.7	51.5			x	
258	13	21	SIIsQETYK	S4(Phospho)	2	574.766	31.64	2.7	31.0			x	
259	14	21	IIsQETYK	S3(Phospho)	2	531.248	24.15	3.2	43.2	x	x	x	5
260	14	22	IIsQETYKQ	S3(Phospho)	2	595.275	24.14	2.7	46.8	x	x		5
261	14	24	IIsQETYKQEK	S3(Phospho)	2	723.847	20.93	2.3	45.8	x	x	x	
262	71	78	ITVDDKHY	none	2	495.747	19.35	2.2	51.7	x	x	x	
263	71	79	ITVDDKHYQ	none	2	559.777	18.20	2.2	51.1	x	x	x	1
264	81	88	ALNEINQF	none	2	474.743	38.83	2.4	45.0			x	
265	81	89	ALNEINQFY	none	2	556.274	45.06	2.3	47.6			x	
266	81	95	ALNEINQFYQKFPQY	none	2	951.975	52.32	2.9	56.6			x	
267	81	98	ALNEINQFYQKFPQYLQY	none	3 (2)	769.721	59.86	4.4	59.7			x	5
268	88	98	FYQKFPQYLQY	none	2	762.880	46.64	3.0	50.0			x	
269	89	95	YQKFPQY	none	2	487.242	28.61	2.2	52.2			x	
270	89	98	YQKFPQYLQY	none	2	689.348	42.20	3.1	64.3			x	
271	90	98	QKFPQYLQY	none	2	607.814	39.81	2.6	53.9			x	
272	98	113	YLYQGPIVLNPWDQVK	none	2	967.015	56.97	4.0	71.2	x	x		5
273	99	113	LYQGPIVLNPWDQVK	none	3 (2)	590.658	53.44	4.4	80.9	x	x	x	7
274	99	114	LYQGPIVLNPWDQVKR	none	2 (3)	963.535	48.82	3.8	95.6	x	x	x	
275	99	115	LYQGPIVLNPWDQVKRN	none	2 (3)	680.707	48.62	3.3	46.4			x	
276	100	112	YQGPIVLNPWDQV	none	2	764.895	58.72	3.0	41.4			x	7
277	100	113	YQGPIVLNPWDQVK	none	2	828.941	50.57	3.8	75.3	x	x	x	7
278	100	114	YQGPIVLNPWDQVKR	none	3	604.996	45.97	3.5	79.5	x	x	x	
279	100	115	YQGPIVLNPWDQVKRN	none	3	643.011	45.69	1.8	42.7			x	
280	101	113	QGPIVLNPWDQVK	none	2	747.409	47.66	2.8	63.9	x	x	x	5
281	101	114	QGPIVLNPWDQVKR	none	3	550.643	42.99	2.7	42.9	x	x	x	
282	102	112	GPIVLNPWDQV	none	2	619.333	55.93	2.1	36.4	x			5
283	102	113	GPIVLNPWDQVK	none	2	683.379	47.32	3.4	68.6	x	x	x	3; 5
284	105	113	VLNPWDQVK	none	2	549.799	37.70	2.2	51.1	x	x	x	1

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
285	115	128	NAVPITPTLNREQL	none	2	783.437	40.03	2.4	59.5		x	x	
286	115	135	NAVPITPTLNREQLSTSEENS	none	2	1150.573	36.88	3.9	85.9	x	x	x	1
287	115	135	NAVPITPTLNREQLSTsEENS	S17(Phospho)	2	1190.556	38.62	4.1	58.5	x	x	x	
288	115	136	NAVPITPTLNREQLSTsEENSK	S17(Phospho)	2	1254.605	35.25	5.0	52.0	x	x	x	
289	115	149	NAVPITPTLNREQLSTsEENSKKTVDMESTEVFTK	S17(Phospho)	3	1335.314	42.34	4.1	32.3	x	x	x	
290	123	135	LNREQLSTSEENS	none	2	753.854	19.61	2.8	53.8	x	x	x	
291	123	136	LNREQLSTsEENSK	S9(Phospho)	2 (3)	857.885	18.43	4.0	51.8	x	x	x	
292	123	137	LNREQLSTsEENSKK	S9(Phospho)	3	614.957	16.25	3.2	18.9	x	x	x	
293	123	149	LNREQLSTsEENSKKTVDMESTEVFTK	S9(Phospho)	4	803.377	34.35	4.9	56.4	x	x	x	5
294	135	149	SKKTVDMEsTEVFTK	S9(Phospho)	3	603.948	28.30	5.7	71.5	x	x	x	
295	137	149	KTVDMESTEVFTK	none	2 (3)	757.873	30.56	4.4	85.5	x	x	x	1; 5
296	137	149	KTVDmESTEVFTK	M5(Ox)	2	510.916	23.93	2.4	42.9	x	x	x	
297	137	149	KTVDMEsTEVFTK	S7(Phospho)	2 (3)	797.857	31.88	5.7	86.5	x	x	x	1; 3; 4; 5
298	137	150	KTVDMESTEVFTKK	none	3	548.281	27.36	5.7	74.0	x	x	x	3; 5
299	137	150	KTVDMEsTEVFTKK	S7(Phospho)	2 (3)	861.905	28.46	5.1	65.3	x	x	x	1; 5
300	138	149	TVDMESTEVFTK	none	2	693.827	35.18	3.8	91.1	x	x	x	1; 3; 5
301	138	149	TVDmESTEVFTK	M4(Ox)	2	701.822	27.51	3.5	76.4	x	x	x	1; 3; 5
302	138	149	TVDMEsTEVFTK	S6(Phospho)	2	733.810	36.40	4.9	75.1	x	x	x	1; 3; 5
303	138	150	TVDmESTEVFTKK	M4(Ox)	2 (3)	765.871	24.32	3.1	53.5	x	x		3
304	139	149	VDMESTEVFTK	none	2	643.301	34.10	3.4	84.6	x	x	x	5
305	139	149	VDMEsTEVFTK	S5(Phospho)	2	683.286	36.36	4.6	70.1	x	x	x	5
306	139	150	VDMESTEVFTKK	none	3	471.901	30.15	2.1	43.3	x	x		
307	139	150	VDmESTEVFTKK	M3(Ox)	3	477.232	22.39	3.1	28.7	x	x		
308	140	149	DmESTEVFTK	M2(Ox)	2	601.764	24.01	2.7	61.1	x	x		
309	140	149	DMEsTEVFTK	S4(Phospho)	2	633.751	33.55	3.4	56.9	x	x	x	
310	141	149	MESTEVFTK	none	2	536.254	25.53	2.2	51.7	x	x	x	
311	141	149	MEsTEVFTK	S3(Phospho)	2	576.238	28.02	3.7	56.6			x	
312	141	150	MEsTEVFTKK	S3(Phospho)	2	640.285	23.57	2.8	42.9	x	x	x	
313	150	163	KTKLTEEEKNRLNF	none	3 (4)	583.987	25.16	3.7	48.0	x	x	x	1

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
314	150	165	KTKLTEEEKNRLNFLK	none	3 (2,4)	664.379	28.24	3.6	48.2	x	x	x	
315	151	161	TKLTEEEKNRL	none	3	454.251	19.23	2.9	48.3	x	x	x	
316	151	162	TKLTEEEKNRLN	none	3 (2)	492.265	17.03	3.2	50.5	x	x	x	1
317	151	163	TKLTEEEKNRLNF	none	3	541.289	29.00	3.5	67.3	x	x	x	1
318	151	164	TKLTEEEKNRLNFL	none	2 (3)	867.971	36.78	4.1	90.9	x	x	x	1
319	151	165	TKLTEEEKNRLNFLK	none	2 (3,4)	932.020	31.80	4.7	87.9	x	x	x	1; 5
320	152	163	KLTEEEKNRLNF	none	3	507.605	26.59	3.1	28.4	x	x	x	1; 5
321	152	164	KLTEEEKNRLNFL	none	3 (2)	545.301	35.24	3.7	78.6	x	x	x	5
322	152	165	KLTEEEKNRLNFLK	none	4 (3)	441.250	29.77	2.8	31.8	x	x		5
323	153	161	LTEEEKNRL	none	2	566.302	16.94	1.9	39.3	x	x	x	1; 5
324	153	164	LTEEEKNRLNFL	none	2 (3)	753.403	38.44	3.5	74.6	x	x	x	1
325	153	165	LTEEEKNRLNFLK	none	3 (2)	545.301	32.01	3.4	44.1	x	x	x	1
326	154	163	TEEEKNRLNF	none	2 (3)	640.317	24.36	3.0	56.3	x	x	x	1
327	154	164	TEEEKNRLNFL	none	2 (3)	696.860	35.53	3.8	69.5	x	x	x	5
328	154	165	TEEEKNRLNFLK	none	3	507.604	27.91	3.1	40.3	x	x	x	5
329	155	164	EEEKNRLNFL	none	2	646.336	35.55	2.2	56.7	x	x	x	1
330	162	169	NFLKKISQ	none	2	489.291	24.74	2.4	44.6			x	
331	170	179	RYQKFALPQY	none	2 (3)	657.354	35.84	2.1	55.8			x	
332	171	179	YQKFALPQY	none	2	579.304	40.61	2.2	56.2			x	
333	171	180	YQKFALPQYL	none	2	635.847	50.00	2.2	49.6	x	x	x	1; 5
334	172	179	QKFALPQY	none	2	497.771	37.54	1.5	43.3			x	
335	172	180	QKFALPQYL	none	2	554.313	47.59	1.8	38.7	x	x	x	5
336	174	181	FALPQYLK	none	2	490.284	44.25	2.3	38.6	x	x	x	1
337	174	187	FALPQYLKTVYQHQ	none	3 (2)	579.310	48.81	3.7	66.7	x	x		1
338	175	188	ALPQYLKTVYQHQK	none	3	572.985	34.66	2.8	40.6	x	x		5
339	176	183	LPQYLKTV	none	2	481.288	35.91	2.7	43.1	x	x		1
340	176	185	LPQYLKTVYQ	none	2	626.849	38.96	2.4	62.6	x	x	x	
341	189	196	AMKPWIQP	none	2	485.761	36.69	2.4	38.2	x	x	x	1
342	189	196	AmKPWIQP	M2(Ox)	2	493.759	30.92	2.0	30.9	x	x		1

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
343	189	197	AMKPWIQPK	none	2	549.808	27.15	2.2	43.6			x	5
344	189	198	AMKPWIQPKT	none	3 (2)	400.557	28.88	3.1	45.9	x	x	x	1
345	189	198	AmKPWIQPKT	M2(Ox)	3 (2)	405.889	23.78	2.6	35.3	x	x		1
346	189	203	AMKPWIQPKTKVIPY	none	4 (3)	450.761	39.31	2.5	29.0			x	
347	191	198	KPWIQPKT	none	2	499.294	21.54	2.1	41.7	x	x		
348	198	204	TKVIPYV	none	2	410.252	34.16	1.9	36.6	x	x	x	1
349	198	205	TKVIPYVR	none	2	488.301	24.73	2.5	37.9	x	x	x	1
350	198	206	TKVIPYVRY	none	2	569.833	32.02	2.4	46.1	x	x	x	1; 5
351	198	207	TKVIPYVRYL	none	3 (2)	417.919	41.48	2.9	52.3	x	x	x	1; 3; 4; 5
352	199	205	KVIPYVR	none	2	437.778	22.91	2.2	21.9	x	x		
353	199	206	KVIPYVRY	none	2	519.310	30.12	1.9	23.4	x	x		
354	199	207	KVIPYVRYL	none	2	575.852	39.86	2.4	39.9	x	x	x	3;
355	200	206	VIPYVRY	none	2	455.263	35.45	1.5	29.7	x	x	x	
356	200	207	VIPYVRYL	none	2	511.804	46.76	1.6	40.6	x	x	x	1; 3; 5
357	201	207	IPYVRYL	none	2	462.271	42.31	1.8	41.4	x	x	x	1; 4
Apolipoprotein A-I (P15497)													
358	235	247	AAIDEASKKLNAQ	none	2	679.868	22.31	3.6	74.7			x	
Beta-1,4-galactosyltransferase 1 (P08037)													
359	69	79	AIGQPSGELRL	none	2	570.822	37.19	2.2	37.5			x	
360	54	69	VGVHPPLQGSSHGAAA	none	3	495.590	22.64	2.8	31.5	x	x		
Beta-2-microglobulin (P01888)													
361	1	10	IQRPPKIQVY	none	2	621.371	29.68	2.1	49.7			x	
Beta-casein (P02666)													
362	1	7	RELEELN	none	2	451.731	20.15	1.7	30.3		x		
363	1	10	RELEELNVPG	none	2	578.302	33.29	1.7	43.5	x	x	x	
364	1	11	RELEELNVPGE	none	2	642.824	34.48	2.5	54.6	x	x	x	1; 4; 6
365	1	14	RELEELNVPGEIVE	none	2	813.425	43.62	2.4	69.3			x	5
366	1	15	RELEELNVPGEIVES	none	2	856.939	43.36	2.6	70.3	x	x	x	1; 5
367	1	16	RELEELNVPGEIVESL	none	2	913.483	58.41	2.5	55.3	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
368	1	16	RELEELNVPGEIVEsL	S15(Phospho)	2	953.466	54.67	3.5	57.2		x	x	3
369	1	22	RELEELNVPGEIVESLSSSEES	none	2	1216.588	58.86	4.3	82.0	x	x	x	1; 5
370	1	25	RELEELNVPGEIVESLSSSEESITR	none	3	934.805	61.58	5.3	76.1	x	x	x	1; 2; 3; 5
371	1	27	RELEELNVPGEIVESLSSSEESITRIN	none	3	1010.515	64.91	4.4	49.8	x	x	x	1; 3; 5
372	1	27	RELEELNVPGEIVESLSSsEESITRIN	S19(Phospho)	3	1037.170	59.61	4.7	66.5	x	x	x	5
373	1	27	RELEELNVPGEIVESLSsSEESITRIN	S18(Phospho)	3	1037.173	62.51	4.7	71.9	x	x	x	5
374	1	28	RELEELNVPGEIVESLSSSEESITRINK	none	3 (4)	1053.213	62.25	7.5	108.7	x	x	x	5
375	1	28	RELEELNVPGEIVESLSSsEESITRINK	S19(Phospho)	4	810.153	56.41	3.0	61.1	x	x	x	5
376	1	28	RELEELNVPGEIVESLsSSEESITRINK	S17(Phospho)	4	810.156	56.89	6.0	83.9	x	x	x	5
377	1	28	RELEELNVPGEIVESLSsSEESITRINK	S18(Phospho)	3 (4)	1079.871	60.17	6.3	23.6	x	x	x	5
378	2	11	ELEELNVPGE	none	2	564.775	39.27	2.1	44.9	x	x	x	5; 7
379	2	15	ELEELNVPGEIVES	none	2	778.888	48.81	2.5	52.2	x	x	x	5
380	7	16	NVPGEIVESL	none	2	528.782	47.86	2.1	56.8			x	
381	16	25	LSSsEESITR	S4(Phospho)	2	594.760	21.90	2.3	29.1	x	x	x	
382	17	27	SSSEESITRIN	none	2	611.797	22.75	1.8	45.8			x	
383	18	27	SSEESITRIN	none	2	568.283	22.23	2.6	48.4			x	
384	26	48	INKKIEKFQSEEQQQTEDELQDK	none	4	709.605	29.21	4.1	24.2	x	x	x	
385	26	48	INKKIEKFQsEEQQQTEDELQDK	S10(Phospho)	3 (4)	972.461	30.94	5.4	54.7	x	x	x	
386	29	39	KIEKFQsEEQQ	S7(Phospho)	2	737.334	17.73	3.1	45.3	x	x	x	
387	29	40	KIEKFQsEEQQQ	S7(Phospho)	2	801.364	18.30	3.7	47.9	x	x	x	
388	29	42	KIEKFQsEEQQQTE	S7(Phospho)	2	916.410	20.81	3.3	43.6	x	x	x	
389	29	43	KIEKFQsEEQQQTED	S7(Phospho)	2 (3)	973.922	21.13	3.9	53.5	x	x	x	
390	29	46	KIEKFQsEEQQQTEDELQ	S7(Phospho)	3 (2)	773.011	30.02	4.6	38.4	x	x	x	
391	29	47	KIEKFQSEEQQQTEDELQD	none	3 (2)	784.699	27.70	5.0	67.4	x	x	x	
392	29	47	KIEKFQsEEQQQTEDELQD	S7(Phospho)	3 (2)	811.356	30.43	5.8	67.3	x	x	x	
393	29	48	KIEKFQSEEQQQTEDELQDK	none	3 (2,4)	827.398	26.72	7.9	98.6	x	x	x	1; 3; 5
394	29	48	KIEKFQsEEQQQTEDELQDK	S7(Phospho)	3 (2,4)	854.054	29.03	7.9	85.7	x	x	x	1; 3; 5
395	29	52	KIEKFQSEEQQQTEDELQDKIHPF	none	4	744.365	40.63	5.4	57.0	x	x	x	5
396	29	52	KIEKFQsEEQQQTEDELQDKIHPF	S7(Phospho)	4 (3)	764.357	42.50	5.8	46.8	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
397	29	53	KIEKFQSEEQQQTEDELQDKIHPFA	none	4	762.125	40.51	6.2	65.4	x	x	x	2
398	29	53	KIEKFQsEEQQQTEDELQDKIHPFA	S7(Phospho)	4 (3)	782.117	42.22	5.4	54.7	x	x	x	
399	29	55	KIEKFQsEEQQQTEDELQDKIHPFAQT	S7(Phospho)	4 (3)	839.395	41.94	6.8	40.4	x	x	x	
400	29	56	KIEKFQSEEQQQTEDELQDKIHPFAQTQ	none	4	851.417	39.67	6.0	43.3	x	x	x	
401	29	56	KIEKFQsEEQQQTEDELQDKIHPFAQTQ	S7(Phospho)	4 (3)	871.409	41.33	6.6	43.8	x	x	x	
402	29	57	KIEKFQSEEQQQTEDELQDKIHPFAQTQS	none	3 (4,5)	1163.900	39.49	6.0	78.7	x	x	x	
403	29	57	KIEKFQsEEQQQTEDELQDKIHPFAQTQS	S7(Phospho)	4 (3)	893.167	41.22	6.0	48.4	x	x	x	
404	30	39	IEKFQsEEQQ	S6(Phospho)	2	673.287	20.70	3.1	39.2	x	x	x	
405	30	40	IEKFQsEEQQQ	S6(Phospho)	2	737.317	21.03	3.7	53.8			x	
406	30	43	IEKFQsEEQQQTED	S6(Phospho)	2	909.874	23.92	3.4	45.0		x	x	7
407	30	47	IEKFQSEEQQQTEDELQD	none	2	1112.498	30.61	4.8	64.7	x	x	x	
408	30	47	IEKFQsEEQQQTEDELQD	S6(Phospho)	2	1152.483	33.60	6.4	74.1	x	x	x	
409	30	48	IEKFQSEEQQQTEDELQDK	none	3 (2)	784.701	28.96	7.4	82.0	x	x	x	3; 5
410	30	48	IEKFQsEEQQQTEDELQDK	S6(Phospho)	3 (2)	811.356	31.54	7.0	71.9	x	x	x	3; 5
411	30	53	IEKFQsEEQQQTEDELQDKIHPFA	S6(Phospho)	3	999.791	44.74	5.9	56.4	x	x	x	
412	30	56	IEKFQsEEQQQTEDELQDKIHPFAQTQ	S6(Phospho)	3	1118.845	43.65	6.1	56.4	x	x	x	
413	30	57	IEKFQsEEQQQTEDELQDKIHPFAQTQS	S6(Phospho)	3	1147.857	43.52	6.2	43.8	x	x	x	
414	32	48	KFQSEEQQQTEDELQDK	none	3 (2)	703.989	24.49	5.6	61.2	x	x	x	1; 3; 5
415	32	48	KFQsEEQQQTEDELQDK	S4(Phospho)	2 (3)	1095.465	28.30	6.8	77.9	x	x	x	3; 5
416	33	48	FQSEEQQQTEDELQDK	none	2 (3)	991.432	26.81	5.6	100.3	x	x	x	3; 5
417	33	48	FQsEEQQQTEDELQDK	S3(Phospho)	2 (3)	1031.416	30.17	7.1	92.6	x	x	x	3; 5
418	33	51	FQSEEQQQTEDELQDKIHP	none	3	777.024	35.99	3.2	35.8	x	x	x	
419	33	53	FQsEEQQQTEDELQDKIHPFA	S3(Phospho)	3	876.382	45.96	4.7	59.7	x	x	x	
420	33	56	FQSEEQQQTEDELQDKIHPFAQTQ	none	3	968.781	41.90	3.8	55.2	x	x		
421	33	57	FQSEEQQQTEDELQDKIHPFAQTQS	none	3	997.794	41.74	4.6	57.4	x	x	x	
422	33	57	FQsEEQQQTEDELQDKIHPFAQTQS	S3(Phospho)	3	1024.448	44.37	4.2	56.3	x	x	x	
423	35	48	SEEQQQTEDELQDK	none	2	853.870	20.82	4.8	98.9	x	x	x	3; 5
424	35	48	sEEQQQTEDELQDK	S1(Phospho)	2	893.854	23.02	5.3	66.0	x	x	x	5
425	36	48	EEQQQTEDELQDK	none	2	810.352	18.76	3.2	72.5	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
426	37	48	EQQQTEDELQDK	none	2	745.834	16.48	2.1	37.3			x	
427	41	49	TEDELQDKI	none	2	545.765	28.47	3.2	52.6	x	x		3; 5
428	43	51	DELQDKIHP	none	2	547.777	25.81	2.2	37.7	x	x		
429	49	56	IHPFAQTQ	none	2	471.244	21.27	2.0	39.8			x	1
430	49	57	IHPFAQTQS	none	2	514.761	21.63	2.0	52.0			x	
431	57	68	SLVYPFPGPIPN	none	2	650.852	55.36	2.1	54.5			x	5; 7
432	57	72	SLVYPFPGPIPNSLPQ	none	2	863.465	59.58	2.2	62.8			x	
433	58	72	LVYPFPGPIPNSLPQ	none	2	819.948	58.52	2.4	62.8			x	
434	69	91	SLPQNIPPLTQTPVVVPPFLQPE	none	2 (3)	1256.203	67.12	2.7	60.7			x	
435	69	105	SLPQNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPK	none	4	992.555	65.99	2.0	22.5	x	x	x	
436	73	91	NIPPLTQTPVVVPPFLQPE	none	3 (2)	696.058	65.52	3.1	58.1			x	
437	83	95	VVPPFLQPEVmGV	M11(Ox)	2	714.384	55.39	1.6	33.8	x	x		5
438	83	98	VVPPFLQPEVMGVSKV	none	2	863.484	56.12	1.9	57.3	x	x	x	5
439	84	95	VPPFLQPEVMGV	none	2	656.852	59.21	1.9	43.6	x	x	x	1; 3; 5; 7
440	84	95	VPPFLQPEVmGV	M10(Ox)	2	664.849	51.70	2.2	48.6	x	x	x	1; 5
441	84	98	VPPFLQPEVMGVSKV	none	2	813.949	52.95	3.3	83.5	x	x	x	5
442	106	123	HKEMPFPKYPVEPFTESQ	none	3	731.024	41.93	3.6	50.7	x	x	x	2; 5
443	106	124	HKEMPFPKYPVEPFTESQS	none	3	760.033	41.43	3.7	59.6	x	x	x	1; 5
444	106	124	HKEmPFPKYPVEPFTESQS	M4(Ox)	3	765.364	37.95	3.6	42.2	x	x	x	5
445	106	125	HKEMPFPKYPVEPFTESQSL	none	3 (4,2)	797.727	46.12	4.2	77.8	x	x	x	1; 2; 3; 5
446	106	125	HKEmPFPKYPVEPFTESQSL	M4(Ox)	3	803.061	43.36	3.4	46.5	x	x	x	5
447	106	132	HKEMPFPKYPVEPFTESQSLTLTDVEN	none	3	1055.181	50.91	3.9	49.4	x	x	x	
448	106	133	HKEMPFPKYPVEPFTESQSLTLTDVENL	none	3 (4)	1092.878	57.53	4.3	37.4	x	x	x	5
449	107	124	KEMPFPKYPVEPFTESQS	none	3	714.347	44.61	3.4	39.8	x	x		
450	107	125	KEMPFPKYPVEPFTESQSL	none	3 (2)	752.040	49.39	4.1	66.8	x	x	x	5
451	107	125	KEmPFPKYPVEPFTESQSL	M3(Ox)	3	757.373	46.60	3.7	38.3	x	x		
452	108	119	EMPFPKYPVEPF	none	2	740.864	53.51	2.9	44.8			x	7
453	108	122	EMPFPKYPVEPFTES	none	2	899.424	51.40	2.4	48.9	x	x	x	7
454	108	123	EMPFPKYPVEPFTESQ	none	2	963.454	50.75	3.8	70.5	x	x	x	7

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
455	108	124	EMPFPKYPVEPFTESQS	none	2 (3)	1006.970	50.30	4.2	89.8	x	x	x	1; 5; 7
456	108	124	EmPFPKYPVEPFTESQS	M2(Ox)	2	1014.968	45.27	3.9	78.9	x	x	x	7; 5
457	108	125	EmPFPKYPVEPFTESQSL	M2(Ox)	2	1071.509	50.77	4.8	84.8	x	x	x	1; 5
458	108	126	EMPFPKYPVEPFTESQSLT	none	2	1114.036	53.94	3.4	56.0	x	x		
459	109	119	MPFPKYPVEPF	none	2	676.342	52.07	3.1	51.9	x		x	7; 5
460	109	120	MPFPKYPVEPFT	none	2	726.864	50.70	3.4	63.0	x	x	x	7
461	109	123	MPFPKYPVEPFTESQ	none	2	898.932	49.28	4.3	77.2	x	x	x	7
462	109	124	MPFPKYPVEPFTESQS	none	2	942.447	48.83	4.3	92.9	x	x	x	1; 5
463	109	124	mPFPKYPVEPFTESQS	M1(Ox)	2	950.446	44.33	3.7	79.9	x	x		
464	109	125	MPFPKYPVEPFTESQSL	none	2	998.991	53.76	4.8	81.9	x	x	x	1; 5
465	109	125	mPFPKYPVEPFTESQSL	M1(Ox)	2 (3)	1006.988	49.86	4.4	76.1	x	x	x	
466	109	126	MPFPKYPVEPFTESQSLT	none	2	1049.514	52.68	3.8	53.4	x	x		
467	111	124	FPKYPVEPFTESQS	none	2	828.402	42.85	3.5	65.3	x	x	x	
468	111	125	FPKYPVEPFTESQSL	none	2	884.943	48.88	4.5	97.3	x	x	x	1; 5; 7
469	114	125	YPVEPFTESQSL	none	2	698.835	46.59	2.3	49.7	x	x	x	1; 5; 7
470	115	123	PVEPFTESQ	none	2	517.245	30.39	1.9	48.8			x	7
471	115	124	PVEPFTESQS	none	2	560.762	30.03	2.3	45.6			x	7
472	115	125	PVEPFTESQSL	none	2	617.305	41.63	2.1	56.8			x	7
473	124	133	SLTLTDVENL	none	2	552.793	51.64	2.4	62.9			x	5
474	126	143	TLTDVENLHLPLPLLQSW	none	2 (3)	1045.073	73.46	3.2	58.7			x	
475	128	143	TDVENLHLPLPLLQSW	none	2	938.005	70.48	3.6	57.9			x	
476	129	139	DVENLHLPLPL	none	2	630.354	59.63	2.3	34.8			x	
477	129	143	DVENLHLPLPLLQSW	none	2	887.482	72.06	3.2	57.8			x	
478	132	143	NLHLPLPLLQSW	none	2	715.912	68.77	2.5	52.1			x	
479	134	143	HLPLPLLQSW	none	2	602.349	61.21	2.6	46.2			x	
480	144	154	MHQPHQPLPPT	none	2	641.821	20.36	2.5	52.3			x	
481	144	162	MHQPHQPLPPTVMFPPQSV	none	3	723.365	45.71	3.4	45.7			x	7
482	144	162	mHQPHQPLPPTVMFPPQSV	M1(Ox)	3	728.696	44.15	2.6	28.9			x	
483	144	163	MHQPHQPLPPTVMFPPQSVL	none	3	761.061	51.23	2.8	46.5			x	7

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
484	144	165	MHQPHQPLPPTVMFPPQSVLSL	none	3	827.764	57.91	3.5	45.2			x	
485	144	165	mHQPHQPLPPTVMFPPQSVLSL	M1(Ox)	3	833.097	57.74	2.7	20.5			x	
486	144	168	MHQPHQPLPPTVMFPPQSVLSLSQS	none	3	928.475	54.60	2.9	38.3			x	
487	161	169	SVLSLSQSK	none	2	474.770	26.09	2.3	53.0			x	
488	163	175	LSLSQSKVLPVPQ	none	2	698.414	40.81	3.0	51.2			x	
489	163	182	LSLSQSKVLPVPQKAVPYPQ	none	3	727.089	42.38	3.7	48.2			x	
490	163	190	LSLSQSKVLPVPQKAVPYPQRDMPIQAF	none	3 (4)	1046.580	50.43	5.0	73.9	x	x	x	
491	164	175	SLSQSKVLPVPQ	none	2	641.872	33.16	2.6	63.0	x		x	
492	164	176	SLSQSKVLPVPQK	none	2 (3)	705.920	27.20	3.8	71.4	x	x	x	1
493	164	182	SLSQSKVLPVPQKAVPYPQ	none	3 (2)	689.394	37.37	3.7	79.8			x	
494	164	190	SLSQSKVLPVPQKAVPYPQRDMPIQAF	none	3 (4)	1008.884	47.49	5.0	70.9	x	x	x	5
495	165	175	LSQSKVLPVPQ	none	2	598.358	31.14	2.5	35.7	x	x	x	
496	166	175	SQSKVLPVPQ	none	2	541.812	26.71	2.5	56.1			x	
497	166	176	SQSKVLPVPQK	none	2 (3)	605.860	20.63	3.3	68.0	x	x	x	
498	166	182	SQSKVLPVPQKAVPYPQ	none	2 (3)	933.533	33.87	2.6	65.6			x	
499	166	190	SQSKVLPVPQKAVPYPQRDMPIQAF	none	3	942.179	45.43	4.6	58.7	x		x	
500	167	175	QSKVLPVPQ	none	2	498.297	26.45	1.7	23.7			x	
501	168	175	SKVLPVPQ	none	2	434.267	26.11	2.3	30.6			x	
502	168	182	SKVLPVPQKAVPYPQ	none	3	550.991	33.37	1.9	56.4			x	
503	170	182	VLPVPQKAVPYPQ	none	2	718.420	36.52	2.2	74.9			x	
504	170	189	VLPVPQKAVPYPQRDMPIQA	none	3	749.748	41.93	3.2	54.9	x	x	x	5
505	170	190	VLPVPQKAVPYPQRDMPIQAF	none	3	798.771	48.74	3.6	66.4	x	x	x	5
506	170	190	VLPVPQKAVPYPQRDmPIQAF	M16(Ox)	3	804.105	44.20	3.3	67.4	x	x	x	
507	171	179	LPVPQKAVP	none	2	474.797	28.99	1.9	39.6		x		
508	171	182	LPVPQKAVPYPQ	none	2	668.884	33.86	1.9	57.1			x	
509	171	186	LPVPQKAVPYPQRDMP	none	3	612.665	36.41	3.3	61.9	x	x	x	5
510	171	189	LPVPQKAVPYPQRDMPIQA	none	3	716.725	40.01	3.4	60.3	x	x	x	
511	171	190	LPVPQKAVPYPQRDMPIQAF	none	3	765.748	47.14	2.5	24.2	x	x	x	5
512	176	182	KAVPYPQ	none	2	401.726	17.58	2.3	32.7			x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
513	176	190	KAVPYPQRDMPIQAF	none	2 (3)	880.961	40.78	3.3	78.0			x	
514	177	188	AVPYPQRDMPIQ	none	2	707.863	34.03	2.3	53.9	x	x	x	7
515	177	189	AVPYPQRDMPIQA	none	2	743.380	36.24	2.7	60.2	x	x	x	
516	177	189	AVPYPQRDmPIQA	M9(Ox)	2	751.378	29.73	2.2	50.8	x	x	x	
517	177	190	AVPYPQRDMPIQAF	none	2	816.914	46.08	2.3	69.2			x	5; 7
518	177	190	AVPYPQRDmPIQAF	M9(Ox)	2	824.913	39.44	2.7	65.3			x	
519	177	191	AVPYPQRDMPIQAFL	none	2	873.458	56.17	2.0	51.9			x	
520	177	209	AVPYPQRDMPIQAFLLYQEPVLGPVRGPFPIIV	none	3	1241.015	76.08	4.9	56.7	x	x	x	5
521	177	209	AVPYPQRDmPIQAFLLYQEPVLGPVRGPFPIIV	M9(Ox)	3	1246.351	73.24	4.2	43.1	x	x	x	
522	178	184	VPYPQRD	none	2	437.723	16.09	1.4	32.5	x	x		
523	178	186	VPYPQRDmP	M8(Ox)	2	559.768	21.20	2.3	42.8	x	x		7
524	178	188	VPYPQRDMPIQ	none	2	672.341	32.40	3.4	60.2	x	x	x	1; 7
525	178	188	VPYPQRDmPIQ	M8(Ox)	2	680.338	25.25	2.9	47.6	x	x		1; 7
526	178	189	VPYPQRDMPIQA	none	2	707.860	34.71	2.8	68.9	x	x	x	1; 4; 5
527	178	189	VPYPQRDmPIQA	M8(Ox)	2	715.858	28.04	2.7	60.1	x	x	x	1
528	178	190	VPYPQRDMPIQAF	none	2	781.395	45.14	3.2	76.2	x	x	x	
529	178	191	VPYPQRDMPIQAFL	none	2	837.938	55.53	3.2	61.7	x	x		1; 2; 5
530	178	191	VPYPQRDmPIQAFL	M8(Ox)	2	845.934	48.70	2.6	35.7	x	x		
531	180	189	YPQRDmPIQA	M6(Ox)	2	617.797	22.13	2.0	38.9	x			
532	180	190	YPQRDMPIQAF	none	2	683.336	41.11	2.4	43.1			x	
533	183	190	RDMPIQAF	none	2	489.247	36.95	1.7	40.9			x	
534	183	190	RDmPIQAF	M3(Ox)	2	497.245	29.32	2.0	36.6			x	
535	191	198	LLYQEPVL	none	2	487.781	47.22	1.6	33.2			x	
536	191	201	LLYQEPVLGPV	none	2	614.354	51.48	2.4	48.9	x		x	5
537	191	206	LLYQEPVLGPVRGPFP	none	2 (3)	891.506	55.05	4.2	89.3			x	6; 7
538	191	207	LLYQEPVLGPVRGPFPI	none	2 (3)	948.046	61.12	3.5	78.7	x	x	x	
539	191	208	LLYQEPVLGPVRGPFPII	none	2 (3)	1004.586	65.35	4.0	80.7	x	x	x	2
540	191	209	LLYQEPVLGPVRGPFPIIV	none	2 (3)	1054.120	67.06	4.2	89.0	x	x	x	1; 5; 6
541	192	206	LYQEPVLGPVRGPFP	none	2	834.960	50.72	4.0	84.4			x	2; 6

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
542	192	207	LYQEPVLGPVRGPFPI	none	2	891.503	57.40	3.2	81.7	x		x	2
543	192	208	LYQEPVLGPVRGPFPII	none	2	948.043	62.13	4.2	88.2	x	x	x	2; 5; 6
544	192	209	LYQEPVLGPVRGPFPIIV	none	2 (3)	997.578	63.95	3.8	82.3	x	x	x	1; 4; 5; 6
545	193	202	YQEPVLGPVR	none	2	579.318	32.25	2.7	57.7	x	x	x	1; 5; 7
546	193	206	YQEPVLGPVRGPFP	none	2	778.417	48.25	3.1	87.7			x	1; 6; 7
547	193	207	YQEPVLGPVRGPFPI	none	2	834.961	55.25	3.8	83.1	x	x	x	7
548	193	208	YQEPVLGPVRGPFPII	none	2	891.501	60.09	4.1	85.1	x	x	x	1; 5
549	193	209	YQEPVLGPVRGPFPIIV	none	2 (3)	941.035	62.19	3.8	91.8	x	x	x	1; 5; 6
550	194	202	QEPVLGPVR	none	2	497.787	26.58	2.0	41.2	x	x		1
551	194	206	QEPVLGPVRGPFP	none	2	696.884	45.81	2.8	66.0	x	x	x	1; 5; 7
552	194	208	QEPVLGPVRGPFPII	none	2	809.969	58.45	2.9	72.1	x	x	x	1; 5; 7
553	194	209	QEPVLGPVRGPFPIIV	none	2	859.503	60.57	3.1	77.1	x	x	x	1; 5
554	195	206	EPVLGPVRGPFP	none	2	632.855	45.94	2.5	61.7	x	x	x	1; 4; 5; 6; 7
555	195	207	EPVLGPVRGPFPI	none	2	689.398	53.30	2.1	47.3	x	x	x	1; 5; 7
556	195	208	EPVLGPVRGPFPII	none	2	745.940	58.53	2.6	62.8	x	x	x	1; 5
557	195	209	EPVLGPVRGPFPIIV	none	2	795.474	60.82	2.7	66.9	x	x	x	1; 2; 4; 5
558	196	209	PVLGPVRGPFPIIV	none	2	730.953	60.32	3.1	65.3	x	x	x	1; 3
559	197	209	VLGPVRGPFPIIV	none	2	682.427	58.12	1.9	46.5		x	x	
560	198	209	LGPVRGPFPIIV	none	2	632.892	56.47	1.8	46.8	x	x	x	5
561	199	208	GPVRGPFPII	none	2	526.815	48.58	2.1	46.6	x	x	x	1
562	199	209	GPVRGPFPIIV	none	2	576.350	51.83	1.7	43.6	x	x	x	1; 4; 5
563	200	209	PVRGPFPIIV	none	2	547.837	51.65	2.1	36.0		x	x	1; 2; 6
Beta-lactoglobulin (P02754)													
564	1	8	LIVTQTMK	none	2	467.274	25.46	2.4	48.2	x	x	x	1; 2
565	1	10	LIVTQTMKGL	none	2	552.328	40.43	2.7	55.7		x	x	
566	1	10	LIVTQTmKGL	M7(Ox)	2	560.326	30.39	2.3	56.8			x	
567	1	11	LIVTQTMKGLD	none	2	609.843	37.95	3.3	71.7		x	x	
568	1	11	LIVTQTmKGLD	M7(Ox)	2	617.840	28.49	2.7	69.5		x	x	
569	1	13	LIVTQTMKGLDIQ	none	2	730.415	45.62	3.6	80.9		x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
570	1	13	LIVTQTmKGLDIQ	M7(Ox)	2	738.412	37.26	3.3	72.2			x	
571	1	17	LIVTQTMKGLDIQKVAG	none	2	908.025	44.70	3.4	51.7		x	x	
572	2	13	IVTQTMKGLDIQ	none	2	673.872	36.76	2.6	51.5			x	
573	9	16	GLDIQKVA	none	2	422.250	29.83	2.0	37.7			x	
574	9	22	GLDIQKVAGTWYSL	none	2	775.914	58.01	3.2	68.3			x	
575	11	22	DIQKVAGTWYSL	none	2	690.863	49.95	3.6	60.5			x	
576	14	22	KVAGTWYSL	none	2	512.776	41.72	2.3	61.5			x	
577	33	42	DAQSAPLRVY	none	2	560.292	30.72	2.6	76.1			x	
578	127	136	EVDDEALEKF	none	2	597.779	37.48	2.0	36.0	x	x		
579	153	162	PTQLEEQCHI	none	2	599.281	29.13	3.0	63.5		x	x	
Butyrophilin subfamily 1 member A1 (P18892)													
580	50	66	VSREGQEQEGEEMAEYR	none	3 (2)	676.297	24.37	5.4	103.8	x	x	x	
581	50	66	VSREGQEQEGEEmAEYR	M13(Ox)	3 (2)	681.629	18.02	5.3	69.8	x	x	x	
582	53	66	EGQEQEGEEMAEYR	none	2	842.840	26.18	3.7	70.2	x	x	x	
583	53	66	EGQEQEGEEmAEYR	M10(Ox)	2	850.838	18.52	2.7	48.9	x	x		
584	67	84	GRVSLVEDHIAEGSVAVR	none	3 (4)	632.009	33.19	4.0	67.8	x	x	x	
585	68	84	RVSLVEDHIAEGSVAVR	none	3	613.001	32.41	3.7	55.1	x	x	x	
586	69	84	VSLVEDHIAEGSVAVR	none	3	560.969	35.23	4.0	65.0	x	x	x	
587	70	84	SLVEDHIAEGSVAVR	none	3 (2)	527.945	32.36	3.9	77.3	x	x		
588	72	82	VEDHIAEGSVA	none	2	563.770	22.24	2.1	47.6	x	x	x	
589	72	84	VEDHIAEGSVAVR	none	3 (2)	461.240	23.63	4.3	66.3	x	x	x	
590	85	97	IQEVKASDDGEYR	none	2	755.361	19.00	3.6	63.5	x	x		
591	102	114	QDENYEEAIVHLK	none	3	529.924	37.79	3.3	35.8	x	x		
592	153	177	THRGEEFPSMSESRNPDEEGLFTVR	none	4 (3,5)	727.589	39.91	5.9	89.2	x	x	x	3; 5
593	153	177	THRGEEFPSmSESRNPDEEGLFTVR	M10(Ox)	4 (3,5)	731.586	34.95	5.4	54.7	x	x	x	3
594	156	177	GEEFPSMSESRNPDEEGLFTVR	none	3	838.380	45.95	4.8	65.2	x	x	x	
595	169	177	DEEGLFTVR	none	2	533.263	38.33	2.6	54.1		x		
596	196	203	NLLLGQEK	none	2	457.767	27.71	2.2	31.5	x	x		
597	287	297	HPHLFLYEDSK	none	3	462.564	31.26	3.4	60.7	x	x		

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
598	467	500	KEIPLSPMGEDSASGDIETLHSKLIPLQPSQGVP	none	3	1190.953	53.65	4.3	48.0	x	x		
599	469	487	IPLSPMGEDSASGDIETLH	none	2	984.967	43.78	5.5	123.4	x	x	x	5
600	469	487	IPLSPmGEDSASGDIETLH	M6(Ox)	2	992.963	38.58	5.0	99.5	x	x	x	
601	472	487	SPmGEDSASGDIETLH	M3(Ox)	2	831.350	27.44	3.3	68.5	x	x	x	
602	475	487	GEDSASGDIETLH	none	2	665.789	25.58	3.7	84.0	x	x	x	
CCAAT/enhancer-binding protein beta (O02755)													
603	161	169	HPPPPPPPP	none	2	466.751	18.19	2.2	48.0	x	x		
DNA-directed RNA polymerases I, II, and III subunit RPABC1 (Q2T9T3)													
604	77	87	PEEPKVGIKTI	none	3 (2)	404.239	29.20	3.2	53.8	x	x		
DnaJ homolog subfamily C member 12 (Q9N287)													
605	185	193	APSELLRKF	none	2	530.811	34.61	2.8	45.6	x	x		
Fatty acid synthase (Q71SP7)													
606	379	389	RPLPVLGGNVG	none	2	539.821	36.20	2.6	53.8	x	x		
607	379	393	RPLPVLGGNVGINSF	none	2	770.435	51.61	3.1	58.6	x	x		
608	1483	1493	SPIPETDPKSL	none	2	592.313	31.30	2.4	61.1	x	x	x	
609	20	38	EDGSDPPSGDFLTEGGGVR	none	2	946.420	37.27	3.3	87.9	x	x	x	
Fibroblast growth factor-binding protein 1 (Q9MZ06)													
610	8	27	RGSKASADESLALGKPGKEP	none	4	500.269	22.06	2.7	32.2	x	x	x	
611	8	28	RGSKASADESLALGKPGKEPR	none	4 (5)	539.295	19.29	5.0	70.4	x	x	x	2; 5
612	9	27	GSKASADESLALGKPGKEP	none	3	614.655	24.30	4.5	59.0	x	x	x	
613	9	28	GSKASADESLALGKPGKEPR	none	3 (2,4,5)	666.691	20.88	3.8	55.0	x	x	x	2; 3; 5
614	9	28	GSKAsADESLALGKPGKEPR	S5(Phospho)	4	520.261	22.73	4.1	31.4	x	x		3
615	12	28	ASADESLALGKPGKEPR	none	3 (4)	575.976	22.88	3.7	55.9	x	x	x	5
616	13	28	SADESLALGKPGKEPR	none	3	552.295	22.11	3.6	36.6	x	x		
617	14	28	ADESLALGKPGKEPR	none	3	523.285	21.58	3.1	29.9	x	x		
FXYD domain-containing ion transport regulator 6 (Q3MHZ5)													
618	1	20	SATEQEKEKDPFHYDYQTLR	none	4 (3)	622.046	32.90	3.4	42.2	x	x	x	
619	1	25	SATEQEKEKDPFHYDYQTLRIGGLV	none	3 (4)	975.486	49.06	4.6	76.6	x	x	x	
Glycosylation-dependent cell adhesion molecule 1 (P80195)													

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
620	1	11	ILNKPEDETHL	none	2 (3)	654.843	25.37	3.4	73.6		x	x	
621	1	12	ILNKPEDETHLE	none	2 (3)	719.364	24.28	3.7	71.4	x	x	x	
622	1	16	ILNKPEDETHLEAQPT	none	2	917.964	26.34	3.3	71.8	x	x	x	
623	1	17	ILNKPEDETHLEAQPTD	none	2	975.475	26.66	4.4	73.7	x	x	x	
624	1	18	ILNKPEDETHLEAQPTDA	none	3 (2)	674.332	27.78	2.3	47.4	x	x	x	
625	1	20	ILNKPEDETHLEAQPTDASA	none	2	1090.030	28.01	3.7	58.1	x	x	x	3
626	1	21	ILNKPEDETHLEAQPTDASAQ	none	2 (3)	1154.065	27.25	3.3	71.3	x	x	x	7
627	1	22	ILNKPEDETHLEAQPTDASAQF	none	2 (3)	1227.595	35.72	4.8	105.5	x	x	x	3; 5; 7
628	1	23	ILNKPEDETHLEAQPTDASAQFI	none	2 (3)	1284.141	41.00	3.6	60.9	x	x	x	5
629	1	24	ILNKPEDETHLEAQPTDASAQFIR	none	3 (2,4)	908.460	36.52	6.1	99.0	x	x	x	3; 5
630	1	24	ILNKPEDETHLEAQPTDAsAQFIR	S19(Phospho)	3	935.114	36.44	4.9	51.7	x	x	x	
631	1	25	ILNKPEDETHLEAQPTDASAQFIRN	none	3	946.474	35.84	6.2	73.4	x	x	x	3; 4; 5
632	1	26	ILNKPEDETHLEAQPTDASAQFIRNL	none	3 (4)	984.169	47.12	7.4	94.4	x	x	x	
633	1	27	ILNKPEDETHLEAQPTDASAQFIRNLQ	none	3 (4)	1026.855	44.88	6.2	86.5	x	x	x	5
634	1	53	ILNKPEDETHLEAQPTDASAQFIRNLQISNEDLSKEPSISREDLI SKEQIVIR	none	6 (5)	1010.530	54.54	5.3	30.0	x	x	x	
635	2	12	LNKPEDETHLE	none	3 (2)	442.217	20.37	3.2	65.4	x	x	x	
636	2	22	LNKPEDETHLEAQPTDASAQF	none	3 (2)	781.038	33.47	4.4	71.4	x	x	x	7
637	2	24	LNKPEDETHLEAQPTDASAQFIR	none	4	653.324	34.72	3.8	44.2	x	x		5
638	12	22	EAQPTDASAQF	none	2	582.761	27.79	2.8	73.9			x	
639	13	22	AQPTDASAQF	none	2	518.240	26.40	2.6	52.4			x	
640	13	26	AQPTDASAQFIRNL	none	2	766.397	46.18	3.1	75.8			x	
641	44	53	LIsKEQIVIR	S3(Phospho)	2	639.862	35.70	3.2	44.0	x	x	x	
642	54	66	SSRQPQSQNPKLP	none	3	489.594	19.71	2.9	45.8	x	x	x	
643	54	67	SSRQPQSQNPKLPL	none	3 (2)	527.289	27.77	3.5	60.7	x	x	x	
644	54	68	SSRQPQSQNPKLPLS	none	3 (2)	556.300	25.69	2.7	49.7	x	x	x	3; 5; 7
645	54	70	SSRQPQSQNPKLPLSIL	none	2 (3)	947.033	45.70	3.2	77.8	x	x	x	5; 7
646	54	71	SSRQPQSQNPKLPLSILK	none	3 (2,4)	674.387	37.70	5.4	71.1	x	x	x	5
647	54	72	SSRQPQSQNPKLPLSILKE	none	4 (3)	538.303	39.06	4.8	61.0	x	x	x	3; 5

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
648	54	73	SSRQPQSQNPKLPLSILKEK	none	4 (3,5)	570.327	34.40	5.8	59.2	x	x	x	2; 3; 5
649	54	75	SSRQPQSQNPKLPLSILKEKHL	none	4 (3,5)	632.862	36.82	5.2	55.9	x	x	x	2; 3; 5
650	55	68	SRQPQSQNPKLPLS	none	3 (2)	527.289	25.48	2.8	38.5	x	x	x	3; 5
651	55	70	SRQPQSQNPKLPLSIL	none	3	602.680	45.70	3.0	24.8	x	x	x	
652	55	71	SRQPQSQNPKLPLSILK	none	4 (3)	484.284	37.75	4.1	60.2	x	x	x	
653	57	68	QPQSQNPKLPLS	none	2	668.864	28.63	2.1	55.3	x	x	x	5
654	57	70	QPQSQNPKLPLSIL	none	2	781.948	50.34	1.9	52.9	x	x	x	5
655	57	71	QPQSQNPKLPLSILK	none	3	564.333	41.21	1.8	30.6	x	x		
656	57	73	QPQSQNPKLPLSILKEK	none	3 (4)	650.046	37.29	3.1	26.5	x	x	x	5
657	57	75	QPQSQNPKLPLSILKEKHL	none	3 (5)	733.426	39.24	2.3	37.1	x	x		5
658	60	67	SQNPKLPL	none	2	448.763	30.54	2.1	42.0			x	
659	60	68	SQNPKLPLS	none	2	492.279	27.81	2.0	45.6			x	
660	60	70	SQNPKLPLSIL	none	2	605.364	50.30	2.4	51.9			x	7
661	62	70	NPKLPLSIL	none	2	497.818	51.03	2.2	35.4			x	
662	63	70	PKLPLSIL	none	2	440.797	50.94	1.9	25.4			x	
663	65	73	LPLSILKEK	none	2	520.839	35.61	1.8	43.7	x	x		3
664	65	74	LPLSILKEKH	none	2	589.368	31.08	2.2	47.5	x	x		
665	65	75	LPLSILKEKHL	none	2 (3)	645.910	37.83	3.5	55.1	x	x	x	
666	109	121	RNLENTVKETIKY	none	3 (2)	536.629	32.85	4.0	61.3		x	x	
667	111	121	LENTVKETIKY	none	2 (3)	669.369	27.69	3.2	66.8			x	
668	112	121	ENTVKETIKY	none	2 (3)	612.827	23.24	2.9	47.2			x	
669	113	121	NTVKETIKY	none	2	548.305	21.05	2.3	46.5			x	
670	122	135	LKSLFSHAFEVVKT	none	3 (4)	535.972	43.57	3.2	70.5			x	
671	123	135	KSLFSHAFEVVKT	none	3	498.276	39.18	3.5	50.7			x	
672	124	135	SLFSHAFEVVKT	none	2	682.864	46.16	3.2	79.8		x	x	
673	126	135	FSHAFEVVKT	none	2	582.805	30.31	2.6	73.2			x	
674	127	135	SHAFEVVKT	none	2	509.270	22.60	2.9	73.2	x	x	x	3; 5
675	128	135	HAFEVVKT	none	2	465.755	21.45	2.2	55.9	x	x	x	
Kappa-casein (P02668)													

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
676	14	24	DERFFSDKIAK	none	3	452.569	29.31	3.4	41.0	x	x	x	
677	31	38	VLSRYPSY	none	2	492.761	26.80	2.4	58.3			x	
678	31	40	VLSRYPSYGL	none	2	577.813	36.76	2.7	65.7			x	
679	31	41	VLSRYPSYGLN	none	2	634.836	32.74	3.1	73.5			x	
680	31	43	VLSRYPSYGLNYY	none	2	797.901	42.57	2.8	65.6			x	
681	33	40	SRYPSYGL	none	2	471.736	30.91	2.2	47.8			x	
682	33	41	SRYPSYGLN	none	2	528.759	26.99	2.5	62.1			x	
683	33	43	SRYPSYGLNYY	none	2	691.824	38.76	3.4	63.3			x	
684	41	50	NYYQQKPVAL	none	2	612.325	31.29	2.8	67.2			x	
685	42	50	YYQQKPVAL	none	2	555.303	28.59	2.7	58.1			x	7
686	42	53	YYQQKPVALINN	none	2	725.889	31.23	3.4	50.9			x	
687	43	50	YQQKPVAL	none	2	473.770	24.17	2.4	47.3			x	
688	43	53	YQQKPVALINN	none	2	644.356	27.79	3.2	45.1			x	
689	49	65	ALINNQFLPYPYYAKPA	none	2	992.023	53.06	3.4	55.7	x	x		5
690	51	65	INNQFLPYPYYAKPA	none	2	899.963	46.66	4.2	65.6			x	
691	52	65	NNQFLPYPYYAKPA	none	2	843.421	44.60	2.9	59.9			x	
692	66	74	AVRSPAQIL	none	2	477.790	33.35	2.2	36.9			x	
693	66	76	AVRSPAQILQW	none	2	634.860	49.07	2.1	49.7			x	
694	69	79	SPAQILQWQVL	none	2	641.862	61.49	1.6	54.8	x			5
695	106	137	MAIPPKKNQDKTEIPTINTIASGEPTSTPTTE	none	4	853.441	38.57	2.9	31.8			x	
696	106	137	mAIPPKKNQDKTEIPTINTIASGEPTSTPTTE	M1(Ox)	4	857.439	37.24	4.1	25.9			x	
697	106	169	MAIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEDsP EVIESPPEINTVQVTSTAV	S44(Phospho)	4	1696.848	62.56	3.8	26.3			x	
698	114	123	QDKTEIPTIN	none	2	579.803	29.01	2.1	41.2			x	
699	148	169	DsPEVIESPPEINTVQVTSTAV	S2(Phospho)	2	1196.565	53.71	3.8	59.2		x	x	
700	149	169	SPEVIESPPEINTVQVTSTAV	none	2	1099.067	48.66	4.2	98.1	x	x	x	
701	149	169	sPEVIESPPEINTVQVTSTAV	S1(Phospho)	2	1139.050	52.01	4.3	82.7	x	x	x	
702	150	169	PEVIESPPEINTVQVTSTAV	none	2	1055.551	48.60	4.1	90.8	x	x	x	
703	151	169	EVIESPPEINTVQVTSTAV	none	2	1007.024	47.36	3.1	68.6		x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UH T[a]	IF[a]	Literature (milk[1-6], colostrum[7])
704	152	160	VIESPPEIN	none	2	499.263	30.82	2.5	62.2			x	
705	152	161	VIESPPEINT	none	2	549.787	33.18	2.4	56.9	x		x	7
706	152	169	VIESPPEINTVQVTSTAV	none	2	942.502	45.84	2.9	64.9		x	x	
707	155	169	SPPEINTVQVTSTAV	none	2	771.905	40.01	2.3	65.2		x	x	
708	159	169	INTVQVTSTAV	none	2	566.813	33.08	2.4	57.2			x	1; 7
709	161	169	TVQVTSTAV	none	2	453.249	25.67	2.6	51.5		x	x	3
Lactoperoxidase (P80025)													
710	1	20	DTIAQAASTTTISDAVSKVK	none	2 (3)	1004.034	42.63	4.3	73.2	x	x	x	
711	35	46	KTTLSSEAPTTQ	none	2	632.325	17.99	2.4	63.4			x	
712	37	53	TLSSEAPTTQQLSEYFK	none	2	965.476	47.25	5.0	93.2	x	x		
713	39	51	SSEAPTTQQLSEY	none	2	720.829	32.42	2.6	75.0			x	
714	40	51	SEAPTTQQLSEY	none	2	677.312	32.40	2.1	47.2			x	
715	61	74	TAIRNGQVWEESLK	none	3	544.289	32.63	3.4	55.2	x	x	x	5
716	61	76	TAIRNGQVWEESLKRL	none	4 (3)	475.765	41.47	5.2	61.8	x	x	x	
717	62	74	AIRNGQVWEESLK	none	3	510.606	31.57	3.9	40.9	x	x	x	3
718	62	76	AIRNGQVWEESLKRL	none	4	450.502	40.52	3.3	24.9	x	x	x	
719	65	74	NGQVWEESLK	none	2	595.296	32.68	2.1	53.4	x	x	x	3
720	66	74	GQVWEESLK	none	2	538.274	32.27	2.8	53.1	x	x	x	5
721	66	76	GQVWEESLKRL	none	2 (3)	672.866	41.64	3.2	57.6	x	x	x	
722	67	74	QVWEESLK	none	2	509.763	30.34	1.6	38.3	x	x	x	
723	67	76	QVWEESLKRL	none	2 (3)	429.906	39.35	1.8	54.1	x	x	x	2
724	68	76	VWEESLKRL	none	2	580.327	35.46	2.4	53.4	x	x	x	
Wiskott-Aldrich syndrome protein family member 2 (A2VDK6)													
725	384	393	APPPPPPPPP	none	2	482.267	24.04	2.8	45.9	x	x		
726	385	393	PPPPPPPPP	none	2	446.748	23.87	2.1	41.1	x	x	x	
727	385	393	PPPPPPPPP	none	2	495.274	25.65	2.4	41.2	x	x	x	
Mucin-1 (Q8WML4)													
728	532	545	SPYEEVSAGNGGSN	none	2	684.288	22.52	2.5	41.8	x	x		
Mucin-15 (Q8MI01)													

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
729	246	257	RLYDDRNEPVLR	none	3	515.942	25.09	2.6	36.3	x	x		
730	247	257	LYDDRNEPVLR	none	2 (3)	695.359	26.02	2.3	47.0	x	x		
731	248	257	YDDRNEPVLR	none	3	426.213	21.04	2.7	36.8	x	x	x	
Myosin regulatory light polypeptide 9 (Q5E9E2)													
732	97	105	TDPEDVIRN	none	2	529.758	24.72	1.8	45.4	x	x		
733	98	105	DPEDVIRN	none	2	479.234	22.25	2.5	47.1	x	x		
Osteopontin (P31096)													
734	20	34	YPDAVATWLKPDPSQ	none	2	844.419	47.19	3.6	69.4	x			
735	249	262	RISHELDSASSEVN	none	2	772.372	21.43	2.7	77.0	x	x	x	3; 5
736	249	262	RISHELDSAsSEVN	S10(Phospho)	2	812.352	21.84	2.8	45.4	x	x	x	
737	249	262	RISHELDsASSEVN	S8(Phospho)	2	812.354	23.41	3.3	50.7	x	x	x	
738	250	262	ISHELDSASSEVN	none	2	694.319	22.59	3.2	64.1	x	x	x	3
739	250	262	ISHELDsASSEVN	S7(Phospho)	2	734.304	25.27	3.3	54.3	x	x	x	
740	250	262	IRIsHELDSASSEVN	S4(Phospho)	2	868.896	34.04	3.8	57.5	x	x	x	
741	250	262	IRISHELDsASSEVN	S9(Phospho)	2	868.896	30.96	3.7	54.7	x	x	x	
742	248	262	IRISHELDSAsSEVN	S11(Phospho)	2	868.896	29.61	3.2	52.5	x	x	x	
743	251	262	SHELDSASSEVN	none	2	637.777	18.34	2.9	56.8	x	x		
744	252	262	HELDSASSEVN	none	2	594.261	16.57	2.0	45.0	x	x	x	
Parathyroid hormone-related protein (P58073)													
745	128	153	VAGTGLEEDYLSDISATsLELNSRRH	S18(Phospho)	3 (4)	971.795	49.90	5.1	30.3			x	
Perilipin-2 (Q9TUM6)													
746	7	15	EPQLSVVTR	none	2	514.789	27.53	1.7	35.8	x	x		5
747	66	76	LPIIQKLEPQIA	none	2	681.920	47.82	3.4	61.0	x	x	x	5
748	191	200	LPLTKDELEK	none	2	593.338	26.60	2.5	56.2	x			
749	431	459	HPKPVPVSNAEGSQPDDSSS	none	3 (2)	678.982	17.44	3.8	49.3	x	x	x	
Poly(rC)-binding protein 1 (Q5E9A3)													
750	317	327	NPVEGSSGRQV	none	2	565.281	15.67	2.5	34.4	x	x		
Polymeric immunoglobulin receptor (P81265)													
751	555	567	QVKAAPAGAAIQS	none	2	606.339	19.41	2.3	53.7	x	x	x	

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
752	556	567	VKAAPAGAAIQS	none	2	542.310	18.18	2.1	45.5	x			
753	558	568	AAPAGAAIQSR	none	2	506.778	15.50	3.0	53.9	x	x		
754	558	574	AAPAGAAIQSRAGEIQN	none	3 (2)	542.283	25.58	3.5	84.6	x	x	x	7
755	558	575	AAPAGAAIQSRAGEIQNK	none	2 (3)	876.970	23.89	4.5	90.0	x	x	x	5
756	559	573	APAGAAIQSRAGEIQ	none	2	720.382	25.55	4.5	78.3	x	x	x	
757	559	574	APAGAAIQSRAGEIQN	none	2	777.405	24.43	4.4	82.8	x	x	x	
758	559	575	APAGAAIQSRAGEIQNK	none	3	561.303	22.72	2.8	45.7	x	x		
759	569	579	AGEIQNKALLD	none	2	586.319	27.50	2.7	58.2	x	x	x	
760	569	583	AGEIQNKALLDPSFF	none	2	825.432	53.46	2.5	49.1			x	
761	569	613	AGEIQNKALLDPSFFAKESVKDAAGGPGAPADPGRPTGYSGSSKA	none	4 (5,6)	1105.058	44.24	4.2	38.5	x	x	x	
762	569	617	AGEIQNKALLDPSFFAKESVKDAAGGPGAPADPGRPTGYSGSSKALVST	none	5	964.290	46.64	3.6	47.3	x	x	x	
763	576	600	ALLDPSFFAKESVKDAAGGPGAPAD	none	3	811.077	50.07	3.3	58.5	x	x	x	
764	576	605	ALLDPSFFAKESVKDAAGGPGAPADPGRPT	none	4	735.630	47.84	4.7	64.3			x	
765	576	613	ALLDPSFFAKESVKDAAGGPGAPADPGRPTGYSGSSKA	none	3 (4)	1226.281	45.69	5.3	54.9	x	x	x	5
766	576	617	ALLDPSFFAKESVKDAAGGPGAPADPGRPTGYSGSSKALVST	none	4	1020.021	48.33	4.1	31.9	x	x	x	
767	576	622	ALLDPSFFAKESVKDAAGGPGAPADPGRPTGYSGSSKALVSTLVPLA	none	4 (3)	1143.353	59.10	3.9	29.9	x	x	x	
768	582	613	FFAKESVKDAAGGPGAPADPGRPTGYSGSSKA	none	4 (3,5)	770.881	28.49	3.9	62.4	x	x	x	3; 5
769	583	613	FAKESVKDAAGGPGAPADPGRPTGYSGSSKA	none	4 (3)	734.112	24.09	4.6	59.5	x	x	x	3
770	587	605	SVKDAAGGPGAPADPGRPT	none	3	574.291	19.15	3.8	64.9			x	
771	587	610	SVKDAAGGPGAPADPGRPTGYSGS	none	3	724.682	22.81	4.1	59.2			x	
772	590	605	DAAGGPGAPADPGRPT	none	2	703.836	19.04	3.0	70.2			x	
773	590	622	DAAGGPGAPADPGRPTGYSGSSKALVSTLVPLA	none	3	1013.193	50.88	3.0	44.0	x	x	x	
774	591	605	AAGGPGAPADPGRPT	none	2	646.322	17.50	2.6	60.8			x	
775	591	613	AAGGPGAPADPGRPTGYSGSSKA	none	3	676.995	20.62	1.8	32.4	x	x	x	
776	601	614	PGRPTGYSGSSKAL	none	3	459.908	19.31	4.2	71.3		x	x	
777	601	622	PGRPTGYSGSSKALVSTLVPLA	none	3	720.067	47.96	1.5	39.5	x	x	x	
Protein canopy homolog 3 (Q0P5N1)													

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
778	31	41	LPAPELGPRQA	none	2	574.823	30.01	2.6	55.2	x	x	x	
Protein OS-9 (Q3MHX6)													
779	3	16	VGSLNLEELSEMRY	none	2	820.406	53.49	3.0	58.0			x	
Ribonuclease pancreatic (P61823)													
780	114	124	PYVPVHFDASV	none	2	615.811	43.25	2.7	71.7		x	x	
Secretoglobin family 1D member (A0JNP2)													
781	72	81	VKAVLNPSSA	none	2	493.287	22.60	2.3	42.5		x		
Serum albumin (P02769)													
782	408	415	FQNALIVR	none	2	480.785	33.47	2.3	43.3	x			
783	419	433	KVPQVSTPTLVEVSR	none	3 (2)	547.317	35.69	4.3	72.5	x			
784	99	112	DPNHFRPAGLPDKY	none	3	542.938	31.70	3.1	45.9	x	x		
Sodium-dependent phosphate transport protein 2B (Q27960)													
785	3	26	PWPELENSQPTSEKYTVKADGEQS	none	3	907.428	37.29	3.0	55.0	x	x		
786	4	16	WPELENSQPTSEK	none	2	772.866	33.22	3.4	63.6	x	x	x	
787	4	25	WPELENSQPTSEKYTVKADGEQ	none	3	846.067	36.08	3.9	56.8	x	x	x	
788	4	26	WPELENSQPTSEKYTVKADGEQS	none	3	875.076	35.82	5.2	68.4	x	x	x	
789	6	26	ELENSQPTSEKYTVKADGEQS	none	3	780.700	23.64	3.1	34.6	x	x	x	
790	26	53	SAKPEKAKETEKDDTGTPITKIELVPSH	none	4 (5)	763.158	30.78	5.2	52.7	x	x	x	
791	27	53	AKPEKAKETEKDDTGTPITKIELVPSH	none	3 (4,5)	988.201	30.74	4.8	60.1	x	x	x	
792	31	53	KAKETEKDDTGTPITKIELVPSH	none	4	635.090	32.21	5.3	57.7	x	x	x	
793	39	47	DTGTPITKI	none	2	473.265	29.26	2.2	50.3	x	x	x	
794	42	53	TPITKIELVPSH	none	3	445.594	35.58	3.6	62.2	x	x	x	
795	666	693	MDKEAQDGVTKSEVDASGTKIVSSVTAL	none	3	956.151	44.54	5.0	51.1	x	x	x	
796	666	693	mDKEAQDGVTKSEVDASGTKIVSSVTAL	M1(Ox)	3	961.483	44.03	4.0	54.0	x	x		
797	667	683	DKEAQDGVTKSEVDASG	none	2	868.401	17.60	2.5	52.0	x	x		
798	667	685	DKEAQDGVTKSEVDASGTK	none	3	655.651	16.50	2.3	36.5	x	x		
799	667	693	DKEAQDGVTKSEVDASGTKIVSSVTAL	none	3	912.470	44.67	4.9	50.8	x	x	x	
Syndecan-2 (Q58DD4)													
800	99	120	KTDPAEEDTNVYTEKHSDNLFK	none	4	646.055	29.65	4.5	33.4	x	x		

Nr.	Start pos.	End pos.	Sequence	Modification	z	*m/z*	t_R (min)	Xcorr	-10lgP	RM[a]	UHT[a]	IF[a]	Literature (milk[1-6], colostrum[7])
Xanthine dehydrogenase/oxidase (P80457)													
801	563	575	PNGQsKEDTVGRP	S5(Phospho)	2	732.827	15.44	2.5	32.1	x	x		

*Phosphorylation sites rely on sequences suggested by Proteome Discoverer 2.2 and PEAKS.

[a] It should be noted that the acquired LC-MS/MS data sets for the different milk types were not statistically different in terms of number of tandem mass spectra acquired per replicate (ranging from 2359 to 2735, with an average of 2541). Additionally, the overall peak area sum (sum of peak areas of all peptides in a sample replicate) was not significantly different between the samples ($p > 0.09$).

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(3) Dallas, D.C.; Guerrero, A.; Parker, E. A.; Garay, L.A.; Bhandari, A.; Lebrilla, C.B. et al. (2014): Peptidomic profile of milk of Holstein cows at peak lactation. In: J. Agric. Food Chem. 62 (1), S. 58–65. DOI: 10.1021/jf4040964.

(4) Sassi, M.; Arena, S.; Scaloni, A. (2015): MALDI-TOF-MS Platform for Integrated Proteomic and Peptidomic Profiling of Milk Samples Allows Rapid Detection of Food Adulterations. In: J. Agric. Food Chem. 63 (27), S. 6157–6171. DOI: 10.1021/acs.jafc.5b02384.

(5) Guerrero, A.; Dallas, D.C.; Contreras, S.; Bhandari, A.; Cánovas, A.; Islas-Trejo, A. et al. (2015): Peptidomic analysis of healthy and subclinically mastitic bovine milk. In: Int. Dairy J. 46, S. 46–52. DOI: 10.1016/j.idairyj.2014.09.006.

(6) Dalabasmaz, S.; Dittrich, D.; Kellner, I.; Drewello, T.; Pischetsrieder, M. (2019): Identification of peptides reflecting the storage of UHT milk by MALDI-TOF-MS peptide profiling. In: J. Proteomics 207, S. 103444. DOI: 10.1016/j.jprot.2019.103444.

(7) Dallas, D.C.; Weinborn, V.; Moura Bell, J.M.L.N. de; Wang, M.; Parker, E.A.; Guerrero, A. et al. (2014): Comprehensive peptidomic and glycomic evaluation reveals that sweet whey permeate from colostrum is a source of milk protein-derived peptides and oligosaccharides. In: Food Res. Int. 63 (Pt B), S. 203–209. DOI: 10.1016/j.foodres.2014.03.021.

Table S3: Modified peptides identified by Proteome Discoverer 2.2 and manual confirmation of the modification sites. If the modified peptide was additionally proposed by PEAKS Studio 10.5, the "-10lgP" value is listed. An "x" indicates that the peptides was present in RM, UHT milk or IF, whereas a "blank" indicates that it was not detected.

Nr.	*Start pos.*	*End pos.*	*Mod. Site*	Annotated Sequence	Modifications	z	*m/z*	t_R (min)	XCorr	-10lgP	RM	UHT	IF
Alpha-S1-casein (P02662)													
1	*1*	*13*	*K7*	RPKHPIkHQGLPQ	K7(Lac)	4	465.754	13.13	1.8				x
2	*1*	*16*	*K7*	RPKHPIkHQGLPQEVL	K7(Lac)	4	551.053	22.65	3.0	18.8			x
3	*1*	*20*	*K7*	RPKHPIkHQGLPQEVLNENL	K7(Lac)	5	535.087	31.77	2.8			x	x
4	*1*	*21*	*K3*	RPkHPIKHQGLPQEVLNENLL	K3(Lac)	5	557.704	37.90	2.3	27.1	x	x	x
5	*1*	*22*	*K3*	RPkHPIKHQGLPQEVLNENLLR	K3(Lac)	4	735.904	34.36	2.2	29.1	x	x	x
6	*1*	*22*	*K3, K7*	RPkHPIkHQGLPQEVLNENLLR	K3(Lac); K7(Lac)	5	653.747	34.04	4.8	28.0			x
7	*1*	*22*	*K7*	RPKHPIkHQGLPQEVLNENLLR	K7(Lac)	5	588.926	34.43	5.4	13.9	x	x	x
8	*1*	*23*	*K3*	RPkHPIKHQGLPQEVLNENLLRF	K3(Lac)	5 (4)	618.339	44.04	5.0	28.0	x	x	x
9	*1*	*23*	*K3, K7*	RPkHPIkHQGLPQEVLNENLLRF	K3(Lac); K7(Lac)	5	683.161	43.40	4.1				x
10	*1*	*23*	*K7*	RPKHPIkHQGLPQEVLNENLLRF	K7(Lac)	5	618.339	44.17	4.4				x
11	*23*	*36*	*K36*	FFVAPFPEVFGKEk	K14(Lac)	3	655.999	53.52	2.5	28.2		x	x
12	*23*	*37*	*K36*	FFVAPFPEVFGKEkV	K14(Lac)	3	689.020	55.98	3.0	37.2			x
13	*23*	*42*	*K36*	FFVAPFPEVFGKEkVNELSK	K14(Lac)	4	659.842	52.29	4.0	37.7			x
14	*24*	*36*	*K36*	FVAPFPEVFGKEk	K13(Hex)	3	552.956	47.39	2.8	28.0			x
15	*24*	*38*	*K34*	FVAPFPEVFGkEKVN	K11(Lac)	3	678.012	47.61	3.2				x
16	*24*	*39*	*K34*	FVAPFPEVFGkEKVNE	K11(Lac)	3	721.026	47.67	2.5	21.6			x
17	*24*	*41*	*K36*	FVAPFPEVFGKEkVNELS	K13(Hex)	3	733.715	51.70	2.6				x
18	*24*	*42*	*K34, K36*	FVAPFPEVFGkEkVNELSK	K11(Hex); K13(Lac)	4	663.588	46.51	3.6	24.3			x
19	*24*	*42*	*K34, K36*	FVAPFPEVFGkEkVNELSK	K11(Lac); K13(Lac)	4	704.101	46.31	3.5	39.6			x
20	*24*	*42*	*K36*	FVAPFPEVFGKEkVNELSK	K13(Lac)	4	623.073	46.72	4.6	63.4			x
21	*24*	*42*	*K36*	FVAPFPEVFGKEkVNELSK	K13(Hex)	4	582.561	47.19	5.6	53.5			x
22	*25*	*36*	*K34*	VAPFPEVFGkEK	K10(Lac)	3	557.952	38.25	1.6	32.2		x	x
23	*25*	*36*	*K34*	VAPFPEVFGkEK	K10(Hex)	3	503.932	39.07	1.8	9.0			x
24	*25*	*37*	*K34, K36*	VAPFPEVFGkEkV	K10(Hex); K12(Lac)	3	644.993	42.19	2.8				x
25	*25*	*40*	*K34*	VAPFPEVFGkEKVNEL	K10(Lac)	3	709.699	47.30	2.7				x

Nr.	*Start pos.*	*End pos.*	*Mod. Site*	Annotated Sequence	Modifications	z	*m/z*	t_R (min)	XCorr	-10lgP	RM	UHT	IF
26	*25*	*42*	*K34*	VAPFPEVFGkEKVNELSK	K10(Lac)	4	586.308	40.86	4.1	49.4			x
27	*25*	*42*	*K36*	VAPFPEVFGKEkVNELSK	K12(Lac)	4	586.307	41.01	3.5	63.0			x
28	*26*	*36*	*K34*	APFPEVFGkEK	K9(Lac)	3	524.926	35.37	2.0	26.2		x	x
29	*26*	*37*	*K34*	APFPEVFGkEKV	K9(Hex)	3	503.933	40.21	2.4	29.6			x
30	*26*	*37*	*K34, K36*	APFPEVFGkEkV	K9(Lac); K11(Lac)	3	665.987	39.25	2.3	33.0			x
31	*28*	*37*	*K34*	FPEVFGkEKV	K7(Lac)	3	501.920	35.84	2.5	27.1			x
32	*80*	*90*	*K83*	HIQkEDVPSER	K4(Lac)	3	554.600	13.76	2.8	12.5	x	x	x
33	*80*	*91*	*K83*	HIQkEDVPSERY	K4(Lac)	3	608.955	18.73	2.7	29.5		x	x
34	*80*	*92*	*K83*	HIQkEDVPSERYL	K4(Lac)	3	646.650	26.26	3.0	30.7			x
35	*80*	*93*	*K83*	HIQkEDVPSERYLG	K4(Lac)	3	665.658	24.37	3.5	32.8		x	x
36	*80*	*94*	*K83*	HIQkEDVPSERYLGY	K4(Lac)	3	720.013	29.80	2.6	23.3			x
37	*80*	*96*	*K83*	HIQkEDVPSERYLGYLE	K4(Lac)	3	800.722	37.83	1.9	10.9			x
38	*80*	*99*	*K83*	HIQkEDVPSERYLGYLEQLL	K4(Lac)	4	689.349	60.43	2.5	17.4		x	x
39	*80*	*100*	*K83*	HIQkEDVPSERYLGYLEQLLR	K4(Lac)	4	728.376	57.22	5.1	51.1		x	x
40	*80*	*100*	*K83*	HIQkEDVPSERYLGYLEQLLR	K4(Hex)	4	687.862	57.64	5.2	51.7			x
41	*80*	*101*	*K83*	HIQkEDVPSERYLGYLEQLLRL	K4(Lac)	4	756.649	66.16	5.1	36.8		x	x
42	*80*	*102*	*K102*	HIQKEDVPSERYLGYLEQLLRLk	K23(Lac)	5 (4)	631.136	59.33	6.7	42.8	x	x	x
43	*80*	*102*	*K83*	HIQkEDVPSERYLGYLEQLLRLK	K4(Lac)	5	631.138	60.64	5.0	26.9	x	x	x
44	*80*	*102*	*K83*	HIQkEDVPSERYLGYLEQLLRLK	K4(Hex)	5	598.726	60.17	6.5	36.4			x
45	*80*	*102*	*K83, K102*	HIQkEDVPSERYLGYLEQLLRLk	K4(Lac); K23(Lac)	5	695.959	58.72	5.8				x
46	*80*	*103*	*K102*	HIQKEDVPSERYLGYLEQLLRLkK	K23(Lac)	5	656.758	55.15	4.7	29.5		x	x
47	*80*	*104*	*K102*	HIQKEDVPSERYLGYLEQLLRLkKY	K23(Lac)	5	689.369	55.84	4.5	25.9		x	x
48	*80*	*104*	*K103*	HIQKEDVPSERYLGYLEQLLRLKkY	K24(Lac)	5	689.370	55.89	4.8	30.6			x
49	*81*	*90*	*K83*	IQkEDVPSER	K3(Lac)	3	508.914	14.69	2.6	15.1		x	x
50	*81*	*90*	*K83*	IQkEDVPSER	K3(Hex)	3	454.896	15.28	2.0				x
51	*81*	*91*	*K83*	QkEDVPSERY	K2(Lac)	3	525.573	17.67	1.6	12.2		x	x
52*	*103*	*123*	*K103*	kYKVPQLEIVPNsAEERLHSM	K1(Lac); S13(Phospho)	4	718.849	44.17	4.0		x	x	x
53*	*103*	*123*	*K103*	kYKVPQLEIVPNsAEERLHSm	K1(Lac); S13(Phospho); M21(Ox)	4	722.849	39.10	3.5		x	x	x
54*	*103*	*123*	*K103, K105*	kYkVPQLEIVPNsAEERLHSM	K1(Hex); K3(Hex); S13(Phospho)	4	718.850	44.18	3.9		x	x	x

Nr.	*Start pos.*	*End pos.*	*Mod. Site*	Annotated Sequence	Modifications	z	*m/z*	t_R (min)	XCorr	-10lgP	RM	UHT	IF
55*	*103*	*123*	*K103, K105*	kYkVPQLEIVPNsAEERLHSm	K1(Hex); K3(Hex); S13(Phospho); M21(Ox)	4	722.849	38.99	3.7			x	x
56*	*103*	*123*	*K103, K105*	kYkVPQLEIVPNsAEERLHSM	K1(Lac); K3(Lac); S13(Phospho)	4	799.878	43.93	2.8				x
57*	*103*	*123*	*K105*	KYkVPQLEIVPNsAEERLHSm	K3(Lac); S13(Phospho); M21(Ox)	4	722.849	39.06	3.5	45.4		x	x
58*	*103*	*123*	*K105*	KYkVPQLEIVPNsAEERLHSM	K3(Hex); S13(Phospho)	4	678.337	44.31	4.2	39.3			x
*59**	*103*	*124*	*K103, K105*	kYkVPQLEIVPNsAEERLHSMK	K1(Hex); K3(Hex); S13(Phospho)	4	750.873	40.28	3.0			x	x
*60**	*103*	*124*	*K105*	KYkVPQLEIVPNsAEERLHSMK	K3(Lac); S13(Phospho)	4	750.872	40.47	2.4			x	x
61	*104*	*123*	*K105*	YkVPQLEIVPNSAEERLHSM	K2(Lac)	4	666.834	45.56	3.3	48.8		x	x
62*	*104*	*123*	*K105*	YkVPQLEIVPNsAEERLHSM	K2(Lac); S12(Phospho)	4	686.826	47.74	3.2	36.2			x
63*	*105*	*123*	*K105*	kVPQLEIVPNsAEERLHSM	K1(Lac); S11(Phospho)	4	646.060	44.37	4.4	39.7			x
64*	*105*	*124*	*K105*	kVPQLEIVPNsAEERLHSMK	K1(Lac); S11(Phospho)	4	678.084	39.97	2.9				x
Alpha-S2-casein (P02663)													
65	*1*	*24*	*K21*	KNTMEHVSSSEESIISQETYkQEK	K21(Lac)	4	784.863	29.54	4.4	44.2		x	x
66*	*1*	*24*	*K21*	KNTMEHVSSSEESIIsQETYkQEK	S16(Phospho); K21(Lac)	4	804.860	30.25	3.4	35.8		x	x
67	*1*	*24*	*K24*	KNTMEHVSSSEESIISQETYKQEk	K24(Lac)	4	784.867	29.46	5.3	40.8		x	x
68	*1*	*24*	*K24*	KNTmEHVSSSEESIISQETYKQEk	M4(Ox); K24(Lac)	4	788.865	26.08	3.2			x	x
69*	*1*	*24*	*K24*	KNTmEHVSSSEESIIsQETYKQEk	M4(Ox); S16(Phospho); K24(Lac)	4	808.858	26.96	3.2			x	x
70*	*1*	*24*	*K24*	KNTMEHVSSSEEsIISQETYKQEk	S13(Phospho); K24(Lac)	4	804.861	30.38	3.2	19.6		x	x
71*	*137*	*150*	*K150*	KTVDMEsTEVFTKk	S7(Phospho); K14(Lac)	3	682.976	26.97	4.2	44.0	x	x	x
72*	*138*	*150*	*K150*	TVDMEsTEVFTKk	S6(Phospho); K13(Lac)	3	640.278	30.53	2.0	21.6		x	x
73	*138*	*150*	*K150*	TVDMESTEVFTKk	K13(Lac)	3	613.620	30.00	2.2	21.3		x	x
74	*150*	*162*	*K150, K152*	kTkLTEEEKNRLN	K1(Lac); K3(Lac)	4	563.528	14.36	2.9	22.2			x
75	*150*	*163*	*K150*	kTKLTEEEKNRLNF	K1(Lac)	4	519.269	24.23	5.5	57.5			x
76	*150*	*163*	*K150, K152*	kTkLTEEEKNRLNF	K1(Lac); K3(Lac)	4	600.297	23.94	3.2				x
77	*150*	*163*	*K152*	KTkLTEEEKNRLNF	K3(Hex)	4	478.756	24.41	3.9				x
78	*150*	*163*	*K152*	KTkLTEEEKNRLNF	K3(Lac)	4	519.272	24.18	4.9				x
79	*150*	*163*	*K152, K158*	KTkLTEEEkNRLNF	K3(Lac); K9(Lac)	4	600.296	24.25	3.4				x
80	*150*	*163*	*K158*	KTKLTEEEkNRLNF	K9(Lac)	3	692.026	24.31	3.0				x
81	*150*	*164*	*K150*	kTKLTEEEKNRLNFL	K1(Lac)	3	729.720	31.77	2.1	9.4		x	x
82	*150*	*164*	*K150, K152*	kTkLTEEEKNRLNFL	K1(Lac); K3(Lac)	4	628.569	31.48	3.4				x

Nr.	*Start pos.*	*End pos.*	*Mod. Site*	Annotated Sequence	Modifications	z	*m/z*	t_R (min)	XCorr	-10lgP	RM	UHT	IF
83	*150*	*164*	*K152*	KTkLTEEEKNRLNFL	K3(Hex)	4	507.027	32.14	4.1	43.7			x
84	*150*	*164*	*K152*	KTkLTEEEKNRLNFL	K3(Lac)	4	547.542	31.69	4.1	48.6	x	x	x
85	*150*	*164*	*K158*	KTKLTEEEkNRLNFL	K9(Lac)	4	547.540	31.96	4.8	36.4	x	x	x
86	*150*	*165*	*K150*	kTKLTEEEKNRLNFLK	K1(Lac)	4 (5)	579.566	27.33	5.6	42.7	x	x	x
87	*150*	*165*	*K150, K152*	kTkLTEEEKNRLNFLK	K1(Lac); K3(Lac)	5	528.674	27.07	5.2				x
88	*150*	*165*	*K152*	KTkLTEEEKNRLNFLK	K3(Lac)	5	463.852	27.56	5.9	34.9		x	x
89	*150*	*165*	*K152, K158*	KTkLTEEEkNRLNFLK	K3(Lac); K9(Lac)	5 (4)	528.674	27.19	5.1	43.5			x
90	*150*	*165*	*K158*	KTKLTEEEkNRLNFLK	K9(Lac)	5	463.853	27.36	5.6	31.8	x	x	x
91	*150*	*165*	*K165*	KTKLTEEEKNRLNFLk	K16(Lac)	4	579.565	27.38	4.7	42.7	x	x	x
92	*151*	*161*	*K152*	TkLTEEEKNRL	K2(Hex)	3	508.269	19.07	2.5	18.1			x
93	*151*	*161*	*K152*	TkLTEEEKNRL	K2(Lac)	3	562.287	18.95	2.5	31.7			x
94	*151*	*161*	*K152, K158*	TkLTEEEkNRL	K2(Lac); K8(Lac)	3	670.324	18.65	3.2	31.7			x
95	*151*	*161*	*K158*	TKLTEEEkNRL	K8(Lac)	3	562.288	18.63	3.1	32.6			x
96	*151*	*162*	*K152, K158*	TkLTEEEkNRLN	K2(Lac); K8(Lac)	4	531.505	16.72	4.1	32.8			x
97	*151*	*162*	*K158*	TKLTEEEkNRLN	K8(Lac)	4 (3)	450.478	16.55	4.6	40.7		x	x
98	*151*	*162*	*K158*	TKLTEEEkNRLN	K8(Hex)	3	546.284	17.00	2.8	17.9			x
99	*151*	*163*	*K152, K158*	TkLTEEEkNRLNF	K2(Lac); K8(Lac)	3	757.362	27.99	2.6	28.0			x
100	*151*	*163*	*K158*	TKLTEEEkNRLNF	K8(Lac)	3	649.325	28.38	3.7	26.2			x
101	*151*	*164*	*K152*	TkLTEEEKNRLNFL	K2(Lac)	3	687.022	35.78	3.3	35.9		x	x
102	*151*	*164*	*K158*	TKLTEEEkNRLNFL	K8(Lac)	4 (3)	515.517	36.11	5.0	33.6		x	x
103	*151*	*164*	*K158*	TKLTEEEkNRLNFL	K8(Hex)	3	633.003	36.19	3.3				x
104	*151*	*165*	*K152*	TkLTEEEKNRLNFLK	K2(Lac)	3	729.719	31.10	2.5	29.4		x	x
105	*151*	*165*	*K158*	TKLTEEEkNRLNFLK	K8(Lac)	4	547.541	31.09	5.0	59.9	x	x	x
106	*151*	*165*	*K158*	TKLTEEEkNRLNFLK	K8(Hex)	4	507.027	31.13	3.4			x	x
107	*151*	*165*	*K158, K165*	TKLTEEEkNRLNFLk	K8(Lac); K15(Lac)	4	628.568	30.73	4.3	34.5			x
108	*151*	*165*	*K165*	TKLTEEEKNRLNFLk	K15(Lac)	4	547.540	30.68	4.6	40.9	x	x	x
109	*151*	*169*	*K152*	TkLTEEEKNRLNFLKKISQ	K2(Lac)	4	661.610	35.50	4.0			x	x
110	*152*	*163*	*K158*	KLTEEEkNRLNF	K7(Lac)	3	615.643	26.00	2.9				x
111	*153*	*162*	*K158*	LTEEEkNRLN	K6(Lac)	3	523.922	14.31	2.6	13.4			x
112	*153*	*163*	*K158*	LTEEEkNRLNF	K6(Lac)	3	572.944	28.00	3.0	28.4			x

Nr.	*Start pos.*	*End pos.*	*Mod. Site*	Annotated Sequence	Modifications	z	*m/z*	t_R (min)	XCorr	-10lgP	RM	UHT	IF
113	*153*	*165*	*K158*	LTEEEkNRLNFLK	K6(Lac)	3	653.336	31.23	1.9	9.8			x
114	*153*	*165*	*K158, K165*	LTEEEkNRLNFLk	K6(Lac); K13(Lac)	4	571.282	30.55	4.3				x
115	*154*	*163*	*K158*	TEEEkNRLNF	K5(Lac)	3	535.251	23.49	2.6				x
116	*154*	*164*	*K158*	TEEEkNRLNFL	K5(Lac)	3	572.945	34.52	2.6	25.8		x	x
117	*154*	*165*	*K158*	TEEEkNRLNFLK	K5(Lac)	4	461.984	26.98	4.5	34.3			x
118	*155*	*163*	*K158*	EEEkNRLNF	K4(Lac)	3	501.567	22.91	2.6	20.3			x
119	*155*	*164*	*K158*	EEEkNRLNFL	K4(Lac)	3	539.262	34.46	2.9	31.3		x	x
120	*170*	*179*	*K173*	RYQkFALPQY	K4(Lac)	3	546.607	34.97	2.2	10.3			x
121	*185*	*197*	*K188*	QHQkAMkPWIQPK	K4(Lac); K7(Lac)	4	567.781	19.03	3.2	18.8			x
122*	*22*	*41*	*T38*	QEKNmAINPsKENLCStFCK	M5(Ox); S10(Phospho); T17(TOx)	4	595.511	34.35	4.1		x	x	
123	*22*	*41*	*T38*	QEKNmAINPSKENLCStFCK	M5(Ox); T17(TOx)	4	575.519	32.24	4.9		x	x	
124*	*22*	*41*	*T38*	QEKNMAINPsKENLCStFCK	S10(Phospho); T17(TOx)	4	591.513	37.73	4.8	8.6	x	x	
125	*22*	*41*	*T38*	QEKNMAINPSKENLCStFCK	T17(TOx)	4	571.520	35.47	5.2	51.1	x	x	
126*	*22*	*45*	*T38*	QEKNmAINPsKENLCStFCKEVVR	M5(Ox); S10(Phospho); T17(TOx)	4	716.332	40.23	4.9		x	x	
127	*22*	*45*	*T38*	QEKNmAINPSKENLCStFCKEVVR	M5(Ox); T17(TOx)	5	557.273	37.97	4.9		x	x	x
128*	*22*	*45*	*T38*	QEKNMAINPsKENLCStFCKEVVR	S10(Phospho); T17(TOx)	4	712.334	42.84	4.7	13.8	x	x	
129	*22*	*45*	*T38*	QEKNMAINPSKENLCStFCKEVVR	T17(TOx)	4 (5)	692.341	40.20	4.7	45.1	x	x	x
130*	*25*	*41*	*T38*	NmAINPsKENLCStFCK	M2(Ox); S7(Phospho); T14(TOx)	3	665.283	37.32	3.0		x	x	x
131	*25*	*41*	*T38*	NmAINPSKENLCStFCK	M2(Ox); T14(TOx)	3	638.625	34.94	3.5		x	x	x
132*	*25*	*41*	*T38*	NMAINPsKENLCStFCK	S7(Phospho); T14(TOx)	3	659.949	41.81	2.5		x	x	x
133	*25*	*41*	*T38*	NMAINPSKENLCStFCK	T14(TOx)	3	633.294	39.11	2.9	24.6	x	x	x
134*	*25*	*45*	*T38*	NmAINPsKENLCStFCKEVVR	M2(Ox); S7(Phospho); T14(TOx)	4	620.032	43.07	4.8		x	x	x
135	*25*	*45*	*T38*	NmAINPSKENLCStFCKEVVR	M2(Ox); T14(TOx)	4	600.041	40.14	4.3		x	x	x
136*	*25*	*45*	*T38*	NMAINPsKENLCStFCKEVVR	S7(Phospho); T14(TOx)	4	616.034	46.37	4.4		x	x	x
137	*25*	*45*	*T38*	NMAINPSKENLCStFCKEVVR	T14(TOx)	4	596.043	43.35	4.8	45.1	x	x	x
Beta-casein (P02666)													
138*	*29*	*40*	*K29*	kIEKFQsEEQQQ	K1(Lac); S7(Phospho)	3	642.614	17.96	2.1	11.4			x
139	*29*	*48*	*K29*	kIEKFQSEEQQQTEDELQDK	K1(Lac)	4	701.828	25.70	3.2	34.3		x	x
140*	*29*	*48*	*K29*	kIEKFQsEEQQQTEDELQDK	K1(Lac); S7(Phospho)	4	721.820	28.68	4.5			x	x
141	*29*	*48*	*K32*	KIEkFQSEEQQQTEDELQDK	K4(Lac)	4	701.829	26.21	4.5	52.7	x	x	x

Nr.	*Start pos.*	*End pos.*	*Mod. Site*	Annotated Sequence	Modifications	z	*m/z*	t_R (min)	XCorr	-10lgP	RM	UHT	IF
142*	*29*	*48*	*K32*	KIEkFQsEEQQQTEDELQDK	K4(Lac); S7(Phospho)	4	721.820	28.48	4.4	42.7	x	x	x
Butyrophilin subfamily 1 member A1 (P18892)													
143	*153*	*177*	*P160*	THRGEEFpSMSESRNPDEEGLFTVR	P8(Ox)	5	585.472	34.45	5.0	32.8	x	x	x
Fibroblast growth factor-binding protein 1 (Q9MZ06)													
144	*6*	*27*	*K22*	NRRGSKASADESLALGkPGKEPR	K17(Lac)	5 (6)	550.488	17.22	3.8	13.2		x	x
145	*8*	*27*	*K25*	RGSKASADESLALGKPGkEPR	K18(Lac)	5	496.459	18.43	5.8	24.0		x	x
146	*9*	*27*	*K22*	GSKASADESLALGkPGKEPR	K14(Lac)	5 (4)	465.239	20.15	4.7	39.3		x	x
147	*9*	*27*	*K25*	GSKASADESLALGKPGkEPR	K17(Lac)	4	581.298	20.10	3.6			x	x
Glycosylation-dependent cell adhesion molecule 1 (P80195)													
148	*1*	*10*	*K4*	ILNkPEDETH	K4(Lac)	3	507.238	14.06	1.9	9.2			x
149	*1*	*11*	*K4*	ILNkPEDETHL	K4(Lac)	3	544.933	24.44	2.3	34.2			x
150	*1*	*12*	*K4*	ILNkPEDETHLE	K4(Lac)	3	587.948	23.42	3.0	32.3			x
151	*1*	*16*	*K4*	ILNkPEDETHLEAQPT	K4(Lac)	3	720.350	25.40	2.7	27.0			x
152	*1*	*24*	*K4*	ILNkPEDETHLEAQPTDASAQFIR	K4(Lac)	4	762.630	35.75	5.4	59.0	x	x	x
153	*1*	*26*	*K4*	ILNkPEDETHLEAQPTDASAQFIRNL	K4(Lac)	4	819.408	46.22	3.9	33.3			x
154	*2*	*13*	*K4*	LNkPEDETHLE	K3(Lac)	3	550.253	19.98	2.4	30.5			x
155	*54*	*67*	*K64*	SSRQPQSQNPkLPL	K11(Hex)	3	581.308	27.54	2.0	16.1			x
156	*54*	*70*	*K64*	SSRQPQSQNPkLPLSIL	K11(Hex)	3	685.710	44.63	3.8	10.1			x
157	*54*	*71*	*K71*	SSRQPQSQNPKLPLSILk	K18(Lac)	4	587.071	36.31	4.5	41.3			x
158	*54*	*73*	*K71*	SSRQPQSQNPKLPLSILkEK	K18(Lac)	5 (4)	521.285	33.40	3.7	10.0		x	x
159	*54*	*73*	*K71, K73*	SSRQPQSQNPKLPLSILkEk	K18(Lac); K20(Lac)	5	586.107	32.73	4.8				x
160	*54*	*73*	*K73*	SSRQPQSQNPKLPLSILKEk	K20(Lac)	5 (4)	521.285	33.30	4.9	31.7		x	x
161	*54*	*75*	*K64, K73*	SSRQPQSQNPkLPLSILkEKHL	K11(Lac); K18(Lac)	5	636.134	35.60	3.1				x
162	*54*	*75*	*K71*	SSRQPQSQNPKLPLSILkEKHL	K18(Lac)	5	571.314	35.94	6.1	47.2			x
163	*54*	*75*	*K73*	SSRQPQSQNPKLPLSILKEkHL	K20(Lac)	5 (4)	571.315	35.40	6.4	37.2			x
164	*109*	*121*	*K116, K120*	RNLENTVkETIkY	K8(Lac); K12(Lac)	3	752.702	32.21	3.0	22.6			x
165	*109*	*121*	*K120*	RNLENTVKETIkY	K12(Lac)	3	644.665	32.31	3.8	42.7			x
166	*111*	*121*	*K116, K120*	LENTVkETIkY	K6(Lac); K10(Lac)	3	662.653	26.84	2.0	17.9			x
167	*111*	*121*	*K120*	LENTVKETIkY	K10(Lac)	3	554.618	27.24	2.8				x
168	*112*	*121*	*K116*	ENTVkETIKY	K5(Lac)	3	516.923	22.96	3.1	35.0			x

Nr.	*Start pos.*	*End pos.*	*Mod. Site*	Annotated Sequence	Modifications	z	*m/z*	t_R (min)	XCorr	-10lgP	RM	UHT	IF
169	*112*	*121*	*K116, K120*	ENTVkETIkY	K5(Lac); K9(Lac)	3	624.958	22.73	2.1	24.9			x
170	*123*	*135*	*K134*	KSLFSHAFEVVkT	K12(Lac)	3	606.313	38.11	2.6				x
171	*126*	*135*	*K134*	FSHAFEVVkT	K9(Lac)	3	496.909	29.14	2.8	41.3			x
172	*126*	*135*	*K134*	FSHAFEVVkT	K9(Hex)	3	442.891	29.73	2.4	43.6			x
173	*127*	*135*	*K134*	SHAFEVVkT	K8(Lac)	3	447.886	21.75	2.1				x
Lactoperoxidase (P80025)													
174	*68*	*76*	*K74*	VWEESLkRL	K7(Lac)	3	495.255	34.81	2.1	27.2		x	x
175	*69*	*76*	*K74*	WEESLkRL	K6(Lac)	3	462.233	30.59	2.1	13.1			x

*Phosphorylation sites rely on software tools without further confirmation of their location.

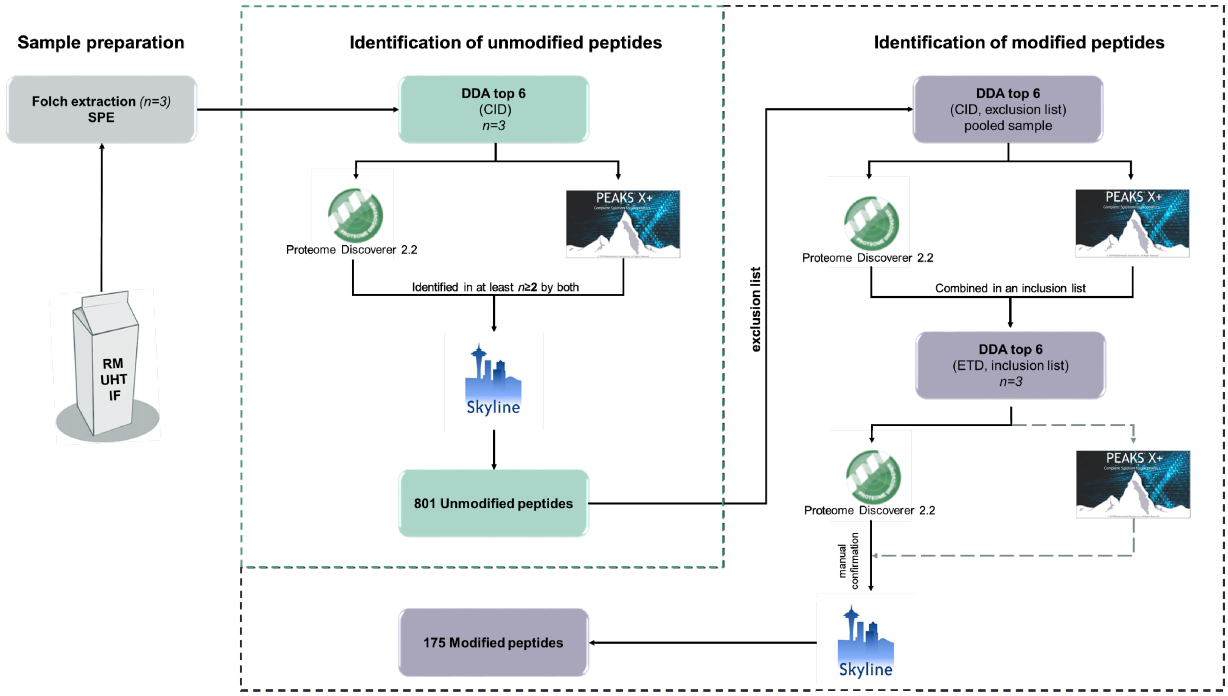


Figure S1: Strategy applied for the identification of unmodified and modified endogenous peptides in RM, UHT milk, and IF relying on software tools Proteome Discoverer 2.2 and PEAKS 10.5 in combination with a spectra library generated within Skyline.

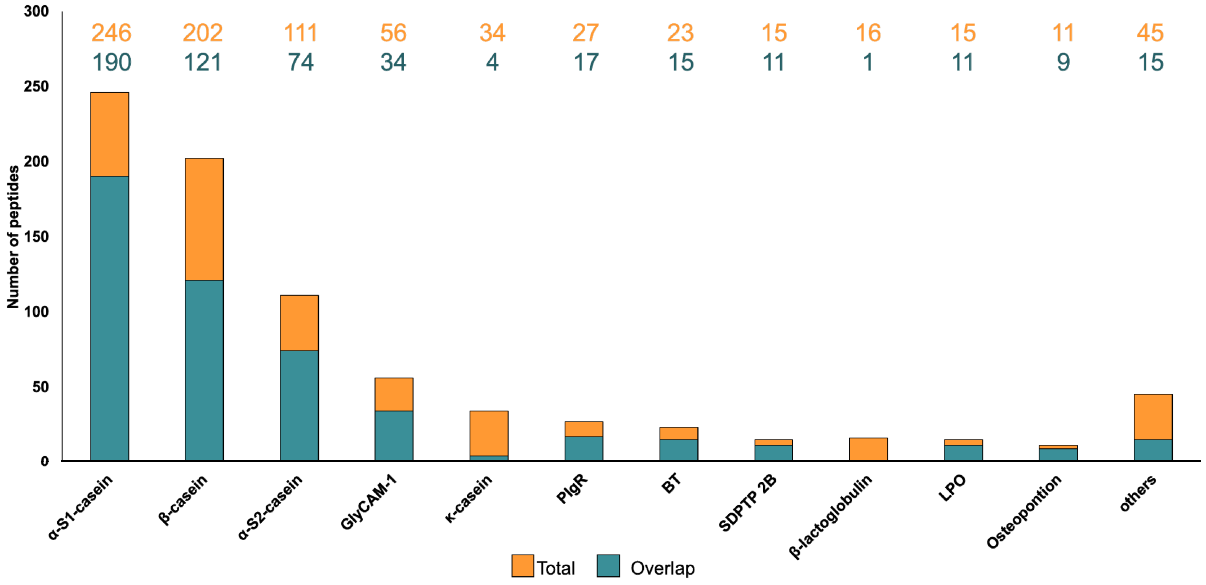


Figure S2: Total number of peptides identified for different proteins (orange) and the number of overlapping peptides (blue) present in RM, UHT milk, and IF. Abbreviations: GlyCAM-1 - glycosylation-dependent cell adhesion molecule 1, PigR - polymeric immunoglobulin receptor, BT - butyrophilin subfamily 1 member A1, SDPTP 2B - sodium-dependent phosphate transport protein 2B, and LPO – lactoperoxidase.

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	Position
AA	R	P	K	H	P	I	K	H	Q	G	L	P	Q	E	V	L	N	E	N	L	L	R	F	F	V	A	P	F	P	E	AA
Total	2	2	2	6	6	6	8	10	14	21	25	25	27	31	33	36	37	35	34	33	31	24	22	18	22	30	33	36	36	36	Total
RM	2	2	2	6	6	6	7	9	10	15	19	19	20	22	24	27	28	27	27	26	24	19	17	17	22	30	33	36	36	36	RM
UHT	2	2	2	6	6	6	7	9	10	15	19	19	20	22	24	27	28	27	27	26	24	19	17	17	22	30	33	36	36	36	UHT
IF	2	2	2	5	5	5	7	9	13	20	23	23	25	29	31	33	34	32	31	30	29	22	19	16	20	27	30	33	33	33	IF

Position	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	Position
AA	V	F	G	K	E	K	V	N	E	L	S	K	D	I	G	S	E	S	T	E	D	Q	A	M	E	D	I	K	Q	M	AA
Total	36	36	34	30	27	23	20	15	15	13	12	8	10	11	11	11	11	11	11	11	11	11	11	10	10	10	10	10	0	0	Total
RM	36	36	34	30	27	23	20	15	15	13	12	8	10	11	11	11	11	11	11	11	11	11	11	10	10	10	10	10			RM
UHT	36	36	34	30	27	23	20	15	15	13	12	8	10	11	11	11	11	11	11	11	11	11	11	10	10	10	10	10			UHT
IF	33	33	31	29	26	23	20	15	15	13	12	8	9	9	9	9	9	9	9	9	9	9	9	8	8	8	8	8			IF

Position	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	Position
AA	E	A	E	S	I	S	S	S	E	E	I	V	P	N	S	V	E	Q	K	H	I	Q	K	E	D	V	P	S	E	R	AA
Total	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	15	20	21	23	24	24	27	27	27	27	26	Total
RM																				15	20	21	23	24	24	27	27	27	27	26	RM
UHT																				13	18	19	21	22	22	25	25	25	25	24	UHT
IF									1	1	1	1	1	1	1	1	1	1	1	15	20	20	21	22	22	24	24	24	24	23	IF

Position	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	Position
AA	Y	L	G	Y	L	E	Q	L	L	R	L	K	K	Y	K	V	P	Q	L	E	I	V	P	N	S	A	E	E	R	L	AA
Total	28	26	28	27	28	27	26	24	22	18	14	10	12	18	25	37	37	42	45	47	48	49	49	50	50	50	50	50	50	36	Total
RM	28	26	28	27	28	27	26	24	22	18	14	10	12	17	22	34	34	39	42	44	45	46	46	47	47	47	47	47	47	33	RM
UHT	26	24	26	25	26	26	26	24	22	18	14	10	12	17	22	34	34	39	42	44	45	46	46	47	47	47	47	47	47	33	UHT
IF	23	20	20	20	21	20	19	17	16	14	10	8	11	18	25	37	37	42	44	46	47	48	48	48	48	48	48	48	48	34	IF

Position	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	Position
AA	H	S	M	K	E	G	I	H	A	Q	Q	K	E	P	M	I	G	V	N	Q	E	L	A	Y	F	Y	P	E	L	F	AA
Total	36	33	29	8	4	4	4	4	4	4	5	5	4	4	4	4	4	4	4	4	4	4	4	4	2	2	2	2	2	2	Total
RM	33	31	27	8	4	4	4	4	4	4	4	3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	RM
UHT	33	31	27	8	4	4	4	4	4	4	4	3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	UHT
IF	34	31	27	8	3	3	3	3	3	3	4	4	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	IF

Position	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	Position
AA	R	Q	F	Y	Q	L	D	A	Y	P	S	G	A	W	Y	Y	V	P	L	G	T	Q	Y	T	D	A	P	S	F	S	AA
Total	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	2	2	2	2	2	3	6	6	9	9	13	15	17	19	26	Total
RM	1	1	1	1												2	2	2	2	2	2	5	5	8	8	11	11	13	14	21	RM
UHT	1	1	1	1												2	2	2	2	2	3	6	6	9	9	13	15	17	19	26	UHT
IF	1	1	1	1												2	2	2	2	2	2	5	5	8	8	11	11	13	14	20	IF

Position	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	Position
AA	D	I	P	N	P	I	G	S	E	N	S	E	K	T	T	M	P	L	W	AA
Total	30	36	38	42	48	51	51	53	55	57	58	59	60	57	55	55	55	43	41	Total
RM	25	29	31	35	39	42	42	44	44	44	46	46	46	44	42	42	42	30	29	RM
UHT	30	36	38	41	47	50	50	52	54	56	57	58	59	56	54	54	54	43	41	UHT
IF	24	28	30	34	38	41	41	43	45	45	47	47	47	46	44	44	44	32	31	IF

Figure S3: Protein sequence of α_{S1}-casein without the signal peptide. The numbers below the sequence indicate how many peptides containing this specific residue were detected over all samples (total) and in RM (sequence coverage 83.9 %), UHT milk (sequence coverage 83.9 %), and IF (sequence coverage 89.4 %). AA denotes amino acid.

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	Position
AA	K	N	T	M	E	H	V	S	S	S	E	E	S	I	I	S	Q	E	T	Y	K	Q	E	K	N	M	A	I	N	P	AA
Total	9	9	9	9	9	9	9	9	10	10	11	11	12	15	15	15	15	15	15	15	13	6	5	4	0	0	0	0	0	0	Total
RM	9	9	9	9	9	9	9	9	10	10	10	10	10	13	13	13	13	13	13	13	11	6	5	4							RM
UHT	9	9	9	9	9	9	9	9	10	10	10	10	10	13	13	13	13	13	13	13	11	6	5	4							UHT
IF	9	9	9	9	9	9	9	9	10	10	11	11	12	15	15	15	15	15	15	15	13	6	5	4							IF

Position	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	Position
AA	S	K	E	N	L	C	S	T	F	C	K	E	V	V	R	N	A	N	E	E	E	Y	S	I	G	S	S	S	E	E	AA
Total	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Total
RM																															RM
UHT																															UHT
IF																															IF

Position	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	Position
AA	S	A	E	V	A	T	E	E	V	K	I	T	V	D	D	K	H	Y	Q	K	A	L	N	E	I	N	Q	F	Y	Q	AA
Total	0	0	0	0	0	0	0	0	0	0	2	2	2	2	2	2	2	2	1	0	4	4	4	4	4	4	4	5	6	6	Total
RM											2	2	2	2	2	2	2	2	1												RM
UHT											2	2	2	2	2	2	2	2	1												UHT
IF											2	2	2	2	2	2	2	2	1		4	4	4	4	4	4	4	5	6	6	IF

Position	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	Position
AA	K	F	P	Q	Y	L	Q	Y	L	Y	Q	G	P	I	V	L	N	P	W	D	Q	V	K	R	N	A	V	P	I	T	AA
Total	6	6	6	6	6	4	4	5	4	8	10	12	12	12	13	13	13	13	13	13	13	13	11	5	7	5	5	5	5	5	Total
RM								1	3	5	7	9	9	9	10	10	10	10	10	10	10	10	9	3	4	4	4	4	4	4	RM
UHT								1	3	5	7	8	8	8	9	9	9	9	9	9	9	9	9	3	5	5	5	5	5	5	UHT
IF	6	6	6	6	6	4	4	4	3	7	9	10	10	10	11	11	11	11	11	11	11	11	10	5	7	5	5	5	5	5	IF

Position	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	Position
AA	P	T	L	N	R	E	Q	L	S	T	S	E	E	N	S	K	K	T	V	D	M	E	S	T	E	V	F	T	K	K	AA
Total	5	5	9	9	9	9	9	9	8	8	8	8	8	8	9	6	9	12	16	18	21	21	21	21	21	21	21	21	21	8	Total
RM	4	4	8	8	8	8	8	8	8	8	8	8	8	8	9	6	9	12	16	18	20	20	20	20	20	20	20	20	20	8	RM
UHT	5	5	9	9	9	9	9	9	8	8	8	8	8	8	9	6	9	12	16	18	20	20	20	20	20	20	20	20	20	8	UHT
IF	5	5	9	9	9	9	9	9	8	8	8	8	8	8	9	6	9	11	13	14	17	17	17	17	17	17	17	17	17	5	IF

Position	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	Position
AA	T	K	L	T	E	E	E	K	N	R	L	N	F	L	K	K	I	S	Q	R	Y	Q	K	F	A	L	P	Q	Y	L	AA
Total	7	10	13	16	17	17	17	17	17	17	17	16	15	11	6	1	1	1	1	1	3	5	5	7	8	10	10	10	10	7	Total
RM	7	10	13	16	17	17	17	17	17	17	17	15	14	10	5						1	2	2	4	5	7	7	7	7	7	RM
UHT	7	10	13	16	17	17	17	17	17	17	17	15	14	10	5						1	2	2	4	5	7	7	7	7	7	UHT
IF	7	9	12	15	16	16	16	16	16	16	16	15	14	10	5	1	1	1	1	1	3	5	5	6	6	7	7	7	7	4	IF

Position	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	Position
AA	K	T	V	Y	Q	H	Q	K	A	M	K	P	W	I	Q	P	K	T	K	V	I	P	Y	V	R	Y	L	AA
Total	5	4	4	3	3	2	2	1	6	6	7	7	7	7	7	7	5	8	8	10	11	11	11	10	9	7	4	Total
RM	5	4	4	3	3	2	2	1	4	4	5	5	5	5	5	5	3	7	7	9	10	10	10	10	9	7	4	RM
UHT	5	4	4	3	3	2	2	1	4	4	5	5	5	5	5	5	3	7	7	9	10	10	10	10	9	7	4	UHT
IF	2	1	1	1	1				4	4	4	4	4	4	4	4	3	6	6	8	9	9	9	8	7	6	4	IF

Figure S4: Protein sequence of α_{S2}-casein without the signal peptide. The numbers below the sequence indicate how many peptides containing this specific residue were detected over all samples (total) and in RM (sequence coverage 66.7 %), UHT milk (sequence coverage 66.7 %), and IF (sequence coverage 75.8 %). AA denotes amino acid.

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	Position
AA	I	L	N	K	P	E	D	E	T	H	L	E	A	Q	P	T	D	A	S	A	Q	F	I	R	N	L	Q	I	S	N	AA
Total	15	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	17	16	15	15	14	13	9	8	5	4	2	1	1	1	Total
RM	14	17	17	17	17	17	17	17	17	17	17	17	15	15	15	15	14	13	12	12	11	10	8	7	4	3	2	1	1	1	RM
UHT	15	18	18	18	18	18	18	18	18	18	18	17	15	15	15	15	14	13	12	12	11	10	8	7	4	3	2	1	1	1	UHT
IF	15	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	16	15	14	14	13	12	8	7	5	4	2	1	1	1	IF

Position	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	Position
AA	E	D	L	S	K	E	P	S	I	S	R	E	D	L	I	S	K	E	Q	I	V	I	R	S	S	R	Q	P	Q	S	AA
Total	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	8	11	11	16	16	16	19	Total
RM	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	8	11	11	16	16	16	16	RM
UHT	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	8	11	11	16	16	16	17	UHT
IF	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	8	11	11	14	14	14	17	IF

Position	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	Position
AA	Q	N	P	K	L	P	L	S	I	L	K	E	K	H	L	R	N	A	T	L	G	S	E	E	T	T	E	H	T	P	AA
Total	19	20	21	21	24	24	23	21	17	17	11	8	7	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Total
RM	16	16	16	16	19	19	18	17	14	14	11	8	7	4	3																RM
UHT	17	17	17	17	20	20	19	17	14	14	11	8	7	4	3																UHT
IF	17	18	19	19	20	20	19	17	13	13	7	5	4	2	2																IF

Position	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	Position
AA	S	D	A	S	T	T	E	G	K	L	M	E	L	G	H	K	I	M	R	N	L	E	N	T	V	K	E	T	I	K	AA
Total	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2	3	4	4	4	4	4	4	4	4	Total
RM																															RM
UHT																			1	1	1	1	1	1	1	1	1	1	1	1	UHT
IF																			1	1	2	3	4	4	4	4	4	4	4	4	IF

Position	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	Position
AA	Y	L	K	S	L	F	S	H	A	F	E	V	V	K	T	AA
Total	4	1	2	3	3	4	5	6	6	6	6	6	6	6	6	Total
RM							1	2	2	2	2	2	2	2	2	RM
UHT	1			1	1	1	2	3	3	3	3	3	3	3	3	UHT
IF	4	1	2	3	3	4	5	6	6	6	6	6	6	6	6	IF

Figure S5: Protein sequence of GlyCAM-1 without the signal peptide. The numbers below the sequence indicate how many peptides containing this specific residue were detected over all samples (total) and in RM (sequence coverage 62.2 %), UHT milk (sequence coverage 74.1 %), and IF (sequence coverage 75.6 %). AA denotes amino acid.

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	Position
AA	Q	E	Q	N	Q	E	Q	P	I	R	C	E	K	D	E	R	F	F	S	D	K	I	A	K	Y	I	P	I	Q	Y	AA
Total	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	Total
RM														1	1	1	1	1	1	1	1	1	1	1							RM
UHT														1	1	1	1	1	1	1	1	1	1	1							UHT
IF														1	1	1	1	1	1	1	1	1	1	1							IF

Position	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	Position
AA	V	L	S	R	Y	P	S	Y	G	L	N	Y	Y	Q	Q	K	P	V	A	L	I	N	N	Q	F	L	P	Y	P	Y	AA
Total	4	4	7	7	7	7	7	7	6	6	5	5	7	5	5	5	5	5	6	6	4	5	5	3	3	3	3	3	3	3	Total
RM																			1	1	1	1	1	1	1	1	1	1	1	1	RM
UHT																			1	1	1	1	1	1	1	1	1	1	1	1	UHT
IF	4	4	7	7	7	7	7	7	6	6	5	5	7	5	5	5	5	5	5	5	3	4	4	2	2	2	2	2	2	2	IF

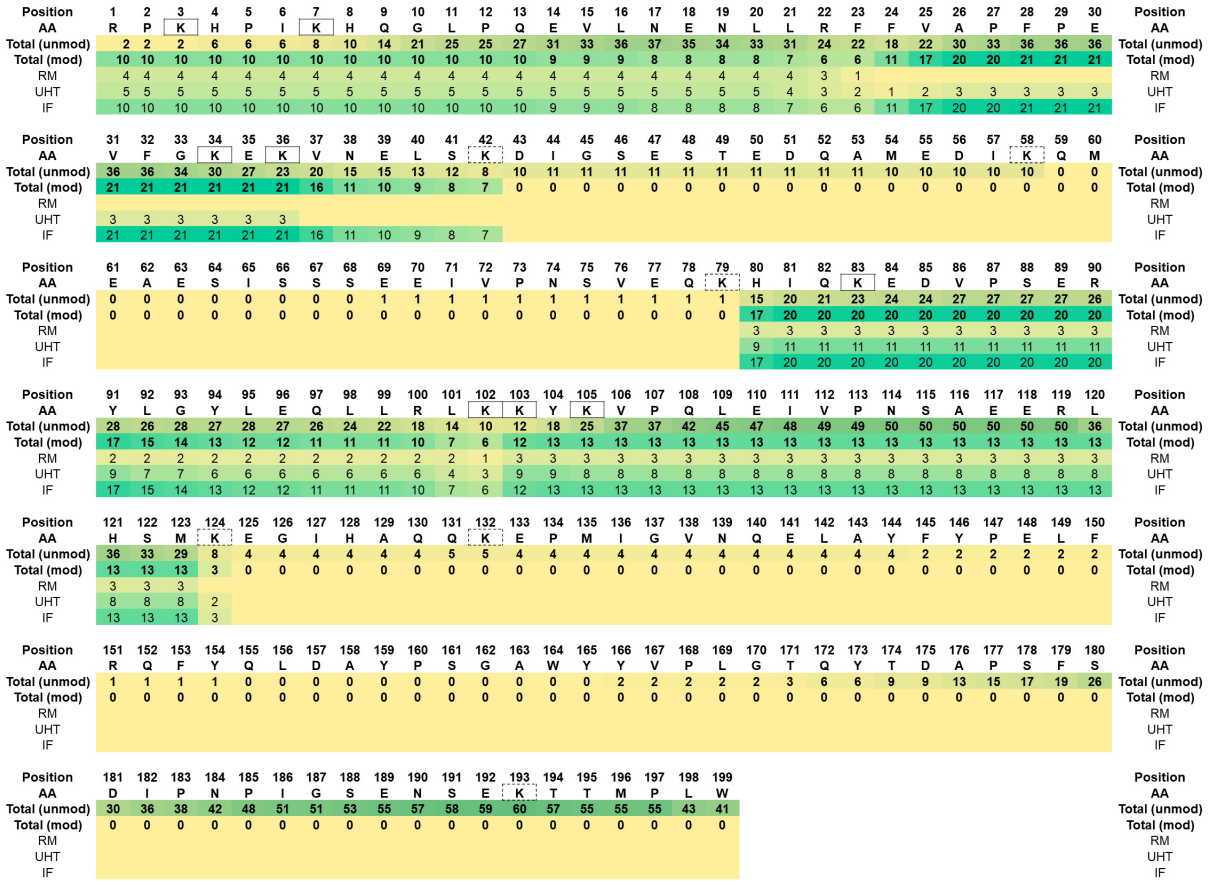
Position	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	Position
AA	Y	A	K	P	A	A	V	R	S	P	A	Q	I	L	Q	W	Q	V	L	S	N	T	V	P	A	K	S	C	Q	A	AA
Total	3	3	3	3	3	2	2	2	3	3	3	3	3	3	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	Total
RM	1	1	1	1	1				1	1	1	1	1	1	1	1	1	1	1												RM
UHT	1	1	1	1	1																										UHT
IF	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1															IF

Position	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	Position
AA	Q	P	T	T	M	A	R	H	P	H	P	H	L	S	F	M	A	I	P	P	K	K	N	Q	D	K	T	E	I	P	AA
Total	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	3	3	3	3	3	4	4	4	4	4	4	4	Total
RM																															RM
UHT																															UHT
IF																3	3	3	3	3	3	3	3	4	4	4	4	4	4	4	IF

Position	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	Position
AA	T	I	N	T	I	A	S	G	E	P	T	S	T	P	T	T	E	A	V	E	S	T	V	A	T	L	E	D	S	P	AA
Total	4	4	4	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	2	4	5	Total
RM																													2	3	RM
UHT																												1	3	4	UHT
IF	4	4	4	3	3	3	3	3	3	3	3	3	3	3	3	3	3	1	1	1	1	1	1	1	1	1	1	2	4	5	IF

Position	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	Position
AA	E	V	I	E	S	P	P	E	I	N	T	V	Q	V	T	S	T	A	V	AA
Total	6	9	9	9	10	10	10	10	11	11	11	10	10	10	10	10	10	10	10	Total
RM	3	4	4	4	4	4	4	4	4	4	4	3	3	3	3	3	3	3	3	RM
UHT	5	6	6	6	7	7	7	7	7	7	8	8	8	8	8	8	8	8	8	UHT
IF	6	9	9	9	10	10	10	10	11	11	11	10	10	10	10	10	10	10	10	IF

Figure S6: Protein sequence of κ-casein without the signal peptide. The numbers below the sequence indicate how many peptides containing this specific residue were detected over all samples (total) and in RM (sequence coverage 36.1 %), UHT milk (sequence coverage 29.6 %), and IF (sequence coverage 71.6 %). AA denotes amino acid.



Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	Position
AA	R	P	K	H	P	I	K	H	Q	G	L	P	Q	E	V	L	N	E	N	L	L	R	F	F	V	A	P	F	P	E	AA
Total (unmod)	2	2	2	6	6	6	8	10	14	21	25	25	27	31	33	36	37	35	34	33	31	24	22	18	22	30	33	36	36	36	Total (unmod)
Total (mod)	10	10	10	10	10	10	10	10	10	10	10	10	10	9	9	9	8	8	8	8	7	6	6	11	17	20	20	21	21	21	Total (mod)
RM	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3	1								RM
UHT	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	4	3	2	1	2	3	3	3	3	3	UHT
IF	10	10	10	10	10	10	10	10	10	10	10	10	10	9	9	9	8	8	8	8	7	6	6	11	17	20	20	21	21	21	IF

Position	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	Position
AA	V	F	G	K	E	K	V	N	E	L	S	K	D	I	G	S	E	S	T	E	D	Q	A	M	E	D	I	K	Q	M	AA
Total (unmod)	36	36	34	30	27	23	20	15	15	13	12	8	10	11	11	11	11	11	11	11	11	11	11	10	10	10	10	10	0	0	Total (unmod)
Total (mod)	21	21	21	21	21	21	16	11	10	9	8	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Total (mod)
RM																															RM
UHT	3	3	3	3	3	3																									UHT
IF	21	21	21	21	21	21	16	11	10	9	8	7																			IF

Position	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	Position
AA	E	A	E	S	I	S	S	S	E	E	I	V	P	N	S	V	E	Q	K	H	I	Q	K	E	D	V	P	S	E	R	AA
Total (unmod)	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	15	20	21	23	24	24	27	27	27	27	26	Total (unmod)
Total (mod)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	20	20	20	20	20	20	20	20	20	20	Total (mod)
RM																				3	3	3	3	3	3	3	3	3	3	3	RM
UHT																				9	11	11	11	11	11	11	11	11	11	11	UHT
IF																				17	20	20	20	20	20	20	20	20	20	20	IF

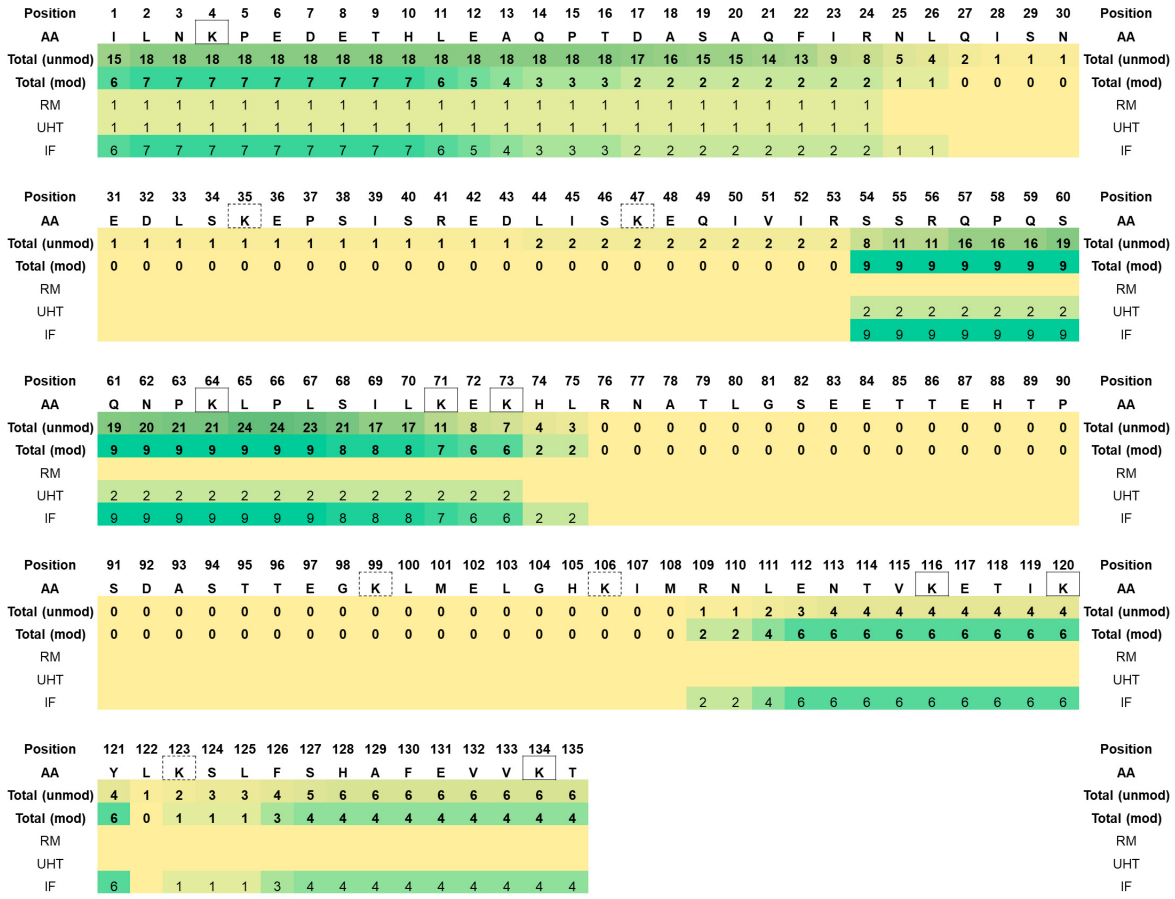
Position	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	Position
AA	Y	L	G	Y	L	E	Q	L	L	R	L	K	K	Y	K	V	P	Q	L	E	I	V	P	N	S	A	E	E	R	L	AA
Total (unmod)	28	26	28	27	28	27	26	24	22	18	14	10	12	18	25	37	37	42	45	47	48	49	49	50	50	50	50	50	50	36	Total (unmod)
Total (mod)	17	15	14	13	12	12	11	11	11	10	7	6	12	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	Total (mod)
RM	2	2	2	2	2	2	2	2	2	2	1	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	RM
UHT	9	7	7	6	6	6	6	6	6	6	4	3	9	9	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	UHT
IF	17	15	14	13	12	12	11	11	11	10	7	6	12	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	IF

Position	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	Position
AA	H	S	M	K	E	G	I	H	A	Q	Q	K	E	P	M	I	G	V	N	Q	E	L	A	Y	F	Y	P	E	L	F	AA
Total (unmod)	36	33	29	8	4	4	4	4	4	4	5	5	4	4	4	4	4	4	4	4	4	4	4	4	2	2	2	2	2	2	Total (unmod)
Total (mod)	13	13	13	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Total (mod)
RM	3	3	3																												RM
UHT	8	8	8	2																											UHT
IF	13	13	13	3																											IF

Position	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	Position
AA	R	Q	F	Y	Q	L	D	A	Y	P	S	G	A	W	Y	Y	V	P	L	G	T	Q	Y	T	D	A	P	S	F	S	AA
Total (unmod)	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	2	2	2	2	2	3	6	6	9	9	13	15	17	19	26	Total (unmod)
Total (mod)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Total (mod)
RM																															RM
UHT																															UHT
IF																															IF

Position	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	Position
AA	D	I	P	N	P	I	G	S	E	N	S	E	K	T	T	M	P	L	W	AA
Total (unmod)	30	36	38	42	48	51	51	53	55	57	58	59	60	57	55	55	55	43	41	Total (unmod)
Total (mod)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Total (mod)
RM																				RM
UHT																				UHT
IF																				IF

Figure S7: Protein sequence of α_{S1}-casein without the signal peptide. The numbers below the sequence indicate how many peptides containing this specific residue were detected in all samples as unmodified (unmod) and/or modified (mod) in RM, UHT milk, and IF. Lysine residues of the protein are framed with a dotted line, and modification sites are fully framed.



Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	Position
AA	I	L	N	K	P	E	D	E	T	H	L	E	A	Q	P	T	D	A	S	A	Q	F	I	R	N	L	Q	I	S	N	AA
Total (unmod)	15	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	17	16	15	15	14	13	9	8	5	4	2	1	1	1	Total (unmod)
Total (mod)	6	7	7	7	7	7	7	7	7	7	6	5	4	3	3	3	2	2	2	2	2	2	2	2	1	1	0	0	0	0	Total (mod)
RM	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1							RM
UHT	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1							UHT
IF	6	7	7	7	7	7	7	7	7	7	6	5	4	3	3	3	2	2	2	2	2	2	2	2	1	1					IF

Position	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	Position
AA	E	D	L	S	K	E	P	S	I	S	R	E	D	L	I	S	K	E	Q	I	V	I	R	S	S	R	Q	P	Q	S	AA
Total (unmod)	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	8	11	11	16	16	16	19	Total (unmod)
Total (mod)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	9	9	9	9	9	9	Total (mod)
RM																															RM
UHT																								2	2	2	2	2	2	2	UHT
IF																								9	9	9	9	9	9	9	IF

Position	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	Position
AA	Q	N	P	K	L	P	L	S	I	L	K	E	K	H	L	R	N	A	T	L	G	S	E	E	T	T	E	H	T	P	AA
Total (unmod)	19	20	21	21	24	24	23	21	17	17	11	8	7	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Total (unmod)
Total (mod)	9	9	9	9	9	9	9	8	8	8	7	6	6	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Total (mod)
RM																															RM
UHT	2	2	2	2	2	2	2	2	2	2	2	2	2																		UHT
IF	9	9	9	9	9	9	9	8	8	8	7	6	6	2	2																IF

Position	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	Position
AA	S	D	A	S	T	T	E	G	K	L	M	E	L	G	H	K	I	M	R	N	L	E	N	T	V	K	E	T	I	K	AA
Total (unmod)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2	3	4	4	4	4	4	4	4	4	Total (unmod)
Total (mod)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	4	6	6	6	6	6	6	6	6	6	Total (mod)
RM																															RM
UHT																															UHT
IF																			2	2	4	6	6	6	6	6	6	6	6	6	IF

Position	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	Position
AA	Y	L	K	S	L	F	S	H	A	F	E	V	V	K	T	AA
Total (unmod)	4	1	2	3	3	4	5	6	6	6	6	6	6	6	6	Total (unmod)
Total (mod)	6	0	1	1	1	3	4	4	4	4	4	4	4	4	4	Total (mod)
RM																RM
UHT																UHT
IF	6		1	1	1	3	4	4	4	4	4	4	4	4	4	IF

Figure S8: Protein sequence of GlyCAM-1 without the signal peptide. The numbers below the sequence indicate how many peptides containing this specific residue were detected in all samples as unmodified (unmod) and/or modified (mod) in RM, UHT milk, and IF. Lysine residues of the protein are framed with a dotted line, and modification sites are fully framed.