

Supplemental Tables and Figures:

Supplemental Table 1: Details of parent proteins from which peptides were derived

Paret Protein names	Gene name	Peptides (n)	Mol. Weight, Parent Protein [kDa]	Sequence length, Parent Protein
β-casein	CSN2	568	25.38	226
polymeric immunoglobulin receptor	PIGR	155	83.28	764
α _{S1} -casein	CSN1S1	128	21.67	185
osteopontin	SPP1	92	35.42	314
κ-casein	CSN3	47	20.31	182
bile salt-activated lipase	CEL	42	79.32	753
clusterin	CLU	16	52.49	449
lactotransferrin	LTF	15	78.18	710
actin, cytoplasmic 1	ACTB	14	41.74	375
butyrophilin subfamily 1 member A1	BTN1A1	12	58.96	526
α-lactalbumin	LALBA	11	16.23	142
histone H1.2	HIST1H1C	2	21.37	213
thymosin β-4	TMSB4	2	5.05	44
14-3-3 protein zeta/delta	YWHAZ	2	27.75	245
protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	POMGNT2	2	66.62	580
14-3-3 protein epsilon	YWHAE	1	29.17	255

Supplemental Table 2: Fold change of peptide intensity by GA and LS indicated from volcano plots

	Sequence	Protein Group	Fold Change	p-value
<i>Gestational Age</i>	ADGSRASVDSGSSEEQGGSS	PIGR	-0.61	0.0003
	ADGSRASVDSGSSEEQGGSSRA	PIGR	-0.45	0.0001
	EESITEYKQKV	β -casein	1.25	0.0012
	ESLSSEESITEYK	β -casein	1.20	0.0013
	ETIESLSSEESITEY	β -casein	0.92	0.0011
	ETIESLSSEESITEYK	β -casein	0.74	0.0014
	ETIESLSSEESITEYKQ	β -casein	1.21	< 0.0001
	ETIESLSSEESITEYKQK	β -casein	0.99	0.0012
	ETIESLSSEESITEYKQKV	β -casein	1.00	0.0010
	LSSEESITEYK	β -casein	1.06	0.0003
	PAVVLVPVPQPEI	β -casein	-0.61	0.0004
	PKAKDTVYT	β -casein	-0.72	0.0009
	RETIESLSSEESITEYKQK	β -casein	1.08	0.0048
	SEESITEYK	β -casein	1.04	0.0001
	SLSSEESITE	β -casein	0.83	0.0003
	SLSSEESITEYK	β -casein	0.88	0.0002
	SSEESITEYK	β -casein	1.17	0.0034
	SSSEESITEYK	β -casein	0.69	0.0011
	SSSEESITEYKQKV	β -casein	0.94	0.0007
	GAKTTFDVYTESWAQDPSQENK	bile salt-activated lipase	0.85	0.0031
<i>Lactational Stage</i>				
	ADTRDQADGSRASVD	PIGR	-0.71	0.0007
	DSGSSEEQGGSSRALVSTLV	PIGR	-1.14	0.0001
	VDSGSSEEQGGSSRA	PIGR	-0.76	0.0020
	AKDTVYTKGRVM	β -casein	-0.65	0.0006
	EESITEYK	β -casein	0.97	< 0.0001
	ESLSSEESITEYK	β -casein	1.39	0.0006
	ETIESLSSEESITEY	β -casein	1.21	0.0000
	ETIESLSSEESITEYKQ	β -casein	1.03	0.0024
	ETIESLSSEESITEYKQK	β -casein	1.33	< 0.0001
	IESLSSEESITEYK	β -casein	1.19	0.0007
	IMEVPAKAKDTVYT	β -casein	0.74	0.0005
	LLNPTHQIYPVTQPLAP	β -casein	-1.36	< 0.0001
	LLNPTHQIYPVTQPLAPVHNPIIS	β -casein	-0.97	< 0.0001
	LLNPTHQIYPVTQPLAPVHNPIISV	β -casein	-0.80	0.0013
	LPIPQQVVPYP	β -casein	0.83	0.0025
	LPVPQPEIMEVPAK	β -casein	0.68	0.0005

	MEVPKAKDTVYTKG	β -casein	-0.80	0.0006
	PLMQQVPQPIPQTL	β -casein	-0.61	0.0004
	RETIESLSSEESITEYK	β -casein	1.59	0.0035
	SEESITEYK	β -casein	1.15	0.0001
	SLSSSEESITE	β -casein	0.81	0.0017
	SLSSSEESITEY	β -casein	0.75	0.0007
	SLSSSEESITEYK	β -casein	1.15	< 0.0001
	SLSSSEESITEYKQKV	β -casein	0.77	0.0005
	SSSEESITEYK	β -casein	0.87	0.0001
	TEYKQKVEKVKHED	β -casein	-0.85	< 0.0001
	VLPIPPQVVPYPQR	β -casein	0.80	0.0013
	VPQPEIMEVPK	β -casein	0.84	< 0.0001
	IPQRQYLPNSHPPTVV	κ -casein	-0.94	0.0014
	NEYNQLQLQAAHAQEQIR	α -S1-casein	1.22	0.0003

Positive values indicate an upregulation and negative values indicate a downregulation in fold change peptide intensity. Bold peptide sequences were significant upregulated in both GA and LS groups.

Supplemental Table 3: Differing peptide sequences by GA, LS and the interaction of GA and LS

Group	Sequence	Protein Group	ANOVA p-value
<i>Preterm vs Term Gestational Age</i>	ETIESLSSEESITEYKQ	β -casein	< 0.0001
	ADGSRASVDSGSSEEQGGSSRA	PIGR	0.0001
	SEESITEYK	β -casein	0.0001
	PKAKDTVYT	β -casein	0.0002
	SLSSSEESITEYK	β -casein	0.0002
	SLSSSEESITE	β -casein	0.0002
	ADGSRASVDSGSSEEQGGSS	PIGR	0.0003
	LSSSEESITEYK	β -casein	0.0004
	ESLSSSEESITEYK	β -casein	0.0005
	SSSEESITEYKQKV	β -casein	0.0006
	ETIESLSSEESITEYKQKV	β -casein	0.0009
	SSSEESITEYK	β -casein	0.0010
	AVADTRDQADGSRASVDSGSSEEQ	PIGR	0.0011
	SRASVDSGSSEEQGGSSRA	PIGR	0.0012
	ETIESLSSEESITEYK	β -casein	0.0012
	AVADTRDQADGSRASVDSG	PIGR	0.0012
	ETIESLSSEESITEYKQK	β -casein	0.0013
	RYPRLQNPSE	α_{s1} -casein	0.0018
	EESITEYKQKV	β -casein	0.0021
	GSRASVDSGSSEEQGGSSRA	PIGR	0.0025
	ETIESLSSEESITEY	β -casein	0.0026
	NQELLNPTHQIYPVT	β -casein	0.0027
	LSSSEESITEYKQKV	β -casein	0.0029
	SSEESITEYK	β -casein	0.0029
	EESITEYK	β -casein	0.0029
	DQADGSRASVDSGSSEEQG	PIGR	0.0031
	ADTRDQADGSRASVDSGSSEEQGGSS	PIGR	0.0036
	PQIPKLT	β -casein	0.0038
	GAKTTFDVYTESWAQDPSQENK	bile salt-activated lipase	0.0039
	SLSSSEESITEYKQKV	β -casein	0.0040
<i>Early vs. Late Lactational Stage</i>	SLSSSEESITEYK	β -casein	< 0.0001
	LLNPTHQIYPVTQPLAP	β -casein	< 0.0001
	VPQPEIMEVPK	β -casein	< 0.0001
	LLNPTHQIYPVTQPLAPVHNPI	β -casein	< 0.0001
	EESITEYK	β -casein	< 0.0001

	ETIESLSSEESITEYKQK	β -casein	< 0.0001
	LPIPQQVVPYP	β -casein	< 0.0001
	SEESITEYK	β -casein	0.0001
	TEYKQKVEKVKHED	β -casein	0.0001
	ETIESLSSEESITEY	β -casein	0.0001
	DSGSSEEQGGSSRALVSTLV	PIGR	0.0001
	SSSEESITEYK	β -casein	0.0001
	NEYNQLQLQAAHAQEQR	α_{s1} -casein	0.0001
	DLENLHLP	β -casein	0.0002
	ESLSSEESITEYK	β -casein	0.0002
	SLSSSEESITEYKQKV	β -casein	0.0002
	SLSSSEESITEY	β -casein	0.0003
	MEVPAKADTVYTKG	β -casein	0.0004
	IMEVPAKADTVYT	β -casein	0.0004
	LNPTHQIYPVTQ	β -casein	0.0004
	ETIESLSSEESITEYKQ	β -casein	0.0006
	LPVPQPEIMEVPAK	β -casein	0.0006
	ADTRDQADGSRASVD	PIGR	0.0008
	PLMQQVPQPIPQTL	β -casein	0.0009
	EDQQQGEDEHQDKIYPS	β -casein	0.0010
	LLNPTHQIYPVTQPLAPVHNPIV	β -casein	0.0011
	VDSGSSEEQGGSSRA	PIGR	0.0012
	AKDTVYTKGRVM	β -casein	0.0012
	VLPIPQQVVPYPQR	β -casein	0.0013
	IESLSSEESITEYK	β -casein	0.0013
	TEYKQKVEKV	β -casein	0.0014
	SGSSEEQGGSSRAL	PIGR	0.0015
	ADTRDQADGSRASVDSGSSEEQGGSS	PIGR	0.0017
	LAQPAVVLPVPQPEIMEVPAK	β -casein	0.0021
	NPTAHENYEKNNVML	α_{s1} -casein	0.0027
	ETIESLSSEESITEYK	β -casein	0.0028
	AVADTRDQADGSRASVD	PIGR	0.0030
	IPQRQYLPNSHPPTVV	κ -casein	0.0031
	PLAPVHNPIV	β -casein	0.0031
	AVADTRDQADGSSRA	PIGR	0.0032
	SLSSSEESITE	β -casein	0.0032
<i>Interaction of GA and LS</i>	SLSSSEESITEYK	β -casein	0.0018
	SEESITEYK	β -casein	0.0045
	LLNPTHQIYPVTQPLAPVHNPIV	β -casein	0.0052
	ETIESLSSEESITEYKQ	β -casein	0.0085

	ETIESLSSEESITEYKQK	β -casein	0.0088
	LLNPTHQIYPVTQPLAP	β -casein	0.0088
	EESITEYK	β -casein	0.0096
	VPQPEIMEVPK	β -casein	0.0131
	SSSEESITEYK	β -casein	0.0137
	ESLSSEESITEYK	β -casein	0.0144
	ETIESLSSEESITEY	β -casein	0.0160
	DLENLHLP	β -casein	0.0186
	TEYKQKVEKVKHED	β -casein	0.0211
	LPIPQQVVPYP	β -casein	0.0232
	ADGSRASVDSGSSEEQGGSSRA	PIGR	0.0246
	SLSSEESITE	β -casein	0.0260
	PKAKDTVYT	β -casein	0.0260
	DSGSSEEQGGSSRALVSTLV	PIGR	0.0262
	SLSSEESITEYKQKV	β -casein	0.0273
	SLSSEESITEY	β -casein	0.0334
	DQADGSRASVDSGSSEEQGGSSRALVSTL	PIGR	0.0345
	MEVPAKDTVYTKG	β -casein	0.0348
	NEYNQLQLQAAHAQEQR	α_{s1} -casein	0.0360
	ADGSRASVDSGSSEEQGGSS	PIGR	0.0384
	LNPTHQIYPVTQ	β -casein	0.0403
	ETIESLSSEESITEYK	β -casein	0.0424
	ADTRDQADGSRASVD	PIGR	0.0429
	LSSSEESITEYK	β -casein	0.0477

Bold peptide sequences were uniquely significant for the designated group, and were not found significant in other groups.

Supplemental Table 4: Prediction of the enzymes responsible for cleavage of human milk parent proteins, ranked by total number of cleavages

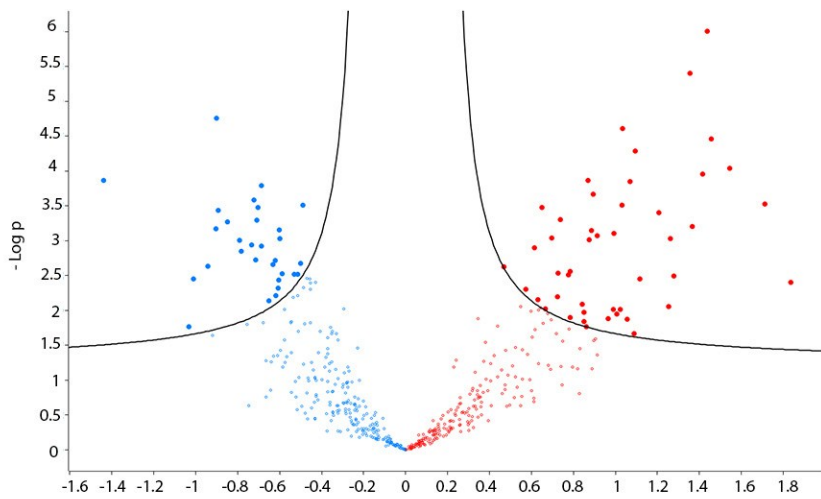
Enzymes	N-terminal cleavage count	C-terminal cleavage count	Total cleavages	Unique cleavage	Number of expected cleavages within the peptide	Number of proteins cleaved	Odds Ratio	Standard Error
trypsin 1 ^a	130	89	219	0	419	7	1.96	1.09
plasmin	130	89	219	0	426	7	1.93	1.09
cathepsin D	93	88	181	0	828	6	0.76	1.09
LysC	77	64	141	0	220	6	2.38	1.12
pepsin (pH 1.3) 1	38	91	129	0	292	8	1.61	1.11
elastase	60	63	123	0	570	5	0.76	1.11
modified chymotrypsin	79	43	122	0	343	8	1.28	1.11
chymotrypsin low 1	76	43	119	0	338	8	1.27	1.12
pepsin (pH > 2) 1	34	82	116	0	209	6	2.04	1.13
Pepsin (pH 1.3) 2	50	30	80	0	262	8	1.09	1.14
AspN								
endopeptidase	68	11	79	0	329	7	0.85	1.14
argcpoteinase	53	25	78	0	206	6	1.36	1.14
clostripain	53	25	78	0	206	6	1.36	1.14
proline								
endopeptidase diff	23	46	69	0	494	5	0.48	1.14
pepsin (pH > 2) 2	40	21	61	0	130	7	1.69	1.17
formic acid	19	37	56	0	351	4	0.56	1.16
staphprotease	28	24	52	0	537	6	0.33	1.16
glutamyl								
endopeptidase ^a	28	24	52	0	537	6	0.33	1.16
staphylococcal								
peptidase I	26	21	47	0	409	6	0.40	1.17
chymotrypsin high 1	21	15	36	0	128	7	1.00	1.21
chymotrypsin low 4	8	5	13	0	125	3	0.37	1.34
CNBr	9	3	12	0	68	2	0.63	1.37
cyanogen bromide	9	3	12	0	68	2	0.63	1.37
chymotrypsin low 3	8	2	10	0	47	2	0.76	1.42
proline								
endopeptidase	4	0	4	0	9	1	1.59	1.82
iodosobenzoic acid	3	0	3	0	5	1	2.14	2.08
iodosobenzoate	3	0	3	0	5	1	2.14	2.08
chymotrypsin low 2	3	0	3	0	5	1	2.14	2.08
chymotrypsin high 2	3	0	3	0	5	1	2.14	2.08
NTCB	0	2	2	0	0	2	17.85	4.71
thrombin 1	1	0	1	1	1	1	3.57	4.11

^aEnzymes that do not have expression in milk, but data indicate the presence of other enzymes with similar activity

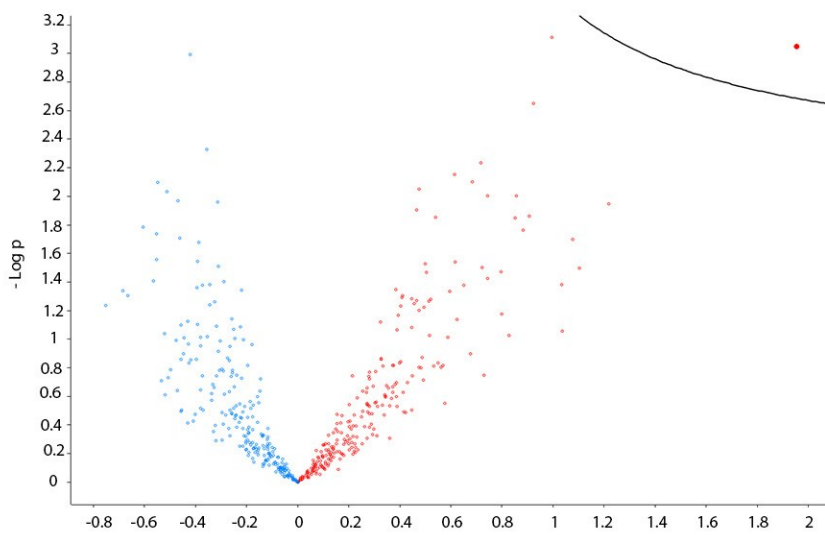
[illegible]

A heatmap visualization showing gene expression profiles across various developmental stages and conditions. The y-axis labels include beta-casein, alpha-S1-casein, PIgR, and other casein-related genes. The x-axis labels represent different developmental stages: Preterm (Late), Term (Early), Term (Late), and Preterm (Late). The color scale ranges from red (high expression) to blue (low expression).

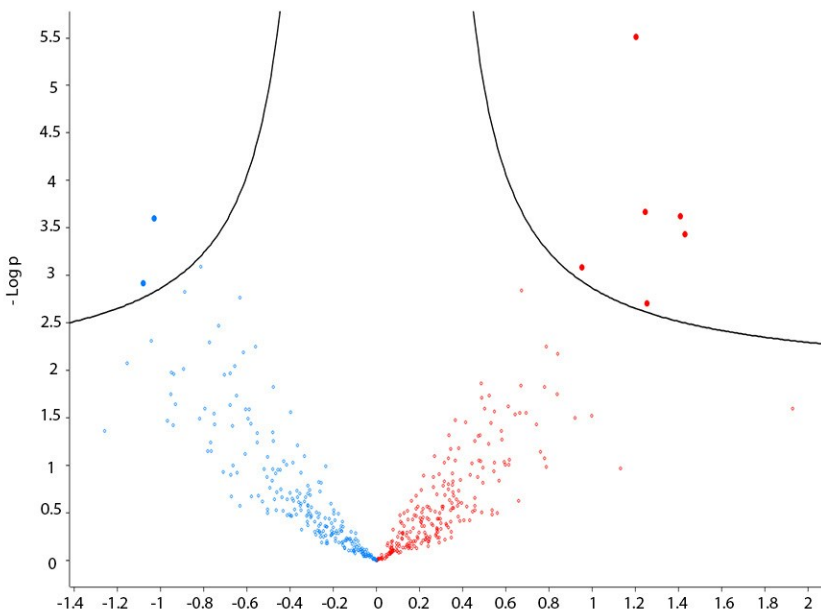
Supplemental Figure 1: Panel A: Quantitative hierarchical k-means clustering shows samples as the column tree and peptide sequences as the row tree, with lower intensities plotted as dark blue with an increasing color scale from gray to dark red as the log₁₀ fold change of the peptide intensity increases. Panel B shows the zoomed in portion of the top of Panel A where peptide intensities were highest, the row tree indicated the parent protein of the most intense peptides.



Panel A



Panel B



Panel C

Supplemental Figure 2: Volcano plots depicting log₁₀ fold change in peptide intensity (x axis) and -log p value (y-axis). All significant peptides are represented as filled circles and non-significant peptides are unfilled. Panel A, peptide intensity distribution between preterm late LS (blue) and term early LS milk (red). Panel B, peptide intensity distribution between preterm late LS (blue) and term late LS milk (red). Panel C, peptide intensity distribution between term early LS (blue) and term late LS milk (red).