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Title	Proteolysis in Danish blue cheese during ripening
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Publication date	2019-06-12
Original Citation	Mane, A., Ciocia, F., Beck, T. K., Lillevang, S. K. and McSweeney, P. L. H. (2019) 'Proteolysis in Danish blue cheese during ripening', International Dairy Journal, 97, pp. 191-200. doi: 10.1016/j.idairyj.2019.05.017
Type of publication	Article (peer-reviewed)
Link to publisher's version	http://www.sciencedirect.com/science/article/pii/S0958694619301396 - 10.1016/j.idairyj.2019.05.017
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Download date	2026-10-13 07:18:30
Item downloaded from	https://hdl.handle.net/10468/8299

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Supplementary Data

Supplementary table 1

First 30 peptides of *Penicillium roqueforti* PR-R was grown in 1:1 ratio of 10% reconstituted low-heat skimmed milk powder and potato dextrose broth for 7 days at 25ºC. This supernatant was aliquoted and further analysed by UPLC and LCMS to identify α_{s1}-casein and β-casein peptides.

Protein	Peptide sequence	start	end	N-terminal cleavage site	C-terminal cleavage site	rel int*100	Retention time (min)
α_{s1}-CN	FVAPFPE	24	30	23-24	30-31	14.36	21.858
α_{s1}-CN	HQGLPQEVLNENLLR FFVAPFPEVFGK	8	34	7-8	34-35	8.53	38.004
α_{s1}-CN	IQKEDVPSERY	81	91	80-81	91-92	4.56	8.202
α_{s1}-CN	LDAYPSGAW	156	164	155-156	164-165	4.26	19.772
α_{s1}-CN	IKHQGLPQE	6	14	5-6	14-15	3.38	6.051
α_{s1}-CN	SEKTTMP	191	197	190-191	191-192	2.91	5.508
α_{s1}-CN	IGSENSEKTTMP	186	197	185-186	186-187	2.12	8.979
α_{s1}-CN	QKEDVPSERYLGYLEQLL	82	99	81-82	99-100	2.1	32.394
α_{s1}-CN	VLNENLLRFFV	15	25	14-15	25-26	1.72	29.818
α_{s1}-CN	DVPSERY	85	91	84-85	91-92	1.62	7.441
α_{s1}-CN	IHAQQKEPM	127	135	126-127	135-36	0.97	4.715
α_{s1}-CN	KHQGLPQEVLNENL	7	20	6-7	20-21	0.88	31.786
α_{s1}-CN	YVPLGTQYT	166	174	165-166	174-175	0.82	22.529
α_{s1}-CN	EGIHAQQKEPM	125	135	124-125	135-136	0.74	25.692
α_{s1}-CN	QAMEDIKQMEA	52	62	51-52	62-63	0.62	8.981
α_{s1}-CN	IHAQQKEPMIG	127	137	126-127	137-138	0.62	8.360
α_{s1}-CN	PNPIGSEN	183	190	182-83	190-191	0.59	23.955
α_{s1}-CN	VEQKHIQKED	76	85	75-76	85-86	0.58	22.529
α_{s1}-CN	QKEDVPSERY	82	91	81-82	91-92	0.58	6.626
α_{s1}-CN	AYPSGAW	158	164	157-158	164-165	0.58	15.471
α_{s1}-CN	IKHQGLPQEV	6	15	5-6	15-16	0.57	9.833
α_{s1}-CN	HQGLPQE	8	14	7-8	14-15	0.57	6.126
α_{s1}-CN	HIQKEDVPSERYLGYL	80	95	79-80	95-96	0.55	28.923
α_{s1}-CN	LDAYPSGA	156	163	155-156	163-164	0.55	10.808
α_{s1}-CN	IGVNQEL	136	142	134-135	142-143	0.54	14.872
α_{s1}-CN	VPNSAEERLH	112	121	111-12	121-122	0.53	6.846
α_{s1}-CN	FSDIPNP	179	185	178-179	185-186	0.53	15.831
α_{s1}-CN	SSEEIVPNSVEQKHIQKED	67	85	66-67	85-86	0.51	32.389
α_{s1}-CN	HIQKEDVPSERY	80	91	79-80	91-92	0.48	7.217
α_{s1}-CN	PQEVLNENLLRFF	12	24	11-12	24-25	0.47	31.812

protein	Protein sequence	Start	End	N-terminal cleavage site	C-terminal cleavage site	Rel int*100	Retention time (min)
β-CN	PYPQRDMP	179	186	178-179	186-187	8.86	13.375
β-CN	VLGPVRGPFPIIV	197	209	196-198	209-210	5.42	29.817
β-CN	MHQPHQPLPPT	144	154	143-144	154-155	5.07	8.841
β-CN	VEPFTES	116	122	115-116	122-123	4.49	13.054
β-CN	LHLPLPL	133	139	132-133	139-140	4.13	27.560
β-CN	LQPEVMG	88	94	87-88	94-95	3.33	13.085
β-CN	VMFPPQS	155	161	154-155	161-162	2.94	17.046
β-CN	AVPYPQRDMP	177	186	176-177	186-187	1.87	13.560
β-CN	TPVVVPPF	80	87	79-80	87-88	1.81	25.291
β-CN	VLGPVRGPFP	197	206	196-197	206-207	1.62	20.206
β-CN	MFPPQSV	156	162	155-165	162-163	1.58	15.370
β-CN	KVLPVPQK	169	176	168-169	176-177	1.48	8.032
β-CN	AMAPKHKEMPFPKYP	101	115	100-101	115-116	1.37	12.905
β-CN	LSQSKVLPVPQK	165	176	164-165	176-177	1.34	11.411
β-CN	VRGPFPI	201	207	200-201	207-208	1.25	19.76
β-CN	WMHQPHQPLPPT	143	154	142-143	154-155	1.2	12.494
β-CN	QPEVMGVSKVKEAMAP	89	104	88-89	104-105	1.13	12.351
β-CN	LNVPGEIVESLSSSEESI	6	23	5-6	23-24	1.02	27.345
β-CN	VLPVPQK	170	176	169-170	176-177	1.02	9.846
β-CN	SKVLPVPQK	168	176	167-168	176-177	0.99	8.711
β-CN	LYQEPVLGPVRGPFP	192	206	191-192	206-207	0.91	25.197
β-CN	VMGVSKVKEAMAPK	92	105	91-92	105-106	0.87	31.713
β-CN	YPFPGPIPNSLPQNIPP	60	76	59-60	76-77	0.79	38.891
β-CN	MAPKHKEMPFPKYPVEPF	102	119	118-119	119-120	0.76	19.652
β-CN	HQPHQPLPPT	145	154	153-154	154-155	0.72	7.123
β-CN	AMAPKHKEMPFPKYPVEP	101	118	117-118	118-119	0.66	15.605
β-CN	WMHQPHQP	143	150	149-150	150-151	0.64	7.744
β-CN	AVPYPQR	177	183	176-177	183-184	0.59	7.507
β-CN	LTDVENL	127	133	126-127	133-134	0.49	15.899
β-CN	VPYPQRDMP	178	186	177-178	186-187	0.47	12.563

Supplementary table (2 A)

List of first 50 peptides in A: α_{s1}-casein from pH 4.6-soluble extracts of Danish blue cheese during 9 w of ripening, with highest values of relative intensity.

OOS				2W				4W				7W				9W			
Seq.	start	end	Rel Int	seq	start	end	Rel Int	Seq.	start	end	Rel Int	Seq.	start	end	Rel Int	Seq.	start	end	Rel Int
FVAPFPE	24	30	20.39	FVAPFPE	24	30	9.13	PSFSDIPNPIGSEN	177	190	9.62	VAPFPEVFGKEK	25	36	3.18	DIPNPIGSENSEK	181	193	3.62
GLPQEVL	10	16	13.78	GLPQEVL	10	16	4.32	QYTDAPSFSDIPNPIGSENSE	172	192	5.83	DIPNPIGSENSEK	181	193	2.07	VAPFPEVFGKEK	25	36	2.14
RPKHPIKHQGLPQEVLN	1	17	4.84	VAPFPEVFGKEK	25	36	3.36	YVPLGTQY	166	173	2.08	YLGYLEQ	91	97	1.91	DIPNPIGSE	181	189	2
RPKHPIKHQGLPQEVL	1	16	3.33	VAPFPEVF	25	32	2.06	SVEQKHIQKEDVPSERYLGYL	75	95	2	PIKHQGLPQEVLNENLLRFFVAPFPEVFGKEKVNEL	5	40	1.61	VNELSKDIGSESTEDQAMEDIKQMEAE	37	63	1.76
RPKHPIKHQGLPQE	1	14	3.07	YLGYLEQ	91	97	2.04	DAYPSGAWYYVPLGTQ	157	172	1.75	ESISSSEEIVPNSVEQKHIQKEDV	63	86	1.61	IPNPIGSENSEK	182	193	1.47
PFPEVFGKEKVNEL	27	40	2.68	HQGLPQE	8	14	2.02	DAYPSGAW	157	164	1.68	FGKEKVNELSKDIGS	32	46	1.48	SVEQKHIQKEDVPSERYLGYL	75	95	1.32
VFGKEKVNEL	31	40	2.14	FVAPFPEVFGK	24	34	1.92	YVPLGTQ	166	172	1.39	FFVAPFPEVFGKEK	23	36	1.36	VPLGTQYTDAPSFSDIPNPI	167	186	1.24
LRLKKYKVPQL	99	109	2.09	PNSVEQKHIQKED	73	85	1.64	EPMIGVNQ	133	140	1.22	VNELSKDIGSESTEDQAMEDIKQMEAE	37	63	1.14	APFPEVFGKEK	26	36	0.97
FVAPFPEVFGKEKVNEL	24	40	2	SVEQKHIQKEDVPSERYLGYLE	75	96	1.31	VFGKEKVNELSK	31	42	1.15	HQGLPQE	8	14	1.09	HIQKEDVPSER	80	90	0.84
LEQLLRLKKYKVPQL	95	109	1.97	APFPEVFGKEK	26	36	1.03	GLPQEVLNENLLRFFVAPFPEVFGKE	10	35	1.14	DIPNPIGSE	181	189	1.06	FFVAPFPEVFGKEK	23	36	0.79
RPKHPIKHQGLPQ	1	13	1.92	GLPQEVLNE	10	18	0.95	FYQLDAYPS	153	161	1.14	EQKHIQKEDVPSERYLGYLEQLL	77	99	1.04	LKKYKVPQLEIVPNSAEE	101	118	0.77
KVPQLEIVPNSAEERLHSMKEGIH	105	128	1.89	RPKHPIKHQGLPQE	1	14	0.88	AYPSGAW	158	164	1.07	VLNENLL	15	21	0.89	LGYLEQL	92	98	0.75
EVLNENL	14	20	1.71	VAPFPEV	25	31	0.76	EIVPNSAEERLHSMKEGIHAQQKEPMIG	110	137	1.01	HIQKEDVPSER	80	90	0.88	VNQELAYFYPELF	138	150	0.64
VAPFPEVFGKEKVNEL	25	40	1.6	SAEERLHSMK	115	124	0.76	EDVPSER	84	90	0.95	RPKHPIKHQGLPQEVLN	1	17	0.76	VAPFPEVF	25	32	0.63
VAPFPEVF	25	32	1.59	AQQKEPMIGVNQELAYFYPELFRQFYQLDA	129	158	0.68	QAMEDIKQMEAESISSSEEIV	52	72	0.9	EDVPSER	84	90	0.7	YLGYLEQ	91	97	0.58
EVLNENLLRF	14	23	1.02	HQGLPQEV	8	15	0.66	HIQKEDV	80	86	0.84	VAPFPEVF	25	32	0.69	HQGLPQE	8	14	0.57
PSERYLGY	87	94	0.81	RPKHPIKHQGLPQEVL	1	16	0.64	LFRQFYQLDA	149	158	0.76	IPNPIGSENSEK	182	193	0.67	EERLHSMKEGIHAQQKEPMIGVQ	117	140	0.55
EQKHIQKEDVPS	77	88	0.64	KHIQKEDVPSERYLG	79	93	0.63	YLGYLEQ	91	97	0.68	FFVAPFPEVFGK	23	34	0.56	PLGTQYTDAPSFSDIPNPIGSEN	168	190	0.54
PNSVEQKHIQKED	73	85	0.6	FFVAPFPEVFGK	23	34	0.6	YYVPLGTQ	165	172	0.68	FFVAPFPEVFGKEKVNEL	23	40	0.56	EDVPSER	84	90	0.52
LGYLEQL	92	98	0.52	PFPEVFGK	27	34	0.57	EQKHIQKEDVPSERYLGYLEQLL	77	99	0.65	LGYLEQL	92	98	0.54	SDIPNPIGSENSEK	180	193	0.51
VLNENLLRF	15	23	0.5	SAEERLHSMKEGIHAQQKEPMI	115	136	0.52	SFSDIPNPIGSENSEK	178	193	0.65	PFPEVFGKEK	27	36	0.52	DAYPSGAW	157	164	0.48

PQEVLN ENLLRFFV	12	25	0.47	KEPMIGVNQELAYFYP ELFR	132	151	0.52	DIPNPIGSENSEK	181	193	0.65	KHIQKEDVPSERYLGY LE	79	96	0.52	FYQLDAYPSGA	153	163	0.43
LEQLLRL	95	101	0.45	RPKHPIKHQGLPQ	1	13	0.51	ENLLRFFVAPFPEVFGK EK	18	36	0.53	PFPEVFGKEKVNEL	27	40	0.49	IPNPIGSEN	182	190	0.43
RLKKYKVPQL	100	109	0.39	LFRQFYQLDA	149	158	0.5	VPNSVEQK	72	79	0.49	FVAPFPEVFGKEKVNE L	24	40	0.45	FFVAPFPEVFGKEKV NEL	23	40	0.42
VLNENLLRFFV	15	25	0.38	NSVEQKHIQKEDVPSER YLGYL	74	95	0.49	KEPMIGVNQELAYFYP ELFR	132	151	0.49	YVPLGTQYTDA	166	176	0.42	SMKEGIHAQQEPMIG VNQELAYFY	122	146	0.42
VAPFPE VFGKEK	25	36	0.37	EVLNENL	14	20	0.48	SISSSEEIVPNSVEQKHI QKEDVPS	64	88	0.47	DAYPSGAW	157	164	0.41	FVAPFPEVFGKEKVN EL	24	40	0.41
PMIGVNQELAYFYPEL FRQFYQLDAYPSGAWY	134	165	0.35	RPKHPIKHQGLPQEVL NEN	1	19	0.46	GIHAQQKEPMIGVNEL AYFYP	126	147	0.46	PQLEIVPNSAEERLHS MKEGIHAQQKEPMI	107	136	0.4	VNELSKDIGSESTEDQ AMEDIKQMEAESIS	37	66	0.41
LGYLEQL LRLKKYKVPQL	92	109	0.33	EVFGKEKVNELSKDIGS ESTEDQAME	30	55	0.45	VNELSKDIGSESTEDQA MEDIKQMEAESIS	37	66	0.45	KEPMIGVNQELAYFYP	132	147	0.4	QAMEDIKQMEAESIS SSEEIV	52	72	0.41
IGVNQEL	136	142	0.33	SVEQKHIQ KEDVPSERYLGYL	75	95	0.44	HQGLPQE	8	14	0.44	VNQELAYFYPELF	138	150	0.4	KHQGLPQEVLNEN	7	19	0.38
VPSERYLGY	86	94	0.32	PFPEVFGKEK	27	36	0.41	IGVNQEL	136	142	0.42	FVAPFPEVFGK	24	34	0.38	QQKEPMIGVNQELA Y	130	144	0.35
QKEPMIGVNQEL	131	142	0.32	EDVPSER	84	90	0.4	VPNSAEERLHSMKEGI HAQQKEPM	112	135	0.41	ISSSEEIVPNSVEQKHIQ KE	65	84	0.34	IPNPIGSE	182	189	0.34
GKEKVNELSKDIGE	33	47	0.3	PQEVLNENLLRFFV	12	25	0.36	SVEQKHIQKE DVPSERYLGYLE	75	96	0.4	KHIQKEDVPSER	79	90	0.33	HIQKEDVPSE RYLGYLEQLR	80	100	0.33
DVPSER YLGYLEQL	85	98	0.3	NSAEERLHSMKEGIHA QQKEPMI	114	136	0.36	FVAPFPEV FGKEK	24	36	0.39	YLGYLEQLLR	91	100	0.3	VPLGTQYTDAPSFSDI PNPIGSENSEK	167	193	0.33
VAPFPEVFGKE	25	35	0.28	SISSSEEIVPNSV	64	76	0.35	QFYQLDAYPS	152	161	0.38	EPMIGVNQ	133	140	0.3	RPKHPIKHQGLPQEV LNE	1	18	0.32
KEGIHAQQK	124	132	0.27	GVNQELAYFYPELFRQ FYQLDA	137	158	0.34	IPNPIGSENSEK	182	193	0.36	VPLGTQYTDAPSFSDIP NPI GSENSEK	167	193	0.29	LFRQFYQLDA	149	158	0.32
QKEPMIGVNQE	131	141	0.27	AWYYVPLGTQYTDAPS FSDIPNPIGSENS	163	191	0.33	LEIVPNSAE ERLHSMKEGIH	109	128	0.35	QKHIQKEDVPSERYLG YLEQ	78	97	0.28	AYPSGAW	158	164	0.32
PFPEVFGKE	27	35	0.25	IVPNSAEERLHSMKEGI HAQQKEPMIGVN	111	139	0.31	VAPFPEV FGKEK	25	36	0.33	RPKHPIKHQGLPQEVL NENL	1	20	0.27	DIPNPIGSE NSEKTTMPL	181	198	0.32
KEGIHAQQKEPMIGVN QELAYFYPELFRQ	124	152	0.25	DIPNPIGSENSEKTTMP LW	181	199	0.31	FPEVFGK	28	34	0.32	DIKQMEAESISSSEEIV	56	72	0.27	RPKHPIKHQGLPQEV LNENLLRF	1	23	0.3
PIKHQGLPQEVLN	5	17	0.24	FFVAPFPE	23	30	0.3	EPMIGVN	133	139	0.3	RPKHPIKQGLPQEVLN ENLLR	1	22	0.26	VLNENLLRFFVAPFP EVFGKEKVNELSKDI GSESTEDQAMEDIKQ MEAESISSSEEIVP	15	73	0.3
DVPSERY	85	91	0.24	NENLLRFFVAPFPEVFG KEK	17	36	0.29	PFPEVFGKE KVNELSKDIGS	27	46	0.29	RPKHPIKHQGLPQEVL NENLLRF	1	23	0.26	PSGAWYYVPLGTQY TDAP	160	177	0.3
KEGIHAQ QKEPMIGVN	124	139	0.24	LKKYKVPQLEIVPNSAE ERLHSMKE	101	125	0.29	DIPNPIGSE	181	189	0.29	QAMEDIKQM EAESISSSEEI	52	71	0.26	VLNENLL	15	21	0.29
QKEPMIG VNQELAY	131	144	0.24	ISSSEEIVPNSVEQKHIQ KEDVPS	65	88	0.28	PFPEVFGKEK VNELSKDIGSE	27	47	0.28	SDIPNPIGSENSEKTTM PLW	180	199	0.25	QQKEPMIGVNQELA	130	143	0.29

DVPSERYLGY	85	94	0.23	FFVAPFPE VFGKEK	23	36	0.27	APFPEVFGKEK	26	36	0.27	QLDAYPSGAWYYVPL GTQYTD APSFSDIPN	155	184	0.24	FVAPFPEVFGKEKVN	24	38	0.28
EGIHAQQKEP	125	134	0.21	APFPEVFK	26	34	0.24	ELAYFYPELFRQ	141	152	0.26	FVAPFPEVFGKE	24	35	0.23	RPKHPIKHQGLPQEV L	1	16	0.27
QGLPQEVLNENLLRFF V	9	25	0.2	PFPEVFGE	27	35	0.24	NELSKDIGSESTEDQA MEDIKQMEAESISSS	38	68	0.23	EDVPSERYLGYLEQLL	84	99	0.23	RPKHPIKHQGLPQEV LNEN	1	19	0.27
APFPEVFGKE	26	35	0.2	GKEKVNL	33	40	0.23	VLNENLLRFF	15	24	0.22	SMKEGIHAQQKEPMI GVNQELAYFY	122	146	0.23	SMKEGIHAQQKEPMI GVNQELAYF	122	145	0.27
ERYLGYLEQL	89	98	0.17	EQKHIQKEDVPSERYL GYLEQLL	77	99	0.23	KEGIHAQQKEP	124	134	0.22	VAPFPEVFG	25	33	0.22	KEPMIGVNQELAYFY P	132	147	0.27
LKKYKVPQLEIVPNSA EERLHSMKE	101	125	0.17	PIKHQGLP QEVLNE	5	18	0.21	NQELA YFYPELF	139	150	0.22	KEGIHAQQKEPMIGVN QELAYF	124	145	0.22	GVNQELAYFYP	137	147	0.27
NENLLRFF	17	24	0.16	HQGLPQEVLNENLLRF FVAPFPEVFGK	8	34	0.21	EAESISSS EEIVPNS	61	75	0.19	QQKEPMI GVNQELA	130	143	0.22	HIQKEDVPSE RYLGYLEQL	80	98	0.26
AEERLHSMKEGIHAQQ KEPMIGVNQELAYFYP ELFRQFYQLDAYPSGA WYYVPLGTQYTD	116	175	0.16	QKEPMIGVNQE	131	141	0.21	VPQLEIVPNSAE	106	117	0.19	RPKHPIKH QGLPQEVLNE	1	18	0.21	NSAEERLHSMKEGIH AQQKEPMIGVNQEL	114	142	0.26

Supplementary table (2 B)

List of first 50 peptides in β-casein from pH 4.6-soluble extracts of Danish blue cheese during 9 w of ripening, with highest values of relative intensity.

OOS				**2W**				**4W**				**7W**				**9W**			
Seq.	**start**	**end**	**Rel Int**	**Seq.**	**start**	**end**	**Rel Int**	**Seq.**	**start**	**end**	**Rel Int**	**Seq.**	**start**	**end**	**Rel Int**	**Seq.**	**start**	**end**	**Rel Int**
YQEPVLGPVR GPFPIIV	193	209	11.89	NVPGEIVE	7	14	8.34	FPGPIPN	62	68	4.54	YQEPVLGPVRGPFPI	193	207	4.65	FPGPIPN	62	68	4.01
NVPGEIVE	7	14	4.56	NSLPQNIPPLTQTPVV	68	83	3.75	YQEPVLGPVRGP	193	204	3.19	NVPGEIVE	7	14	4.63	YQEPVLGPVRGPFPII	193	208	3.43
LTQTPVVVPPFLQP	77	90	3.98	ELQDKIHPFAQTQSLVY PFPGPI	44	66	3.72	PPFLQPEV MGVS	85	96	2.94	YQEPVLGPVRGPFPII	193	208	3.5	SLSQSKVLPVPQKAV PYPQR	164	183	2.48
QEPVLGPVRGPFP	194	206	2.7	YQEPVLGPVRGPFPII	193	208	3.09	TQTPVVVPPFLQPEVM	78	93	2.63	SLSQSKVLPVPQKAVPY PQR	164	183	3.3	NVPGEIVE	7	14	2.41
VLGPVRGPFPIIV	197	209	2.5	QEPVLGPVRGPFPI	194	207	2.53	YQEPVLGPVRGPFP	193	206	2.58	QEPVLGPVRGPFPIIV	194	209	3.04	DMPIQAF	184	190	2.18
YQEPVLGPVRGPFP	193	206	1.84	NIPPLTQTPVVVPPF	73	87	2.19	QEPVLGPVRGPFPI	194	207	2.54	DMPIQAF	184	190	2.71	LYQEPVLGPVRGPFP IIV	192	209	2.1
LYQEPVLG PVRGPFPIIV	192	209	1.79	SLPQNIPPL	69	77	1.96	VLPVPQK	170	176	2.28	LTDVENLHLPLPLLQS WMHQPHQPLPPTVMF PP	127	159	2.44	TPVVVPP	80	86	1.86
MAPKHKEMPFPKY	102	114	1.73	QEPVLGPVRGPFP	194	206	1.79	NVPGEIVE	7	14	2.23	TPVVVPP	80	86	2.16	YPFPGPIP	60	67	1.59
KVLPVPQ	169	175	1.56	VYPFPGPI	59	66	1.78	QDKIHPFAQT	46	55	1.99	QEPVLGPVRGPFPI	194	207	2.12	YQEPVLGVRGP	193	204	1.58
SLSQSKVLPVPQKAVP YPQ	164	182	1.55	PLTQTPVVVPPFLQ	76	89	1.67	DKIHPFAQTQSL	47	58	1.9	YPFPGPIP	60	67	2.06	ITRINKKIEKFQSEEQ	23	38	1.42
EPVLGPV RGPFPIIV	195	209	1.5	YQEPVLGPVRGPFP	193	206	1.32	PFTESQSL	118	125	1.41	PVPQKAVPYPQR	172	183	1.71	DKIHPFAQTQSL	47	58	1.38

DELQDKIHPF	43	52	1.29	FAQTQSLVYPF	52	62	1.27	YPFPGPIP	60	67	1.35	LHLPLPLLQSWMHQPHQPLP	133	152	1.6	PVPQKAVPYPQR	172	183	1.36
MHQPHQPLPPTVMFPPQSVLSLSQSKVLPVPQKAVPYPQ	144	182	1.21	DKIHPFAQTQSL	47	58	1.02	VLGPVRGPFPI	197	207	1.24	YQEPVLGPVRGP	193	204	1.37	NSLPQNIPPLTQTPV	68	82	1.16
LLYQEPVLGPVRGPFP	191	206	1.1	QPLPPTVMFPPQSVLSLSQ	149	167	0.98	QEPVLGPVRGPFP	194	206	1.23	YPFPGPI	60	66	1.36	VLPVPQKAVPYPQ	170	182	1.12
LPQNIPPL	70	77	0.97	PFAQTQSLVYPFP	51	63	0.97	VENLHLPLPLLQS	130	142	1.21	VENLHLPLPLLQS	130	142	1.28	YQEPVLGPVRGPFP	193	206	0.92
EPVLGPVRGPFP	195	206	0.96	KVLPVPQ	169	175	0.95	DKIHPFAQTQS	47	57	1.09	VLPVPQKAVPYPQ	170	182	1.19	ESQSLTLTDVENLHLPLPLLQSWMHQP	121	147	0.88
EDELQDKIH	42	50	0.93	PPFLQPE	85	91	0.87	FPGPIPNSL	62	70	1.04	SQSKVLPVPQKAVPYPQR	166	183	1.04	EPVLGPVRGPFPI	195	207	0.86
KAVPYPQ	176	182	0.86	VLPVPQKAVPYPQ	170	182	0.82	PFPGPIPNSLPQNIP	61	75	0.88	VLPVPQKAVPYPQR	170	183	0.81	QPLPPTVMFPPQSVLSLSQ	149	167	0.81
SLSQSKVLPVPQ	164	175	0.66	VLGPVRGPFPIIV	197	209	0.78	HQPLPPTVMFPPQSV	148	162	0.81	YQEPVLGPVRGPFP	193	206	0.8	SLSQSKVLPVPQK	164	176	0.74
PPFLQPE	85	91	0.59	DELQDKIHPFAQTQSLVYPFPGPIPNSLP	43	71	0.76	YPFPGPI	60	66	0.78	VLGPVRGPFPIIV	197	209	0.77	VLGPVRGPFPIIV	197	209	0.74
LSLSQSKVLPVPQKAVPYPQ	163	182	0.56	KAVPYPQ	176	182	0.74	EVMGVSK	91	97	0.7	SLSQSKVLPVPQK	164	176	0.76	EPVLGPVRGPFPIIV	195	209	0.73
MHQPHQPLPPTVMFPPQSVLSLSQSKVLPVPQKAVPYPQRDMPIQAF	144	190	0.49	RDMPIQAFLLYQEPVLGPVRGP	183	204	0.74	KEAMAPKHK	99	107	0.7	EPVLGPVRGPFPI	195	207	0.7	VENLHLPLPLLQS	130	142	0.72
VPGEIVE	8	14	0.45	DELQDKIHPF	43	52	0.65	ELQDKIHPFAQTQSLVYPFPGPI	44	66	0.62	EPVLGPVRGPFPIIV	195	209	0.68	LYQEPVLGPVRGPFPI	192	207	0.69
EESITRINKKIEKFQSEEQQQTEDELQDKIHPF	20	52	0.45	EPVLGPVRGPFPIIV	195	209	0.58	GPIPNSL	64	70	0.59	DKIHPFAQTQ	47	56	0.6	SQSKVLPVPQKAVPYPQR	166	183	0.68
GVSKVKEAMAPKHKEMPFPKYPVEPF	94	119	0.42	IQAFLLYQE	187	195	0.57	QEPVLGPVRGP	194	204	0.59	PFPGPIPNSLPQNIP	61	75	0.57	VLPVPQKAVPYPQR	170	183	0.66
LHLPLPLLQSW	133	143	0.41	LQDKIHPF	45	52	0.55	VLGPVRGPFPIIV	197	209	0.59	TPVVVPPF	80	87	0.53	SKVLPVPQKAVPYPQR	168	183	0.62
PVEPFTESQSLTLTDVENLHLPLPLLQSWMHQPHQPLPPTVMFPPQSVL	115	163	0.4	LNVPGEIVE	6	14	0.49	TPVVVPPF	80	87	0.58	SKVLPVPQKAVPYPQR	168	183	0.52	YPFPGPI	60	66	0.58
PVLGPVRGPF	196	205	0.4	YPFPGPI	60	66	0.49	TPVVVPP	80	86	0.57	NVPGEIV	7	13	0.48	PFPGPIPNSLPQNIP	61	75	0.57
DKIHPFAQTQSL	47	58	0.38	NVPGEIV	7	13	0.48	VLGPVRGP	197	204	0.5	QEPVLGPVRGPFP	194	206	0.48	QEPVLGPVRGPFP	194	206	0.53
QTEDELQ	40	46	0.35	NSLPQNIPPLTQTPVVVPPFLQPEVMG	68	94	0.48	QPHQPLPPTVMFPPQSVL	146	163	0.49	TQTPVVVPPFLQPEVM	78	93	0.47	GPFPIIV	203	209	0.46
NLHLPLPLLQSW	132	143	0.34	LPQNIPPL	70	77	0.47	YQEPVLGPVRGPF	193	205	0.46	GPFPIIV	203	209	0.46	DKIHPFAQTQ	47	56	0.45
LLQSWMHQPHQPLPPTVMFPP	139	159	0.34	PVPQKAVPYPQR	172	183	0.46	NVPGEIV	7	13	0.44	VLPVPQK	170	176	0.42	LLYQEPVLGPVRGPFPI	191	207	0.45
GVSKVKEA	94	101	0.33	DMPIQAF	184	190	0.46	SWMHQPHQPLPPT	142	154	0.42	VYPFPGPI	59	66	0.4	QEPVLGPVRGP	194	204	0.44
DVENLHLPLPLLQS	129	143	0.32	LHLPLPL	133	139	0.43	VYPFPGPI	59	66	0.41	QEPVLGPVRGP	194	204	0.4	QPHQPLPPTVMFPPQSVL	146	163	0.4
SQSKVLPVPQKAVPYPQ	166	182	0.32	YQEPVLGPVRGP	193	204	0.43	VLPVPQKAVPYPQ	170	182	0.41	AMAPKHKEMPFPKYPVEPFTESQSLTLTDVENLHLPLPLLQS	101	142	0.38	VPYPQRDMPIQAFLLYQEPV	178	197	0.4

LYQEPVLGPVRGPFP	192	206	0.32	EPVLGPVRGPFPI	195	207	0.43	PVLGPVRGPFPIIV	196	209	0.41	VPYPQRDMPIQAFLLYQEPV	178	197	0.38	VLPVPQK	170	176	0.34
TQTPVVVPPFLQPE	78	91	0.29	VENLHLPLPLLQS	130	142	0.41	SKVLPVPQ	168	175	0.37	VVPPFLQPEVMGVSKVKEAMAPKHKEMPFPKYPV	83	116	0.37	PPTVMFPPQS	152	161	0.32
QNIPPLTQTP	72	81	0.27	DKIHPFAQTQS	47	57	0.38	KVLPVPQ	169	175	0.37	SQSKVLPVPQKAVPYPQ	166	182	0.37	SLSQSKVLPVPQ	164	175	0.31
ITRINKKIEKFQ	23	34	0.26	VPPFLQPEVMGVSKVKEAM	84	102	0.38	LYQEPVLGPVRGPFPI	192	207	0.37	DMPIQAFL	184	191	0.37	TPVVVPPF	80	87	0.3
HLPLPLL	134	140	0.26	SLSQSKVLPVPQ	164	175	0.38	GPIPNSLPQNIPPLTQTPVVVPPFLQPE	64	91	0.36	GPVRGPFPIIV	199	209	0.34	KHKEMPFPKYPVEPFTESQSLTLTDV	105	130	0.3
DELQDKIH	43	50	0.25	DKIHPFAQTQ	47	56	0.37	SQSKVLPVPQK	166	176	0.34	LVYPFPGPIPNSLPQNIPPLTQTPVVVPPFLQPEVMGVSK	58	97	0.31	LYQEPVLGPVRGPFPII	192	208	0.3
IPPLTQTPVVVPPFLQ	74	89	0.25	RDMPIQA	183	189	0.36	GPFPIIV	203	209	0.34	ELNVPGE	5	11	0.3	PVLGPVRGPFPIIV	196	209	0.3
VMGVSKVKEAMAPKHK	92	107	0.25	NLHLPLPL	132	139	0.35	MAPKHKEMPFPKYPVE	102	117	0.32	AVPYPQR	177	183	0.3	SKVLPVPQ	168	175	0.29
GVSKVKEAMAPKHKEMPFPKYPVEPFTESQS	94	124	0.25	MHQPHQPLPPT	144	154	0.35	GPVRGPF	199	205	0.31	EPVLGPVRGPFP	195	206	0.29	AVPYPQR	177	183	0.29
GVSKVKEAMAPKHKEMPFPKYPVEPFTESQSLTLTDVENLHLPLPLLQSW	94	143	0.24	LTQTPVVVPPFLQP	77	90	0.33	EAMAPKHKEMPFKYPV	100	116	0.3	EVMGVSK	91	97	0.28	EPVLGPVRGPFP	195	206	0.29
DMPIQAF	184	190	0.22	LLYQEPVLGPVRGPFPI	191	207	0.32	DMPIQAF	184	190	0.29	SLSQSKVLPVPQ	164	175	0.28	LVYPFPGPIPNSLPQNI	58	74	0.27
PQNIPPLT	71	78	0.2	QEPVLGPVRGPF	194	205	0.31	EELNVPGE	4	11	0.28	LLYQEPVLGPVRGPFPI	191	207	0.28	TLTDVENLHLPLPL	126	139	0.27
VLGPVRGPFPI	197	207	0.2	EPVLGPVRGPFPII	195	208	0.3	MAPKHKEMPFPKYPV	102	116	0.28	LLYQEPVLGPVRGPFPII	191	208	0.27	PQKAVPYPQR	174	183	0.27
VPYPQRDMP	178	186	0.19	LYQEPVLGPVRGPFPII	192	208	0.29	LYQEPVLGPVRGP	192	204	0.28	LYQEPVLGPVRGPFPII	192	208	0.27	KKIEKFQSEEQQQ	28	40	0.26
QEPVLGPVRGPFPI	194	207	0.19	SLSQSKVLPVPQK	164	176	0.28	QEPVLGPVRGPFPIIV	194	209	0.28	NSLPQNIPPLTQTPVVVPPFLQPEVM	68	93	0.26	VKEAMAPKHKEMPFPKYPVEPFTESQSLTLTDVENLHLPLPLLQS	98	142	0.26

Seq.: sequence of the peptide fragment, start: start of peptide fragment, end: end of peptide fragment; Rel Int: LCMS Relative intensity.