

Supplemental Information

Figure S1. 2D gel electrophoresis of *ipt*-transgenic broccoli at harvesting and after cooking. Protein composition of *ipt*-transgenic broccoli lines 102 and 103 and non-transgenic control were compared at harvesting and after cooking. The relative molecular weight of protein is indicated at the left and the pH value at the bottom of each gel. The *ipt* transgenic broccoli-specific protein spots are marked with arrows and an Arabic number.

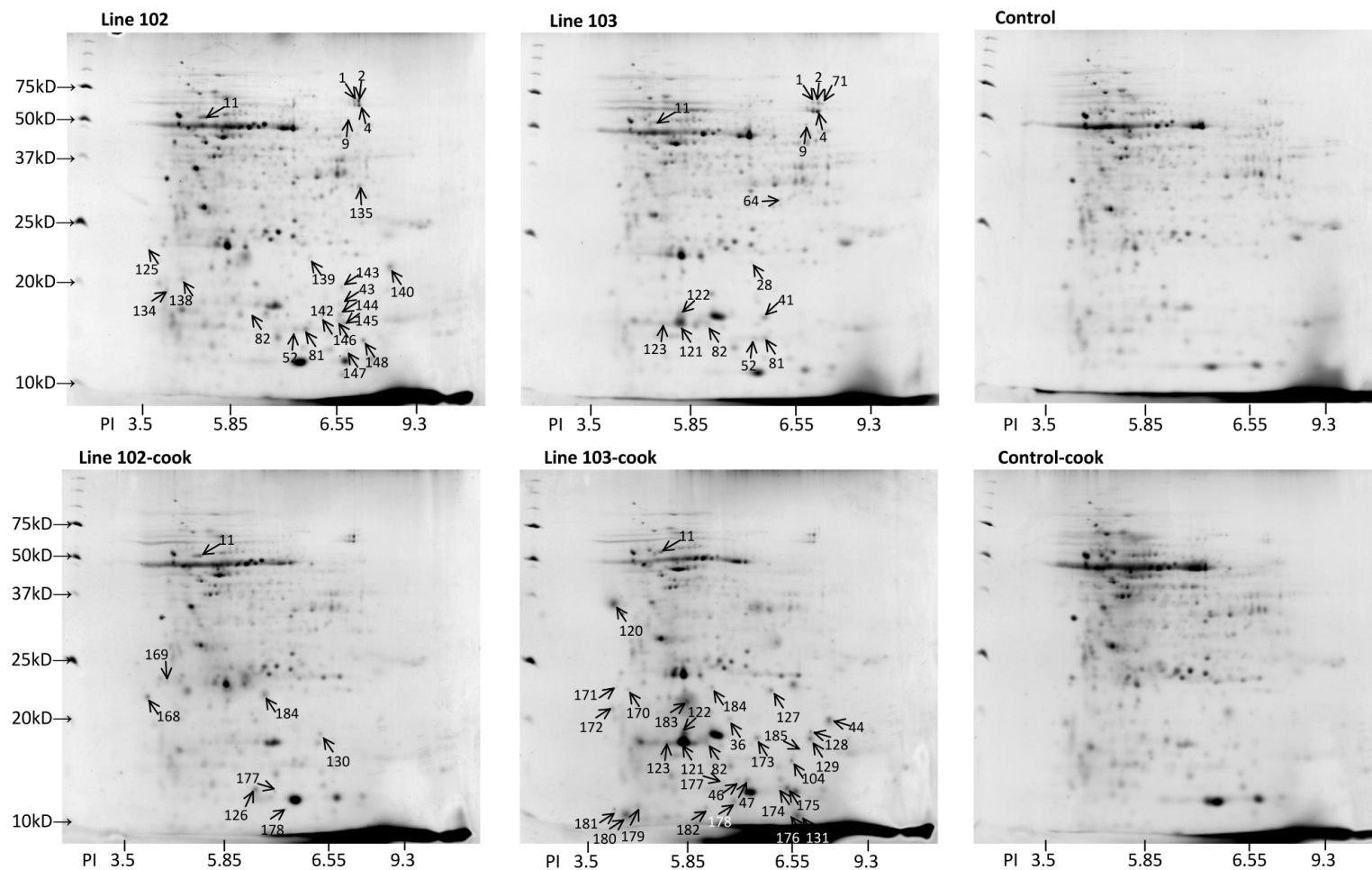


Table S1. MS/MS match peptide of proteins specifically detected in *ipt*-transgenic broccoli.

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
1	18	1	K.IEAIAK.S	4	2
			K.FMNIK.C	9	2
			K.RSFSDIMFR.R	7	2
			K.TQYSFSDHASK.	47	2
			R.LDIDPASITWR.R	10	2
		2	K.SYGASGVEYSDQAEK.Q	91	2
		1	R.YSGLTPQCAIVVATVR.A	86	2
			K.STTTVGLCQALGAYLDK.K	25	3
			K.STTTVGLCQALGAYLDKK.V	33	3
		1	K.AGDPITADDLGVGALTVMK.D	5	3
4	5	2	K.LVGPGGFVVTEAGFGSDIGTEK.F	136	2
		1	K.ACQNITQPLR.F	2.96	2
			K.STTTVGLCQALGAYLDKK.V	2.55	3
			K.SYGASGVEYSDQAEK.Q	4.94	2
			R.SFSDIM*FR.R	2.28	2
2	13	2	R.ELELSR.R	19	2
			R.AVEALNGKK.F	12	2
			K.VSEALDVLR.N	11	2
			R.RSGVGNLFVK.N	13	2
			K.VMRDPSGTSK.G	4	3
			R.RYEQGSSDGGNK.F	16	3
			K.LNYSYLNKGK.MIR.I	6	3
		1	R.ELFAEFGTITSCK.V	82	2
		1	R.GYGFVQFDTEDSAK.N	44	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
9	50	1	-.ILGVHIM*APNAGELIHEAVLAINYDASSEDIAIAR.-	6.54	3
			-.LTVEPAEGGEQSILEADVVLVSAGR.-	2.56	2
			-.VCHAHPTMSEALK.-	2.47	2
			K.AEEDGVACVEFIAGK.H	4.14	2
			K.AIDNAEGLVK.I	3.52	2
		2	K.ALLHSSHMYHEAK.H	4.10	2
			K.EAAM*ATYDKPIHI.-	3.10	2
		1	K.EAAMATYDKPIHI.-	3.29	2
			K.FPFMANSR.A	2.42	2
		2	K.GKHIIIVATGSDVK.S	4.24	2
		1	K.HGHVDYDKVPGVVYTHPEVASVGK.T	7.63	3
		2	K.HIIIVATGSDVK.S	3.47	2
		1	K.IVSSTGALSLSEVPK.K	3.83	2
		1	K.IVSSTGALSLSEVPKK.L	4.17	2
		1	K.KIVSSTGALSLSEVPK.K	5.52	2
			K.KIVSSTGALSLSEVPKK.L	4.64	3
		1	K.KIVSSTGALSLSEVPKK.L	5.22	2
			K.KLIVIGAGYIGLEM*GSVWGR.L	5.60	2
			K.KLIVIGAGYIGLEMGSVWGR.L	2.97	3
		2	K.LIVIGAGYIGLEM*GSVWGR.L	6.85	2
		1	K.LIVIGAGYIGLEM*GSVWGR.L	5.67	3
		1	K.SLPGITIDEKK.I	2.70	2
		1	K.VPGVVYTHPEVASVGK.T	4.77	2
		1	K.VSSVEVDLPAMLAQK.D	3.98	2
			R.FLSNVPGVYAIGDVIPGPMLAHK.A	2.37	2
			R.GALGGTCLNVGCIPSK.A	4.70	2
		1	R.TPFTSGLDLEK.I	3.19	2
			R.VGKFPPM*ANSR.A	2.59	3
		1	R.VGKFPPMANSR.A	2.37	2

Table S1. Cont.

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
11	74		-.DPSNHPYVSK.-	2.45	2
			-.KQSGPASAEIK.-	2.91	2
		4	K.AAAELSSQSPPIFLAK.I	4.51	2
			K.ANVVVDQIESWM*K.D	4.32	2
			K.ANVVVDQIESWM*KDFKDGK.V	3.18	3
		1	K.ANVVVDQIESWMK.D	4.67	2
			K.DPSNHPYVSK.F	2.13	2
			K.ESSIPLVTVFDKDP SNHPYVSK.F	3.10	3
			K.FVKESSIPLVTVFDKDP SNHPYVSK.F	4.79	3
		1	K.GQDLAFLVGDAESSQGALQYFGL EESQVPLIIQTSDSKK.Y	6.39	3
		1	K.IDASEESNKGIANEYK.I	4.53	2
		1	K.IDASEESNKGIANEYK.I	4.33	3
		1	K.IDASEESNKGIANEYKIQGFPTIK.I	6.38	3
		1	K.KQSGPASAEIKSADGAAEVIG EK.S	4.44	3
		1	K.LAPILDEVALAFQNDPSVIVAK.L	4.98	3
		1	K.LAPILDEVALAFQNDPSVIVAK.L	5.39	2
			K.LDATANDIPS DTFDVK.G	5.38	2
		1	K.LRADYDFAHTLDAK.F	4.15	2
		5	K.LSGEEFDSFM*AVAEK.L	5.05	3
		2	K.LSGEEFDSFM AVAEK.L	5.90	3
			K.NVLIEFYAPWCGHCQK.L	5.13	2
			K.QSGPASAEIKSADGAAEVIG EK.S	3.81	3
			K.SADGAAEVIG EK.S	2.82	2
			K.SADGAAEVIG EK.S	2.24	2
			K.SIQDYNGPR.E	2.05	2
		4	K.SIQDYNGPR.E	2.12	2
		2	K.SQPIPAENNEPVK.V	3.20	2
			K.SQPIPAENNEPVKV VVAESLDDM*VFNSGK.N	5.20	3

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
		1	K.SQIPAENNEPVKVVVAESLDDMVFNSGK.N	4.73	3
			K.SVVAVGVPFK.L	2.84	2
		3	K.VVVAESLDDM*VFNSGK.N	5.33	2
		3	K.VVVAESLDDMVFNSGK.N	4.78	2
		1	K.VVVEGSR.T	2.31	2
			R.LFKPFDELFDVDSKDFNGEALEK.F	3.59	3
		1	R.SADGKVVEGSR.T	4.01	3
			R.SGEHKTEESAACKDEL.-	3.78	3
			R.SGEHKTEESAACKDEL.-	3.01	2
		1	R.TKEDFISFIEK.N	4.01	2
			-YASEVYEK.-	2.17	2
			K.FNGGGHVNHSIFWK.N	2.59	2
28	8	1	K.HHPTYVTNYYNNALEQLDQAVNK.G	4.39	3
			K.KLVVDTTANQDPLVTK.G	5.24	2
			K.LVVDTTANQDPLVTK.G	4.43	2
36	1		K.NPDQVTENDFAFTGLGK.A	4.8	2
41	14	1	-SWDEGVSSK.-	2.56	2
			-VVIFGLPGAYTGVCSQQHVPSYK.-	2.58	3
		1	K.AVNVEEAPSDFK.V	3.41	2
			K.DLSAALLGPR.S	3.15	2
		1	K.SLGLDKDLSAALLGPR.S	4.91	2
			K.VTGAEVILGQI.-	3.11	2
		1	K.VVIFGLPGAYTGVCSQQHVPSYK.S	4.19	2
		2	R.WSAYVEDGKVK.A	3.24	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
43	16		-.SLGLDKDLSAALLGPR.-	3.59	3
		1	K.AVNVEEAPSDFK.V	3.94	2
		1	K.AVNVEEAPSDFK.V	3.20	1
		1	K.DLSAALLGPR.S	3.43	2
		1	K.LSEGTDITSAAPGVSLQK.A	5.48	2
		1	K.SLGLDKDLSAALLGPR.S	5.19	2
			K.VTGAEVILGQI.-	2.82	2
		1	R.WSAYVEDGK.V	2.67	1
		1	R.WSAYVEDGKVK.A	3.45	2
44	12	1	K.FADENFER.K	2.81	2
		1	K.HVVFGQVVEGLDVVK.A	4.49	3
		2	K.IVM*ELYTDKTPK.T	3.23	2
		1	K.IVMELYTDKTPK.T	3.27	2
			K.TDWLDGKHVVFGQVVEGLDVVK.A	2.64	3
		1	R.IVMELYTDK.T	3.15	2
46	14		-.TEYPNAFIR.-	2.12	2
			K.FETLSYLPDLTEVELGK.E	3.24	2
			K.KFETLSYLPDLTEVELGK.E	4.12	3
		1	K.KFETLSYLPDLTEVELGK.E	5.87	2
		1	K.KKFETLSYLPDLTEVELGK.E	4.59	3
			K.KKFETLSYLPDLTEVELGK.E	3.32	2
		1	K.LPLFGCTDSAQVLK.E	4.85	2
			K.TEYPNAFIR.I	2.57	2
			R.IIGFDNNR.Q	2.04	2
		1	R.QVQCISFIAYKPPSFTGA.-	3.74	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
47	8	1	K.KFETLSYLPDLTEVELGK.E	3.32	3
			K.KKFETLSYLPDLTEVELGK.E	4.12	3
			K.LPLFGCTDSAQVLK.E	4.74	2
		1	K.TEYPNAFIR.I	2.19	2
			R.EHGSTPGYYDGR.Y	2.97	3
			R.QVQCISFIA YKPPSFTGA.-	4.73	2
131	3		R.IIGFDNNR.Q	2.51	2
			K.LPLFGCTDSAQVLK.E	4.57	2
			R.QVQCISFIA YKPPSFTGA.-	3.08	2
147	13		K.KFETLSYLPDLTEVELGK.E	4.7	2
			K.KKFETLSYLPDLTEVELGK.E	3.7	3
		1	K.KKFETLSYLPDLTEVELGK.E	4.4	3
		1	K.LPLFGCTDSAQVLK.E	4.9	2
			K.TEYPNAFIR.I	2.3	2
			R.EHGSTPGYYDGR.Y	3	2
		1	R.IIGFDNNR.Q	2.6	2
		1	R.QVQCISFIA YKPPSFTGA.-	4.6	2
174	10		-.EVDYLLR.-	2.23	1
			-.TEYPNAFIR.-	1.85	1
			K.EVQECKTEYPNAFIR.I	3.36	2
		1	K.KKFETLSYLPDLTEVELGK.E	4.33	3
			K.LPLFGCTDSAQVLK.E	4.76	2
			R.EHGSTPGYYDGR.Y	3.09	2
			R.QVQCISFIA YKPPSFTGA.-	4.52	2
175	9	1	-.EVDYLLR.-	2.2	1
			K.EVQECKTEYPNAFIR.I	3.5	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
177	14	1	K.LPLFGCTDSAQVLK.E	4.9	2
			R.EHGSTPGYYDGR.Y	3.4	2
			R.IIGFDNNR.Q	2.4	2
		1	R.QVQCISFIA YKPPSFTGA.-	4.5	2
			-.KKFETLSYLPDLTEVELGK.-	4.1	3
			K.FETLSYLPDLTEVELGK.E	4.3	2
		1	K.KFETLSYLPDLTEVELGK.E	4.2	3
		1	K.KFETLSYLPDLTEVELGK.E	5.7	2
			K.KKFETLSYLPDLTEVELGK.E	4.3	3
		1	K.LPLFGCTDSAQVLK.E	2.9	2
		1	K.TEYPNAFIR.I	2.5	2
			R.EHGSTPGYYDGR.Y	2.7	2
		1	R.QVQCISFIA YKPPSFTGA.-	4.4	2
			-.M*IMGSVSNHVNNVACPVTVVK.-	6.66	3
52	14	1	K.ICEAAEHIPLSSLVIGNR.G	5.04	2
		1	K.YGVKPDAETLDIANTAAR.Q	4.86	2
		1	R.IGVA VDFSECSK.K	3.23	2
		1	R.M*IM*GSVSNHVNNVACPVTVVK.A	5.01	3
			R.M*IMGSVSNHVNNVACPVTVVK.A	3.93	3
		1	R.MIM*GSVSNHVNNVACPVTVVK.A	6.66	3
			R.RIGVA VDFSECSK.K	3.52	3
			-.DDL FNINAGIVK.-	0.14	2
		2	-.SQVVG YM*GDDNLAK.-	0.45	2
		1	-.SQVVG YMGDDNLAK.-	0.57	2
64	73	1	-.VAILGAAGGIGQPLALLM*K.-	0.23	2
		3	K.ALEGADLVIIIPAGVPR.K	0.50	1
		10	K.ALEGADLVIIIPAGVPR.K	0.46	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
		3	K.ALEGADLVIIIPAGVPR.K	0.33	3
			K.GLNGVPDVVECSYVQSTITELPFFASK.V	0.56	2
			K.KLFGVTTLDVVR.A	0.32	1
		3	K.KLFGVTTLDVVR.A	0.42	2
		1	K.LFGVTTLDVVR.A	0.30	2
		1	K.LNPLVSSLSLYDIANTPGVAADVGHINTR.S	0.60	2
		4	K.LNPLVSSLSLYDIANTPGVAADVGHINTR.S	0.68	3
		3	K.NGVVEVLDLGPLSDFEK.E	0.56	2
		4	K.VAILGAAGGIGQPLALLM*K.L	0.57	2
		1	K.VAILGAAGGIGQPLALLMK.L	0.56	2
		5	K.YCPHALVNM*ISNPVNSTVPAAEIFK.K	0.62	3
		2	K.YCPHALVNM*ISNPVNSTVPAAEIFKK.A	0.37	3
			K.YCPHALVNMISNPVNSTVPAAEIFK.K	0.54	3
			K.YCPHALVNMISNPVNSTVPAAEIFKK.A	0.57	3
		5	R.DDLFNINAGIVK.N	0.28	2
		1	R.KVAILGAAGGIGQPLALLM*K.L	0.36	3
			R.KVAILGAAGGIGQPLALLMK.L	0.41	3
			K.KLPFDR.H	14	2
			R.AFDKIFK.E	12	2
			M.ESLIGLVNR.I	12	2
71	13	1	R.LIEGALGYFR.G	63	2
		1	R.IYGVFDNQLPAALK.K	75	2
			K.DVDPTGERTFGVLTK.L	5	3
		1	R.IASNVSA Y VNMVSDTLR.N	7	3
			R.LVDMESAYLTAEFFRK.L	11	3
		1	K.IVSEADGYQPHLIAPEQGYR.R	65	3

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
81	12		-.MIM*GSVSNHVNNVACPVTVVK.-	4.58	3
		1	K.ICEAAEHIPLSSLVIGNR.G	4.72	2
		1	K.KYGVKPDAETLDIANTAAAR.Q	5.28	3
		1	K.YGVKPDAETLDIANTAAAR.Q	4.71	2
		1	R.IGVAVDFSECSK.K	4.64	2
			R.M*IM*GSVSNHVNNVACPVTVVK.A	5.26	3
			R.M*IMGSVSNHVNNVACPVTVVK.A	4.52	3
			R.MIMGSVSNHVNNVACPVTVVK.A	4.68	3
82	24		-.FALLIDNLK.-	2.93	2
			-.LLGLELDLKD.K.-	2.61	3
			K.FVADGSGEYTK.L	2.42	2
		1	K.FVADGSGEYTK.L	3.00	2
		1	K.GVDEIICFSVNDPFVM*K.A	5.29	2
		1	K.GVDEIICFSVNDPFVMK.A	5.43	2
		1	K.KVILFGVPGAFTPTCSMK.H	3.42	2
		1	K.LLGLELDLKD.D	3.33	2
		1	K.LLGLELDLKD.K.G	3.75	2
		1	K.VILFGVPGAFTPTCSM*K.H	4.02	2
		1	K.VILFGVPGAFTPTCSMK.H	4.48	2
		2	K.VTVANVESGGEFTVSSADDILK.A	6.96	2
		1	R.FALLIDNLK.V	2.76	2
123	20	1	-.FALLIDNLK.-	2.7	2
			-.VILFGVPGAFTPTCSM*KHVPGFIEK.-	3	3
		2	K.FVADGSGEYTK.L	3.4	2
			K.GVDEIICFSVNDPFVM*K.A	5.1	2
			K.GVDEIICFSVNDPFVMK.A	4.7	2
		1	K.KVILFGVPGAFTPTCSMKHVPGFIEK.A	4.5	3
		1	K.LLGLELDLKD.D	3.2	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
104	14	2	K.VILFGVPGAFTPTCSM*K.H	3.8	2
			K.VILFGVPGAFTPTCSMK.H	4.4	2
			K.VILFGVPGAFTPTCSMKHVPGFIEK.A	2.9	3
		1	K.VTVANVESGGEFTVSSADDILK.A	6.6	2
			R.FALLIDNLK.V	2.6	1
104	14	1	-.GM*IGMVSIGDVVR.-	3.38	2
			-.VGDIM*TEENKLITVTPETK.-	3.18	2
		1	K.DKGM*IGM*VSIGDVVR.A	3.90	2
			K.DKGM*IGMVSIGDVVR.A	3.90	3
		1	K.GMIGM*VSIGDVVR.A	4.25	2
		1	K.VGDIM*TEENKLITVTPETK.V	5.56	3
		1	K.VGDIMTEENK.L	3.33	2
144	9	1	K.VGDIMTEENKLITVTPETK.V	5.84	3
		1	K.DKGM*IGM*VSIGDVVR.A	3.89	2
		1	K.GM*IGM*VSIGDVVR.A	4.40	2
		1	K.VGDIM*TEENKLITVTPETK.V	5.17	3
144	9	1	K.VGDIM*TEENKLITVTPETK.V	4.06	2
			R.AM*QLM*TDNR.I	2.98	2
145	26	1	-.DKGM*IGMVSIGDVVR.-	3.09	3
			-.DKGMIGM*VSIGDVVR.-	3.07	2
			-.GM*IGMVSIGDVVR.-	3.09	2
			-.LITVTPETK.-	2.39	2
			K.DKGM*IGM*VSIGDVVR.A	3.82	2
		1	K.DKGM*IGM*VSIGDVVR.A	3.96	3
			K.DKGM*IGMVSIGDVVR.A	4.30	2
		1	K.GM*IGM*VSIGDVVR.A	4.88	2
		1	K.GMIGM*VSIGDVVR.A	4.04	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
		1	K.LITVTPETK.V	2.32	1
			K.VGDIM*TEENK.L	2.88	2
			K.VGDIM*TEENKLITVTPETK.V	5.02	3
		1	K.VGDIM*TEENKLITVTPETK.V	4.13	2
		1	K.VGDIMTEENK.L	3.35	2
		1	R.LNAFIQGGY.-	2.22	1
		1	R.LNAFIQGGY.-	2.84	2
146	24	1	-.GM*IGMVSIGDVVR.-	3.14	2
		1	K.DKGM*IGM*VSIGDVVR.A	4.32	2
		1	K.GM*IGM*VSIGDVVR.A	4.51	2
		1	K.GMIGM*VSIGDVVR.A	3.95	2
		1	K.GMIGMVSIGDVVR.A	4.22	2
		1	K.LITVTPETK.V	2.37	1
		1	K.VGDIM*TEENK.L	3.71	2
		1	K.VGDIM*TEENKLITVTPETK.V	4.06	2
		1	K.VGDIMTEENK.L	3.51	2
		1	R.LNAFIQGGY.-	2.58	2
		3	R.LNAFIQGGY.-	2.67	1
185	5		K.DKGM*IGM*VSIGDVVR.A	3.41	2
		1	K.GM*IGM*VSIGDVVR.A	4.35	2
			K.VGDIM*TEENKLITVTPETK.V	4.85	3
			R.LNAFIQGGY.-	2.45	1
120	35		-.DELDIVIPTIR.-	3.14	2
			-.DLIGPAM*YFGLMGDGQPIGR.-	2.94	2
		1	-.GTLFPM*CGMNLAHDR.-	3.83	2
			-.LSSLDPYFDK.-	3.00	2
			-.YVDAVM*TIPK.-	3.79	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
			K.ASCISFK.D	2.26	2
			K.AVNALEQHIK.N	2.79	2
			K.DELDIVIPTIR.N	3.20	2
		1	K.EAVTVQQCYIELSK.M	4.02	2
		1	K.GTLFPM*CGM*NLAFLDR.E	3.85	2
		1	K.GTLFPMCGM*NLAFLDR.E	4.64	2
		1	K.GTLFPMCGMNLAFLDR.E	4.58	2
		1	K.IHVPEGYDYELYNR.N	4.70	2
		1	K.KIHVPEGYDYELYNR.N	4.91	3
		1	K.KYIFTIDDDCFVAK.D	4.33	3
			R.DLIGPAM*YFGLM*GDGQPIGR.Y	4.98	2
		1	R.DLIGPAM*YFGLM*GDGQPIGR.Y	5.03	3
		1	R.DLIGPAMYFGLM*GDGQPIGR.Y	4.88	2
		1	R.EGVSTAVSHGLWLNIPDYDAPTQLVKPK.E	6.76	3
			R.YDDM*WAGWCIK.V	3.69	2
			R.YDDMWAGWCIK.V	3.37	2
			R.YVDAVM*TIPK.G	3.05	2
		1	R.YVDAVMTIPK.G	4.41	2
121	114		-.DSNGNPVKR.-	2.59	2
		1	-.EPAIIGGER.-	2.60	2
		6	-.IEEATGAHTYK.-	2.98	2
			-.IEEATGAHTYK.-	2.79	3
			K.EPAIIGGER.T	2.52	1
		9	K.IEEATGAHTYK.L	3.19	2
		4	K.LTTSSGTVGTIPGPWLGAPQLIATNDDAK.T	5.70	3
		40	K.LWAVDVSSSAK.E	4.48	2
		13	K.LWAVDVSSSAAKEPAIIGGER.T	6.45	2
			K.YFIQPAK.S	2.45	1

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
129	4	30	R.SEIWPVCNELSK.L	3.81	2
		1	-.IEEATGAHTYK.-	2.73	3
			K.LWAVDVSSSAK.E	3.59	2
			R.SEIWPVCNELSK.L	3.02	2
122	70	1	-.DGNDCIDVGK.-	2.47	2
			-.GSYYVLPVIR.G	2.85	2
			-.NGNQCPLFIGQER.-	2.56	2
			-.SAFIAVGPKPEAGGEDSSR.-	3.05	3
		1	K.FVFCRDGNDCIDVGK.N	3.83	3
		1	K.FVFCRDGNDCIDVGKNEEGGVR.G	5.55	3
		1	K.MDIEPTFCAQSTYWVTTAPSPWR.S	3.55	3
			R.DGNDCIDVGK.N	3.55	2
			R.DGNDCIDVGKNEEGGVR.G	4.80	3
			R.GPEGGGLTLTTR.N	3.83	2
		5	R.NGNQCPLFIGQER.S	3.74	2
		10	R.SAFIAVGPKPEAGGEDSSR.S	4.80	3
		2	R.VGFVPESENLIK.M	2.59	1
173	7	1	R.GPEGGGLTLTTR.N	3.66	2
			R.SAFIAVGPKPEAGGEDSSR.S	5.19	3
			R.SAFIAVGPKPEAGGEDSSR.S	5.07	2
			R.VGFVPESENLIK.M	3.34	2
184	7	1	R.DGNDCIDVGK.N	2.90	2
			R.GPEGGGLTLTTR.N	3.49	2
		1	R.SAFIAVGPKPEAGGEDSSR.S	5.20	3
		1	R.VGFVPESENLIK.M	3.40	2
125	2		K.FLDGIYVSEK.S	2.90	2
			K.HLNLDLFQLIK.D	2.71	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
168					
126	10		-.IETVDLENK.-	2.60	2
		1	K.NFKEIDEYLLK.Q	3.68	2
		1	K.TM*QVLAGDGNSPGSIR.L	5.35	2
		1	K.TMQVLAGDGNSPGSIR.L	4.98	2
			R.IETVDLENK.S	2.76	2
		1	R.LIIYGEGSPLVK.V	3.59	2
127	6	1	K.NFLSLLAENGK.L	4.45	2
		1	K.VLVTTVM*PLPPAEEK.E	4.72	2
		1	R.LAAIVDVCDK.A	3.19	2
139	27	1	K.ELKETLQEII GEGK.K	3.65	2
			K.ELKETLQEII GEGKK.V	4.59	2
			K.ETLQEII GEGK.K	2.68	2
			K.ETLQEII GEGKK.V	3.28	2
			K.FM*QLTTAHR.G	3.27	2
			K.FMQLTTAHR.G	2.49	2
		1	K.IESDLSELVEAM*K.A	4.92	2
		1	K.IESDLSELVEAM*K.A	3.67	3
			K.KFM*QLTTAHR.G	3.07	2
			K.NFLSLLAENGK.L	4.10	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
128	11	1	K.NFLSLLAENGK.L	3.17	1
			K.NFLSLLAENGK.LK.N	2.99	2
		3	K.VLVTTVM*PLPPAEEK.E	5.02	2
		1	K.VLVTTVMPLPPAEEK.E	4.47	2
		2	R.LAAIVDVCDK.A	2.99	1
		1	R.LLREPVDLSNL.-	3.41	2
			K.LIEEQETDR.G	3.01	2
		1	K.VYFDISVGNPVGK.L	4.55	2
		1	R.DFM*IQGGDFDK.G	3.27	2
		1	R.HVVFGQVIEGM*DVVR.L	4.23	2
		2	R.IVIGLFGDDVPQTVENFR.A	5.13	2
130	14		R.IVIGLFGDDVPQTVENFR.A	4.03	3
		1	K.LIEEQETDR.G	3.03	2
		1	K.VVIADCGQLPM*SEA.-	3.25	2
		1	K.VYFDISVGNPVGK.L	4.29	2
		1	R.DFM*IQGGDFDK.G	3.57	2
		1	R.HVVFGQVIEGM*DVVR.L	5.05	2
			R.HVVFGQVIEGMDVVR.L	2.05	2
		1	R.IVIGLFGDDVPQTVENFR.A	4.70	2
			R.IVIGLFGDDVPQTVENFR.A	3.37	3
		1	R.IIFIGQPINAQVAQR.V	4.59	2
		1	R.VISQLVTLASIDDK.S	4.83	2
135	12		-.DRPALAM*VADAEK.-	3.81	2
		1	K.DRPALAM*VADAEKK.N	5.01	3
			K.EAEAM*KPVSV.D.-	2.69	2
		1	K.RDASLLIGR.T	3.17	2
		1	R.IIM*TM*PSYTSLER.R	4.01	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
138	6	1	R.TPLVFLNR.V	2.84	2
		1	R.VTEGCGAYIAAK.Q	4.09	2
		3	K.EIENGILWEVEGK.W	3.88	2
			K.LTPEQQEEFKK.G	2.74	2
			K.VVDIVDTFR.L	3.24	2
140	4	1	R.VNQAIFLLTTGAR.E	4.47	2
		1	K.TIAECLADELINAAG.K	5.08	2
142	6	1	K.DFPSSSSFSR.E	2.34	2
		1	K.VEIEDDSVLK.I	3.18	2
		1	R.HVEKEDKNDTWHR.V	3.80	3
143	4		K.DTDSEEELKEAFR.V	3.38	2
			K.EADVVDGDGQINYDEFVK.V	5.58	2
		1	K.EAFSLFDKDGDCITTK.E	4.28	2
		1	R.GDFAIDIGR.N	2.60	2
169	7		-.FWAIFIDEK.-	2.98	2
			K.IFGSLEAVGGAK.D	4.06	2
		1	K.LIGSWASPFSSR.A	3.50	2
		1	K.LM*ENLAILEEAFQK.S	5.38	2
			R.FWAIFIDEK.I	2.79	2
170	3		K.KKDETKPEETIDSEFEQK.V	5.36	3
		1	K.VATEESSTATGEVTDR.G	5.52	2
178	9	1	K.DHPYDPAHDSVLSR.V	3.31	2
		1	K.TNYLIVDSK.T	3.31	2
		1	K.YLFSAESVSQR.-	3.76	2
		1	R.FLVDSYNKPVPAILEIPSK.D	4.25	3
			R.KTNYLIVDSK.T	2.91	2

Table S1. *Cont.*

Spot No.	Peptide Matched Number	Dupes	Peptide Sequence	Peptide Score	Peptide Charge
179	3		K.EPAIIIIGGER.T	2.6	1
		1	-.LWAVDVSSSAK.-	3	1
183	15		-.DRNEAWIR.-	3.25	2
		1	K.GGM*IVLPAGIYHR.F	2.96	3
		1	K.GGM*IVLPAGIYHR.F	3.42	2
		1	K.KGGM*IVLPAGIYHR.F	4.63	3
		1	K.LAELGVLSWR.L	3.92	2
		1	R.FTVDSDNLIK.A	2.96	2
		1	R.LDADNYETDEELK.K	4.97	2
		1	R.LDADNYETDEELKK.I	4.21	2

Proteins have been analyzed using LC-MS/MS (LTQ XL Linear Ion Trap Mass Spectrometer, Thermo Scientific) and the acquired MS/MS data were processed for sequence identification using Mascot v 2.3 (Matrix Sciences) search engine against *Brassica* database (347,992 protein entries) downloaded from UniProtKB/Swiss-Prot with significant threshold $p = 0.05$. * represents Oxidation methionine.