

## Supplemental Tables

**Supplemental Table S1: Identified serine hydrolases labeled with FP-biotin in senescent cotyledons of oilseed rape (cv. Ténor) after 5 days of LN treatment.** To characterize the serine hydrolases observed in Figure 2, labeling with FP-biotin was performed and followed by a pull-down of biotinylated proteins (Figure 3). LC-MS/MS spectra were searched against the *Viridiplantae* database focusing on *Brassica napus* L. using MASCOT 2.5.0 and only scores higher or equal to 41 were considered. The assigned protein with the best match is provided alongside the Uniprot accession number (if available) or NCBI/GenBank accession number. Score, queries matched, peptide matches, different peptide matches, experimental mass, theoretical mass and classification of serine hydrolases are also presented.

Zone (kDa)	Protein [ <i>Brassica napus</i> ] UniProt or NCBI accession no.	Score	Queries Matched	Peptides matched	Different matched peptides	Exp. Mass (Da)	Theo. Mass (Da)	Theo. pI	Classification
1 (70)	PREDICTED: serine carboxypeptidase-like 49 XP_013676539	100	12	6	5	58335	58372.2	5.03	S10
	Lipase_GDSL A0A078JNT9	81	5	4	3	34584	34605.51	8.59	Lipase
	PREDICTED: subtilisin-like protease SBT1.7 XP_013654072	77	5	4	4	73353	73398.89	7.57	Subtilisin S8
	Carboxypeptidase A0A078EDE5	59	2	2	2	56843	56878.91	5.35	S10
	Carboxypeptidase A0A078GRW5	54	2	2	2	53488	53521.41	5.43	S10
2 (65)	PREDICTED: serine carboxypeptidase-like 49 XP_013676539.1	62	5	5	5	58335	58372.2	5.03	S10
3 (60)	Probable carboxylesterase 12 A0A078CLX0	90	4	4	4	34316	34337.89	5.23	CXEs
	Carboxypeptidase A0A078BZ09	71	10	4	4	53907	53941.01	6.43	S10
	PREDICTED: subtilisin-like protease SBT1.7 XP_013654072.1	61	5	4	4	73353	73398.89	7.57	Subtilisin S8
4 (55)	GDSL esterase/lipase A0A078H579	195	12	8	8	48149	48180.03	7.2	Lipase
	alpha-L-fucosidase 3-like A0A078FHK0	186	12	8	8	48820	48851.72	6.69	Lipase
	GDSL esterase/lipase A0A078HX36	165	9	7	7	42221	42247.84	6.44	Lipase
	PREDICTED: serine carboxypeptidase-like 35 A0A078G963	146	22	7	6	54114	54148.29	6.83	S10
	PREDICTED: subtilisin-like protease SBT1.7 XP_013654072.1	125	8	6	6	73353	73398.89	7.57	Subtilisin S8
	PREDICTED: probable carboxylesterase 12 A0A078HJQ8	103	6	5	5	35528	35550.37	5.16	CXEs
	PREDICTED: probable carboxylesterase 12 partial XP_013704469.1	84	5	4	4	29451	29469.5	5.38	CXEs
5 (50)	PREDICTED: probable carboxylesterase 12 A0A078HJQ8	360	24	12	11	35528	35550.37	5.16	CXEs

	PREDICTED: protease Do-like 1, chloroplastic XP_013644609.1	81	5	5	5	46206	46234.66	6	Deg protease
	Serine-type carboxypeptidase-like 35 A0A078BZ09	61	4	3	3	53907	53941.01	6.43	S10
	PREDICTED: probable carboxylesterase 13 A0A078JMY7	55	2	2	2	12594	12601.54	9.51	S10
6 (45)	PREDICTED: probable carboxylesterase 12 A0A078HJQ8	129	10	10	5	35528	35550.37	5.16	CXEs
	PREDICTED: subtilisin-like protease SBT1.7 XP_013654072.1	65	4	4	4	73353	73398.89	7.57	Subtilisin S8
	PREDICTED: serine carboxypeptidase-like 35 A0A078G963	41	2	2	2	54114	54148.29	6.83	S10
7 (40)	PREDICTED: serine carboxypeptidase-like 29 A0A078IYZ5	131	6	6	4	53001	53035	6.02	S10
	PREDICTED: probable carboxylesterase 12 A0A078HJQ8	122	7	7	5	35528	35550.37	5.16	CXEs
	PREDICTED: serine carboxypeptidase-like 29 A0A078GRW5	108	8	8	3	53488	53521.41	5.43	S10
	PREDICTED: serine carboxypeptidase-like 35 A0A078G963	62	6	6	5	54114	54148.29	6.83	S10
	PREDICTED: serine carboxypeptidase-like 20 A0A078HQ25	52	6	6	3	56619	56655.77	6.21	S10
8 (35)	Serine carboxypeptidase-like 29 A0A078BV89	199	22	6	6	53413	53447.24	5.28	S10
	PREDICTED: serine carboxypeptidase-like 29 A0A078GRW5	165	20	6	6	53488	53521.41	5.43	S10
	PREDICTED: probable carboxylesterase 12 A0A078HJQ8	105	7	4	4	35528	35550.37	5.16	CXEs
	PREDICTED: methylesterase 10-like A0A078EN16	91	5	3	3	30212	30231.68	5.79	MEs
	PREDICTED: serine carboxypeptidase-like 29 A0A078GF58	79	3	3	3	53131	53164.05	5.87	S10
	PREDICTED: serine carboxypeptidase-like 51 A0A078GVN3	78	3	3	3	51093	51125.51	6.74	S10
9 (33)	PREDICTED: methylesterase 9-like A0A078BY50	315	20	9	9	28749	28768.08	5.23	MEs
	PREDICTED: methylesterase 9-like A0A078CFS2	216	13	7	7	28614	28632.94	5.23	MEs
	PREDICTED: probable carboxylesterase 12 A0A078HJQ8	163	8	6	6	35528	35550.37	5.16	CXEs
	PREDICTED: acyl-protein thioesterase 2-like XP_013730870.1	98	4	4	4	26707	26723.43	6.15	Thiol-esterase
	PREDICTED: probable carboxylesterase 12 partial XP_013704469.1	96	6	5	5	29451	29469.5	5.38	CXEs
	PREDICTED: serine carboxypeptidase-like 29 A0A078GRW5	91	5	2	2	53488	53521.41	5.43	S10
	PREDICTED: methylesterase 9-like isoform X2 A0A078IOV8	77	6	3	3	13001	130009.93	4.77	MEs

10 (30)	PREDICTED: probable carboxylesterase 12 XP_013701961.1	298	22	22	9	35535	35557.41	5.24	CXEs
	PREDICTED: probable carboxylesterase 12 A0A078HJQ8	295	22	22	9	35528	35550.37	5.16	CXEs
	PREDICTED: serine carboxypeptidase-like 29 A0A078GRW5	85	7	7	2	53488	53521.41	5.43	S10
	PREDICTED: methylesterase 9-like A0A078BY50	73	4	4	4	28749	28768.08	5.23	MEs
11 (25)	PREDICTED: probable carboxylesterase 12 A0A078HJQ8	211	14	7	7	35528	35550.37	5.16	CXEs
	PREDICTED: serine carboxypeptidase-like 29 A0A078GRW5	93	9	3	3	53488	53521.41	5.43	S10
	PREDICTED: methylesterase 9-like A0A078BY50	83	4	4	4	28749	28768.08	5.23	MEs
	PREDICTED: serine carboxypeptidase-like 20 XP_013696030.1	55	4	3	3	57750	57787.39	6.32	S10
	PREDICTED: probable carboxylesterase SOBER1-like isoform X2 A0A078ECJ1	51	3	2	2	54591	54625.41	5.39	Thiol-esterase
12 (20)	PREDICTED: serine carboxypeptidase-like 29 A0A078GRW5	269	18	8	8	53488	53521.41	5.43	S10
	PREDICTED: serine carboxypeptidase-like 20 XP_013696030.1	155	7	5	5	57750	57787.39	6.32	S10
	PREDICTED: serine carboxypeptidase-like 35 A0A078BZ09	61	5	3	3	53907	53941.01	6.43	S10

**Supplemental Table S2: Identified Cysteine proteases (CPs) labeled with DCG04 in senescent cotyledons of oilseed rape (cv. Ténor) after 5 days of LN treatment.** To characterize CPs observed in Figure 4, labeling with DCG04 was carried out and followed by a pull-down of biotinylated proteins (Figure 3). LC-MS/MS spectra were searched against the *Viridiplantae* database focusing on *Brassica napus* L. using MASCOT 2.5.0 and only scores higher or equal to 41 were considered. The assigned protein with the best match is provided alongside the Uniprot accession number (if available) or NCBI/GenBank accession number. Score, queries matched, peptide matches, different peptide matches, experimental mass and theoretical mass are also presented. Finally, CPs were classified according to the classification of Richau *et al.* (2012) [37].

Zone (kDa)	Protein accession no [ <i>Brassica napus</i> ] / NCBI accession no.	Score	Queries Matched	Peptides matched	Different matched peptides	Exp. Mass (Da)	Theo. Mass (Da)	Theo. pI	Classification
<b>1 (40)</b>	PREDICTED: cysteine proteinase RD21a-like A0A078FVG4	161	7	7	6	50625	50657.95	5.23	RD21-like
	PREDICTED: cysteine proteinase RD21a A0A078EXH0	158	10	10	6	50452	50484.76	5.3	RD21-like
	cysteine proteinase RD21a A0A078FXL6	146	10	10	6	50534	50566.84	5.23	RD21-like
	PREDICTED: cysteine proteinase RD21a-like A0A078G7A3	64	3	3	2	50506	50539.07	5.57	RD21-like
<b>2 (35)</b>	PREDICTED: cysteine proteinase RD21a-like A0A078G7A3	120	5	5	3	50506	50539.07	5.57	RD21-like
	PREDICTED: cysteine proteinase RD21a-like A0A078EXH0	97	4	4	4	50452	50484.76	5.3	RD21-like
	PREDICTED: cysteine proteinase RD21a-like A0A078FVG4	94	5	5	4	50625	50657.95	5.23	RD21-like
<b>3 (30)</b>	PREDICTED: cysteine proteinase RD21a-like A0A078FVG4	74	3	3	3	50625	50657.95	5.23	RD21-like
	PREDICTED: cysteine proteinase RD21a-like A0A078EXH0	71	3	3	3	50452	50484.76	5.3	RD21-like
<b>4 (25)</b>	Senescence-specific cysteine protease SAG12-like Q9SQH3	143	8	8	7	38333	38357.54	6.99	SAG12-like
	PREDICTED: cysteine proteinase RD21a-like A0A078EXH0	68	5	5	4	50452	50484.76	5.3	RD21-like
	PREDICTED: cysteine proteinase RD21a-like A0A078FVG4	63	4	4	4	50625	50657.95	5.23	RD21-like
	PREDICTED: cysteine proteinase RD21a-like A0A078G7A3	47	3	3	2	50506	50539.07	5.57	RD21-like