



**Appendix A** Two-dimensional electrophoresis (2-DE) page gel images of proteins extracted from the lamina (A, B and C) and mid-vein (D, E and F) during senescence.

**Appendix B** Differentially abundant proteins identified from the mid-vein and leaf lamina by mass spectrometry (MS)

Biological process	Match ID <sup>1</sup>	Identified protein <sup>2</sup>	Accession no. <sup>3</sup>	Pi/Mr <sup>4</sup>	MO <sup>5</sup>	PM <sup>6</sup>	SC% <sup>7</sup>	Variation <sup>n</sup>	
Metabolism	Amimo acid	37	Cysteine synthase [ <i>Oryza sativa</i> .L Japonica]	Q9XEA6.2	5.39/33.93	32	29	9	Up
		104	PREDICTED: glutamine synthetase, chloroplastic [ <i>Oryza sativa</i> .L Japonica Group]	XP_015635322.1	5.96/46.96	132	59	13	Down
		58	putative precursor chloroplastic glutamine synthetase [ <i>Oryza sativa</i> .L Japonica Group]	AAL87183.1	6.18/49.77	85	38	8	Down
Citrate cycle		60	PREDICTED: malate dehydrogenase, mitochondrial [ <i>Oryza sativa</i> .L Japonica Group]	XP_015639465.1	8.22/35.64	73	26	7	Up
		150	PREDICTED: dihydrolipoyl dehydrogenase 1, mitochondrial [ <i>Oryza sativa</i> .L Japonica Group]	XP_015611017.1	7.21/53.01	68	45	8	Up
Energy	Photosynthesis	38	Ribulose biphosphate carboxylase large chain precursor, putative [ <i>Oryza sativa</i> .L Japonica Group]	ABA96140.2	9.04/56.55	88	32	6	Up
		69	glyceraldehyde-3-phosphate dehydrogenase, partial [ <i>Oryza sativa</i> .L Indica Group]	ABR25332.1	6.95/23.79	87	44	20	Up
		70	RuBisCO activase small isoform precursor [ <i>Oryza sativa</i> .L]	BAA97584.1	5.85/48.13	89	36	8	Up
		73	PREDICTED: glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic [ <i>Oryza sativa</i> .L Japonica Group]	XP_015630808.1	6.22/47.54	80	30	6	Up
		92	ribulose-1,5-bisphosphate carboxylase/oxygenase activase [ <i>Oryza sativa</i> .L Japonica Group]	AAC28134.1	5.85/48.06	111	67	15	Down

		123	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial [ <i>Oryza sativa</i> .L]	ADD48129.1	7.00/26.50	70	31	13	Down
		125	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial [ <i>Oryza sativa</i> .L]	AFK09923.1	7.00/24.23	71	32	14	Down
		128	Os12g0207600 [ <i>Oryza sativa Japonica</i> Group]	BAF29408.1	9.01/59.56	48	32	6	Down
		134	atpB gene product [ <i>Oryza sativa</i> .L]	AAA84588.1	5.30/53.98	150	55	11	Up
		135	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial [ <i>Oryza sativa</i> .L]	CAG34174.1	6.23/63.33	71	32	6	Down
		157	Putative rbcL; RuBisCO large subunit from chromosome 10 chloroplast insertion [ <i>Oryza sativa</i> .L Japonica Group]	AAM08604.1	6.45/53.43	57	32	6	Up
		185	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial [ <i>Oryza sativa</i> .L Japonica Group]	XP_015630641.1	6.15/88.21	172	69	8	Down
		265	PREDICTED: short-chain type dehydrogenase/reductase [ <i>Oryza sativa</i> .L Japonica Group]	XP_015613174.1	6.17/26.85	43	35	13	Up
	Glyoxylate	33	PREDICTED: phosphoglycolate phosphatase 1B, chloroplastic [ <i>Oryza sativa</i> .L Japonica Group]	XP_015636788.1	6.75/39.81	77	45	12	Up
Protein synthesis and storage	Translation factor	108	chloroplast translational elongation factor Tu [ <i>Oryza sativa</i> .L Japonica Group]	AAF15312.1	6.05/50.55	90	45	9	Up
		109	PREDICTED: elongation factor Tu, chloroplastic	XP_015627061.1	6.19/50.61	50	31	5	Up

			[ <i>Oryza sativa</i> .L Japonica Group]							
	Translation control	247	PREDICTED: probable mediator of RNA polymerase II transcription subunit 37c [Oryza sativa.L Japonica Group]	XP_015618966	5.10/71.32	41	28	4		Down
	Folding	179	PREDICTED: stromal 70 kDa heat shock-related protein (Hsp70) [Oryza sativa.L Japonica Group]	XP_015639965	5.12/73.68	105	40	5		Down
		183	PREDICTED: heat shock cognate 70 kDa protein 2 (Hsp70) [Oryza sativa.L Japonica Group]	XP_015630538	5.10/71.46	69	39	6		Up
Signal transduction		50	PREDICTED: guanine nucleotide-binding protein subunit beta-like protein A [Oryza sativa.L Japonica Group]	XP_015620921	5.95/36.67	56	36	10		Up
	Stress response	24	PREDICTED: L-ascorbate peroxidase 2, cytosolic [Oryza sativa.L Japonica Group]	XP_015646556	5.21/27.22	106	39	15		Down
Disease/defense		34	PREDICTED: thioredoxin-like protein CDSP32, chloroplastic [Oryza sativa Japonica Group]	XP_015646731	6.27/32.48	46	26	8		Down
		61	hypothetical protein OsI_29063 [Oryza sativa Indica Group]	EAZ06824.1	5.88/31.98	96	41	13		Down
	Unkown	23	PREDICTED: thylakoid lumenal 29 kDa protein, chloroplastic [Oryza sativa.L Japonica Group]	XP_015636056	8.67/38.44	109	56	15		Up
		29	PREDICTED: uncharacterized protein At5g02240 [Oryza sativa.L Japonica Group]	XP_015632967	6.34/27.95	66	24	9		Up

84	unknown protein [ <i>Oryza sativa</i> .L Japonica Group]	BAD16990.1	11.86/43.7 5	45	18	4	Up
226	hypothetical protein OsI_07899 [ <i>Oryza sativa</i> .L Indica Group]	EEC73516.1	5.68/55.76	63	28	5	Down

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<sup>1)</sup> Protein spot IDs as denoted in Figure 5.

<sup>2)</sup> Protein identification (protein ID [reference organism], accession no. and matched peptide sequences) was determined by database searches using the MASCOT software ([www.matrixscience.com](http://www.matrixscience.com)) in the NCBI nr, Swiss Prot and EST databases.

<sup>3)</sup> Accession no., accession number.

<sup>4)</sup> Pi/Mr, theoretical Mr/pI, molecular weight (Mr, expressed in Kilodalton) and isoelectric point (pI) of the identified proteins.

<sup>5)</sup> Mo, MOWSE score.

<sup>6)</sup> PM, number of peptides matched.

<sup>7)</sup> SC, percentage of sequence coverage (%).