

**Table S1.** Identification of protein bands (I-VII) from SOD activity native gels (cv. 'Picual') by nano-LC-ESI-MS/MS analysis.

Gel band	Identified protein (Species)	Accession no.	Coverage (%)	Score <sup>a</sup>	m/z meas.	$\Delta$ m/z [ppm]	Range	Peptides
I	Superoxide dismutase [Mn], mitochondrial ( <i>Hevea brasiliensis</i> )	P35017	11.2	95	1417.67	-7.27	59-69	K.HHQTYITNYNK.A
					1626.88	-1.70	167-181	K.LVVETTANQDPLVTK.G
II	Superoxide dismutase [Cu-Zn] 2 ( <i>Olea europaea</i> )	Q8L5E0-1	17	78	1378.68	-4.72	102-114	K.QIPLTGPHSIIGR.A
						-20.81	115-127	R.AVVVHSDPDDLGR.G
III	Superoxide dismutase [Mn], mitochondrial ( <i>Pisum sativum</i> )	P27084	4.7	32	1417.67	2.62	68-78	K.HHQTYITNYNK.A
						-4.64	68-78	K.HHQTYITNYNK.A
IV	Superoxide dismutase [Cu-Zn] 2 ( <i>Olea europaea</i> )	Q8L5E0-1	17	78	1378.68	-4.72	102-114	K.QIPLTGPHSIIGR.A
						-20.81	115-127	R.AVVVHSDPDDLGR.G
VII	Superoxide dismutase [Cu-Zn] 2 ( <i>Olea europaea</i> )	Q8L5E0-1	8.6	57	1387.79	-21.91	102-114	K.QIPLTGPHSIIGR.A
							Superoxide dismutase [Cu-Zn] ( <i>Paulownia kawakamii</i> )	O49073

<sup>a</sup>Protein scores greater than 31 are significant (p<0.05). Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.