

**Peroxidases identified in a subtractive cDNA library approach show tissue-specific transcript abundance and enzyme activity during seed germination of *Lepidium sativum***

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*Journal of Experimental Botany* 2009 (JEXBOT/2009/040063)

**Table S1.** Cress sequences of the subtractive library were deposited in the GenBank database and are available via the NCBI website ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)). Putative gene function was based on the highest BLAST hit, usually Arabidopsis otherwise the closest homologue is indicated next to the percentage nucleotide identity.

GenBank accession number	Locus of closest homologue	Putative gene product function	Sequence similarity to Arabidopsis (%) if not indicated otherwise
GR972444	AT1G01300	aspartyl protease family	87.6
GR972418	AT1G07890	ascorbate peroxidase	87.6
GR972448	AT1G14290	acid phosphatase, SBH2 (sphingoid base hydroxylase 2)	92.6
GR972432	AT1G32900	starch synthase	84.1
GR972464	AT1G64970	gamma-tocopherol-methyltransferase	90.7 <i>Brassica napus</i>
GR972445	AT1G66200	glutamine synthase	89.2
GR972417	AT1G75040	PR5	82.2
GR972433	AT1G79050	DNA repair recA	87.1
GR972468	AT2G18980	putative peroxidase	84.3
GR972415	AT2G33150	KAT2 (also known as peroxisome defective 1)	83.7 <i>Brassica napus</i>
GR972452	AT2G34040	API5 apoptosis inhibitory	85.4
GR972441	AT2G34470	UREG (urease accessory protein G)	89.6
GR972466	AT2G36530	phosphopyruvate hydratase	89.6 <i>Brassica rapa</i>
GR972424	AT3G12620	PP2C family (protein phosphatase)	91.6
GR972456	AT3G13920	EIF4A1 (eukaryotic translation initiation factor)	87.5
GR972423	AT3G16640	TCTP (translationally controlled tumor)	90.9
GR972414	AT3G20820	leucine-rich repeat family	86.4
GR972460	AT3G21720	isocitrate lyase	90.3
GR972462	AT3G46740	TOC75-III	88.2
GR972446	AT3G52960	Peroxiredoxin Type 2	85.9
GR972442	AT3G53500	nucleic acid binding	89.1

GR972457	AT3G55120	TT5 (transparent testa)	80.5 <i>Brassica rapa</i>
GR972449	AT3G55430	beta-1,3-glucanase	88.1
GR972421	AT4G02890	UBQ14 (ubiquitin)	87.6
GR972453	AT4G05050	UBQ11 (ubiquitin)	89.2
GR972469	AT4G05320	UBQ10 (ubiquitin)	88.8 <i>Boechea divaricarpa</i>
GR972463	AT4G13510	ammonium transporter	82.8
GR972436	AT4G21150	ribophorin II family	88.7
GR972426	AT4G31990	cationic amino acid transporter	80.8
GR972434	AT4G32410	cellulose synthase	86.6
GR972425	AT5G05750	DNAJ	87.7
GR972431	AT5G09440	phosphate-responsive	87.4
Gr972422	AT5G13930	chalcone synthase (TT4)	81.5
GR972427	AT5G14030	TRAPB family (translocon-associated)	89.7
GR972440	AT5G17920	cobalmin-independent methionine synthase	94.2
GR972461	AT5G19780	tubulin alpha-5	95.6
GR972467	AT5G25350	EIN3-binding F-box protein	85.5
GR972455	AT5G37600	glutamine synthase	91.3
GR972435	AT5G37770	calmodulin-related	84.7
GR972450	AT5G48930	anthranilate N-benzoyltransferase	92.3
GR972447	AT5G57300	methyltransferase	90.3
GR972454	AT5G60390	elongation factor	96.5
GR972451	AT5G62700	tubulin beta-3	79.5
GR972439	AT3G49910	putative 60S ribosomal protein	89.6
GR972419	AT4G09800	S18.A ribosomal protein	91.5
GR972459	AT2G18020	60S ribosomal protein L2	94.1

**Fig S1** . Detailed germination kinetics of fresh *Arabidopsis* seeds at 24 °C in continuous light of the three peroxidase-SALKlines and the corresponding WT. Three times 50 seeds were used per line. Means +/- SE are shown. TR = testa rupture, ER = endosperm rupture.

