amino acid	ALD1 in vitro assay				in planta detection
	% in vitro activity	% trans-amination (30 min)	possible ketoacid / product	in vitro detection of product	
L-Lys	100	77.75 ± 6.58	2,3-DP	yes	yes
L-Ala[1]	0.7	0.53 ± 0.16	pyruvic acid	no	yes[2]
L-Asp	0.1	0.11 ± 0.01	oxaloacetic acid	no	no
L-Tyr	0.3	0.20 ± 0.05	4-hydroxy-phenyl pyruvic acid	no	no
L-Ser	0.7	0.58 ± 1.06	(R)-3-hydroxy-2-oxobutanoic acid	no	no
L-Thr	0.1	0.05 ± 0.02	hydroxypyruvic acid	no	no
L-Cys	1.2	0.93 ± 0.36	3-mercapto-2-oxopropanoic acid	no	no
Gly	0.01	0.01 ± 0.01	glyoxylic acid	no	no
L-Pro	0.02	0.02 ± 0.01	-	no	no
L-Pip	0.3	0.22 ± 0.05	-	no	no
L-Arg	60.0	46.65 ± 7.92	5-guanidino-2-oxopentanoic acid	no[3]	no[3]
L-His	12.7	9.88 ± 1.06	3-(1H-imidazol-4-yl)-2-oxopropanoic acid	no[3]	no[3]

Supplemental Table S1. ALD1 in vitro activity towards additional amino acids (compare Table 1 for experimental details).

[1] For L-Ala, α-ketoglutarate was used as the acceptor oxoacid and Glu was quantified as the resulting product amino acid. For all other substrate amino acids, pyruvate was employed as the acceptor oxoacid and Ala quantified as the corresponding product amino acid.

[2] Pyruvate was detected to substantial and similar levels in both Col-0 wild-type and *ald1* mutant plants.

[3] The L-Arg- and L-His-derived transamination products could not be detected be the employed GC-MS-based methods.

Gene	Primer name	Primer sequence (5' to 3')	Usage
ALD1	ALD1_p32_SP20_F1	TAT GAT TCC CAA GGC TAG TTT GGA CTT	**pET32b cloning by sticky-end technique for fusion protein expression**
	ALD1_p32_SP20_F2	TGA TTC CCA AGG CTA GTT TGG ACT T	
	ALD1_p32_SP39_F1	TAT GGT TCG GAA CGT GAA TTT GGA GAA	
	ALD1_p32_SP39_F2	TGG TTC GGA ACG TGA ATT TGG AGA A	
	ALD1_p32_R1	G ATT GGT ATT AGA AGT GGA AGA GAG AT	
	ALD1_p32_R2	TCGAG ATT GGT ATT AGA AGT GGA AGA G	
SARD4	SARD4_p32b_F1	TAT GGC TGC ATT ACC AGT ATT CAT ACC	
	SARD4_p32b_F2	TGG CTG CAT TAC CAG TAT TCA TAC CA	
	SARD4_p32b_S42_F1	TAT GCA AAA CTA CAC CGT TTC ATC ACC	
	SARD4_p32b_S42_F2	TGC AAA ACT ACA CCG TTT CAT CAC CT	
	SARD4-p32b-R1	GAC AAC GGC TGA GGT AAG TCT C	
	SARD4-p32b-R2	TCGAG AC AAC GGC TGA GGT AAG T	
CRYM (Isoform 1)	CRYM_p32b_F1	TAT GAG CCG GGT ACC AGC GTT	
	CRYM_p32b_F2	TGA GCC GGG TAC CAG CGT TC	
	CRYM_p32b_R1	G TT TAC CAG ATG ACC AGG AAT CAT AG	
	CRYM_p32b_R2	TCGAGTTT ACC AGA TGA CCA GGA ATC	
SARD4	GSP01F	ATGATGACTGGTGGGTAGCAG	**Genotyping**
	GSP01R	ATGTGAAATATTCGCAAACGC	
Actin2	Act2_for	TCGCCATCCAAGCTGTTCTCT	
	Act2_rev	CCTGGACCTGCCTCATCATACTC	
SARD4	SARD4_qPCR_01F	GTGTTTAAGTCCGTCGGTTCG	**qPCR**
	SARD4_qPCR_01R	AACGGCTGAGGTAAGTCTCG	
	SARD4_qPCR_02F	AAGGGCTCAGGAGTTAGCTG	
	SARD4_qPCR_02R	TCTAGCGAATCGTGGCTATCG	

Supplemental Table S2. List of primers used in this study.

µg g^{-1} FW	inoculated leaves (2 dpi)	
amino acid	µg g^{-1} FW	
	$MgCl_2$	*Psm*
Lys[1]	5.1 ± 1.1	28.8 ± 11.7 **
Leu[1]	3.3 ± 0.6	49.2 ± 26.7 **
Orn[1]	0.7 ± 0.1	1.1 ± 0.2 *
Met	0.8 ± 0.1	3.9 ± 1.0 **
DAP	not detected	not detected

Supplemental Table S3. Levels of free amino acids in the leaves of *Psm*-inoculated and mock-treated Arabidopsis Col-0 plants.

Leaves were harvested 2 days after inoculation (dpi). Mean values are given in µg g^{-1} fresh weight (FW) ± SD from a minimum of three replicate samples. Mock treatments were performed by infiltration of leaves with a 10 mM $MgCl_2$ solution. Asterisks denote statistically significant differences between *Psm*-inoculated and mock-treated samples (two-tailed *t* test; **: $P < 0.01$, *: $P < 0.05$).

[1] taken from Návarová et al. (2012)