Zusätzliche Informationen zur Dissertation von Yvonne Gäbler, 2007

Tabelle 7-79: Liste von Genen, deren Expression durch flg22-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.

Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	AGI	Beschreibung	flg22
261050_at	AT1G01260	basic helix-loop-helix (bHLH) family protein	2,0
263165_at	AT1G03060	WD-40 repeat family protein / beige-related	2,1
261815_at	AT1G08320	bZIP family transcription factor	2,6
264669_at	AT1G09630	ATRAB11C (ARABIDOPSIS RAB GTPASE HOMOLOG A2A); GTP binding	3,7
264522_at	AT1G10050	glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein	2,1
261832_at	AT1G10650	protein binding / zinc ion binding	3,5
260466_at	AT1G10900	phosphatidylinositol-4-phosphate 5-kinase family protein	2,6
260468_at	AT1G11100	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related	2,1
261033_at	AT1G17380	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G72450.1); similar to PnFL-2 [Ipomoea nil] (GB:AAG49896	2,0
256013_at	AT1G19270	ubiquitin interaction motif-containing protein / LIM domain-containing protein	2,6
260671_at	AT1G19310	zinc finger (C3HC4-type RING finger) family protein	2,0
261458_at	AT1G21080	DNAJ heat shock N-terminal domain-containing protein	2,0
260878_at	AT1G21450	SCL1 (SCARECROW-LIKE 1); transcription factor	2,6
245660_at	AT1G28240	similar to hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in linear amides [Arabidopsis thaliana] (TAIR:AT1	2,0
260026_at	AT1G29970	RPL18AA (60S RIBOSOMAL PROTEIN L18A-1)	2,5
256159_at	AT1G30135	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G34600.1); similar to ZIM [Medicago truncatula] (GB:ABE8	2,5
261216_at	AT1G33030	O-methyltransferase family 2 protein	2,5
245765_at	AT1G33600	leucine-rich repeat family protein	2,1
262540_at	AT1G34260	phosphatidylinositol-4-phosphate 5-kinase family protein	2,5
262565_at	AT1G34320	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G08660.1); similar to Os05g0430300 [Oryza sativa (japonica	2,0
260722_at	AT1G48040	protein phosphatase type 2C	2,1
261852_at	AT1G50440	zinc finger (C3HC4-type RING finger) family protein	2,0
	AT1G51280	similar to Toll-Interleukin-Resistance (TIR) domain-containing protein [Arabidopsis thaliana] (TAIR:At5g45000.1); simila	2,1
262090_at	AT1G55970	histone acetyltransferase 4 (HAC4)	4,3
262896_at	AT1G59820	haloacid dehalogenase-like hydrolase family protein	2,3
264886_at	AT1G61120	terpene synthase/cyclase family protein	2,1
260243_at	AT1G63720	similar to hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] (TAIR:AT4G25620.1); similar to unknow	2,8
264685_at	AT1G65610	endo-1,4-beta-glucanase, putative / cellulase, putative	2,8
262926_s_at	AT1G65800;A	[AT1G65800, ARK2 (Arabidopsis Receptor Kinase 2); kinase];[AT1G65790, ARK1 (A. THALIANA RECEPTOR KINAS	2,3

264232_at	AT1G67470	protein kinase family protein	2,3
259642_at	AT1G69030	similar to BSD domain-containing protein [Arabidopsis thaliana] (TAIR:AT1G26300.1); similar to Os04g0662000 [Oryza s	2,0
260411_at	AT1G69890	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1); similar to Cytosolic fatty-acid binding; Actin-cro	2,3
264313_at	AT1G70410	carbonic anhydrase, putative / carbonate dehydratase, putative	2,6
256337_at	AT1G72070;A	[AT1G72070, DNAJ heat shock N-terminal domain-containing protein];[AT1G72060, serine-type endopeptidase inhibitor]	2,3
259852_at	AT1G72280	AERO1 (ARABIDOPSIS ENDOPLASMIC RETICULUM OXIDOREDUCTINS 1)	2,1
245777_at	AT1G73540	ATNUDT21 (Arabidopsis thaliana Nudix hydrolase homolog 21); hydrolase	3,5
260394_at	AT1G74080	MYB122 (myb domain protein 122); DNA binding / transcription factor	2,3
260227_at	AT1G74450	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G18740.1); similar to Protein of unknown function DUF793		2,1
259876_at	AT1G76700	DNAJ heat shock N-terminal domain-containing protein	2,8
266203_at	AT2G02230	ATPP2-B1 (Phloem protein 2-B1)	2,0
266235_at	AT2G02360	ATPP2-B10 (Phloem protein 2-B10)	2,5
266182_at	AT2G02370	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G12450.1); similar to At2g02370/T16F16.16 [Medicago trun	2,6
263722_at	AT2G13650	GONST1 (GOLGI NUCLEOTIDE SUGAR TRANSPORTER 1); nucleotide-sugar transporter	2,3
267112_at	AT2G14750	APK (APS KINASE); ATP binding / kinase/ transferase, transferring phosphorus-containing groups	2,3
263072_at	AT2G17530	protein kinase family protein	2,0
263613_at	AT2G25250	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G32020.1)	2,1
266835_at	AT2G29990	NDA2 (ALTERNATIVE NAD(P)H DEHYDROGENASE 2); NADH dehydrogenase	2,1
267248_at	AT2G30120	transcription factor	2,0
267246_at	AT2G30250	WRKY25 (WRKY DNA-binding protein 25); transcription factor	2,1
266476_at	AT2G31090	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G20562.1); similar to hypothetical protein MtrDRAFT_AC1	2,3
266360_at	AT2G32250	FRS2 (FAR1-RELATED SEQUENCE 2); zinc ion binding	2,3
266609_at	AT2G35510	SRO1 (SIMILAR TO RCD ONE 1); NAD+ ADP-ribosyltransferase	2,8
263928_at	AT2G36330	similar to integral membrane protein, putative [Arabidopsis thaliana] (TAIR:AT5G62820.1); similar to Os01g0640700 [Ory	3,5
265208_at	AT2G36690	oxidoreductase, 2OG-Fe(II) oxygenase family protein	6,1
266964_at	AT2G39480	PGP6; ATPase, coupled to transmembrane movement of substances	2,6
267064_at	AT2G41110	ATCAL4 (calmodulin-related protein 4); calcium ion binding	2,3
260560_at	AT2G43590	chitinase, putative	2,6
260556_at	AT2G43620	chitinase, putative	2,1
267393_at	AT2G44500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07900.1); similar to Plant protein family, putative [Medicag	3,0
265454_at	AT2G46530	ARF11 (AUXIN RESPONSE FACTOR 11); transcription factor	2,5
258855_at	AT3G02070	OTU-like cysteine protease family protein	2,0
256328_at	AT3G02360	6-phosphogluconate dehydrogenase family protein	2,3
257536_at	AT3G02800	phosphoprotein phosphatase	3,0
259325_at	AT3G05320	similar to protein-O-fucosyltransferase 1 [Saccharum officinarum] (GB:CAH40838.1)	2,1
259298_at	AT3G05370	disease resistance family protein	2,0

258743_s_at	AT3G05840;	[AT3G05840, ATSK12 (Arabidopsis thaliana SHAGGY-like kinase 12); protein kinase]; [AT5G26751, ATSK11 (Arabido	2,1
258557_at	AT3G05990	leucine-rich repeat family protein	2,5
258544_at	AT3G07040	RPM1 (RESISTANCE TO P. SYRINGAE PV MACULICOLA 1)	2,1
259040_at	AT3G09270	ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau) 8); glutathione transferase	2,6
259033_at; 25903	AT3G09410	pectinacetylesterase family protein	2,5
257700_at	AT3G12740	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein	2,1
256958_at	AT3G13430	zinc finger (C3HC4-type RING finger) family protein	3,5
257206_at	AT3G16530	legume lectin family protein	2,0
257038_at	AT3G19260	LAG1 HOMOLOG 2 (LONGEVITY ASSURANCE GENE1 HOMOLOG 2)	2,8
258176_at	AT3G21650	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative	2,5
258125_s_at;2571	AT3G23530;A	[AT3G23530, cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative];[AT3G23510, cyclopropane fatty ac	2,1
257623_at	AT3G26210	CYP71B23 (cytochrome P450, family 71, subfamily B, polypeptide 23); oxygen binding	2,0
257829_at	AT3G26680	SNM1 (SENSITIVE TO NITROGEN MUSTARD 1)	3,5
256633_at	AT3G28340	GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring	2,3
257902_at	AT3G28450	leucine-rich repeat transmembrane protein kinase, putative	2,5
252602_at	AT3G45040	phosphatidate cytidylyltransferase family protein	2,3
252592_at	AT3G45640	ATMPK3 (MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein kinase	2,6
252383_at	AT3G47780	ATATH6 (ABC2 homolog 6); ATPase, coupled to transmembrane movement of substances	2,3
256674_at	AT3G52360	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G35850.1)	2,0
252018_at	AT3G53000	ATPP2-A15 (Phloem protein 2-A15)	2,0
251971_at	AT3G53160	UGT73C7 (UDP-glucosyl transferase 73C7); UDP-glycosyltransferase/ transferase, transferring glycosyl groups	2,1
251821_at	AT3G55050	serine/threonine protein phosphatase 2C (PP2C6)	2,0
251624_at	AT3G57280	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G20510.1); similar to hypothetical protein 11 [Plantago majo	2,1
251594_at	AT3G57630	exostosin family protein	2,6
251475_at	AT3G59660	C2 domain-containing protein / GRAM domain-containing protein	2,1
255596_at	AT4G01720	WRKY47 (WRKY DNA-binding protein 47); transcription factor	2,1
255553_at	AT4G01960	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G02380.1); similar to hypothetical protein MtrDRAFT_AC1	2,1
255381_at	AT4G03510	RMA1 (Ring finger protein with Membrane Anchor 1); protein binding / ubiquitin-protein ligase/ zinc ion binding	2,0
255306_at	AT4G04740	CPK23 (calcium-dependent protein kinase 23); calcium- and calmodulin-dependent protein kinase/ kinase	2,0
255116_at	AT4G08850	leucine-rich repeat family protein / protein kinase family protein	2,0
245265_at	AT4G14400	ACD6 (ACCELERATED CELL DEATH 6); protein binding	2,1
245308_at	AT4G17486	Identical to UPF0326 protein At4g17486 [Arabidopsis Thaliana] (GB:Q93VG8;GB:O23591;GB:Q9FPJ0); similar to unkno	2,3
	AT4G17900	zinc-binding family protein; similar to zinc-binding family protein [Arabidopsis thaliana] (TAIR:AT1G32700.1); similar to	2,0
254409_at	AT4G21400	protein kinase family protein	4,9
	AT4G21865	unknown protein	3,0
254256_at	AT4G23180	CRK10 (CYSTEINE-RICH RLK10); kinase	6,1

254167_at	AT4G24400	CIPK8 (CBL-INTERACTING PROTEIN KINASE 8); kinase	2,0
254082_at	AT4G25720	glutamine cyclotransferase family protein	2,3
253925_at	AT4G26690	MRH5/SHV3 (morphogenesis of root hair 5); glycerophosphodiester phosphodiesterase/ kinase	2,3
253898_s_at	AT4G27027	[AT4G27070, TSB2 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT); tryptophan synthase]; [AT5G54810, TSB1 (TRYP	2,3
253637_at	AT4G30390	unknown protein	2,1
253625_at	AT4G30600	signal recognition particle receptor alpha subunit family protein	2,3
253582_at	AT4G30670	unknown protein	2,0
253457_at	AT4G32060	calcium-binding EF hand family protein	2,0
253467_at	AT4G32140	similar to membrane protein [Arabidopsis thaliana] (TAIR:AT3G07080.1); similar to H0811D08.4 [Oryza sativa (indica cul	2,0
253476_at	AT4G32300	lectin protein kinase family protein	3,7
253392_at	AT4G32650	ATKC1 (ARABIDOPSIS THALIANA K+ RECTIFYING CHANNEL 1); cyclic nucleotide binding / inward rectifier potas	2,6
246213_at	AT4G36480	ATLCB1 (ARABIDOPSIS THALIANA SPHINGOLIPID LONGCHAIN BASE 1); serine C-palmitoyltransferase	2,1
252928_at	AT4G38940	kelch repeat-containing F-box family protein	2,3
252939_at	AT4G39230	isoflavone reductase, putative	3,0
251086_at	AT5G01450	protein binding / zinc ion binding	2,1
251028_at	AT5G02230	haloacid dehalogenase-like hydrolase family protein	2,8
250990_at	AT5G02290	NAK; kinase	2,3
250818_at	AT5G04930	ALA1 (AMINOPHOSPHOLIPID ATPASE1); ATPase, coupled to transmembrane movement of ions, phosphorylative mec	2,5
245879_at	AT5G09420	chloroplast outer membrane translocon subunit, putative	2,0
250463_at	AT5G10030	TGA4 (TGACG MOTIF-BINDING FACTOR 4); DNA binding / calmodulin binding / transcription factor	2,0
246528_at	AT5G15640	mitochondrial substrate carrier family protein	2,0
246460_at	AT5G16910	ATCSLD2 (Cellulose synthase-like D2); cellulose synthase/ transferase, transferring glycosyl groups	2,3
246422_at	AT5G17060	ADP-ribosylation factor, putative	2,1
250090_at	AT5G17330	GAD (Glutamate decarboxylase 1); calmodulin binding	2,0
249987_at	AT5G18490	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G04090.1); similar to unknown protein [Arabidopsis thaliana	3,2
249872_at	AT5G23130	peptidoglycan-binding LysM domain-containing protein	2,1
249625_at	AT5G37480	similar to Os03g0748600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001051270.1)	2,1
249417_at	AT5G39670	calcium-binding EF hand family protein	2,3
249418_at;249423	AT5G39785	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69610.1); similar to conserved hypothetical protein [Medica	2,1
249411_at	AT5G40390	SIP1 (SEED IMBIBITION 1-LIKE); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compoun	2,6
249140_at	AT5G43190	F-box family protein (FBX6)	2,1
249057_at	AT5G44480	DUR (DEFECTIVE UGE IN ROOT); catalytic	2,1
249021_at;254521	AT5G44820	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G19970.1); similar to H0307D04.3 [Oryza sativa (indica cult	2,1
249024_at	AT5G44860	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G19950.1); similar to conserved hypothetical protein [Medica	2,3
249029_at	AT5G44870	disease resistance protein (TIR-NBS-LRR class), putative	2,3
248968_at	AT5G45280	pectinacetylesterase, putative	2,1

248848_at	AT5G46520	ATP binding / nucleoside-triphosphatase/ nucleotide binding / protein binding / transmembrane receptor	2,0
248568_at	AT5G49760	leucine-rich repeat family protein / protein kinase family protein	2,0
248581_at	AT5G49900	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G33700.2); similar to unknown protein [Arabidopsis thaliana	3,2
248477_at	AT5G50900	armadillo/beta-catenin repeat family protein	2,3
248243_at	AT5G53590	auxin-responsive family protein	2,1
248134_at	AT5G54860	integral membrane transporter family protein	2,0
248142_at	AT5G55030	similar to DNA-binding bromodomain-containing protein [Arabidopsis thaliana] (TAIR:AT1G20670.1); similar to Hypothe	2,6
247934_at	AT5G57000	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G72690.1); similar to Os09g0363700 [Oryza sativa (japonica	3,2
247776_at	AT5G58700	phosphoinositide-specific phospholipase C family protein	2,1
247617_at	AT5G60270	lectin protein kinase family protein	2,1
247525_at	AT5G61380	TOC1 (TIMING OF CAB1 1); transcription regulator	2,1
247545_at	AT5G61530	small G protein family protein / RhoGAP family protein	2,0
247492_at	AT5G61890	AP2 domain-containing transcription factor family protein	2,3
247438_at	AT5G62460	zinc finger (C3HC4-type RING finger) family protein	2,1
247389_at	AT5G63490	CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein	2,3
247213_at	AT5G64900	ATPEP1/PROPEP1 (Elicitor peptide 1 precursor)	3,7

Tabelle 7-80: Liste von Genen, deren Expression durch HrpZ$_{Psph}$-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	AGI	Beschreibung	HrpZ$_{Psph}$
261405_at	AT1G18740	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74450.1); similar to Protein of unknown function DUF793 [Medicago	2,1
265170_at	AT1G23730	carbonic anhydrase, putative / carbonate dehydratase, putative	2,3
246287_at	AT1G31870	similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G29210.1); similar to Os08g0178300 [Ory	2,0
254839_at	AT4G12400	stress-inducible protein, putative	2,0
246944_at	AT5G25450	ubiquinol-cytochrome C reductase complex 14 kDa protein, putative	2,0
247346_at	AT5G63770	ATDGK2 (DIACYLGLYCEROL KINASE 2); diacylglycerol kinase	2,1
247197_at	AT5G65240	leucine-rich repeat family protein / protein kinase family protein	2,0

Tabelle 7-81: Liste von Genen, deren Expression durch NLP_{Pp}-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	AGI	Beschreibung	NLP_{Pp}
259443_at	AT1G02360	chitinase, putative	16,0
259447_s_at	AT1G02430;A	[AT1G02430, ATARFD1B (ADP-ribosylation factor D1B); GTP binding];[AT1G02440, ATARFD1A (ADP-ribosylation factor	2,5
262731_at	AT1G16420	latex-abundant protein, putative (AMC8) / caspase family protein	2,3
264202_at	AT1G22810	AP2 domain-containing transcription factor, putative	2,6
264867_at	AT1G24150	ATFH4/FH4 (FORMIN HOMOLOGUE 4); actin binding / protein binding	3,0
245641_at	AT1G25370	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68340.1); similar to conserved hypothetical protein [Medicago t	2,3
261005_at	AT1G26420	FAD-binding domain-containing protein	7,0
256192_at	AT1G30110	diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase, putative	2,5
246627_s_at	AT1G48860;A	[AT1G48860, 3-phosphoshikimate 1-carboxyvinyltransferase, putative / 5-enolpyruvylshikimate-3-phosphate, putative / EPSP s	2,0
245840_at	AT1G58420	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10140.1); similar to Os07g0123800 [Oryza sativa (japonica cult	2,1
262324_at	AT1G64170	ATCHX16 (CATION/H+ EXCHANGER 16); monovalent cation:proton antiporter	2,5
264635_at	AT1G65500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65490.1)	2,0
	AT1G67520	lectin protein kinase family protein; similar to CES101 (CALLUS EXPRESSION OF RBCS 101), carbohydrate binding / kinase	2,6
260439_at	AT1G68340	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G25370.1); similar to conserved hypothetical protein [Medicago t	2,3
262228_at	AT1G68690	pseudogene, protein kinase family, similar to protein kinase 1 GB:BAA94509 GI:7573596 from (Populus nigra); blastp match o	2,8
261899_at	AT1G80820	CCR2 (CINNAMOYL COA REDUCTASE)	3,5
267436_at	AT2G19190	FRK1 (FLG22-INDUCED RECEPTOR-LIKE KINASE 1); kinase	7,5
267288_at	AT2G23680	stress-responsive protein, putative	2,1
263800_at	AT2G24600	ankyrin repeat family protein	10,6
267199_at	AT2G30990	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G29240.1); similar to Protein of unknown function DUF688 [Me	2,0
265725_at	AT2G32030	GCN5-related N-acetyltransferase (GNAT) family protein	2,1
263948_at	AT2G35980	YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	4,6
258606_at	AT3G02840	immediate-early fungal elicitor family protein	3,7
258796_at	AT3G04630	WDL1 (WVD2-LIKE 1)	2,0
258351_at	AT3G17700	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1); calmodulin binding / cyclic nucleotide binding / ion channe	2,1
257978_at	AT3G20860	protein kinase family protein	3,2
256911_at	AT3G24090	transaminase	2,0
257784_at; 25778	AT3G26980	ubiquitin family protein	3,7

251248_at	AT3G62150	PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances	3,2
255564_s_at	AT4G01770;A	[AT4G01770, RGXT1 (RHAMNOGALACTURONAN XYLOSYLTRANSFERASE 1); UDP-xylosyltransferase];[AT4G0175	4,6
245566_at	AT4G14610	pseudogene, disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a d	2,5
254673_at	AT4G18430	AtRABA1e (Arabidopsis Rab GTPase homolog A1e); GTP binding	2,0
254571_at	AT4G19370	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G31720.1); similar to Os06g0114700 [Oryza sativa (japonica cult	2,1
253654_at	AT4G30060	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G19160.1); similar to Protein of unknown function DUF266, plan	2,0
253181_at	AT4G35180	LHT7 (LYS/HIS TRANSPORTER 7); amino acid permease	3,0
250983_at	AT5G02780	In2-1 protein, putative	5,7
246955_at	AT5G04870	CPK1 (calcium-dependent protein kinase isoform AK1); calcium- and calmodulin-dependent protein kinase/ kinase	2,1
250025_at	AT5G18290	SIP1;2 (SMALL AND BASIC INTRINSIC PROTEIN1B)	2,0
249841_at	AT5G23520	similar to Os04g0442100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001052880.1); similar to P0076O17.10 [Oryza sativ	2,0
249618_at	AT5G37490	U-box domain-containing protein	2,8
249188_at	AT5G42830	transferase family protein	4,3
249032_at	AT5G44910	Toll-Interleukin-Resistance (TIR) domain-containing protein	4,6
248090_at	AT5G55090	MAPKKK15 (Mitogen-activated protein kinase kinase kinase 15); kinase	2,8
247940_at	AT5G57190	phosphatidylserine decarboxylase, putative	3,5
247215_at	AT5G64905	PROPEP3 (Elicitor peptide 3 precursor)	16,0
244979_at	ATCG00750	30S chloroplast ribosomal protein S11	2,3

Tabelle 7-82: Liste von Genen, deren Expression durch LPS-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.

Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	AGI	Beschreibung	LPS
264834_at	AT1G03730	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G03600.1); similar to expressed protein [Oryza sativa (japonica	2,1
264608_at	AT1G04710	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative	2,0
264566_at	AT1G05270	TraB family protein	2,1
256058_at	AT1G07240	UDP-glucoronosyl/UDP-glucosyl transferase family protein	2,3
261064_at	AT1G07510	FTSH10 (FtsH protease 10); ATPase	2,0
261413_at	AT1G07630	PLL5 (POL-like 5); protein phosphatase type 2C	2,1
264255_at	AT1G09140	ATSRP30.1 (ARABIDOPSIS THALIANA SERINE/ARGININE PROTEIN 30.1); RNA binding	2,6
264708_at	AT1G09740	ethylene-responsive protein, putative	2,1
260477_at	AT1G11050	protein kinase family protein	2,1
261023_at	AT1G12200	flavin-containing monooxygenase family protein / FMO family protein	2,3
262656_at	AT1G14200	zinc finger (C3HC4-type RING finger) family protein	2,5
261838_at	AT1G16030	HSP70B (heat shock protein 70B); ATP binding	2,0
262521_at	AT1G17130	cell cycle control protein-related	2,0
261232_at	AT1G20220	nucleic acid binding	2,0
255941_at	AT1G20350	ATTIM17-1 (Arabidopsis thaliana translocase inner membrane subunit 17-1); protein translocase	2,5
259543_at	AT1G20580	small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative	2,1
264868_at	AT1G24090	RNase H domain-containing protein	2,3
245633_at	AT1G25280	AtTLP10 (TUBBY LIKE PROTEIN 10); phosphoric diester hydrolase/ transcription factor	2,1
245667_at	AT1G28200	FIP1 (FH INTERACTING PROTEIN 1)	2,0
261443_at	AT1G28480	glutaredoxin family protein	2,6
260885_at	AT1G29230	CIPK18 (CIPK18); kinase	2,3
259826_at	AT1G29340	PUB17 (PLANT U-BOX17); ubiquitin-protein ligase	2,3
245768_at	AT1G33590	disease resistance protein-related / LRR protein-related	2,0
260761_at	AT1G49150	unknown protein	2,3
245750_at	AT1G51060	histone H2A, putative	2,1
264190_at	AT1G54830	CCAAT-box binding transcription factor Hap5a, putative	2,0
259655_at	AT1G55210	disease resistance response	2,5
259648_at; 25966	AT1G55310	SR33 (SC35-like splicing factor 33); RNA binding	2,1
259664_at	AT1G55330	AGP21 (ARABINOGALACTAN PROTEIN 21)	2,1

264539_at	AT1G55590	F-box family protein	2,0
256024_at	AT1G58340	ZF14; transporter	2,3
262911_s_at	AT1G59860;A	[AT1G59860, 17.6 kDa class I heat shock protein (HSP17.6A-CI)];[AT1G07400, 17.8 kDa class I heat shock protein (HSP17.	2,6
262691_at	AT1G62740	stress-inducible protein, putative	2,0
	AT1G64950	member of CYP89A	2,5
262925_at	AT1G65730	YSL7 (YELLOW STRIPE LIKE 7); oligopeptide transporter	2,0
256518_at	AT1G66080	similar to Hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAO06975.1); similar to expressed protein [Oryz	2,5
256407_at	AT1G66570	ATSUC7 (SUCROSE-PROTON SYMPORTER 7); carbohydrate transporter/ sucrose:hydrogen symporter/ sugar porter	2,0
259856_at	AT1G68440	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G25400.1); similar to IMP dehydrogenase/GMP reductase [Mec	2,0
262229_at	AT1G68620	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16080.1); similar to CXE carboxylesterase [Actinidia deliciosa	2,8
260039_at	AT1G68795	CLE12 (CLAVATA3/ESR-RELATED 12); receptor binding	2,0
260304_at	AT1G70480	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23560.1); similar to OBP32pep (GB:AAA79703.1); contains I	2,0
260310_at	AT1G70590	F-box family protein	2,3
259749_at	AT1G71100	RSW10 (RADIAL SWELLING 10); ribose-5-phosphate isomerase	2,8
259890_at	AT1G72750	ATTIM23-2 (Arabidopsis thaliana translocase inner membrane subunit 23-2); protein translocase	2,1
260386_at	AT1G74010	strictosidine synthase family protein	2,6
260251_at	AT1G74250	DNAJ heat shock N-terminal domain-containing protein	2,0
262948_at	AT1G75560	zinc knuckle (CCHC-type) family protein	2,3
262685_at	AT1G76010	nucleic acid binding	2,0
261749_at	AT1G76180	ERD14 (EARLY RESPONSE TO DEHYDRATION 14)	2,0
259979_at	AT1G76600	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21010.1); similar to TMV response-related gene product [Nico	2,5
264948_at	AT1G77050	DEAD/DEAH box helicase, putative	2,0
259710_at	AT1G77670	aminotransferase class I and II family protein	2,1
262133_at	AT1G78000	SULTR1;2 (SULFATE TRANSPORTER 1;2); sulfate transporter	2,0
260807_at	AT1G78310	VQ motif-containing protein	2,3
263128_at	AT1G78600	zinc finger (B-box type) family protein	2,1
262939_s_at	AT1G79530;A	[AT1G79530, GAPCP-1; glyceraldehyde-3-phosphate dehydrogenase];[AT1G16300, GAPCP-2; glyceraldehyde-3-phosphate	2,0
262054_s_at	AT1G79920;A	[AT1G79920, heat shock protein 70, putative / HSP70, putative];[AT1G79930, HSP91 (Heat shock protein 91)]	2,1
266328_at	AT2G01600	epsin N-terminal homology (ENTH) domain-containing protein	2,5
267483_at	AT2G02810	ATUTR1/UTR1 (UDP-GALACTOSE TRANSPORTER 1); UDP-galactose transporter/ UDP-glucose transporter/ pyrimidine	2,1
266037_at	AT2G05940	protein kinase, putative	2,0
265375_at	AT2G06530	SNF7 family protein	2,3
244922_s_at	AT2G07674;A	[AT2G07674, Identical to Hypothetical mitochondrial protein AtMg01010 (ORF118) [Arabidopsis Thaliana] (GB:P92535;GB	2,1
266013_s_at	AT2G07702;A	[AT2G07702, Identical to Hypothetical mitochondrial protein AtMg00440/AtMg01140 (ORF152a/ORF152b) [Arabidopsis Th	2,0
266014_s_at	AT2G07722;A	[AT2G07722, Identical to Hypothetical mitochondrial protein AtMg00170/AtMg00620 (ORF139b/ORF139a) [Arabidopsis Th	2,0
266385_at	AT2G14610	PR1 (PATHOGENESIS-RELATED GENE 1)	2,0

265501_at	AT2G15490	UGT73B4; UDP-glycosyltransferase/ transferase, transferring glycosyl groups	3,2
	AT2G16590	?	2,1
263076_at	AT2G17520	IRE1A (Yeast endoribonuclease/protein kinase IRE1-like gene); kinase	2,0
264619_at	AT2G17760	aspartyl protease family protein	2,3
265930_at	AT2G18510	EMB2444 (EMBRYO DEFECTIVE 2444); RNA binding	2,0
266949_s_at	AT2G18840;A	[AT2G18840, integral membrane Yip1 family protein];[AT4G30260, integral membrane Yip1 family protein]	2,0
267489_s_at	AT2G19120;A	[AT2G19120, tRNA-splicing endonuclease positive effector-related];[AT4G30100, tRNA-splicing endonuclease positive effe	2,5
265259_at	AT2G20330	transducin family protein / WD-40 repeat family protein	2,0
263374_at	AT2G20560	DNAJ heat shock family protein	3,2
263716_at	AT2G20580	AtRPN1a/RPN1A (26S proteasome regulatory subunit S2 1A); binding	2,0
265384_at	AT2G20760	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40060.1); similar to conserved hypothetical protein [Medicag	2,1
264003_at	AT2G22475	GRAM domain-containing protein / ABA-responsive protein-related	2,3
263799_at	AT2G24550	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G31510.1); similar to putative KID-containing protein [Brassica	2,0
263538_at	AT2G25010	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G17930.1); similar to Os07g0507600 [Oryza sativa (japonica cu	2,0
266261_at	AT2G27580	zinc finger (AN1-like) family protein	2,0
267496_at	AT2G30550	lipase class 3 family protein	2,6
265675_at	AT2G32120	HSP70T-2; ATP binding	2,1
263938_at	AT2G35900	similar to Mal d 1-associated protein [Malus x domestica] (GB:AAP86780.1)	2,3
263901_at	AT2G36320	zinc finger (AN1-like) family protein	2,0
267032_at	AT2G38490	CIPK22 (CBL-INTERACTING PROTEIN KINASE 22); kinase	2,0
266170_at	AT2G39050	hydroxyproline-rich glycoprotein family protein	2,1
265721_at	AT2G40090	ATATH9 (ABC2 homolog 9)	2,0
266053_at	AT2G40730	HEAT repeat-containing protein	2,0
245101_at	AT2G40890	CYP98A3 (cytochrome P450, family 98, subfamily A, polypeptide 3); p-coumarate 3-hydroxylase	2,1
260522_x_at	AT2G41730	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G24640.1)	2,8
266437_at; 26643	AT2G43160	epsin N-terminal homology (ENTH) domain-containing protein	2,8
266447_at	AT2G43290	MSS3 (MULTICOPY SUPPRESSORS OF SNF4 DEFICIENCY IN YEAST 3); calcium ion binding	2,1
260586_at	AT2G43630	similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:AT3G59640.2); similar to glycine-rich protein, related [Medicago	2,3
260571_at	AT2G43790	ATMPK6 (MAP KINASE 6); MAP kinase/ kinase	2,1
267389_at	AT2G44460	glycosyl hydrolase family 1 protein	2,0
267559_at	AT2G45570	CYP76C2 (cytochrome P450, family 76, subfamily C, polypeptide 2); oxygen binding	2,0
265451_at	AT2G46490	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G35110.1)	2,0
265450_at	AT2G46620	AAA-type ATPase family protein	2,1
266752_at	AT2G47000	PGP4 (P-GLYCOPROTEIN 4, P-GLYCOPROTEIN4); ATPase, coupled to transmembrane movement of substances / xenobi	2,8
263320_at	AT2G47180	ATGOLS1 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 1); transferase, transferring hexosyl groups	3,0
266514_at	AT2G47890	zinc finger (B-box type) family protein	2,0

257519_at	AT3G01210	nucleic acid binding	2,1
259272_at	AT3G01290	band 7 family protein	2,8
259194_at	AT3G01540	DRH1 (DEAD box RNA helicase 1)	2,0
258879_at	AT3G03270	universal stress protein (USP) family protein / early nodulin ENOD18 family protein	2,3
258805_at	AT3G04010	glycosyl hydrolase family 17 protein	2,8
258840_at	AT3G04620	nucleic acid binding	2,1
258792_at	AT3G04640	glycine-rich protein	2,6
259312_at	AT3G05200	ATL6 (Arabidopsis T?xicos en Levadura 6); protein binding / zinc ion binding	3,2
259106_at	AT3G05490	RALFL22 (RALF-LIKE 22)	2,5
258501_at	AT3G06780	glycine-rich protein	2,1
258982_at	AT3G08870	lectin protein kinase, putative	2,3
259205_at	AT3G09030	potassium channel tetramerisation domain-containing protein	2,1
258939_at	AT3G10020	similar to Os12g0147200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001066153.1); similar to Os11g0149200 [Oryza sa	2,8
258926_s_at	AT3G10490;A	[AT3G10490, ANAC051/ANAC052 (Arabidopsis NAC domain containing protein 51, Arabidopsis NAC domain containing p	2,3
259071_at	AT3G11650	NHL2 (NDR1/HIN1-like 2)	2,3
256663_at	AT3G12050	Aha1 domain-containing protein	2,0
256258_at	AT3G12480	transcription factor, putative	2,0
256245_at	AT3G12580	HSP70 (heat shock protein 70); ATP binding	2,1
257654_at	AT3G13310	DNAJ heat shock N-terminal domain-containing protein	2,1
258201_at	AT3G13910	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G19460.1); similar to hypothetical protein MtrDRAFT_AC1525	2,0
258207_at	AT3G14050	RSH2 (RELA-SPOT HOMOLOG); catalytic	2,1
258119_at	AT3G14720	ATMPK19 (Arabidopsis thaliana MAP kinase 19); MAP kinase	2,1
257266_at	AT3G15010	RNA recognition motif (RRM)-containing protein	2,0
258336_at	AT3G16050	A37 (PYRIDOXINE BIOSYNTHESIS 1.2); protein heterodimerization	3,0
258338_at	AT3G16150	L-asparaginase, putative / L-asparagine amidohydrolase, putative	2,5
258425_at	AT3G16760	tetratricopeptide repeat (TPR)-containing protein	2,3
257880_at	AT3G16910	AAE7/ACN1 (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase	2,0
	AT3G17615	hypothetical protein	2,1
257719_at	AT3G18440	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G18420.1); similar to Putative expressed protein [Brassica olera	2,0
257022_at	AT3G19580	AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2); nucleic acid binding / transcription factor/ zinc ion binding	3,2
258167_at	AT3G21560	UGT84A2; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase	2,0
257951_at	AT3G21700	GTP binding	2,3
256916_at	AT3G24050	GATA transcription factor 1 (GATA-1)	2,3
258133_at	AT3G24500	ATMBF1C/MBF1C (MULTIPROTEIN BRIDGING FACTOR 1C); DNA binding / transcription coactivator/ transcription fac	2,1
256757_at	AT3G25620	ABC transporter family protein	2,0
257643_at	AT3G25730	AP2 domain-containing transcription factor, putative	2,0

258277_at	AT3G26830	PAD3 (PHYTOALEXIN DEFICIENT 3); oxygen binding	2,3
252745_at	AT3G43230	zinc finger (FYVE type) family protein	2,1
252679_at	AT3G44260	CCR4-NOT transcription complex protein, putative	2,5
252475_s_at	AT3G46640;A	[AT3G46640, PCL1 (PHYTOCLOCK 1); DNA binding / transcription factor];[AT5G59570, myb family transcription factor]	2,1
252421_at	AT3G47540	chitinase, putative	2,1
252400_at	AT3G48020	similar to F-box family protein-related [Arabidopsis thaliana] (TAIR:AT5G62860.1); similar to IS10 transposase, putative [Ly	2,5
252214_at	AT3G50260	ATERF#011/CEJ1 (COOPERATIVELY REGULATED BY ETHYLENE AND JASMONATE 1); DNA binding / transcriptic	2,5
252029_s_at	AT3G52660;A	[AT3G52660, RNA recognition motif (RRM)-containing protein];[AT5G28390, RNA recognition motif (RRM)-containing pr	2,1
252009_at	AT3G52800	zinc finger (AN1-like) family protein	2,3
251975_at	AT3G53230	cell division cycle protein 48, putative / CDC48, putative	2,1
251917_at	AT3G53970	proteasome inhibitor-related	2,1
251904_at	AT3G54130	josephin family protein	2,5
251879_at	AT3G54200	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G05975.1); similar to Harpin-induced 1 [Medicago truncatula] (	2,0
251839_at	AT3G54950	PLA IIIA/PLP7 (Patatin-like protein 7)	2,3
246293_at	AT3G56710	SIB1 (SIGMA FACTOR BINDING PROTEIN 1); binding	2,3
251658_at	AT3G57020	strictosidine synthase family protein	2,0
251422_at	AT3G60540	sec61beta family protein	2,0
251351_s_at	AT3G61030;A	[AT3G61030, C2 domain-containing protein];[AT3G60950, C2 domain-containing protein];[AT3G61050, calcium-dependent	2,0
251336_at	AT3G61190	BAP1 (BON ASSOCIATION PROTEIN 1)	3,0
251300_at	AT3G61980	serine protease inhibitor, Kazal-type family protein	2,0
251192_at	AT3G62720	ATXT1; UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups	3,5
251176_at	AT3G63380	calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)	2,0
255599_at	AT4G01010	ATCNGC13 (cyclic nucleotide gated channel 13); calmodulin binding / cyclic nucleotide binding / ion channel	2,6
255382_at	AT4G03430	STA1 (STABILIZED1); RNA splicing factor, transesterification mechanism	2,0
255259_at	AT4G05020	NDB2 (NAD(P)H DEHYDROGENASE B2); disulfide oxidoreductase	2,1
255171_at	AT4G07990	DNAJ heat shock N-terminal domain-containing protein	2,0
255151_at	AT4G08180	oxysterol-binding family protein	2,3
255037_at	AT4G09460	ATMYB6 (myb domain protein 6, myb domain protein 8); DNA binding / transcription factor	2,5
254858_at	AT4G12070	similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD12897.1); similar to Os02g0717600 [Oryza s	2,3
254812_at	AT4G12250	GAE5 (UDP-D-GLUCURONATE 4-EPIMERASE 5); catalytic	2,0
254759_at	AT4G13180	short-chain dehydrogenase/reductase (SDR) family protein	2,1
245554_at	AT4G15380	CYP705A4 (cytochrome P450, family 705, subfamily A, polypeptide 4); oxygen binding	2,0
245334_at	AT4G15800	RALFL33 (RALF-LIKE 33)	3,0
245477_at	AT4G16110	ARR2 (ARABIDOPSIS RESPONSE REGULATOR 2); transcription factor/ two-component response regulator	2,0
245247_at	AT4G17230	SCL13 (SCARECROW-LIKE 13); transcription factor	2,1
245252_at	AT4G17500	ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription factor/ transcription	2,5

254608_at	AT4G18910	NIP1;2/NLM2 (NOD26-like intrinsic protein 1;2); water channel	2,3
254559_at	AT4G19200	proline-rich family protein	2,0
254477_at	AT4G20380	LSD1 (LESION SIMULATING DISEASE)	2,3
254453_at	AT4G21120	AAT1 (CATIONIC AMINO ACID TRANSPORTER 1); cationic amino acid transporter	2,0
254318_at	AT4G22530	embryo-abundant protein-related	2,3
254248_at	AT4G23270	protein kinase family protein	2,1
254200_at	AT4G24110	similar to Hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAO17020.1)	3,0
254204_at	AT4G24160	hydrolase, alpha/beta fold family protein	2,5
253838_at	AT4G27880	seven in absentia (SINA) family protein	2,0
253824_at	AT4G27940	mitochondrial substrate carrier family protein	2,0
253778_at	AT4G28480	DNAJ heat shock family protein	2,1
253735_at	AT4G29160	SNF7 family protein	2,5
253663_at	AT4G30160	VLN4 (ARABIDOPSIS THALIANA VILLIN 4); actin binding	2,1
253631_at	AT4G30440	GAE1 (UDP-D-GLUCURONATE 4-EPIMERASE 1); UDP-glucuronate 4-epimerase/ catalytic	3,0
253577_at;253555	AT4G31080	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24330.1); similar to Os02g0631000 [Oryza sativa (japonica cu	2,0
253259_at	AT4G34410	AP2 domain-containing transcription factor, putative	2,0
253104_at	AT4G36010	pathogenesis-related thaumatin family protein	2,0
246253_at	AT4G37260	AtMYB73/MYB73 (myb domain protein 73); DNA binding / transcription factor	2,0
252832_at	AT4G39910	ATUBP3 (UBIQUITIN-SPECIFIC PROTEASE 3); ubiquitin-specific protease	2,0
252831_at	AT4G39980	DHS1 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1); 3-deoxy-7-phosphoheptulonate synth	2,0
251138_at	AT5G01160	e-cadherin binding protein-related	2,0
251090_at	AT5G01340	mitochondrial substrate carrier family protein	2,0
250896_at	AT5G03560	nucleobase:cation symporter	2,0
245714_at	AT5G04280	glycine-rich RNA-binding protein	2,0
250833_at	AT5G04540	inositol or phosphatidylinositol phosphatase/ phosphoric monoester hydrolase	2,0
250803_at	AT5G04980	endonuclease/exonuclease/phosphatase family protein	2,5
245882_at	AT5G09470	mitochondrial substrate carrier family protein	2,0
250451_at	AT5G10270	CDKC;1 (CYCLIN-DEPENDENT KINASE C;1); kinase	2,0
250399_at	AT5G10750	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G24990.1); similar to Os10g0455900 [Oryza sativa (japonica cu	2,3
250449_at	AT5G10830	embryo-abundant protein-related	2,3
250335_at	AT5G11650	hydrolase, alpha/beta fold family protein	2,1
250357_at	AT5G11730	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25970.1); similar to expressed protein [Oryza sativa (japonica	2,3
245207_at	AT5G12310	zinc finger (C3HC4-type RING finger) family protein	2,0
250193_at	AT5G14540	proline-rich family protein	2,0
246584_at	AT5G14730	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G01513.1); similar to conserved hypothetical protein [Medicago	2,3
246511_at	AT5G15490	UDP-glucose 6-dehydrogenase, putative	2,0

250114_s_at	AT5G16370;A	[AT5G16370, AMP-binding protein, putative];[AT5G16340, AMP-binding protein, putative]	2,0
246453_at	AT5G16830	SYP21 (syntaxin 21); t-SNARE	2,5
246147_s_at	AT5G20000;A	[AT5G20000, RPT6A (regulatory particle triple-A 6A); ATPase];[AT5G19990, ATSUG1; ATPase]	2,0
246001_at	AT5G20790	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G43110.1); similar to conserved hypothetical protein [Medicag	2,1
245686_at	AT5G22060	ATJ2 (Arabidopsis thaliana DnaJ homologue 2)	2,3
249944_at	AT5G22290	ANAC089 (Arabidopsis NAC domain containing protein 89); transcription factor	2,0
249765_at	AT5G24030	C4-dicarboxylate transporter/malic acid transport family protein	2,1
249748_at	AT5G24620	thaumatin-like protein, putative	2,1
249752_at	AT5G24660	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G24655.1); similar to unknown protein [Brassica rapa subsp. pe	2,8
246961_at; 24696	AT5G24710	similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:AT5G38560.1); similar to Os01g0653800 [Oryza sativa	2,0
246607_at	AT5G35370	carbohydrate binding / kinase	2,3
249583_at	AT5G37770	TCH2 (TOUCH 2); calcium ion binding	2,0
249415_at	AT5G39660	CDF2 (CYCLING DOF FACTOR 2); DNA binding / protein binding / transcription factor	2,1
249123_at	AT5G43760	beta-ketoacyl-CoA synthase, putative	2,6
249072_at	AT5G44060	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G04000.1); similar to Os02g0621600 [Oryza sativa (japonica cu	2,5
248905_at	AT5G46250	RNA recognition motif (RRM)-containing protein	2,1
248865_at	AT5G46790	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17870.1); similar to Streptomyces cyclase/dehydrase family p	2,5
248826_at	AT5G47080	CKB1 (casein kinase II beta chain 1); protein kinase CK2 regulator	2,1
248774_at	AT5G47830	similar to hypothetical protein MtrDRAFT_AC150207g26v1 [Medicago truncatula] (GB:ABD32636.1)	3,0
248551_at	AT5G50200	WR3 (WOUND-RESPONSIVE 3); nitrate transporter	2,0
248434_at	AT5G51440	23.5 kDa mitochondrial small heat shock protein (HSP23.5-M)	3,7
248304_at	AT5G53180	polypyrimidine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative	2,0
248253_at	AT5G53290	CRF3 (CYTOKININ RESPONSE FACTOR 3); DNA binding / transcription factor	2,1
253890_s_at	AT5G54100;A	[AT5G54100, band 7 family protein];[AT4G27585, band 7 family protein]	2,0
248205_at	AT5G54300	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61260.1); similar to Protein of unknown function DUF761, pl	2,6
248100_at	AT5G55180	glycosyl hydrolase family 17 protein	2,3
247996_at	AT5G56170	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G20700.1); similar to GPI-anchored protein [Vigna radiata] (G	2,1
247964_at	AT5G56600	PFN3/PRF3 (PROFILIN 3); actin binding	2,0
247979_at	AT5G56750	Ndr family protein	2,1
247899_at	AT5G57345	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54520.1); similar to conserved hypothetical protein [Medicag	2,0
247874_at	AT5G57710	heat shock protein-related	2,3
247825_at	AT5G58470	zinc finger (Ran-binding) family protein	2,0
247795_at	AT5G58620	zinc finger (CCCH-type) family protein	2,0
247655_at	AT5G59820	RHL41 (RESPONSIVE TO HIGH LIGHT 41); nucleic acid binding / transcription factor/ zinc ion binding	5,3
247629_at;24763	AT5G60410	ATSIZ1/SIZ1; DNA binding / SUMO ligase	2,5
247393_at	AT5G63130	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	2,3

247305_at	AT5G63905	similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABA99036.2)	2,0
247328_at	AT5G64130	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69510.2); similar to Os01g0249300 [Oryza sativa (japonica cu	2,3
247325_at	AT5G64200	ATSC35 ("Arabidopsis thaliana arginine/serine-rich splicing factor 35, 35 kDa protein"); RNA binding	2,1
247282_at	AT5G64240	latex-abundant family protein (AMC3) / caspase family protein	2,5
247272_at	AT5G64300	ATGCH (Arabidopsis thaliana GTP cyclohydrolase II); 3,4-dihydroxy-2-butanone-4-phosphate synthase/ GTP cyclohydrolase	2,1
247177_at	AT5G65300	similar to Avr9/Cf-9 rapidly elicited protein 75 [Nicotiana tabacum] (GB:AAG43558.1)	2,6
247033_at	AT5G67250	SKIP2 (SKP1 INTERACTING PARTNER 2); ubiquitin-protein ligase	2,0
244994_at	ATCG01010	Chloroplast encoded NADH dehydrogenase unit.	2,6
244950_at	ATMG00160	cytochrome c oxidase subunit 2	2,0

Tabelle 7-83: Liste von Genen, deren Expression durch flg22- und HrpZ$_{Psph}$-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	**AGI**	**Beschreibung**	**flg22**	**HrpZ$_{Psph}$**
262455_at	AT1G11310	MLO2 (MILDEW RESISTANCE LOCUS O 2); calmodulin binding	4,6	2,6
261526_at	AT1G14370	APK2A (PROTEIN KINASE 2A); kinase	2,6	2,5
255967_at	AT1G22280	protein phosphatase 2C, putative / PP2C, putative	3,5	2,1
257401_at	AT1G23550	SRO2 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribosyltransferase	2,6	2,1
245662_at	AT1G28190	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12340.1); similar to expressed protein [Oryza sativa	2,6	2,0
262026_at	AT1G35670	ATCDPK2 (CALCIUM-DEPENDENT PROTEIN KINASE 2); calcium- and calmodulin-dependent protein kinase/	2,8	2,3
260126_at	AT1G36370	SHM7 (serine hydroxymethyltransferase 7); glycine hydroxymethyltransferase	2,6	2,1
259626_at	AT1G42990	ATBZIP60 (BASIC REGION/LEUCINE ZIPPER MOTIF 60); DNA binding / transcription factor	2,6	2,0
256185_at	AT1G51700	ADOF1 (Arabidopsis dof zinc finger protein 1); DNA binding / transcription factor	2,1	2,1
260975_at	AT1G53430	leucine-rich repeat family protein / protein kinase family protein	4,0	3,0
262933_at	AT1G65840	ATPAO4 (POLYAMINE OXIDASE 4); amine oxidase	2,6	2,5
264951_at	AT1G76970	VHS domain-containing protein / GAT domain-containing protein	3,5	2,6
261402_at	AT1G79670	RFO1 (RESISTANCE TO FUSARIUM OXYSPORUM 1); kinase	3,5	2,0
266428_at	AT2G07180	protein kinase, putative	2,8	2,0
263419_at	AT2G17220	protein kinase, putative	3,0	2,5
265583_at	AT2G20010	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25800.1); similar to unknown protein [Oryza sativa	2,6	2,0
266800_at	AT2G22880	VQ motif-containing protein	3,0	2,5
245041_at	AT2G26530	AR781	2,6	2,1
267470_at	AT2G30490	ATC4H (CINNAMATE-4-HYDROXYLASE)	2,3	2,3
245167_s_at	AT2G33120;A	[AT2G33120, SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1)];[AT2G33110, ATVAMP723 (Arabidopsis tha	2,6	2,1
267140_at	AT2G38250	DNA-binding protein-related	2,0	2,1
245119_at	AT2G41640	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57380.1); similar to glycosyltransferase [Medicago	2,3	2,0
266580_at	AT2G46260	BTB/POZ domain-containing protein	2,8	2,1
263776_s_at	AT2G46440;A	[AT2G46440, ATCNGC11 (cyclic nucleotide gated channel 11); calmodulin binding / cyclic nucleotide binding / io	3,5	2,3
258566_at	AT3G04110	GLR1 (GLUTAMATE RECEPTOR 1)	3,0	2,5
259133_at	AT3G05400	sugar transporter, putative	3,0	2,6
258852_at	AT3G06300	AT-P4H-2 (A. THALIANA P4H ISOFORM 2); oxidoreductase, acting on paired donors, with incorporation or redu	2,5	2,1
258682_at	AT3G08720	ATPK19/ATPK2 (ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 19, ARABIDOPSIS	3,2	2,6

256922_at	AT3G19010	oxidoreductase, 2OG-Fe(II) oxygenase family protein	3,0	2,1
256627_at	AT3G19970	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18245.1); similar to Os06g0730300 [Oryza sativa (j	2,6	2,0
258125_s_at; 257	AT3G23530;A	[AT3G23530, cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative];[AT3G23510, cyclopropane	2,6	2,5
252739_at	AT3G43250	cell cycle control protein-related	2,3	2,0
252474_at	AT3G46620	zinc finger (C3HC4-type RING finger) family protein	2,0	2,3
252058_at	AT3G52470	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein	2,6	2,5
251862_at	AT3G54850	armadillo/beta-catenin repeat family protein / U-box domain-containing family protein	3,2	2,3
251752_at	AT3G55740	ProT2 (PROLINE TRANSPORTER 2); amino acid permease	2,6	2,8
251684_at	AT3G56410	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G61670.1); similar to cell wall-anchored protein [Sta	3,2	2,5
251636_at	AT3G57530	CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE 32); calcium- and calmodulin-dependent protein kinase/ ki	3,0	2,3
251479_at	AT3G59700	ATHLECRK (ARABIDOPSIS THALIANA LECTIN-RECEPTOR KINASE); kinase	3,5	2,8
251379_at	AT3G60680	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45260.1); similar to expressed protein [Oryza sativa	3,5	2,0
255250_at	AT4G05100	AtMYB74 (myb domain protein 74); DNA binding / transcription factor	3,7	2,3
254905_at	AT4G11170	disease resistance protein (TIR-NBS-LRR class), putative	5,7	2,3
245251_at	AT4G17615	CBL1 (CALCINEURIN B-LIKE PROTEIN 1); calcium ion binding	3,5	2,0
254416_at	AT4G21380	ARK3 (Arabidopsis Receptor Kinase 3); kinase	2,8	2,1
254413_at	AT4G21440	ATM4/ATMYB102 (ARABIDOPSIS MYB-LIKE 102); DNA binding / transcription factor	3,5	2,8
254289_at	AT4G22980	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G51920.1); similar to Os03g0765800 [Oryza sativa (j	2,6	3,0
254103_at	AT4G25030	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45410.3); similar to Os07g0159500 [Oryza sativa (j	2,5	2,0
253522_at	AT4G31290	ChaC-like family protein	2,0	2,0
253401_at	AT4G32870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25770.2); similar to conserved hypothetical protein	2,0	2,0
245976_at	AT5G13080	WRKY75 (WRKY DNA-binding protein 75); transcription factor	3,2	2,0
246146_at	AT5G20050	protein kinase family protein	2,8	2,5
246071_at	AT5G20150	SPX (SYG1/Pho81/XPR1) domain-containing protein	2,0	2,0
246870_at	AT5G26030	ferrochelatase I	2,1	2,0
249050_at	AT5G44290	protein kinase family protein	2,5	2,1
248936_at	AT5G45710	AT-HSFA4C (Arabidopsis thaliana heat shock transcription factor A4C); DNA binding / transcription factor	3,0	2,3
248701_at	AT5G48410	ATGLR1.3 (Arabidopsis thaliana glutamate receptor 1.3)	3,7	2,6
248657_at	AT5G48570	peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative	2,5	2,5
248164_at	AT5G54490	PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding	4,0	3,0
248106_at	AT5G55100	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein	2,1	2,0
247913_at	AT5G57510	similar to Os08g0448100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001061936.1)	2,8	2,3
247790_at	AT5G58720	PRLI-interacting factor, putative	3,0	2,1
246989_at	AT5G67350	similar to hypothetical protein MtrDRAFT_AC144765g16v1 [Medicago truncatula] (GB:ABE87032.1)	2,5	2,3

Tabelle 7-84: Liste von Genen, deren Expression durch flg22- und NLP_{Pp}-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	**AGI**	**Beschreibung**	**flg22**	**NLP_{Pp}**
255923_at	AT1G22180	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	2,3	2,3
262254_at	AT1G53920	GLIP5 (GDSL-motif lipase 5); carboxylic ester hydrolase	2,8	2,0
256376_s_at	AT1G66690;A	[AT1G66690, S-adenosyl-L-methionine:carboxyl methyltransferase family protein];[AT1G66700, S-adenosyl-	2,5	2,1
255881_at	AT1G67070	DIN9 (DARK INDUCIBLE 9); mannose-6-phosphate isomerase	3,5	2,0
260015_at	AT1G67980	CCoAMT (caffeoyl-CoA 3-O-methyltransferase); caffeoyl-CoA O-methyltransferase	3,7	2,0
263075_at	AT2G17570	undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein	2,6	2,0
267411_at	AT2G34930	disease resistance family protein	2,6	2,0
266962_at	AT2G39440	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61280.1); similar to hypothetical protein MtrD	2,6	2,1
245089_at	AT2G45290	transketolase, putative	2,1	2,0
266326_at	AT2G46650	B5 #1 (cytochrome b5 family protein #1); heme binding / transition metal ion binding	2,6	2,0
252311_at	AT3G49370	calcium-dependent protein kinase, putative / CDPK, putative	2,3	2,0
255411_at	AT4G03110	RNA-binding protein, putative	2,8	2,1
254788_at	AT4G12790	ATP-binding family protein	2,1	2,0
245370_at	AT4G16840	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G61630.1)	2,3	2,1
250692_at	AT5G06560	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11850.2); similar to expressed protein [Oryza	3,5	2,0
	AT5G44810	?	2,3	2,1
248091_at	AT5G55120	similar to VTC2 (VITAMIN C DEFECTIVE 2) [Arabidopsis thaliana] (TAIR:AT4G26850.1); similar to unkn	3,2	2,1
247864_s_at	AT5G57890;A	[AT5G57890, anthranilate synthase beta subunit, putative];[AT1G25155, anthranilate synthase beta subunit, p	2,8	2,5

Zusätzliche Informationen zur Dissertation von Yvonne Gäbler, 2007

Tabelle 7-85: Liste von Genen, deren Expression durch flg22- und LPS-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.

Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	AGI	Beschreibung	flg22	LPS
259439_at	AT1G01480	ACS2 (1-Amino-cyclopropane-1-carboxylate synthase 2)	2,0	2,3
264467_at	AT1G10140	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G58420.1); similar to Os07g0123800 [Oryza sat	2,5	2,6
262762_at	AT1G10700	ribose-phosphate pyrophosphokinase 3 / phosphoribosyl diphosphate synthetase 3 (PRS3)	2,1	2,0
262845_at	AT1G14740	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G63500.2); similar to Potyvirus VPg interacting	2,3	2,6
261029_at	AT1G17330	metal-dependent phosphohydrolase HD domain-containing protein-related	2,3	2,1
259461_at	AT1G18900	pentatricopeptide (PPR) repeat-containing protein	2,1	2,1
259540_at	AT1G20640	RWP-RK domain-containing protein	2,0	2,0
257407_at	AT1G27100	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69890.1); similar to Cytosolic fatty-acid bindir	2,5	2,6
261501_at	AT1G28390	protein kinase family protein	4,0	2,5
261242_at	AT1G32960	subtilase family protein	2,0	2,6
	AT1G62420	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G12030.1); similar to hypothetical protein [Oryz	2,0	2,1
261973_at	AT1G64610	WD-40 repeat family protein	2,5	2,0
259825_at	AT1G66260	RNA and export factor-binding protein, putative	2,0	2,8
259859_at	AT1G68410	protein phosphatase 2C-related / PP2C-related	2,5	2,3
262678_at	AT1G75810	unknown protein	2,0	2,3
259879_at	AT1G76650	calcium-binding EF hand family protein	2,8	2,0
259734_at	AT1G77500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21740.1); similar to hypothetical protein [Oryz	2,3	2,5
263241_at	AT2G16500	ADC1 (ARGININE DECARBOXYLASE 1)	2,1	2,3
266685_at	AT2G19710	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G29440.1); similar to MAPK activating protein-	2,0	2,0
264005_at	AT2G22470	AGP2 (ARABINOGALACTAN-PROTEIN 2)	2,1	2,5
266316_at	AT2G27080	harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	2,1	2,1
265620_at	AT2G27310	F-box family protein	3,2	2,8
267202_s_at	AT2G31020;A	[AT2G31020, oxysterol-binding family protein];[AT2G31030, oxysterol-binding family protein]	2,1	2,6
263475_at	AT2G31945	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05575.1); similar to hypothetical protein [Oryz	2,6	2,8
265796_at	AT2G35730	heavy-metal-associated domain-containing protein	3,0	2,3
267034_at	AT2G38310	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G05440.1); similar to hypothetical protein [Nico	2,0	2,3
267026_at	AT2G38340	AP2 domain-containing transcription factor, putative (DRE2B)	2,0	2,3
267357_at	AT2G40000	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55840.1); similar to putative Hs1pro-1-like rec	2,1	2,8
259309_at	AT3G05050	protein kinase family protein	2,0	2,0

258896_at	AT3G05710	SYP43 (syntaxin 43); t-SNARE	2,0	2,0
258683_at	AT3G08760	ATSIK; kinase	2,5	3,2
259216_at	AT3G09000	proline-rich family protein	2,3	2,5
256443_at	AT3G10960	xanthine/uracil permease family protein	2,1	3,0
257235_at	AT3G15060	AtRABA1g (Arabidopsis Rab GTPase homolog A1g); GTP binding	2,1	2,8
257887_at	AT3G17090	protein phosphatase 2C family protein / PP2C family protein	2,5	2,0
	AT3G18920	unknown protein	2,5	2,0
258132_at	AT3G24550	ATPERK1 (PROLINE EXTENSIN-LIKE RECEPTOR KINASE 1); ATP binding / protein kinase	2,5	2,3
252422_at	AT3G47550	zinc finger (C3HC4-type RING finger) family protein	2,3	2,8
252131_at	AT3G50930	AAA-type ATPase family protein	2,1	2,6
252121_at	AT3G51160	MUR1 (MURUS 1)	2,1	2,0
251922_at	AT3G54030	protein kinase family protein	2,1	3,5
251804_at	AT3G55430	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative	2,1	2,8
251683_at	AT3G57120	protein kinase family protein	2,3	2,5
255280_at	AT4G04960	lectin protein kinase, putative	2,1	2,5
254843_at	AT4G11860	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22960.1); similar to hypothetical protein LOC	2,1	2,5
254331_s_at	AT4G22710;A	[AT4G22710, CYP706A2 (cytochrome P450, family 706, subfamily A, polypeptide 2); oxygen binding];[AT4	2,3	2,3
254040_at	AT4G25900	aldose 1-epimerase family protein	2,3	2,1
253915_at	AT4G27280	calcium-binding EF hand family protein	2,0	3,7
253919_at	AT4G27350	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G54240.1); similar to membrane lipoprotein lipi	2,1	2,3
253814_at	AT4G28290	unknown protein	2,5	2,3
253796_at	AT4G28460	unknown protein	4,0	2,0
253696_at	AT4G29740	CKX4 (CYTOKININ OXIDASE 4); cytokinin dehydrogenase	2,6	2,8
253534_at	AT4G31500	CYP83B1 (CYTOCHROME P450 MONOOXYGENASE 83B1); oxygen binding	2,0	2,0
253455_at	AT4G32020	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25250.1); similar to Os02g0797600 [Oryza sat	2,1	2,6
253124_at	AT4G36030	armadillo/beta-catenin repeat family protein	2,0	2,5
252940_at	AT4G39270	leucine-rich repeat transmembrane protein kinase, putative	2,3	2,5
250944_at	AT5G03380	heavy-metal-associated domain-containing protein	2,0	2,1
250809_at	AT5G05140	transcription elongation factor-related	2,3	2,1
250676_at	AT5G06320	NHL3 (NDR1/HIN1-like 3)	2,5	3,7
250398_at	AT5G11000	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25200.1); similar to Os08g0439600 [Oryza sat	2,6	2,0
245981_at	AT5G13100	similar to Os01g0102500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001041749.1); contains domain no	2,1	2,5
249942_at	AT5G22300	NIT4 (NITRILASE 4)	2,3	2,6
246653_at	AT5G35200	epsin N-terminal homology (ENTH) domain-containing protein	2,5	2,3
	AT5G39780	putative protein	2,0	2,3
248689_at	AT5G48150	PAT1 (PHYTOCHROME A SIGNAL TRANSDUCTION 1); transcription factor	2,3	2,0

248392_at	AT5G52050	MATE efflux protein-related	2,5	4,0
248393_at	AT5G52060	ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); protein binding	2,6	2,1
247811_at	AT5G58430	ATEXO70B1 (exocyst subunit EXO70 family protein B1); protein binding	2,5	2,6
247708_at	AT5G59550	zinc finger (C3HC4-type RING finger) family protein	2,1	3,0
247693_at	AT5G59730	ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding	2,6	3,2
247500_at	AT5G61910	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32910.1); similar to expressed protein [Oryza s	2,0	2,0
247125_at	AT5G66070	zinc finger (C3HC4-type RING finger) family protein	2,0	2,6
247132_at	AT5G66200	armadillo/beta-catenin repeat family protein	2,5	2,0

Tabelle 7-86: Liste von Genen, deren Expression durch HrpZ$_{Psph}$- und NLP$_{Pp}$-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	AGI	Beschreibung	HrpZ$_{Psph}$	NLP$_{Pp}$
247293_at	AT5G64510	similar to ORF; able to induce HR-like lesions [Nicotiana tabacum] (GB:AAC49976.1); similar to Os01g0767600 [Oryza	2,1	2,0

Tabelle 7-87: Liste von Genen, deren Expression durch HrpZ$_{Psph}$- und LPS-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	AGI	Beschreibung	HrpZ$_{Psph}$	LPS
255884_at	AT1G20310	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76070.1); similar to syringolide-induced protein	2,6	3,7
261637_at	AT1G49950	ATTRB1/TRB1 (TELOMERE REPEAT BINDING FACTOR 1); DNA binding / transcription factor	2,0	2,1
260248_at	AT1G74310	ATHSP101 (HEAT SHOCK PROTEIN 101); ATP binding / ATPase	2,5	2,6
265499_at	AT2G15480	UGT73B5 (UDP-glucosyl transferase 73B5); UDP-glycosyltransferase/ transferase, transferring glycosyl groups	2,1	3,0
266775_at	AT2G29060	scarecrow transcription factor family protein	2,0	2,5
263931_at	AT2G36220	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G52710.1); similar to Os11g0153300 [Oryza sativ	2,0	4,9
266184_s_at	AT2G38940;A	[AT2G38940, ATPT2 (PHOSPHATE TRANSPORTER 2); carbohydrate transporter/ phosphate transporter/ sug	2,0	2,3
267008_at	AT2G39350	ABC transporter family protein	2,1	3,0
267624_at	AT2G39660	BIK1 (BOTRYTIS-INDUCED KINASE1); kinase	2,0	2,6
266368_at	AT2G41380	embryo-abundant protein-related	2,0	2,8
266590_at	AT2G46240	ATBAG6/BAG6 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 6); calmodulin bindin	2,6	3,0
252042_at	AT3G51990	protein kinase family protein	2,3	2,0
251584_at	AT3G58620	TTL4 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 4); binding	2,5	2,0
254447_at	AT4G20860	FAD-binding domain-containing protein	2,1	2,8
254159_at	AT4G24240	WRKY7 (WRKY DNA-binding protein 7); transcription factor	2,8	2,3
253316_s_at	AT4G33930;A	[AT4G33930, glycine-rich protein];[AT4G34300, glycine-rich protein]	2,0	3,5
250351_at	AT5G12030	AT-HSP17.6A (Arabidopsis thaliana heat shock protein 17.6A)	2,3	5,7
250279_at	AT5G13200	GRAM domain-containing protein / ABA-responsive protein-related	2,0	2,8
247933_at	AT5G56980	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G26130.1); similar to cDNA-5-encoded protein (	2,0	2,8

Tabelle 7-88: Liste von Genen, deren Expression durch flg22-, HrpZ$_{Psph}$- und NLP$_{Pp}$-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	**AGI**	**Beschreibung**	**flg22**	**HrpZ$_{Psph}$**	**NLP$_{Pp}$**
259428_at	AT1G01560	ATMPK11 (Arabidopsis thaliana MAP kinase 11); MAP kinase/ kinase	8,0	2,6	2,6
264351_at	AT1G03370	C2 domain-containing protein / GRAM domain-containing protein	4,0	2,3	2,3
262457_at	AT1G11200	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G21570.1); similar to unknown [Medicago	4,0	2,1	2,1
259512_at	AT1G12360	KEU (KEULE); protein transporter	3,2	2,1	2,0
246327_at	AT1G16670	protein kinase family protein	4,0	2,0	2,6
261378_at	AT1G18890	ATCDPK1; calcium- and calmodulin-dependent protein kinase/ kinase/ protein kinase	3,7	2,8	2,3
264774_at	AT1G22890	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G44568.1); contains domain FAMILY NOT	3,5	3,2	2,8
255740_at	AT1G25390	protein kinase family protein	5,3	3,2	2,5
262408_at	AT1G34750	protein phosphatase 2C, putative / PP2C, putative	4,0	3,0	2,5
246631_at	AT1G50740	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G20510.1); similar to hypothetical protein 1	11,3	4,9	5,3
246368_at	AT1G51890	leucine-rich repeat protein kinase, putative	9,2	5,7	3,7
260153_at	AT1G52760	esterase/lipase/thioesterase family protein	2,6	2,6	3,2
246405_at	AT1G57630	disease resistance protein (TIR class), putative	2,6	2,3	2,0
264923_s_at	AT1G60740;A	[AT1G60740, peroxiredoxin type 2, putative];[AT1G65970, TPX2 (THIOREDOXIN-DEPENDENT PER	3,7	2,5	2,1
264883_s_at	AT1G61250;A	[AT1G61250, SC3 (SECRETORY CARRIER 3); carrier];[AT1G11180, secretory carrier membrane prote	2,8	2,1	2,0
264757_at	AT1G61360	S-locus lectin protein kinase family protein	9,2	4,6	4,0
264636_at	AT1G65490	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65500.1)	4,0	3,7	2,1
255880_at	AT1G67060	similar to Os02g0221600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046323.1); similar to hypo	4,9	2,0	2,3
245200_at	AT1G67850	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13000.2); similar to Protein of unknown f	2,8	2,6	2,0
260005_at	AT1G67920	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G24600.1)	3,2	2,6	2,1
260405_at	AT1G69930	ATGSTU11 (Arabidopsis thaliana Glutathione S-transferase (class tau) 11); glutathione transferase	4,3	2,3	2,1
261506_at	AT1G71697	ATCK1 (CHOLINE KINASE)	4,3	2,6	2,3
261754_at	AT1G76130	AMY2/ATAMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase	3,5	2,1	2,5
266231_at	AT2G02220	ATPSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine	7,0	4,6	2,1
266071_at	AT2G18680	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18690.1); similar to Os08g0107100 [Oryz	4,3	2,3	2,0
266017_at	AT2G18690	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18680.1); similar to Os08g0107100 [Oryz	4,3	3,7	3,0
265306_at	AT2G20320	DENN (AEX-3) domain-containing protein	4,0	2,8	2,3
267289_at	AT2G23770	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	7,5	3,7	3,2

266615_s_at	AT2G29720;A	[AT2G29720, CTF2B; monooxygenase];[AT2G35660, CTF2A; monooxygenase]	6,5	2,5	2,3
267547_at	AT2G32670	ATVAMP725 (Arabidopsis thaliana vesicle-associated membrane protein 725)	2,8	2,1	2,5
266101_at	AT2G37940	similar to phosphatidic acid phosphatase-related / PAP2-related [Arabidopsis thaliana] (TAIR:AT3G5402(	6,5	4,0	3,7
266977_at	AT2G39420	esterase/lipase/thioesterase family protein	6,5	4,6	4,0
259134_at	AT3G05390	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G01240.1); similar to Os06g0474300 [Oryz	5,3	2,3	2,3
259230_at	AT3G07780	protein binding / zinc ion binding	2,1	2,0	2,0
259224_at	AT3G07800	thymidine kinase, putative	4,0	2,3	2,5
258665_at	AT3G08710	ATH9 (thioredoxin H-type 9); thiol-disulfide exchange intermediate	4,9	2,5	2,5
258650_at	AT3G09830	protein kinase, putative	3,7	2,3	2,3
258203_at	AT3G13950	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G13266.1); similar to conserved hypothetica	3,7	3,7	2,0
258364_at	AT3G14225	GLIP4 (EMBRYO DEFECTIVE 1474); carboxylic ester hydrolase	9,8	2,6	3,5
257088_at	AT3G20510	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50740.1); similar to hypothetical protein 1	2,8	2,1	2,3
258173_at	AT3G21630	protein kinase family protein	4,0	2,6	2,3
256616_at	AT3G22260	OTU-like cysteine protease family protein	4,6	3,0	2,1
256933_at	AT3G22600	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	5,3	2,5	2,8
252234_at	AT3G49780	ATPSK4 (PHYTOSULFOKINE 4 PRECURSOR); growth factor	2,3	2,0	2,0
252170_at	AT3G50480	HR4 (HOMOLOG OF RPW8 4)	2,1	2,0	2,1
251884_at	AT3G54150	embryo-abundant protein-related	5,3	3,2	2,8
251790_at	AT3G55470	C2 domain-containing protein	8,0	3,7	3,7
251634_at	AT3G57480	zinc finger (C2H2 type, AN1-like) family protein	4,0	2,8	2,5
251643_at	AT3G57550	AGK2 (GUANYLATE KINASE-ENCODING GENE 1)	8,6	4,6	3,0
251494_at	AT3G59350	serine/threonine protein kinase, putative	2,3	2,0	2,0
255511_at	AT4G02075	PIT1 (PITCHOUN 1); protein binding / zinc ion binding	4,3	2,1	2,5
255284_at	AT4G04610	APR1 (PAPS REDUCTASE HOMOLOG 19)	3,0	2,5	2,0
254924_at	AT4G11330	ATMPK5 (MAP KINASE 5); MAP kinase/ kinase	4,9	2,5	3,0
254857_at	AT4G12120	SEC1B; protein transporter	4,3	3,0	2,6
254784_at	AT4G12720	AtNUDT7 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 7); hydrolase	3,0	2,5	3,0
245533_at	AT4G15130	cholinephosphate cytidylyltransferase, putative / phosphorylcholine transferase, putative / CTP:phosphoch	4,6	2,3	2,5
254592_at	AT4G18880	AT-HSFA4A (Arabidopsis thaliana heat shock transcription factor A4A); DNA binding / transcription fac	3,0	2,5	2,0
254487_at	AT4G20780	calcium-binding protein, putative	6,1	2,5	2,6
254410_at	AT4G21410	protein kinase family protein	4,3	3,2	2,1
254321_at	AT4G22590	trehalose-6-phosphate phosphatase, putative	3,5	2,8	2,6
253827_at	AT4G28085	unknown protein	13,0	2,0	2,8
253780_at	AT4G28400	protein phosphatase 2C, putative / PP2C, putative	2,3	2,1	2,3
253664_at	AT4G30210	ATR2 (ARABIDOPSIS P450 REDUCTASE 2)	4,6	2,8	2,5
253321_at	AT4G33910	oxidoreductase, 2OG-Fe(II) oxygenase family protein	2,6	2,0	2,1

253257_at	AT4G34390	XLG2 (extra-large GTP-binding protein 2); signal transducer	4,6	3,0	2,1
253173_at	AT4G35110	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G16900.1); similar to pEARLI 4 gene produ	4,6	2,3	3,0
253063_at	AT4G37640	ACA2 (CALCIUM ATPASE 2); calmodulin binding	5,7	3,2	2,8
245181_at	AT5G12420	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16350.1); similar to Protein of unknown f	4,9	2,6	2,3
250323_at	AT5G12880	proline-rich family protein	4,6	2,6	2,0
246529_at	AT5G15730	serine/threonine protein kinase, putative	3,2	2,1	2,5
250018_at	AT5G18150	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G58375.1); similar to hypothetical protein	7,5	2,6	2,6
249835_s_at	AT5G23490;A	[AT5G23490, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G08440.1); similar to Os05g	3,7	2,1	2,1
249780_at	AT5G24240	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	3,5	2,8	2,3
246943_at	AT5G25440	protein kinase family protein	2,8	3,2	2,0
249372_at	AT5G40760	G6PD6 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 6); glucose-6-phosphate 1-dehydrogenase	2,0	2,0	2,0
248934_at	AT5G46080	protein kinase family protein	7,0	4,0	2,6
248698_at	AT5G48380	leucine-rich repeat family protein / protein kinase family protein	4,0	3,2	2,5
248129_at	AT5G54780	RAB GTPase activator	3,7	2,0	2,5
248118_at	AT5G55050	GDSL-motif lipase/hydrolase family protein	2,5	2,6	2,0
248060_at	AT5G55560	protein kinase family protein	3,5	2,0	2,3
247912_at	AT5G57480	AAA-type ATPase family protein	3,0	2,5	2,1
247925_at	AT5G57560	TCH4 (TOUCH 4); hydrolase, acting on glycosyl bonds	5,3	3,0	2,0
247571_at	AT5G61210	SNAP33 (synaptosomal-associated protein 33); t-SNARE	5,3	3,0	3,5

Tabelle 7-89: Liste von Genen, deren Expression durch flg22-, HrpZ$_{Psph}$- und LPS-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	**AGI**	**Beschreibung**	**flg22**	**HrpZ$_{Psph}$**	**LPS**
264178_at	AT1G02170	LOL3 (LSD ONE LIKE 3); caspase/ cysteine-type endopeptidase	2,3	2,1	2,0
259445_at	AT1G02400	ATGA2OX6/DTA1 (GIBBERELLIN 2-OXIDASE 6); gibberellin 2-beta-dioxygenase	5,7	4,3	4,9
260904_at	AT1G02450	NIMIN-1/NIMIN1; protein binding	3,2	3,7	3,7
264841_at	AT1G03740	protein kinase family protein	3,0	2,0	2,6
262630_at	AT1G06520	ATGPAT1/GPAT1 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 1); 1-acylglycerol-3-	3,2	3,2	2,6
	AT1G07135	glycine-rich protein; similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:AT3G04640.2);	2,6	2,5	3,7
261525_at	AT1G14330	kelch repeat-containing F-box family protein	2,8	2,0	3,2
262571_at	AT1G15430	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80220.1); similar to Os01g06126	2,5	2,3	3,0
261763_at	AT1G15520	ATPDR12/PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembra	2,8	2,0	3,2
261429_at	AT1G18860	WRKY61 (WRKY DNA-binding protein 61); transcription factor	2,8	3,0	2,6
262801_at	AT1G21010	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76600.1); similar to TMV respons	2,3	2,1	2,6
261933_at	AT1G22410	2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phos	2,3	2,0	2,0
264773_at	AT1G22900	similar to disease resistance-responsive family protein [Arabidopsis thaliana] (TAIR:AT5G42500.	2,0	2,0	2,8
265184_at	AT1G23710	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G70420.1); similar to Os01g06396	4,0	2,6	3,2
255733_at	AT1G25400	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68440.1); similar to IMP dehydro	2,5	2,1	3,5
261648_at	AT1G27730	STZ (SALT TOLERANCE ZINC FINGER); nucleic acid binding / transcription factor/ zinc ion b	2,3	2,3	3,5
263221_at	AT1G30620	MUR4 (MURUS 4); catalytic	3,0	2,3	3,2
245794_at	AT1G32170	XTR4 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 4); hydrolase, acting on glycosyl bonds	3,7	2,6	4,9
261193_at	AT1G32920	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G32928.1)	2,1	2,0	3,0
245757_at	AT1G35140	PHI-1 (PHOSPHATE-INDUCED 1)	4,9	2,3	6,5
256169_at	AT1G51800	leucine-rich repeat protein kinase, putative	4,3	4,3	2,3
262901_at	AT1G59910	formin homology 2 domain-containing protein / FH2 domain-containing protein	5,7	3,5	5,3
264746_at	AT1G62300	WRKY6 (WRKY DNA-binding protein 6); transcription factor	2,5	2,1	2,5
256356_s_at	AT1G66500;A	[AT1G66500, zinc finger (C2H2-type) family protein];[AT5G43620, S-locus protein-related]	2,3	2,3	3,2
264717_at	AT1G70140	ATFH8 (FORMIN 8); actin binding / actin filament binding / profilin binding	3,7	2,8	3,2
260303_at	AT1G70520	protein kinase family protein	3,0	2,5	2,1
260362_at	AT1G70530	protein kinase family protein	4,3	2,5	2,0
260239_at	AT1G74360	leucine-rich repeat transmembrane protein kinase, putative	4,6	3,7	2,5

261748_at	AT1G76070	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G20310.1); similar to syringolide-in	2,6	2,1	3,0
260276_at	AT1G80450	VQ motif-containing protein	3,0	4,0	4,3
261892_at	AT1G80840	WRKY40 (WRKY DNA-binding protein 40); transcription factor	4,0	2,8	3,2
265737_at	AT2G01180	ATPAP1 (PHOSPHATIDIC ACID PHOSPHATASE 1); phosphatidate phosphatase	4,3	2,8	4,3
263565_at	AT2G15390	FUT4 (fucosyltransferase 4); fucosyltransferase/ transferase, transferring glycosyl groups	4,9	3,2	2,5
266536_at	AT2G16900	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35110.3); similar to pEARLI 4 ge	3,5	2,8	4,0
267490_at	AT2G19130	S-locus lectin protein kinase family protein	4,3	2,8	2,5
245051_at	AT2G23320	WRKY15 (WRKY DNA-binding protein 15); transcription factor	2,5	2,0	2,3
266000_at	AT2G24180	CYP71B6 (CYTOCHROME P450 71B6); oxygen binding	2,6	2,0	2,3
257377_at	AT2G28890	PLL4 (POLTERGEIST LIKE 4); protein phosphatase type 2C	2,8	3,5	2,8
266294_at	AT2G29500	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	2,0	2,3	3,5
266834_s_at	AT2G30020;A	[AT2G30020, protein phosphatase 2C, putative / PP2C, putative];[AT3G27140, protein phosphata	4,0	3,0	4,0
255844_at	AT2G33580	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	2,5	2,0	2,1
266995_at	AT2G34500	CYP710A1 (cytochrome P450, family 710, subfamily A, polypeptide 1); C-22 sterol desaturase/ o	3,7	3,5	4,6
267055_at	AT2G38360	prenylated rab acceptor (PRA1) family protein	3,2	2,5	3,0
267028_at	AT2G38470	WRKY33 (WRKY DNA-binding protein 33); transcription factor	4,3	3,2	3,5
266992_at	AT2G39200	MLO12 (MILDEW RESISTANCE LOCUS O 12); calmodulin binding	7,0	6,5	7,0
266993_at	AT2G39210	nodulin family protein	3,0	3,2	3,7
267623_at	AT2G39650	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07350.1); similar to unknown prot	2,6	2,6	3,7
263379_at	AT2G40140	CZF1/ZFAR1; transcription factor	3,7	2,5	3,5
265852_at	AT2G42350	zinc finger (C3HC4-type RING finger) family protein	2,5	2,0	4,0
265853_at	AT2G42360	zinc finger (C3HC4-type RING finger) family protein	4,3	4,3	6,1
267392_at	AT2G44490	PEN2 (PENETRATION 2); hydrolase, hydrolyzing O-glycosyl compounds	3,0	2,6	3,0
266552_at	AT2G46330	AGP16 (ARABINOGALACTAN PROTEIN 16)	3,7	3,0	4,3
260581_at	AT2G47190	MYB2 (myb domain protein 2); DNA binding / transcription factor	2,3	2,1	2,6
259178_at	AT3G01650	copine-related	2,3	2,0	2,1
258616_at	AT3G02880	leucine-rich repeat transmembrane protein kinase, putative	3,0	2,6	3,0
258516_at	AT3G06490	MYB108 (BOTRYTIS-SUSCEPTIBLE1, myb domain protein 108); DNA binding / transcription	2,6	2,5	3,7
259213_at	AT3G09010	protein kinase family protein	3,0	2,0	3,5
256442_at	AT3G10930	unknown protein	2,0	2,5	4,6
256664_at	AT3G12040	DNA-3-methyladenine glycosylase (MAG)	3,0	2,1	2,6
256763_at	AT3G16860	phytochelatin synthetase-related	4,3	2,5	3,2
258415_at	AT3G17390	MTO3 (S-adenosylmethionine synthase 3); methionine adenosyltransferase	2,0	2,1	2,3
258463_at	AT3G17410	serine/threonine protein kinase, putative	3,5	2,1	2,6
257061_at	AT3G18250	unknown protein	2,6	2,5	3,2
257751_at	AT3G18690	MKS1 (MAP KINASE SUBSTRATE 1)	3,0	2,3	3,5

257621_at	AT3G20410	CPK9 (CALMODULIN-DOMAIN PROTEIN KINASE 9); calcium- and calmodulin-dependent p	2,5	2,1	2,8
257950_at	AT3G21780	UGT71B6 (UDP-glucosyl transferase 71B6); UDP-glycosyltransferase/ abscisic acid glucosyltrans	3,2	2,8	3,7
257925_at	AT3G23170	similar to ATBET12 [Arabidopsis thaliana] (TAIR:AT4G14450.1)	2,8	2,5	4,3
257619_at	AT3G24810	ICK3 (kip-related protein 5); cyclin-dependent protein kinase inhibitor	2,6	2,5	2,8
257840_at	AT3G25250	AGC2-1 (OXIDATIVE SIGNAL-INDUCIBLE1); kinase	2,0	2,1	3,5
256755_at	AT3G25600	calmodulin, putative	3,5	2,8	5,3
256756_at	AT3G25610	haloacid dehalogenase-like hydrolase family protein	4,9	3,2	6,5
258084_at	AT3G26020	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative	2,8	2,3	2,6
258282_at	AT3G26910	hydroxyproline-rich glycoprotein family protein	5,7	3,0	4,6
256735_at	AT3G29400	ATEXO70E1 (exocyst subunit EXO70 family protein E1); protein binding	3,5	2,3	2,8
252652_at	AT3G44720	prephenate dehydratase family protein	4,0	2,0	3,2
252511_at	AT3G46280	protein kinase-related	7,5	8,6	7,0
252470_at	AT3G46930	protein kinase family protein	2,5	2,0	3,0
252331_s_at	AT3G48790;A	[AT3G48780, serine C-palmitoyltransferase, putative];[AT3G48790, serine C-palmitoyltransferas	2,1	2,0	2,5
252334_at	AT3G48850	mitochondrial phosphate transporter, putative	2,6	2,0	2,3
252310_at	AT3G49350	RAB GTPase activator	3,5	2,3	2,6
252269_at	AT3G49580	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49570.1); similar to unknown prot	2,3	2,1	3,5
251895_at	AT3G54420	ATEP3 (Arabidopsis thaliana chitinase class IV); chitinase	2,3	2,6	2,8
251861_at	AT3G54810	BME3/BME3-ZF (BLUE MICROPLYLAR END3); transcription factor	3,5	2,3	3,7
251789_at	AT3G55450	protein kinase, putative	3,0	2,3	2,8
251797_at	AT3G55560	DNA-binding protein-related	3,0	2,1	3,2
251745_at	AT3G55980	zinc finger (CCCH-type) family protein	4,0	3,5	6,5
251640_at	AT3G57450	similar to Hypothetical protein [Oryza sativa] (GB:AAM08779.1); similar to Os07g0185900 [Oryz	4,0	2,6	4,3
255716_at	AT4G00330	CRCK2 (calmodulin-binding receptor-like cytoplasmic kinase 2); kinase	2,5	2,0	2,0
255647_at	AT4G00900	ECA2 ("calcium-transporting ATPase 2, endoplasmic reticulum-type"); calcium-transporting ATP	2,3	2,0	2,0
255568_at	AT4G01250	WRKY22 (WRKY DNA-binding protein 22); transcription factor	10,6	9,2	10,6
255502_at	AT4G02410	lectin protein kinase family protein	2,3	2,3	3,2
254926_at	AT4G11280	ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6)	2,6	2,1	4,0
254861_at	AT4G12040	zinc finger (AN1-like) family protein	2,8	2,0	3,5
254723_at	AT4G13510;A	[AT4G13510, AMT1;1 (AMMONIUM TRANSPORT 1); ammonium transporter]	3,5	2,6	3,2
254652_at	AT4G18170	WRKY28 (WRKY DNA-binding protein 28); transcription factor	3,2	2,3	2,3
254432_at	AT4G20830	FAD-binding domain-containing protein	2,0	2,0	2,5
254347_at	AT4G22070	WRKY31 (WRKY DNA-binding protein 31); transcription factor	2,3	2,3	3,7
254243_at	AT4G23210	protein kinase family protein	4,3	2,3	2,3
254215_at	AT4G23700	ATCHX17 (CATION/H+ EXCHANGER 17); monovalent cation:proton antiporter	3,7	3,0	4,6
254120_at	AT4G24570	mitochondrial substrate carrier family protein	7,0	3,7	11,3

253643_at	AT4G29780	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to Os01g05826	3,2	2,5	3,7
253578_at	AT4G30340	ATDGK7 (DIACYLGLYCEROL KINASE 7); diacylglycerol kinase	2,8	2,6	3,2
253614_at	AT4G30350	heat shock protein-related	3,0	2,6	3,2
253414_at	AT4G33050	EDA39 (embryo sac development arrest 39); calmodulin binding	4,3	2,6	2,8
253416_at	AT4G33070	pyruvate decarboxylase, putative	2,0	2,0	3,0
253338_at	AT4G33430	BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); kinase	3,0	2,5	2,5
253323_at	AT4G33920	protein phosphatase 2C family protein / PP2C family protein	4,3	3,0	4,0
253284_at	AT4G34150	C2 domain-containing protein	3,5	3,2	3,0
253140_at	AT4G35480	RHA3B (RING-H2 finger A3B); protein binding / zinc ion binding	2,3	2,5	3,0
246214_at	AT4G36990	HSF4 (HEAT SHOCK FACTOR 4); DNA binding / transcription factor	2,3	2,0	2,8
253046_at	AT4G37370	CYP81D8 (cytochrome P450, family 81, subfamily D, polypeptide 8); oxygen binding	2,8	2,5	3,2
252908_at	AT4G39670	similar to ACD11 (ACCELERATED CELL DEATH 11) [Arabidopsis thaliana] (TAIR:AT2G346	4,9	3,7	7,0
251054_at	AT5G01540	lectin protein kinase, putative	5,3	4,3	5,3
251073_at	AT5G01750	Identical to Protein At5g01750 [Arabidopsis Thaliana] (GB:Q9LZX1;GB:Q8LEK9); similar to un	2,1	2,0	2,0
250994_at	AT5G02490	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)	2,5	2,5	2,6
250909_at	AT5G03700	PAN domain-containing protein	3,2	2,6	2,5
246018_at	AT5G10695	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G57123.1); similar to conserved hy	2,3	2,0	3,2
250339_at	AT5G11670	ATNADP-ME2 (NADP-MALIC ENZYME 2); malate dehydrogenase (oxaloacetate-decarboxylati	2,6	2,0	2,0
250296_at	AT5G12020	17.6 kDa class II heat shock protein (HSP17.6-CII)	2,1	3,0	6,5
246597_at	AT5G14760	AO (L-ASPARTATE OXIDASE); L-aspartate oxidase	3,2	2,5	2,1
249984_at	AT5G18400	similar to Protein of unknown function DUF689 [Medicago truncatula] (GB:ABE78163.1); contai	3,0	2,3	3,0
246099_at	AT5G20230	ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding	2,1	2,3	2,6
249928_at	AT5G22250	CCR4-NOT transcription complex protein, putative	3,7	2,5	5,7
249719_at	AT5G35735	auxin-responsive family protein	2,3	2,0	2,3
249339_at	AT5G41100	DNA binding	5,3	2,8	3,5
249252_at	AT5G42010	WD-40 repeat family protein	3,2	2,0	2,8
248868_at	AT5G46780	VQ motif-containing protein	3,5	2,1	3,2
248799_at	AT5G47230	ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcrip	4,3	2,1	4,3
248686_at	AT5G48540	33 kDa secretory protein-related	4,3	3,2	2,8
248611_at	AT5G49520	WRKY48 (WRKY DNA-binding protein 48); transcription factor	3,0	2,3	3,0
248298_at	AT5G53110	similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:AT	2,5	2,3	2,6
248176_at	AT5G54650	Fh5 (FORMIN HOMOLOGY5); actin binding	2,8	2,5	2,5
247611_at	AT5G60710	zinc finger (C3HC4-type RING finger) family protein	3,2	2,3	3,7
247532_at	AT5G61560	protein kinase family protein	2,5	2,1	3,2
247493_at	AT5G61900	BON1 (BONZAI1); calcium-dependent phospholipid binding	2,8	2,5	2,5
247322_at	AT5G64090	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G21050.1); similar to Os11g01696	2,5	2,0	2,6

247327_at	AT5G64120	peroxidase, putative	3,2	3,7	4,3
247279_at	AT5G64310	AGP1 (ARABINOGALACTAN-PROTEIN 1)	3,0	2,6	4,0
247239_at	AT5G64640	pectinesterase family protein	2,8	2,5	3,2
247086_at	AT5G66320	zinc finger (GATA type) family protein	2,5	2,1	3,2

Tabelle 7-90: Liste von Genen, deren Expression durch flg22-, NLP$_{Pp}$- und LPS-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird. *Microarray* -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	**AGI**	**Beschreibung**	**flg22**	**NLP$_{Pp}$**	**LPS**
256044_at	AT1G07160	protein phosphatase 2C, putative / PP2C, putative	21,1	4,0	16,0
261020_at	AT1G26390	FAD-binding domain-containing protein	2,8	2,3	2,5
260255_at	AT1G74330	ATP binding / protein kinase	4,3	2,0	3,2
260051_at	AT1G78210	hydrolase, alpha/beta fold family protein	3,2	2,5	3,2
265424_at	AT2G20780	mannitol transporter, putative	2,8	2,1	2,3
267567_at	AT2G30770	CYP71A13 (cytochrome P450, family 71, subfamily A, polypeptide 13); oxygen binding	2,1	2,3	2,1
267209_at	AT2G30930	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G06540.1)	2,1	2,0	2,0
250493_at	AT5G09800	U-box domain-containing protein	6,5	2,6	5,3

Tabelle 7-91: Liste von Genen, deren Expression durch flg22-, HrpZ$_{Psph}$-, NLP$_{Pp}$- und LPS-Behandlung nach 1 h in *A. thaliana* -Protoplasten induziert wird.
Microarray -Analyse mit unveröffentlichten Daten aus Jen Sheen's Labor.

Datensatz ID	**AGI**	**Beschreibung**	**flg22**	**HrpZ$_{Psph}$**	**NLP$_{Pp}$**	**LPS**
261027_at	AT1G01340	ATCNGC10 (CYCLIC NUCLEOTIDE GATED CHANNEL 10); calmodulin binding / cyclic nu	4,3	2,8	2,1	3,5
264580_at	AT1G05340	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32210.1); similar to conserved h	3,2	2,5	2,0	3,2
263182_at	AT1G05575	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G31945.1); similar to hypothetica	6,1	4,6	2,5	4,6
256050_at	AT1G07000	ATEXO70B2 (exocyst subunit EXO70 family protein B2); protein binding	6,1	3,5	4,0	2,6
260648_at	AT1G08050	zinc finger (C3HC4-type RING finger) family protein	3,5	3,0	2,5	3,7
264624_at	AT1G08930	ERD6 (EARLY RESPONSE TO DEHYDRATION 6); carbohydrate transporter/ sugar porter	3,5	3,0	2,3	2,8
264645_at	AT1G08940	phosphoglycerate/bisphosphoglycerate mutase family protein	6,1	3,5	3,0	4,6
264660_at	AT1G09940	HEMA2; glutamyl-tRNA reductase	4,3	2,5	2,3	2,1
262793_at	AT1G13110	CYP71B7 (cytochrome P450, family 71, subfamily B, polypeptide 7); oxygen binding	18,4	11,3	6,5	4,6
262772_at	AT1G13210	haloacid dehalogenase-like hydrolase family protein	8,6	3,2	2,5	4,0
259410_at	AT1G13340	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35730.1); similar to unknown pr	3,2	2,1	2,1	3,0
261474_at	AT1G14540	anionic peroxidase, putative	73,5	17,1	14,9	14,9
262832_s_at	AT1G14870;A	[AT1G14870, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G35525.1); similar	4,9	4,0	2,3	5,3
261719_at	AT1G18380	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G67025.1); similar to Ser/Thr pro	6,5	4,3	2,1	5,7
261718_at	AT1G18390	protein kinase family protein	4,9	3,7	2,1	4,3
255753_at	AT1G18570	MYB51 (myb domain protein 51); DNA binding / transcription factor	5,7	2,5	2,3	3,0
259479_at	AT1G19020	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G48180.1); similar to conserved h	4,3	3,2	2,1	6,1
260656_at	AT1G19380	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G65650.1); similar to unknown [V	6,1	4,6	3,0	4,0
261450_s_at	AT1G21110;A	[AT1G21110, O-methyltransferase, putative];[AT1G21120, O-methyltransferase, putative]	9,2	3,5	4,6	4,6
261449_at	AT1G21120	O-methyltransferase, putative	7,5	3,0	4,3	3,0
261453_at	AT1G21130	O-methyltransferase, putative	7,5	4,0	3,7	7,5
264866_at	AT1G24140	matrixin family protein	7,0	3,7	2,1	8,6
261021_at	AT1G26380	FAD-binding domain-containing protein	12,1	4,0	6,1	4,0
261445_at	AT1G28380	NSL1 (NECROTIC SPOTTED LESIONS 1)	4,9	3,2	2,0	2,6
262744_at	AT1G28680	transferase family protein	3,2	2,3	2,5	2,0
259792_at	AT1G29690	CAD1 (CONSTITUTIVELY ACTIVATED CELL DEATH 1); oxidoreductase	3,2	2,1	2,0	4,6
263228_at	AT1G30700	FAD-binding domain-containing protein	9,2	8,6	2,3	10,6
246312_at	AT1G31930	XLG3 (extra-large GTP-binding protein 3); signal transducer	4,0	2,6	2,1	2,0

260706_at	AT1G32350	AOX1D (ALTERNATIVE OXIDASE 1D); alternative oxidase	4,9	2,5	2,6	5,3
256177_at	AT1G51620	protein kinase family protein	11,3	6,5	3,2	2,8
256186_at	AT1G51680	4CL1 (4-COUMARATE:COA LIGASE 1); 4-coumarate-CoA ligase	9,2	7,5	6,1	4,0
256170_at	AT1G51790	leucine-rich repeat protein kinase, putative	8,0	8,6	2,6	7,0
256181_at	AT1G51820	leucine-rich repeat protein kinase, putative	7,5	7,5	2,3	2,5
260978_at	AT1G53540	17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156)	2,6	3,5	2,1	9,2
265075_at	AT1G55450	embryo-abundant protein-related	11,3	9,2	4,3	5,3
262085_at	AT1G56060	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32190.1); similar to conserved h	4,6	2,8	2,6	3,5
262082_s_at	AT1G56140;A	[AT1G56140, leucine-rich repeat family protein / protein kinase family protein];[AT1G56130, le	5,3	3,7	2,5	3,5
245866_s_at	AT1G57990;A	[AT1G57990, ATPUP18 (Arabidopsis thaliana purine permease 18); purine transporter];[AT1G5	6,5	3,5	2,1	4,9
265008_at	AT1G61560	MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding	16,0	7,5	4,6	3,0
257466_at	AT1G62840;A	[AT1G62840, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G12320.1); similar	3,2	2,8	2,0	4,0
261545_at	AT1G63530	similar to hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] (TAIR:AT1G6	3,5	3,2	2,5	3,2
264213_at;264153	AT1G65390	ATPP2-A5; transmembrane receptor	36,8	24,3	7,0	3,0
	AT1G65400	hypothetical protein	19,7	13,9	6,1	4,0
262930_at	AT1G65690	harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	4,3	4,0	2,0	3,0
256526_at	AT1G66090	disease resistance protein (TIR-NBS class), putative	5,7	4,3	2,1	3,7
256522_at	AT1G66160	U-box domain-containing protein	6,5	4,0	2,0	7,0
257583_at	AT1G66480	PMI2 (plastid movement impaired 2)	4,6	2,1	2,8	2,5
256366_at	AT1G66880	serine/threonine protein kinase family protein	7,5	5,3	3,2	4,9
264314_at	AT1G70420	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23710.1); similar to Protein of u	7,0	4,3	2,5	5,3
260399_at	AT1G72520	lipoxygenase, putative	21,1	13,9	8,6	12,1
262360_at	AT1G73080	PEPR1 (PEP1 RECEPTOR 1); ATP binding / kinase/ protein binding / protein serine/threonine k	3,2	2,8	2,1	2,0
262220_at	AT1G74740	CPK30 (calcium-dependent protein kinase 30); calcium- and calmodulin-dependent protein kinas	4,9	3,7	2,1	3,7
264279_s_at	AT1G78820;A	[AT1G78820, curculin-like (mannose-binding) lectin family protein / PAN domain-containing pr	4,0	2,6	2,3	2,8
264299_s_at	AT1G78860;A	[AT1G78860, curculin-like (mannose-binding) lectin family protein];[AT1G78850, curculin-like	12,1	7,0	7,5	4,9
261394_at	AT1G79680	wall-associated kinase, putative	11,3	5,3	6,1	2,3
265221_s_at	AT2G02000;A	[AT2G02000, glutamate decarboxylase, putative];[AT2G02010, glutamate decarboxylase, putati	9,8	6,1	3,7	6,1
264107_s_at	AT2G13790;A	[AT2G13790, ATSERK4 (SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 4); pro	4,3	3,2	3,0	2,8
264616_at	AT2G17740	DC1 domain-containing protein	16,0	12,1	3,5	5,3
265440_at	AT2G20960	pEARLI4	7,0	3,2	2,0	3,0
264000_at	AT2G22500	mitochondrial substrate carrier family protein	6,5	4,3	2,5	5,3
263797_at	AT2G24570	WRKY17 (WRKY DNA-binding protein 17); transcription factor	10,6	10,6	3,0	8,6
266658_at	AT2G25735	unknown protein	13,0	5,7	3,2	5,3
267381_at	AT2G26190	calmodulin-binding family protein	5,3	2,0	2,0	2,0
245038_at	AT2G26560	PLP2 (PHOSPHOLIPASE A 2A); nutrient reservoir	9,2	5,7	4,9	2,8

266247_at	AT2G27660	DC1 domain-containing protein	8,6	8,6	2,6	7,0
267493_at	AT2G30400	ATOFP2/OFP2 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 2)	2,6	2,0	2,1	2,0
267565_at	AT2G30750	CYP71A12 (cytochrome P450, family 71, subfamily A, polypeptide 12); oxygen binding	4,9	2,6	3,2	2,5
263478_at	AT2G31880	leucine-rich repeat transmembrane protein kinase, putative	5,7	3,7	2,3	3,7
265670_s_at	AT2G32190;A	[AT2G32190, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32210.1); similar	6,5	3,0	2,8	6,1
265670_s_at	AT2G32210;A	[AT2G32210, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32190.1); similar	5,7	3,5	2,1	6,1
265679_at	AT2G32240	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05320.3); similar to kinesin, put	4,9	2,6	2,6	2,0
267548_at	AT2G32660	disease resistance family protein / LRR family protein	7,5	4,6	3,2	4,6
267550_at	AT2G32800	AP4.3A; ATP binding / protein kinase	3,2	2,0	2,5	2,3
267451_at	AT2G33710	AP2 domain-containing transcription factor family protein	3,7	2,8	2,1	5,3
263935_at	AT2G35930	U-box domain-containing protein	19,7	9,8	4,0	14,9
263838_at	AT2G36880	MAT3 (METHIONINE ADENOSYLTRANSFERASE 3); methionine adenosyltransferase	2,3	2,5	2,5	2,1
263845_at	AT2G37040	PAL1 (PHE AMMONIA LYASE 1); phenylalanine ammonia-lyase	5,3	4,9	4,3	3,2
266010_at	AT2G37430	zinc finger (C2H2 type) family protein (ZAT11)	18,4	13,9	4,0	17,1
266167_at	AT2G38860	YLS5 (yellow-leaf-specific gene 5)	3,2	2,0	2,1	2,8
266975_at	AT2G39380	ATEXO70H2 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H2); protein binding	11,3	11,3	3,7	6,5
266983_at	AT2G39400	hydrolase, alpha/beta fold family protein	13,9	6,5	4,9	6,1
266967_at	AT2G39530	integral membrane protein, putative	8,6	6,1	3,7	4,3
267083_at	AT2G41100	TCH3 (TOUCH 3)	3,0	3,2	3,0	2,8
265260_at	AT2G43000	ANAC042 (Arabidopsis NAC domain containing protein 42); transcription factor	4,9	2,5	3,0	4,3
260568_at	AT2G43570	chitinase, putative	3,0	2,0	2,0	2,1
266884_at	AT2G44790	UCC2 (UCLACYANIN 2); copper ion binding	13,0	4,6	6,1	5,7
245148_at	AT2G45220	pectinesterase family protein	5,3	4,6	2,8	5,7
266761_at	AT2G47130	short-chain dehydrogenase/reductase (SDR) family protein	3,0	2,5	2,0	2,6
266737_at	AT2G47140	short-chain dehydrogenase/reductase (SDR) family protein	7,0	3,5	2,5	2,0
245151_at	AT2G47550	pectinesterase family protein	16,0	8,0	4,3	9,8
258947_at	AT3G01830	calmodulin-related protein, putative	7,5	5,3	2,8	3,7
258856_at	AT3G02040	SRG3 (SENESCENCE-RELATED GENE 3); glycerophosphodiester phosphodiesterase	2,0	2,6	2,3	2,8
259120_at	AT3G02240	unknown protein	8,0	4,3	2,8	2,8
259018_at	AT3G07390	AIR12 (Auxin-Induced in Root cultures 12); extracellular matrix structural constituent	4,6	4,0	2,3	4,3
258786_at	AT3G11820	SYP121 (syntaxin 121); t-SNARE	4,0	2,8	2,0	3,5
258787_at	AT3G11840	U-box domain-containing protein	4,3	3,7	2,5	3,5
257697_at	AT3G12700	aspartyl protease family protein	5,7	4,9	3,7	6,5
256787_at	AT3G13790	ATBFRUCT1/ATCWINV1 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 1); beta	3,2	2,3	2,1	3,0
256799_at	AT3G18560	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G49000.1); similar to Os02g0711	2,8	2,5	2,3	2,5
256968_at	AT3G21070	NADK1 (NAD kinase 1); NAD+ kinase/ NADH kinase/ calmodulin binding	13,9	7,5	4,0	6,1

258037_at	AT3G21230	4CL5 (4-COUMARATE:COA LIGASE 5); 4-coumarate-CoA ligase	13,9	8,6	5,7	9,8
257264_at	AT3G22060	receptor protein kinase-related	4,3	3,7	2,0	5,3
257919_at	AT3G23250	AtMYB15/AtY19/MYB15 (myb domain protein 15); DNA binding / transcription factor	13,0	9,2	5,3	3,5
257644_at	AT3G25780	AOC3 (ALLENE OXIDE CYCLASE 3)	2,5	2,6	2,0	2,5
258075_at	AT3G25900	ATHMT-1/HMT-1; homocysteine S-methyltransferase	6,5	3,5	3,2	3,7
256583_at	AT3G28850	glutaredoxin family protein	5,3	2,6	2,5	2,0
252515_at	AT3G46230	ATHSP17.4 (Arabidopsis thaliana heat shock protein 17.4)	3,2	4,9	2,5	9,8
252126_at	AT3G50950	disease resistance protein (CC-NBS-LRR class), putative	5,3	3,7	3,5	2,1
252037_at	AT3G51920	CAM9 (CALMODULIN 9); calcium ion binding	9,2	5,7	4,0	2,0
252053_at	AT3G52400	SYP122 (syntaxin 122); t-SNARE	11,3	5,7	3,0	9,2
252045_at	AT3G52450	U-box domain-containing protein	17,1	12,1	2,8	4,9
251984_at	AT3G53260	PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase	4,0	3,2	3,2	2,8
251987_at	AT3G53280	CYP71B5 (CYTOCHROME P450 71B5); oxygen binding	6,5	4,6	2,6	4,6
251906_at	AT3G53720	ATCHX20 (CATION/H+ EXCHANGER 20); monovalent cation:proton antiporter	8,6	8,0	3,7	10,6
251769_at	AT3G55950	protein kinase family protein	5,3	2,8	2,3	3,2
251507_at	AT3G59080	aspartyl protease family protein	6,1	3,2	2,1	4,6
255714_at	AT4G00300	fringe-related protein	4,0	3,0	2,5	3,0
255595_at	AT4G01700	chitinase, putative	18,4	7,5	5,7	5,7
254922_at	AT4G11370	RHA1A (RING-H2 finger A1A); protein binding / zinc ion binding	4,6	2,6	2,3	4,6
245329_at	AT4G14365	zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein	14,9	7,5	5,7	2,1
245363_at	AT4G15120	VQ motif-containing protein	4,3	3,7	2,1	4,6
254605_at	AT4G18950	ankyrin protein kinase, putative	7,0	4,3	2,3	2,1
254575_at	AT4G19460	glycosyl transferase family 1 protein	5,7	4,6	3,0	6,1
254543_at	AT4G19810	glycosyl hydrolase family 18 protein	5,7	3,2	2,6	3,5
254468_at	AT4G20460	NAD-dependent epimerase/dehydratase family protein	5,7	3,7	2,3	4,3
254408_at	AT4G21390	B120; protein kinase/ sugar binding	5,7	3,5	2,3	4,0
254291_at	AT4G23010	ATUTR2/UTR2 (UDP-GALACTOSE TRANSPORTER 2)	3,5	2,6	2,0	2,1
254241_at	AT4G23190	CRK11 (CYSTEINE-RICH RLK11); kinase	9,8	4,6	3,0	4,9
254249_at	AT4G23280	protein kinase, putative	7,0	4,0	2,8	3,5
253819_at	AT4G28350	lectin protein kinase family protein	8,0	4,6	3,0	5,7
253535_at	AT4G31550	WRKY11 (WRKY DNA-binding protein 11); transcription factor	9,2	7,0	2,1	5,7
253204_at	AT4G34460	AGB1 (GTP BINDING PROTEIN BETA 1); nucleotide binding	5,7	2,5	2,3	2,3
246270_at	AT4G36500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18210.1); similar to hypothetica	6,1	3,5	2,5	2,3
253044_at	AT4G37290	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23270.1)	6,5	4,6	3,5	7,0
252976_s_at	AT4G38550	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G20950.3); similar to pEARLI 4 g	8,0	4,6	2,8	5,7
252906_at	AT4G39640	GGT1; gamma-glutamyltransferase/ glutathione gamma-glutamylcysteinyltransferase	18,4	12,1	7,0	10,6

252862_at	AT4G39830	L-ascorbate oxidase, putative	10,6	3,0	2,1	2,3
252870_at	AT4G39940	AKN2 (APS-KINASE 2); ATP binding / kinase/ transferase, transferring phosphorus-containing	7,0	4,0	4,3	3,7
251096_at	AT5G01550	lectin protein kinase, putative	8,0	5,3	3,0	9,2
250941_at	AT5G03320	protein kinase, putative	4,0	3,0	2,1	3,2
250918_at	AT5G03610	GDSL-motif lipase/hydrolase family protein	9,8	6,1	3,7	8,0
246982_s_at	AT5G04860;A	[AT5G04860, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11760.1); similar	3,5	3,5	2,0	2,1
250821_at	AT5G05190	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G61670.1); similar to Os02g0464	8,6	5,7	2,5	6,5
250575_at	AT5G08240	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23160.1)	6,1	3,5	3,0	4,3
250301_at	AT5G11970	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G19460.1); similar to hypothetica	5,3	3,5	2,3	4,6
245209_at	AT5G12340	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G28190.1); similar to putative pro	10,6	4,6	2,5	2,1
245156_at	AT5G12480	CPK7 (CALMODULIN-DOMAIN PROTEIN KINASE 7); calcium- and calmodulin-dependent	4,0	2,1	2,3	2,1
250267_at	AT5G12930	unknown protein	5,3	3,0	3,7	3,0
250289_at	AT5G13190	similar to LITAF-domain-containing protein [Pisum sativum] (GB:AAY40471.1); similar to Os	3,0	2,6	2,5	2,1
250149_at	AT5G14700	cinnamoyl-CoA reductase-related	9,2	2,6	2,8	4,0
246532_at	AT5G15870	glycosyl hydrolase family 81 protein	6,1	2,6	2,6	3,0
250098_at	AT5G17350	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar to conserved h	3,5	2,1	2,0	3,2
249918_at	AT5G19240	Identical to Putative GPI-anchored protein At5g19240 precursor [Arabidopsis Thaliana] (GB:Q8	9,8	8,6	7,5	2,3
246041_at	AT5G19290	esterase/lipase/thioesterase family protein	5,3	3,0	3,2	2,8
249941_at	AT5G22270	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11600.1); similar to H0913C04.	5,3	3,7	2,0	2,5
249730_at	AT5G24430	calcium-dependent protein kinase, putative / CDPK, putative	6,5	4,0	2,8	3,7
246927_s_at	AT5G25260;A	[AT5G25260, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25250.1); similar	10,6	6,5	4,6	4,3
246858_at	AT5G25930	leucine-rich repeat family protein / protein kinase family protein	4,9	4,0	2,1	4,6
246821_at	AT5G26920	calmodulin binding	5,7	3,7	2,1	4,6
246777_at	AT5G27420	zinc finger (C3HC4-type RING finger) family protein	5,7	3,5	2,1	8,0
249527_at	AT5G38710	proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative	3,0	2,5	2,0	2,6
249481_at	AT5G38900	DSBA oxidoreductase family protein	4,0	2,5	2,5	2,6
249459_at	AT5G39580	peroxidase, putative	11,3	9,2	4,0	8,0
249264_s_at	AT5G41740;A	[AT5G41740, disease resistance protein (TIR-NBS-LRR class), putative];[AT5G41750, disease	4,9	4,0	2,0	3,2
249197_at	AT5G42380	calmodulin-related protein, putative	6,1	4,0	2,5	4,3
249078_at	AT5G44070	CAD1 (CADMIUM SENSITIVE 1)	12,1	7,0	5,3	2,1
248914_at	AT5G45750	AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding	2,1	2,1	2,0	2,0
248896_at	AT5G46350	WRKY8 (WRKY DNA-binding protein 8); transcription factor	6,1	3,5	3,0	2,3
248814_at	AT5G46910	transcription factor jumonji (jmj) family protein	4,9	3,0	2,8	2,6
248819_at	AT5G47050	ATP binding / protein binding / shikimate kinase/ zinc ion binding	6,1	3,2	2,3	6,5
248769_at	AT5G47730	SEC14 cytosolic factor, putative / polyphosphoinositide-binding protein, putative	8,0	4,3	3,5	2,3
248719_at	AT5G47910	RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)	9,8	4,9	3,0	6,5

248700_at	AT5G48400	ATGLR1.2 (Arabidopsis thaliana glutamate receptor 1.2)	7,0	4,6	2,6	3,7
248703_at	AT5G48430	similar to extracellular dermal glycoprotein, putative / EDGP, putative [Arabidopsis thaliana] (T	16,0	7,0	5,3	5,7
248486_at	AT5G51060	RHD2 (ROOT HAIR DEFECTIVE 2)	3,5	3,2	2,0	3,2
248276_at	AT5G53550	YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	4,6	2,8	2,6	2,0
248163_at	AT5G54510	DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase	3,2	2,5	2,8	2,8
247949_at	AT5G57220	CYP81F2 (cytochrome P450, family 81, subfamily F, polypeptide 2); oxygen binding	19,7	6,5	5,7	7,5
247610_at	AT5G60630	similar to hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] (TAIR:AT3G4	4,6	3,5	2,0	4,0
247487_at	AT5G62150	peptidoglycan-binding LysM domain-containing protein	9,2	5,3	3,0	3,7
247240_at	AT5G64660	U-box domain-containing protein	8,0	4,9	3,0	8,6
247137_at	AT5G66210	CPK28 (calcium-dependent protein kinase 28); calcium- and calmodulin-dependent protein kina	7,0	3,5	3,5	2,5
247044_at	AT5G66850	MAPKKK5 (Mitogen-activated protein kinase kinase kinase 5); kinase	2,6	2,1	2,0	2,1
246988_at	AT5G67340	armadillo/beta-catenin repeat family protein / U-box domain-containing protein	11,3	5,7	4,0	2,5