Table 1, supplementary data. Annotation of Arabidopsis LRXs and related proteins in databases. Results from query with "extensin AND "repeat" as key words at NCBI Map Viewer (http://www.ncbi.nlm.nih.gov/map/search.cgi?chr=arabid.inf). Twelve genes labelled with pink boxes were found with with search. The 11 LRX genes annotated by Baumberger et al. (2003) are labelled with violet boxes. Functional domains were found using InterProScan (http://www.eb.ac.uk/Tools/InterProScan/) and ScanProsite (http://www.expasy.ch/tools/scanprosite/). Names of domains (IPR: InterProScan; PF: PFAM; PR: SPRINT; PS: PROSITE) are indicated as well as the corresponding scores and positions on the amino acid sequence between square brackets.

	Annotations in databases	Interproscan and Prosite results		Annotation by Baumberger et al. (2003)
		•		
At1g12040	NCBI	IPR001611: Leucine-rich repeat		AtLRX1
		PF00560: LRR 1	6000.000322506199 [148-170]T, 32.999983317480 [172-191]T, 2100.0003726265404 [243-265]T, 3500.00043291567 [267-289]T, 39.999997148235 [291-313]T	
	LRX1 (LEUCINE-RICH REPEAT/EXTENSIN 1) similar to LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2), protein binding / structural constituent of cell wall [Arabidopsis thaliana] (TAIR:AT1662440.1)	IPR013210: Leucine-rich repeat, N-termina		-
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210) contains InterPro domain Leucine-rich repeat (IPR001611)	PF08263: LRR_NT unintegrated	0.04300000526153389 [51-90]T	
	TAIR	PR01217: PRICHEXTENSN	4.8E-14 [383-395]T, 4.8E-14 [406- 427]T, 4.8E-14 [428-444]T, 4.8E-14 [457-482]T	
	LEUCINE-RICH REPEAT/EXTENSIN 1, LRX1 encodes a a chimeric leucine-rich repeat/extensin protein that regulates root hair morphogenesis and elongation. Null mutants develop root hairs that frequently abort, swell, or branch. Gene is expressed in root hair cells and protein is specifically localized in the wall of the hair proper.			
	Leucine-rich repeat (N-terminal:IPR013210)	PS50099: PRO_RICH Proline-rich region profile	score = 104.855 [383 - 741]	
	Leucine-rich repeat;Molecular Function: protein bi (IR001611) TIGR			
	leucine-rich repeat family protein / extensin family protein (LRX1) similar to extensin-like protein [Lycopersicon esculentum] gi]5917664]gb AAD55979 contains leucine-rich repeats (PF00560)			
	contains proline rich extensin domains (IPR002965) MIPS			
	leucine-rich repeat/extensin 1 (LRX1)			
At1g49490	NCBI	IPR001611: Leucine-rich repeat		AtPEX2
	leucine-rich repeat family protein / extensin family protein	PF00560: LRR 1	1899.9996417184002 [180-202]T 3399.99972437719 [250-272]T 6000.000322506199 [274-296]T 58.999994304626 [288-320]T	
	similar to leucine-rich repeat family protein / extensin family protein similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] (TAIR:AT3G19020.1)	IPR003882: Pistil-specific extensin-like pro		
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210) contains InterPro domain Pistil-specific extensin-like protein (IPR003882)	PR01218: PSTLEXTENSIN IPR013210: Leucine-rich repeat, N-termina	1.4E-5 [530-553]T 1.4E-5 [565-583]T al	-
	contains InterPro domain Leucine-rich repeat (IPR001611) TAIR leucine-rich repeat family protein / extensin family protein	PF08263: LRR_NT	2.0000006595059 [59-98]T	-
	similar to leucine-rich repeat family protein / extensin family protein thaliana] (TAIR:AT3G19020.1) contains Inter/Pro domain Leucine-rich repeat, N-terminal (IPR013210)	PS50099: PRO_RICH Proline-rich region profile	score = 86.183 [394 - 842]	
	contains InterPro domain Pistil-specific extensin-like protein (IPR003882) contains InterPro domain Leucine-rich repeat (IPR001611) TIGR			
	leucine-rich repeat family protein / extensin family protein contains similarity to disease resistance protein GI:3894383 from [Lycopersicon esculentum] contains leucine-rich repeats (PF00560)			
	contains proline rich extensin domains (IPR002965) MIPS hypothetical protein			

		-			
At1g62440	NCBI	IPR001611: Leucine-rich repeat			AtLRX2
			0.022 [214-233]T, 4.1 [285-307]T,		
	LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2)	PF00560: LRR_1	0.029 [309-331]T, 0.029 [333-355]T		
	similar to LRX1 (LEUCINE-RICH REPEAT/EXTENSIN 1), protein binding /				
		IPR003883: Extensin-like protein			
		in Receden Exteriori into protoni			
	contains InterPro domain Extensin-like protein (IPR003883)	PF02095: Extensin 1	5.9 [636-645]T, 63 [664-673]T, 2.9 [679-688]T, 22 [693-702]T, 6.6 [722- 731]T, 22 [737-746]T	Extensins are plant cell-wall proteins; they can account for up to 20% of the dry weight of the cell wall. They are highly-glycosylated, possibly reflecting their interactions with cell-wall carbohydrates. Amongst their functions is cell wall strengthening in response to mechanical stress (e.g., during attack by pests, plant-bending in the wind, etc.). This repeat occurs within extensin-like proteins.	
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)		10111, 22 [101 1 10]1	otoly. The report occurs within extension and protonic.	
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)				
		DOFOCO DEC DICIL Decline data estas			
		PS50099: PRO_RICH Proline-rich region	100 1 10 1 10 5 00 11		
		profile	score = 108.140 [425 - 824]		
	LEUCINE-RICH REPEAT/EXTENSIN 2, LRX2 encodes a paralog of LRX1 (LEUCINE-RICH REPEAT/EXTENSIN 1) which acts synergistically with LRX1 in root hair cell morphogenesis. Leucine-rich repeat, N-terminal (IPR013210) Extensin-like protein;Molecular Function: structur (IPR003883) Leucine-rich repeat;Molecular Function: protein bi (IPR001611) TIGR leucine-rich repeat family protein / extensin family protein similar to extensin-like protein [Lycopersicon esculentum] gi[5917664[gb]AAD55979 contains leucine-rich repeats (PF00560) contains proline rich extensin domains (IPR002965) MIPS putative extensin-like protein (gnl]PID[e1310400)				
At2g15880	NCBI	IPR001611: Leucine-rich repeat			AtPEX3
		PF00560: LRR 1	51.9999946268774 [299-321]T		
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis	IPR003882: Pistil-specific extensin-like pr	otein		
1			4.1E-10 [514-537]T, 4.1E-10 [549-		
1	contains InterPro domain Pistil-specific extensin-like protein (IPR003882)	PR01218: PSTLEXTENSIN	567]T, 4.1E-10 [663-684]T		4

Inalianaj (TAIR:A14G33970.1)	iPR003662: Pistii-specific extensin-like p	rotein	
		4.1E-10 [514-537]T, 4.1E-10 [549-	
contains InterPro domain Pistil-specific extensin-like protein (IPR003882)	PR01218: PSTLEXTENSIN	567]T, 4.1E-10 [663-684]T	
contains InterPro domain Leucine-rich repeat (IPR001611)	unintegrated		
		2.7E-11 [390-402]T, 2.7E-11 [404-	
		420]T, 2.7E-11 [424-436]T, 2.7E-11	
TAIR	PR01217: PRICHEXTENSN	[442-463]T, 2.7E-11 [465-481]T	
leucine-rich repeat family protein / extensin family protein			
leucine-rich repeat family protein / extensin family protein; similar to leucine-rich			
repeat family protein / extensin family protein [Arabidopsis thaliana]			
(TAIR:AT4G33970.1)			
	PS50099: PRO_RICH Proline-rich region		
contains InterPro domain Pistil-specific extensin-like protein (IPR003882)	profile	score = 109.004 [394 - 722]	
contains InterPro domain Leucine-rich repeat (IPR001611)			
TIGR			
leucine-rich repeat family protein / extensin family protein			
similar to extensin-like protein [Lycopersicon esculentum]			
gi 5917664 gb AAD55979			
contains leucine-rich repeats (PF00560)			
contains proline rich extensin domains (IPR002965)			
MIPS			
unknown protein			

At2g19780	NCBI	IPR001611: Leucine-rich repeat		none
			4.599999811982681 [134-156]T,	
			20.000020319536 [158-178]T,	
			5.9000024020674 [182-201]T,	
			6099.99977126217 [205-224]T,	
	leucine-rich repeat family protein / extensin family protein	PF00560: LRR 1	45.000003473935095 [301-323]T	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
		IPR013210: Leucine-rich repeat, N-termina		
		PF08263: LRR_NT	8.29999581180007E-5 [68-107]T	
	contains InterPro domain Leucine-rich repeat (IPR001611)			
	TAIR			
	leucine-rich repeat family protein / extensin family protein			
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT4G29240.1)			
	similar to hypothetical protein [Vitis vinifera] (GB:CAN62837.1)			
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)			
	contains inter to domain Leucine-rich repeat (IPR001611)			
	TIGR			
	leucine-rich repeat family protein / extensin family protein			
	contains leucine rich-repeat (LRR) domains (PF00560, IPR001611)			
	similar to leucine-rich repeat/extensin 1 (GI:13809918) [Arabidopsis thaliana]			
	contains similarity to disease resistance protein [Lycopersicon esculentum]			
1	gi 3894383 gb AAC78591			
1	MIPS	1		
	putative disease resistance protein			

At3g19020	NCBI	IPR001611: Leucine-rich repeat		AtPEX1
		· · · · · · · · · · · · · · · · · · ·	4000.00081278147 [193-215]T,	
			7300.001901602701 [263-285]T,	
	leucine-rich repeat family protein / extensin family protein	PF00560: LRR_1	3800.00071256818 [287-309]T	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT1G49490.1)	IPR003882: Pistil-specific extensin-like pro	otein	
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)	PR01218: PSTLEXTENSIN	8.7E-6 [675-698]T, 8.7E-6 [710-728]T, 8.7E-6 [811-832]T	
		IPR013210: Leucine-rich repeat, N-termina	al	
		PF08263: LRR_NT	5.3000002124871 [72-111]T	
	TAIR	unintegrated		
		PR01217: PRICHEXTENSN	6.4E-9 [406-418]T, 6.4E-9 [423-444]T, 6.4E-9 [446-462]T, 6.4E-9 [470-487]T	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT1G49490.1)			
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)			
		PS50099: PRO_RICH Proline-rich region		
		profile	score = 132.344 [407 - 954]	
	contains InterPro domain Leucine-rich repeat (IPR001611)			
	TIGR			
	leucine-rich repeat family protein / extensin family protein			
	similar to extensin-like protein [Lycopersicon esculentum]			
	gi 5917664 gb AAD55979			
	contains leucine-rich repeats (PF00560)			
	contains proline rich extensin domains (IPR002965)			
	MIPS			
	hypothetical protein			

At3g22800 NCBI IPR001611: Leucine-rich repeat 2200.0002175608097 [148-170]T, 38.999996884611306 [172-194]T, 1499.99977583351 [268-290]T, leucine-rich repeat family protein / extensin family protein PF00560: LRR_1 32.9999983317489 [292-314]T similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] (TAIR:AT3G24480.1) IPR003882: Pistil-specific extensin-like protein similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis 1.2E-5 [400-423]T, 1.2E-5 [435-453]T thaliana] (TAIR:AT4G13340.1) PR01218: PSTLEXTENSIN contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210) IPR013210: Leucine-rich repeat, N-termina contains InterPro domain Pistil-specific extensin-like protein (IPR003882) PF08263: LRR_NT 0.0989999902584295 [51-90]T contains InterPro domain Leucine-rich repeat (IPR001611) unintegrated 3.6E-14 [374-386]T, 3.6E-14 [386-407]T, 3.6E-14 [414-430]T PR01217: PRICHEXTENSN TAIR leucine-rich repeat family protein / extensin family protein similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] (TAIR:AT4G13340.1) PS50099: PRO_RICH Proline-rich region contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210) profile score = 52.470 [376 - 467] contains InterPro domain Pistil-specific extensin-like protein (IPR003882) contains InterPro domain Leucine-rich repeat (IPR001611) TIGR leucine-rich repeat family protein / extensin family protein similar to extensin-like protein [Lycsimilar to extensin-like protein [Lycopersicon esculentum] gi[5917664]gb[AAD55979 contains leucine-rich repeats (PF00560) contains proline rich extensin domains (IPR002965) MIPS hypothetical protein

At3g24480	NCBI	IPR001611: Leucine-rich repeat		AtLRX4
			2100.0003726265404 [195-214]T,	
			5099.9988243997805 [289-311]T,	
	leucine-rich repeat family protein / extensin family protein	PF00560: LRR_1	3099.99945899369 [313-335]T	
	similar to leucine-rich repeat family protein /extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT4G18670.1)	IPR013210: Leucine-rich repeat, N-termi	nal	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT4G13340.1)	PF08263: LRR_NT	0.0739999967908919 [74-113]T	
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)	unintegrated		
		-	5.4E-16 [411-432]T, 5.4E-16 [434-	
	contains InterPro domain Leucine-rich repeat (IPR001611)	PR01217: PRICHEXTENSN	450]T, 5.4E-16 [456-473]T	
	TAIR			
	leucine-rich repeat family protein / extensin family protein			
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis	PS50099: PRO_RICH Proline-rich region		
	thaliana] (TAIR:AT4G18670.1)	profile	score = 34.144 [403 - 492]	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT4G13340.1)			
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)			
	contains InterPro domain Leucine-rich repeat (IPR001611)			
	TIGR			
	leucine-rich repeat family protein / extensin family protein			
	similar to extensin-like protein [Lycopersicon esculentum]			
	gi 5917664 gb AAD55979			
	contains leucine-rich repeats (PF00560)			
	contains proline rich extensin domains (IPR002965)			
	MIPS	1		
	disease resistance protein, putative	1		

t4g06744	NCBI	IPR001611: Leucine-rich repeat	none
		2700.00035356384 [143-165]T,	
		4100.000492084209 [167-189]T,	
		8199.9995664553 [215-238]T,	
		5200.00089003336 [264-286]T,	
		PF00560: LRR_1 48.9999951782359 [314-335]T	
	Identical to Uncharacterized protein At4g06744 precursor [Arabidopsis Thaliana] (GB:Q8W3M4)		
	similar to leucine-rich repeat family protein [Arabidopsis thaliana]		
	(TAIR:AT3G19320.1)		
	similar to leucine-rich repeat family protein [Arabidopsis thaliana]		
	(TAIR:AT1G49750.1)		
	similar to Leucine-rich repeat, plant specific [Medicago truncatula]		
	(GB:ABD32635.1)		
	contains InterPro domain Leucine-rich repeat (IPR001611)		
	TAIR		
	leucine-rich repeat family protein / extensin family protein		
	Identical to Uncharacterized protein At4g06744 precursor [Arabidopsis Thaliana]		
	(GB:Q8W3M4)		
	similar to leucine-rich repeat family protein [Arabidopsis thaliana] (TAIR:AT3G19320.1)		
	similar to Leucine-rich repeat, plant specific [Medicago truncatula]		
	(GB:ABD32635.1)		
	contains InterPro domain Leucine-rich repeat (IPR001611)		
	TIGR		
	leucine-rich repeat family protein / extensin family protein		
	similar to leucine-rich repeat/extensin 1 (GI:13809918) {Arabidopsis thaliana}		
	contains PF00560: Leucine Rich Repeat domains		
	MIPS		
	not found		

At4g13340	NCBI	IPR001611: Leucine-rich repeat		AtLRX3
, ang loo lo			2100.0003726265404 [187-206]T, 7199.99952919347 [281-303]T,	
		PF00560: LRR_1	1599.99977185865 [305-327]T	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis	IPR003882: Pistil-specific extensin-like pro	tein	
			6.2E-5 [416-439]T, 6.2E-5 [449-467]T	
		IPR013210: Leucine-rich repeat, N-termina		
			0.00230000061930563 [66-105]T	
	contains InterPro domain Leucine-rich repeat (IPR001611)	unintegrated		
			1.0E-14 [392-413]T, 1.0E-14 [425-	
		PR01217: PRICHEXTENSN	441]T, 1.0E-14 [443-460]T	
	leucine-rich repeat family protein / extensin family protein			
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT3G24480.1)	DOCODO DIOLI DISTINUISTA SIST		
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] (TAIR:AT4G18670.1)		score = 153.609 [394 - 758]	
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)	profile	SCOTE = 153.609 [394 - 756]	-
	contains InterPro domain Pistil-specific extensin-like protein (IPR03882)			
	contains InterPro domain Leucine-rich repeat (IPR001611)			
	TIGR			
	leucine-rich repeat family protein / extensin family protein			
	similar to extensin-like protein [Lycopersicon esculentum]			
	ail5917664 ab AAD55979			
	contains leucine-rich repeats (PF00560)			
	contains proline rich extensin domains (IPR002965)			
	MIPS			
	extensin-like protein			
	strong similarity to known protein : extensin-like protein, Zea mays,			
	PIR2:S49915			

4g18670	NCBI	IPR001611: Leucine-rich repeat		AtLRX5
			3200.00074719642 [199-218]T,	
			3099.99945899369 [293-315]T,	
	leucine-rich repeat family protein / extensin family protein	PF00560: LRR_1	4600.00044330866 [317-339]T	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT3G24480.1)	IPR002951: Atrophin		
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
		PR01222: ATROPHIN	2.1E-5 [410-438]T, 2.1E-5 [759-780]T	
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)	IPR013210: Leucine-rich repeat, N-termina		
	contains InterPro domain Leucine-rich repeat (IPR001611)	PF08263: LRR_NT	0.0739999967908919 [78-117]T	
	contains InterPro domain Atrophin (IPR002951)	unintegrated		
			2.4E-11 [402-423]T, 2.4E-11 [426-	
			442]T, 2.4E-11 [446-463]T, 2.4E-11	
	TAIR	PR01217: PRICHEXTENSN	[465-490]T	
	leucine-rich repeat family protein / extensin family protein			
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT3G24480.1)			
	thaliana] (TAIR:AT4G13340.1)	profile	score = 99.495 [406 - 837]	
		PS50324: SER_RICH Serine-rich region		
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)	profile	score = 13.379 [418 - 596]	
		PS50316 HIS_RICH Histidine-rich region		
	contains InterPro domain Leucine-rich repeat (IPR001611)	profile	score = 13.990 [628 - 674]	
	contains InterPro domain Atrophin (IPR002951)			
	TIGR			
	leucine-rich repeat family protein / extensin family protein			
	similar to extensin-like protein [Lycopersicon esculentum]			
	gi 5917664 gb AAD55979			
	contains leucine-rich repeats (PF00560)			
	contains proline rich extensin domains (IPR002965)			
	MIPS			
	extensin-like protein			
	strong similarity to known protein : extensin-like protein - maize, PIR2:S49915			

At4g29240	NCBI	IPR001611: Leucine-rich repeat		none
			31.0000030991121 [139-161]T,	
			31.9999986882983 [163-183]T,	
			29.9999985646001 [187-206]T,	
			6899.99963379704 [210-232]T,	
	leucine-rich repeat family protein / extensin family protein	PF00560: LRR 1	3099.99945899369 [306-328]T	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
		IPR013210: Leucine-rich repeat, N-termina	al	
		PF08263: LRR NT	0.016000002110419 [73-112]T	
	contains InterPro domain Leucine-rich repeat (IPR001611)	1100203. ERR_N1	0.010000002110413[13-112]1	-
	TAIR			
		PS50315 GLY RICH Glycine-rich region		-
			44.050 [04.04]	
		profile	score = 14.253 [21 - 61]	-
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT2G19780.1)			
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210)			
	contains InterPro domain Leucine-rich repeat (IPR001611)			
	TIGR			
	leucine-rich repeat family protein / extensin family protein			
	contains PF00560: Leucine Rich Repeat domains			
	similar to leucine-rich repeat/extensin 1 (GI:13809918) [Arabidopsis thaliana]			
	MIPS			
	extensin-like protein			

t4g33970	NCBI	IPR001611: Leucine-rich repeat		AtPEX4
	leucine-rich repeat family protein / extensin family protein	PF00560: LRR_1	31.0000030991121 [325-347]T	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
		IPR013210: Leucine-rich repeat, N-termina		
		PF08263: LRR_NT	0.52000001763605 [86-125]T	
	contains InterPro domain Leucine-rich repeat (IPR001611)	unintegrated		
			4.0E-14 [418-430]T, 4.0E-14 [434-	
			450]T, 4.0E-14 [454-466]T, 4.0E-14	
		PR01217: PRICHEXTENSN	[467-488]T, 4.0E-14 [490-506]T	
	leucine-rich repeat family protein / extensin family protein			
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis			
	thaliana] (TAIR:AT2G15880.1)	DOCODO DO DIOLI DISTINUISTI IN		
		PS50099: PRO_RICH Proline-rich region		
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210) contains InterPro domain Leucine-rich repeat (IPR001611)	profile	score = 82.898 [419 - 694]	
	TIGR			
	leucine-rich repeat family protein / extensin family protein			
	similar to extensin-like protein [Lycopersicon esculentum]			
	gi 5917664 gb AAD55979			
	contains leucine-rich repeats (PF00560)			
	contains proline rich extensin domains (IPR002965)			
	MIPS			
	extensin-like protein			
	strong similarity to known protein : extensin-like protein, Zea mays,			
	PIR2:S49915			

t5g25550	NCBI	IPR001611: Leucine-rich repeat		AtLRX7
	leucine-rich repeat family protein / extensin family protein	PF00560: LRR_1	0.034 [172-191]T, 7.8 [218-240]T, 2.2 [267-289]T, 0.011 [291-313]T	
	similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] (TAIR:AT3G24480.1)	IPR013210: Leucine-rich repeat, N-termina	l l	
	contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210) contains InterPro domain Leucine-rich repeat (IPR001611)	PF08263: LRR_NT	6.5e-05 [51-90]T	-
	TAIR			
		PS50099: PRO_RICH Proline-rich region		
	leucine-rich repeat family protein / extensin family protein similar to leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] (TAIR:AT3G24480.1) contains InterPro domain Leucine-rich repeat, N-terminal (IPR013210) contains InterPro domain Leucine-rich repeat (IPR001611)	profile	score = 16.337 [382 - 430]	
	TIGR			
	leucine-rich repeat family protein / extensin family protein similar to leucine-rich repeat/extensin 1 (GI:13809918) [Arabidopsis thaliana] contains PF00560: Leucine Rich Repeat domains			
	MIPS			
	extensin-like protein strong similarity to known protein : Pex1 extensin-like protein, Lycopersicon esculentum, EMBL:AF159296			

Table 2, supplementary data. Annotation of some cell wall proteins in databases. Functional domains were found using InterProScan (http://www.ebi.ac.uk/Tools/InterProScan/) and ScanProsite (http://www.expasy.ch/tools/scanprosite/). Names of domains are as follows: IPR: InterProScan; PF: PFAM; PR: SPRINT; PTHR: PANTHER; PS: PROSITE; SSF: Superfamily. The corresponding scores are given as well as the positions on the amino acid sequence between square brackets.

	Annotations in databases	Interproscan and Prosite results			Annotation by experts
Some exten	sin genes				Johnson et al. (2003)
At1g21310	NCBI	IPR006706: Extensin-like region		Extensins are homologous hydroxyproline-rich glycoproteins (HRGPs) found in the plant extracellular matrix. The key to the role of HRGPs in cell wall self-	extensin (ROOT SHOOT HYPOCOTYL DEFECTIVE) (RSH)
	AtEXT3 (ROOT SHOOT HYPOCOTYL DEFECTIVE) contains InterPro domain Extensin-like region (IPR006706) TAIR	PF04554: Extensin-like region	1.9e-40 [9-220]T, 1.9e-33 [221-428]T	assembly and cell extension lies in their chemistry, which is dependent on extensive post-translatio	-
	AtEXT3 (ROOT SHOOT HYPOCOTYL DEFECTIVE) contains InterPro domain Extensin-like region (IPR006706) TIGR	PS50099: PRO_RICH Proline-rich region profile	score = 95.519 [34 - 428]		
	proline-rich extensin-like family protein contains extensin-like region (PF04554) MIPS extensin 3 (atExt3)(AtExt5)				

At1g26240	NCBI	IPR006706: Extensin-like region		extensin
			1.10000150671643E-32 [10-143]T,	
			2.10000267834025E-23 [144-243]T,	
			4.0999959904575E-28 [244-362]T,	
	proline-rich extensin-like family protein	PF04554: Extensin-like region	9.70001793430386E-24 [364-478]T	
	contains InterPro domain Extensin-like region (IPR006706)	unintegrated		
			2.5E-10 [28-44]T, 2.5E-10 [50-62]T,	
	TAIR	PR01217: PRICHEXTENSN	2.5E-10 [63-84]T, 2.5E-10 [88-104]T	
	proline-rich extensin-like family protein			
	contains InterPro domain Extensin-like region (IPR006706)			
		PS50099: PRO_RICH Proline-rich region		
	TIGR	profile	score = 150.151 [32 - 476]	
		PS50328: TYR_RICH Tyrosine-rich region		
	proline-rich extensin-like family protein	profile	score = 32.719 [28 - 470]	
	similar to hydroxyproline-rich glycoprotein precursor gi 727264 gb AAA87902			
	contains proline-rich extensin domains (IPR002965)			
	MIPS			
	hypothetical protein			

At1g26250	NCBI	IPR006706: Extensin-like region		extensin
			5.89998809405682E-29 [9-163]T,	
			1.99999636034536E-24 [164-273]T,	
	proline-rich extensin, putative	PF04554: Extensin-like region	7.300005909151711E-16 [274-443]T	
	contains InterPro domain Extensin-like region (IPR006706)	unintegrated		
			5.5E-10 [24-40]T, 5.5E-10 [44-56]T,	
	TAIR	PR01217: PRICHEXTENSN	5.5E-10 [63-84]T, 5.5E-10 [88-104]T	
	proline-rich extensin, putative			
	contains InterPro domain Extensin-like region (IPR006706)			
		PS50099: PRO_RICH Proline-rich region		
	TIGR	profile	score = 131.825 [29 - 441]	
		PS50328: TYR_RICH Tyrosine-rich region		
	proline-rich extensin, putative	profile	score = 37.973 [17 - 435]	
	similar to extensin gi 1165322 gb AAB53156			
	contains proline-rich extensin domains (IPR002965)			
	MIPS			
	hypothetical protein			

Some poller	Some pollen Ole e1 allergen and extensin family proteins						
At1g78040	NCBI	IPR006041: Pollen Ole e 1 allergen and extens	in		none		
	pollen Ole e 1 allergen and extensin family protein	PF01190: Pollen_Ole_e_I	9.70001793430386E-27 [32-153]T	These proteins are most probably secreted and consist of about 145 residues. There are six cysteines which are conserved in the sequence of these proteins. They seem to be involved in disulphide bonds			
	similar to unknown [Populus trichocarpa] (GB:ABK94215.1) contains InterPro domain Pollen Ole e 1 allergen and extensin (IPR006041) TAIR						
	pollen Ole e 1 allergen and extensin family protein similar to unknown [Populus trichocarpa] (GB:ABK92993.1) contains InterPro domain Pollen Ole e 1 allergen and extensin (IPR006041)						
	TIGR						
	pollen Ole e 1 allergen and extensin family protein PF01190 : Pollen proteins Ole e I family						
	MIPS	TonB box, conserved site					
	phosphoglycerate mutase 1 like protein Prosite motif: 1-6 TonB-dependent receptor proteins signatures	PS00430: TONB_DEPENDENT_REC_1	0.0 [1-35]?				

At3g33790	NCBI	IPR006041: Pollen Ole e 1 allergen and extensin		AtAGP30
		PF01190: Pollen_Ole_e_I	9.09992432541697E-68 [112-239]T	
	similar to AGP31 (ARABINOGALACTAN-PROTEIN 31) structural constituent of cell wall (AT1G28290.1)			
	contains InterPro domain Pollen Ole e 1 allergen and extensin (IPR006041)			
		PS50099: PRO_RICH Proline-rich region		
	TAIR	profile	score = 16.164 [30 - 103]	
	pollen Ole e 1 allergen protein containing 14.6% proline residues			
	similar to arabinogalactan protein (Daucus carota) (11322245)			
	contains PF01190: Pollen proteins Ole e I family			
	TIGR			
	pollen Ole e 1 allergen and extensin family protein			
	similar to arabinogalactan protein (Daucus carota) (11322245)			
	contains PF01190: Pollen proteins Ole e I family			
	MIPS			
	putative proline-rich protein			

others				
At2g15770	NCBI	IPR003245: Plastocyanin-like		AtEN23
	glycine-rich protein	PF02298: Cu_bind_like	0.026000001808627 [154-184]T	Nersissian and Shipp (2002)
		IPR008972: Cupredoxin		
		SSF4953: Cupredoxins superfamily	4.0E-17 [141-258]T	
	contains InterPro domain Plastocyanin-like (IPR003245)			
	TAIR			
		PS50324: SER_RICH Serine-rich region		
	glycine-rich protein	profile	score = 18.782 [21 - 136]	
		PS50315: GLY_RICH Glycine-rich region		
	contains InterPro domain Cupredoxin (IPR008972)	profile	score = 8.908 [35 - 96]	
	contains InterPro domain Plastocyanin-like (IPR003245)			
	TIGR			
	glycine-rich protein			
	contains a domain related to blue copper-binding protein			
	similar to Stellacyanin (SP:P00302) {Rhus vernicifera}			
	MIPS			
	hypothetical protein			

		PS50099: PRO_RICH Proline-rich region		
At1g15825	NCBI	profile	score = 24.463 [2 - 123]	none
	hydroxyproline-rich glycoprotein family protein			
	similar to leucine-rich repeat family protein / extensin family protein			
	(AT3G19020.1)			
	TAIR			
	hydroxyproline-rich glycoprotein family protein			
	similar to leucine-rich repeat family protein / extensin family protein			
	(AT3G19020.1)			
	TIGR			
	hydroxyproline-rich glycoprotein family protein			
	contains proline-rich extensin domains (IPR002965)			
	MIPS			
	putative protein			

At1g12090	NCBI	IPR003612: Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	none
	ELP, EXTENSIN-LIKE PROTEIN	PF00234: Tryp_alpha_amyl 6.09999977126231E-23 [55-137]T	
	similar to protease inhibitor/seed storage/lipid transfer protein (LTP) family	· ·	7
		IPR001450: 4Fe-4S ferredoxin, iron-sulphur binding	
		PF00198: 4FE4S_FERREDOXIN 0.0 [23-34]?	
	contains InterPro domain Plant lipid transfer protein/seed storage/trypsin-		
	alpha amylase inhibitor (IPR003612)		
	contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed		
	storage (IPR016140)		
	contains InterPro domain Plant lipid transfer protein and hydrophobic protein		
	helical (IPR013770)		
	TAIR		
	ELP, EXTENSIN-LIKE PROTEIN		
	Plant lipid transfer protein/seed storage/trypsin (IPR003612		
	Bifunctional inhibitor/plant lipid transfer protein (IPR016140)		
	Plant lipid transfer protein and hydrophobic protein (IPR013770)		
	TIGR		
	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein		
	similar to 14 kDa polypeptide [Catharanthus roseus] (407410)		
	similar to 14 kba polypeptide [Catharantinus loseds] (40/410)		
1	contains Pfam protease inhibitor/seed storage/LTP family domain (PF00234)		
	MIPS		
	pEARLI 1-like protein		
	4Fe-4S ferredoxins, iron-sulfur binding region signature		
	· · · · ·		•
	NCBI	IPR003612: Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	
Brassica			
napus		PF00234: Tryp_alpha_amyl 1.3999989204989E-19 [55-137]T	
		IPR001450: 4Fe-4S ferredoxin, iron-sulphur binding	
		PF00198: 4FE4S_FERREDOXIN 0.0 [23-34]?	
	98% identity with At1g12090		