

	Signal peptide	Domain I	
LiEXPA1	-----MALLALLVVGFIAMAASAEYGG-----	GGWINAHATFYGGSDASGTMGGACGYGNLYSQG	YGTNTAALSTALFNNGLS 73
LiEXPA2	-----MALAGLLMVGFLATAAYTEADG-----	GGWINAHATFYGGSDASGTMGGACGYGNLYSQG	YGTNTAALSTALFNNGLS 73
LiEXPA3	-----MAAASGSPSLVGIIVSLALF-----LALAEARIPSG-----	SPWQSAHATFYGGSDASGTMGGACGYGNLYSQG	YGVNTAALSTALFNNGLS 81
LiEXPA4	-----MILPGLLLFGLISLVASHVVDGYG-----	GGWTNAHATFYGGSDASGTMGGACGYGNLYSQG	YGTNTAALSTALFDSGLS 74
LiEXPA5	-----MKDMERKRFVNSTGLVLFGLLSVSHVVDGYG-----	GGWTNAHATFYGGSDASGTMGGACGYGNLYSQG	YGTNTAALSTALFDNGLS 84
LiEXPA6	-----MVLSDLASMTGREDMACLGILLMGLLSLIPCAHSNG-----	EGWTDAAHATFYGGSDASGTMGGACGYGNLYDEG	YGTDTAALSTALFNDGLS 87
LiEXPA7	-----MAVVGGSFLVLFALLSFCNIHGSYGDY-----	GGWQGGHATFYGGSDASGTMGGACGYGNLYSQG	YGTNTAALSTALFNNGLS 78
LiEXPA8	-----MSRTSALSVLFVFLGSCCLRIAVSDD-----	GGWQGGHATFYGGSDASGTMGGACGYGNLYSQG	YGTNTAALSTALFNNGLS 76
LiEXPA9	-----MAMARISISALILVLGSCIGGTGDN-----	GGWESGHATFYGGSDASGTMGGACGYGNLYSQG	YGTNTAALSTALFNNGLS 78
LiEXPA10	-----MAGTASVVTGIVLLAAFLAVAEARIPSS-----	GPWQKAHATFYGGSDASGTMGGACGYGNLYSHG	YGVSTAALSTALFRNGFS 79
LiEXPA11	-----MAAASALSAIVISLVAF-----LSVAEARIPSG-----	SPWQSAHATFYGGSDASGTMGGACGYGNLYSQG	YGVNTAALSTALFNNGFS 80
LiEXPA12	-----MAAASGSPSLVGIIVSLLAFLALAEARIPSG-----	SPWQSAHATFYGGSDASGTMGGACGYGNLYSQG	YGVNTAALSTALFNNGFS 81
LiEXPA13	-----MAPSGTIVTCGIGTLLCLL-----AAAEARIPSG-----	GPWQKAHATFYGGSDASGTMGGACGYGNLYSQG	YGVNTAALSTALFNNGFS 79
LiEXPA14	-----MARFQTVPSIVTLTLLCLAAEGRIPTG-----	GSWQDAHATFYGGSDASGTMGGACGYGNLYSQG	YGVNTAALSTALFNNGLS 79
LiEXPA15	-----MLHMLLVWLVLASPATSTHTPTSTPPA-----	SEWRSARATYYAASDPRDAVGACGYGDLVKAG	YGMATVGLSESIIFERGOV 78
LiEXPA16	-----MATVVSCTAAGIAYIVMAMMAAEARIPSG-----	GSWQNAHATFYGGSDASGTMGGACGYGNLYSQG	YGVNTAALSTALFNNGLS 82
LiEXPA17	-----MASMTVLSTALFLLSLMCAEGRIPRG-----	SSWQTAHATFYGGSDASGTMGGACGYGNLYSQG	YGVNTAALSTALFNNGFS 78
LiEXPA18	-----MESLFAKKVTSFLLYVGLLIVMENSKGAS-----	AAWLKAHATFYGGSDASGTMGGACGYGNLYTDG	YGTRTAALSTALFNNGKS 80
LiEXPA19	-----MNMERSIFALVTLALLRRTYSVAFAA-----	TGWTKAHATFYGGSDASGTMGGACGYGNLYAAG	YGTRTAALSTALFDDGAS 78
LiEXPA20	-----MAASIVALVLLGLNLYFNLTVTNGFTA-----	TGWTKAHATFYGGSDASGTMGGACGYGNLYYQTG	YGTRTAALSTALFNDGNS 78
LiEXPA21	-----MGLPLQAPSHPLALLLVLLISALALVQVAAKNDNGHHHPKFKPG	PPWKAQAYATFYQG--GSQTFGACGYQDVVVEG	YGLQTAALSVLFFNNQGT 93
LiEXPA22	MNRERERSGSAESEPANSSSSKDPQMGLLLTLVGLMIMVDRCKPFNE	GEWKSATATYTKETNGPIINEGACGYGDLHRRAS	YGEYSAGLSTMLFNRGST 98
LiEXPB1	-----MQPQRRMGFLFGLWALLVYSTRLVSAQLAHAA-----	QWQKAHATFYGGSPGSDGGACGYGDLVDVKPLRARVGA	YSPVLFMNGEG 86
LiEXPB2	-----MALLPOHPHALLFLALLALISLNPSSAFNPFSRVQSNSTD	WSPAGATWYGGANGDSGGACGYGNVAGQPPFSMSI	SAGPSLFFKSGKS 95
LiEXLA1	-----MRSISSTQSPSTLSHKLFSATMVIFLCEFFLLVSSATACD-----	RCLHRSKAAFYFNKASSLS--GACGYGSAAMEL	SAGQLAAVPSLYKDGAG 90
LiEXLA2	-----MAAIFLSHVFFLLVSSATACD-----	RCLHRSKAAHSSSMASALPSAGSCGYGSLAVDL	NSNQIILAAVPSLYKDGAG 73
LiEXLB1	-----MGSHSNSHNNFLLCLLLLPVACYCQ-----	DSFVPSRATYGYSPDCYGTANGACGYGYDGRTV	NDGYVTGVSKLYKDGSG 77
		Domain I	Domain II
LiEXPA1	CGSCYIEIRCMND--GKWLQSG--SIVVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 165		
LiEXPA2	CGSCYIEIRCMND--GKWLQSG--SIVVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 165		
LiEXPA3	CGSCYIEIRCMND--GKWLQSG--SIVVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 173		
LiEXPA4	CGACYELRCVKD--PQWCLPG--SIVVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 158		
LiEXPA5	CGACYELRCVKD--PQWCLPG--SIVVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 168		
LiEXPA6	CGACFEIKCTGE--PKWCLPG--SIVVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YKAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 179		
LiEXPA7	CGSCYEMRCND--PRWCLPG--TITVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 170		
LiEXPA8	CGACYEMRCND--PQWCLPG--TITVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 168		
LiEXPA9	CGACYEMRCND--PQWCLPG--TITVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 170		
LiEXPA10	CGACFEIKCTDD--PKWGRGSPSIFIVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 173		
LiEXPA11	CGACFEIKCTDD--PKWGRGSPSIFIVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 173		
LiEXPA12	CGACFEIKCTDD--PQWCHSGSPSIFIVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 174		
LiEXPA13	CGACFEIKCTDD--PQWCHSGSPSIFIVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 175		
LiEXPA14	CGACFEIKCTDD--PQWCHSGSPSIFIVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 173		
LiEXPA15	CGACFEIKCTDD--PRWGNPNPSIFIVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 173		
LiEXPA16	CGACFEIKCTDD--LRWCIPGT--SIIITATNFCAPNYGFPADGGGHCNPPNQHFLPIEAFKIAI-----WKAGNMPVQYRRIKORKEG--GIRFTINGHS--Y 171		
LiEXPA17	CGACFEIKCTDD--PRWCHSGSPSIFIVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 176		
LiEXPA18	CGACFEIKCTDD--PQWCHSGSPSIFIVTATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 172		
LiEXPA19	CGGQYQIICDAAQVQWCLKG--TYIITATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 175		
LiEXPA20	CGGQYQIICDAAQVQWCLKG--VSVTITATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 173		
LiEXPA21	CGGQYQIICDAAQVQWCLKG--VSVTITATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 173		
LiEXPA22	CGACYIEIRCMND--AQWQPGQASLKITATNFCPPNNALPNNAGGWCNPPLOHFDLSQPVFQRIAQ-----YKAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 188		
LiEXPB1	CGACYIEIRCMND--IRWCLPGSPTVILATDFCPNNYGLSADYGGWCNPPLOHFDLSQPVFQRIAQ-----YRAGIVPVAYRRVPCRRRG--GIRFTINGHS--Y 192		
LiEXPB2	CGACYIEIRCMND--SISRRRAVTVITDE--CP-----GGYQSGGRVHFDLSGAAGFARMATGDDGQLRDRGVIPVYRRTQCKYPGKNIIFRVNNGS--TN 178		
LiEXLA1	CGACYIEIRCMND--EAGGNPATVITDE--CP-----GGPCTSESIVHFDLSGAAGFARMATGDDGQLRDRGVIPVYRRTQCKYPGKNIIFRVNNGS--TN 188		
LiEXLA2	CGACFKVRCNE--KLSCKEGTQVITDLDN-----KSNATDFVLSRRFAAMANKGMSQDILKLGIVDIIEYKRVPGCEFNQNLAIIRVEESSQKPH 178		
LiEXLB1	CGACFKVRCNE--KLSCKEGARVITDLD-----RGNSTDFVLSRRRAAMANKGMSQDILKLGIVDIIEYKRVPGCEFNQNLAIIRVEESSQKPH 161		
	CGACYQVRCKTP--EDTEDGANVVVTD-----YGEDRTDFVLSRRRAAMANKGMSQDILKLGIVDIIEYKRVPGCEFNQNLAIIRVEESSQKPH 164		
		Domain II	
LiEXPA1	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 247		
LiEXPA2	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 249		
LiEXPA3	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 255		
LiEXPA4	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 240		
LiEXPA5	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 252		
LiEXPA6	FPLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 263		
LiEXPA7	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 254		
LiEXPA8	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 252		
LiEXPA9	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 254		
LiEXPA10	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 257		
LiEXPA11	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 258		
LiEXPA12	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 259		
LiEXPA13	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 257		
LiEXPA14	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 257		
LiEXPA15	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 255		
LiEXPA16	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 260		
LiEXPA17	FNLVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 256		
LiEXPA18	FELVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 259		
LiEXPA19	FELVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 257		
LiEXPA20	FELVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 257		
LiEXPA21	FELVLTITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 271		
LiEXPA22	YYQVLVITNVGGAGDVHSVSVKGSR--TG--WQPMMSRNWGNWQ--SNSYLNGQ--SLSFVVTAS--DGRSIVSYNVAPAGWSFGQTFTGA--QL----- 274		
LiEXPB1	WLSSLVEFEDDGGDVGSMHIREAG--SSEWEMKHLWGANWCIIGGTLQG--PFSVKLTITLSTRTLSARDVIRNWSPTTYTSLRNLFS----- 264		
LiEXPB2	F--ASLIEYEDDGGDLSVALVELQALDSDSVPMRQSGYAVVK--LDSGALGAPFSIRLTAAQSGKTLVANNVIRPAGWQPGQTYRSLVNF----- 274		
LiEXLA1	YLAIKVLVYGGQTEIFVLDVAQVG--SSNRVMSRKYGAVVDS--TSRVPDGLQFRFVVTAGYDGKWWAKSVLPADKWKVGGIYDAGVQITDIAREGYSKCDGDSWR 281		
LiEXLA2	YLAIKVLVYGGQTEIFVLDVAQVG--SPNWRVMSRKYGAVVDS--TSRVPDGLQFRFVVTAGYDGKWWAKSVLPADKWKVGGIYDAGVQITDIAREGYSKCDGDSWR 264		
LiEXLB1	YMALVILVYAGRNIDMAVQISPAD--CQWRQMRRAYGAVFD--IATPPKEDIIVRFQSGSNGLNWVQPKGTIPRDWKAGATYTTTELQNL----- 251		

Supplementary Fig S3: Amino acid sequence comparison of members of the LiEXPs gene family.