Table S1 The list of 46 ABF genes identified in *Medicago sativa* L..

Gene ID	Gene Name	Protein
MS.gene88920.t1	MsABF1	MASSKLMPSSDPPSSPSPKPHFTTANFLDDQISLADAVATPRTVDDVWREIVAGDVISGDRECKEEISDEMMTLEDFLVKAGAVEDEEEGEDVKMTIPLSETLSGSGMFSLDSSFQGIENVDGSVIGFGNGNGNGNVNGVEMVEGGGRGKRGRPVMEQLDKAAQQRQRRMIKNRESAARSRERKQAYQVELESLAVKLEEENDKLMKEKAERKKERFKQLMEKVIPVVEQRRPPRLLRRLSHSTTILVDGSSEWKNPTVSIGDSITFKHKQNYNLYIFKNQKAFNLCNFTQANLLTDPSTTSYTWHPSRVGFFYFTFSNDSLKACQDSQKLAIKVTPTKASAPEASSPMPTTPGPSSGGDIQSSPSFPWPFRPHQGSSPGPAPTPEASSPITLPLVPYKGSGDGMPFINSNPAVPLPTGEVDSATIHPLATSGHQGQVPILFSHSLLF
MS.gene60690.t1	MsABF2	MASSKLMPSSDPPSSPSPKPHFTTANFLDDQISLADAVATPRTVDNVWREIVAGDVISGDRECKEEISDEMMTLEDFLVKAGAVEDEEEGEDVKMTIPLSETLSGSGMFSLDSSFQGIENVDGSVIGFGNGNGNGNGNVNGVEMVEGGGRGKRGRPVMEQLDKAAQQRQRRMIKNRESAARSRERKQAYQVELESLAVKLEEENDKLMKEKAERKKERFKQLMEKVIPVVEQRRPPRLLRRVRSLQWHPGLTPVQTANVLVEGKGDCRRLYDVVTV
MS.gene59225.t1	MsABF3	MASSKLMPSSDPPSSPSPKPHFTTANFLDDQISLADAVATPRTVDDVWREIVAGDVISGDRECKEEISDEMMTLEDFLVKAGAVEDEEEGEDVKMTIPLSETLSGSGMFSLDSSFQGIENVDGSVIGFGNGNGNGNVNGVEMVEGGGRGKRGRPVMEQLDKAAQQRQRRMIKNRESAARSRERKQAYQVELESLAVKLEEENDKLMKEKVMLRGKRRGSSRY
MS.gene006156.t1	MsABF4	MASSKLMPSSDPPSSPSPKPHFTTANFLDDQISLADAVATPRTVDDVWREIVAGDVISGDRECKEEISDEMMTLEDFLVKAGAVEDEEEGEDVKMTIPLSETLSGSGMFSLDSSFQGIENVDGSVIGFGNGNGNGNGNVNGVEMVEGGGRGKRGRPVMEQLDKAAQQRQRRMIKNRESAARSRERKQAYQVELESLAVKLEEENDKLMKEKAERKKERFKQLMEKVIPVVEQRRPPRLLRRLSHSTTILVDGSSEWKNPTVSIGDSITFKHKQNYNLYIFKNQKAFNLCNFTQANLLTDPSTTSYTWHPSRVGFFYFTFSNDSLKACQDSQKLAIKVTPTKASAPEASSPMPTTPGPSSG

		GDIQSSPSFPWPFRPHQGSSPGPAPTPEASSPITLPLVPYKGSGDGMPFINSNPAVPLPTGEVDSATIHPLATSGHQGQVPILFSHSLLF
MS.gene35405.t1	MsABF5	MALQQLDQEDSYPSNQNALTLDDFKNFDSLNMDEFLASIWSSSDEATTQTHNNIESVVATEHTSSQQLGDSVSVPPPVCKKTSDEVWSEIHKNQPQFKEENNLKRNETLKKQETPGEMTFEDFLVKAGVVQQSSSLSFQNHSGNVSNNMRPLNIASSGLTSNSPATYQMTSGAESSGAATRKRIIDGPPEVLLERKQRRMMKNRESAARSRARRQAYTIELEAELNLLQEENKMLKQFLAEAENKRKQELLQRKQSAKVQKGTEKSSSSTTW
MS.gene84329.t1	MsABF6	MALQQLDQEDSYPSNQNALTLDDFKNFDSLNMDEFLASIWSSSDEATTQTHNNIESVVTTEHTSSQQLGDSVSVPPLVCKKTSDEVWSEIHKNQPQFKEENNLKRNETLKKQETPGEMTFEDFLVKAGVVQQSSSLSFQNHSGNVSNNMRPLNIASSGLTSNSPATYQMTSGAESSGAATRKRIIDGPPEVLLERKQRRMMKNRESAARSRARRQAYTIELEAELNLLQEENKMLKQFLAEAENKRKQELLQRKQSAKVQKGTEKSSSSTTW
MS.gene034460.t1	MsABF7	MALQQLDQEDSHPTNQNALTLDDFKNFDSLNMDEFLASIWSSSDEATTQTHNNIESVVTTEHTSSQQLGDSVSVPPPVCKKTSDEVWSEIHKNQPQFKEENNLKRNETLKKQETPGEMTFEDFLVKAGVVQQSSSLSFQNHSGNVSNNMRPLNIASSGLTSNSPATYQMTSGAESSGAATRKRIIDGPPEVLLERKQRRMMKNRESAARSRARRQAYTIELEAELNLLQEENKMLKQFLAEAENKRKQELLQRKQSAKVQKGTEKSSSSTTW
MS.gene43043.t1	MsABF8	MALQQLDQEDSHPSNQNALTLDDFKNFDSLNMDEFLASIWSSSDEATTQTHNNIESVVTTEHTSSQQLGDSVSVPPPVCKKTSDEVWSEIHKYQPQFKEENNLKRNETLKKQETPGEMTFEDFLVKAGVVQQSSSLSFQNHSGNVSNNMRPLNIASSGLTSNSPATYQMTSGAESSGAATRKRIIDGPPEVLLERKQRRMMKNRESAARSRARRQAYTIELEAELNLLQEENKMLKQFLAEAENKRKQELLQRKQSAKVQKGTEKSSSSTTW
MS.gene56338.t1	MsABF9	MGSQVVDESNNENQPQFQPLARQNSMYNLTLDEVQNHLGDLGKPLSSMNLDELLKNVWTVEANQSIRMENEDTAQAGQVVFQRQPNLSLTGPLSKKTVDEVWRDIQQNNDHEEVKSQEMQSTLGEMTLEDFLVKAGVVSAASSNRKNTNSPTPKVSVVESNVALPQFSPHGPWIQYAQPHYQHPQQSVMATYVPSQIIAQSLHMAAGAPSGGVPYTDGQVALASPVVGNLSDTQKSARKR

		GPEDMIERTVERKQKRMIKNRESAARSRARKQAYTTELEIKVSRLEEENEKLRKEKELENMLVNAPPPEPKCQLRRVSSASF
MS.gene48512.t1	MsABF10	MNFKGFGNDPGASAAGAGNGGGRIAAGNFPLTRQPSVYSLTVDEFMNSMGGSGKDFGSMNMDELLKNIWSAEEVQTMGGEEAINNHLQRQGSLTLPRTLSQKTVDEVWKDISKDYGGPNLAAPMTQRQPTLGEMTLEEFLVRAGVVREDAKPNDGVFLDLGNVGNNGNLGLAFQAQQMNKVAGFMGNGSRINGNDDPLVGLQSPTNLPLNVNGIRSTNQQQQMQNSQSQAQQQHQNQQLQQLQQQHQQQQQQQQQQIFPKQPGLNYATQMPLSNNQGMRGGIVGLSPDQGLNGNLVQGGGIGMVGLAPGAVQIGAVSPANQISSDKMGKSNGDTSSVSPVPYVFNGGMRGRKGNGAVEKVIERRQRRMIKNRESAARSRARKQAYTMELEAEVAKLKEENEELQKKQEEIMELQKNQVPSYNMLICHPPPRAIEGSTKVIVKITFGQKLC
MS.gene38353.t1	MsABF11	MNFKGFGNDQGASAGNGGGRIAAGNFPLTRQPSVYSLTVDEFMNSMGGSGKDFGSMNMDELLKNIWSAEEVQTMGGEEAISNHLQRQGSLTLPRTLSQKTVDEVWKDISKDYGGPNLAAPMTQRQPTLGEMTLEEFLVRAGVVREDAKPNDGVFLDLGNVGNNGNLGLAFQAQQMNKVAGFMGNGSRINGNDDPLVGLQSPTNLPLNVNGIRSTNQQQQMQNSQSQAQQQHQNQQLQQLQQQHQQQQQQQIFPKQPGLNYATQMPLSNNQGMRGGIVGLSPDQGLNGNLVQGGGIGMVGLAPGAVQIGAVSPANQISSDKMGKSNGDTSSVSPVPYVFNGGMRGRKGNGAVEKVIERRQRRMIKNRESAARSRARKQAYTMELEAEVAKLKEENEELQKKQEEIMELQKNQLVRNMFKGLTYQCP
MS.gene62039.t1	MsABF12	MGSQVVDESNNENQPQFQPLARQNSMYNLTLDEVQNHLGDLGKPLSSMNLDELLKNVWTVEANQSIRMENEDTAQAGQVVFQRQPNLSLTGPLSKKTVDEVWRDIQQNNDHEEVKSQEMQSTLGEMTLEDFLVKAGVVSAASSNRKNTNSPTPKVSVVESNVALPQFSPHGPWIQYAQPHYQHPQQSVMATYVPSQIIAQSLHMAAGAPSDGVPYTDGQVALASPVVGNLSDTQKSARKRGPEDMVERTVERKQKRMIKNRESAARSRARKQAYTTELEIKVSRLEEENEKLRKEKELENMLANAPPPEPKCQLRRGHRSLP
MS.gene38710.t1	MsABF13	MNFKGFGNDQGASAGNGGGRIAAGNFPLTRQPSVYSLTVDEFMNSMGGSGKDFGSMNMDELLKNIWSAEEVQTMGGEEAISNHLQRQGSLTLPRTLSQKTVDEVWKDISKDYGGPNLAAP

		MTQRQPTLGEMTLEEFLVRAGVVREDAKPNDGVFLDLGNVGNNGNLGLAFQAQQMNKVAGFMGNGSRINGNDDPLVGLQSPTNLPLNVNGIRSTNQQQQMQNSQSAQQQHQNQQLQQLQQQHQQQQQQQIFPKQPGLNYATQMPLSNNQGMRGGIVGLSPDQGLNGNLVQGGGIGMVGLAPGAVQIGAVSPANQISSDKMGKSNGDTSSVSPVPYVFNGGMRGRKGNGAVEKVIERRQRRMIKNRESAARSRARKQAYTMELEAEVAKLKEENEELQKKQEEIMELQKNQVPSYNMLICHPPPRAIEGSTKVIVKITFGQKLC
MS.gene51984.t1	MsABF14	MGSQVVDESNNENQPQFQPLARQNSMYNLTLDEVQNHLGDLGKPLSSMNLDELLKNVWTVEANQSIRMENEDTAQAGQVVFQRQPNLSLTGPLSKKTVDEVWRDIQQNSDHEEVKSQEMQSTLGEMTLEDFLVKAGVVSAASSNRKNTNSPTPKVSVVESNVALPQFSPHGPWIQYAQPHYQHPQQSVMATYVPSQIIAQSLHMAAGAPSDGVPYTDGQVALASPVVRNLSDTQKSARKRGPEDMIERTVERKQKRMIKNRESAARSRARKQAYTTELEIKVSRLEEENEKLRKEKELENMLANAPPPEPKCQLRRVSSASF
MS.gene51703.t1	MsABF15	MGSQVVDESNNENQPQFQPLARQNSMYNLTLDEVQNHLGDLGKPLSSMNLDELLKNVWTVEANQSIRMENEDTAQAGQVVFQRQPNLSLTGPLSKKTVDEVWRDIQQNNDHEEVKSQEIQSTLGEMTLEDFLVKAGVVSAASSNRKNTNGPTPKVSVVESNVALPQFSPHGPWIQYAQPHYQHPQQSVMATYVPSQIIAQSLHMTAGAPSDGVPYTDGQVALASTVIGNLSDTQKSARKRGPEDMIERTVERKQKRMIKNRESAARSRARKQAYTTELEIKVSRLEEENEKLRKEKELENMLANAPPPEPKCQLRRVSSASF
MS.gene012975.t1	MsABF16	MNFKGFGNDQGASAGNGGGRIAAGNFPLTRQPSVYSLTVDEFMNSMGGSGKDFGSMNMDELLKNIWSAEEVQTMGGEEAISNHLQRQGSLTLPRTLSQKTVDEVWKDISKDYGGPNLAAPMTQRQPTLGEMTLEEFLVRAGVVREDAKPNDGVFLDLGNVGNNGNLGLAFQAQQMNKVAGFMGNGSRINGNDDPLVGLQSPTNLPLNVNGIRSTNQQQQMQNSQSAQQQHQNQQLQQLQQQHQQQQQQQIFPKQPGLNYATQMPLSNNQGMRGGIVGLSPDQGLNGNLVQGGGIGMVGLAPGAVQIGAVSPANQISSDKMGKSNGDTSSVSPVPYVFNGGMRGRKGNGAVEKVIERRQRRMIKNRESAARSRARKQAYTMELEAEVAKLKEENEELQKKQEEIMELQKNQVPSYNMLICHPPPRAIEGSTKVIVKITFGQKLC

MS.gene012973.t1	MsABF17	GFGNDQGASAGNGGGRIAAGNFPLTRQPSVYSLTVDEFMNSMGGSGKDFGSMNMDELLKNIWSAEEVQTMGGEEAISNHLQRQGSLTLPRTLSQKTVDEVWKDISKDYGGPNLAAPMTQRQPTLGEMTLEEFLVRAGVVREDAKPNDGVFLDLGNVGNNGNLGLAFQAQQMNKVAGFMGNGSRINGMRGGIVGLSPDQGLNGNLVQGGGIGMVGLAPGAVQIGAVSPANQISSDKMGKSNGDTSSVSPVPYVFNGGMRGRKGNGAVEKVIERRQRRMIKNRESAARSRARKQAYTMELEAEVAKLKEENEELQKKQEEIMELQKNQLVRNMFKGLTYQCP
MS.gene26446.t1	MsABF18	MNFAWDAMSVKTPGSVNLASQSSIYSLTFDELQSTIGGVGKDFGSMNMDELLKNIWNVEETQALTSLTGGGVGEGPNNPNGGSLQKQGSLTLPRTLSQRKVDEVWRDLMKDSGSSMPQRQPTLGEVTLEEFLVRAGVVKEDTPNHAQQIERPNNNEWFSDFSRSNNNTNLLGFQQPNGNNGDMSDNNNLVPKHVPLPPSSINLNHSQRPPPLFPKPTTVAFSSPIHLLNNAQLGNNGRSVVPGVGMHGLSASNVTAPVTSPGSKMSPDLITKRNLDPTLLSPVPYAINRGRKCVPVEKGVERRQKRMIKNRESAARSRARKQAYTVELEAEVAKLKEVNEELQRKQAEFMEMQKSKEDLVRTNKIKYLRRTLTGPW
MS.gene28750.t1	MsABF19	MDEILKNIFPAAIEAAKQHHQEEQQSNNNNNNIDDVWTDIVAEGGANHLHHQQHYHHPSSDEGFSACGAGGGDEVTLEDFLVKAGAVPYPHHQYPSSSSAVDDGSHSLQVALGKRKTVDETLDKAALQKQKRMIKNRESAARLILLSLRVWLSIWR
MS.gene053517.t1	MsABF20	MNFAWDAMSVKTPGSVNLASQSSIYSLTFDELQSTIGGVGKDFGSMNMDELLKNIWNVEETQALTSLTGGGVGEGPNNPNGGSLQKQGSLTLPRTLSQRKVDEVWRDLMKDSGSSMPQRQPTLGEVTLEEFLVRAGVVKEDTPNHAQQIERPNNNEWFSDFSRSNNNTNLLGFQQPNGNNGDMSDNNNLVPKHVPLPPSSINLNHSQRPPPLFPKPTTVAFSSPIHLLNNAQLGNNGRSVVPGVGMHGLSASNVTAPVTSPGSKMSPDLITKRNLDPTLLSPVPYAINRGRKCVPVEKGVERRQKRMIKNRESAARSRARKQAYTVELEAEVAKLKEVNEELQRKQAEFMEIQKSKEDLVRTNKIKYLRRTLTGPW
MS.gene35075.t1	MsABF21	MDEILKNIFPAAIEAAKQHHQEHHQEEQQSNNNNNNIDDVWTDIVAEGGANHLHHQQHYHHPSSDEGFSACGAGGGDEVTLEDFLVKAGAVPYPHHQYPSSSSAVDDGSHSLQVALGKRKTVDETLDKAALQKQKRMIKNRESAARLILLSLRVWLSIWR

MS.gene028382.t1	MsABF22	MDEILKNIFPAAIEAAKQHHQEHHQEEQQSNNNNNNIDDVWTDIVAEGGANHLHHQQHYHHPSSDEGFSACGAGGGDEVTLEDFLVKAGAVPYPHHQYPSSSSAVDDGSHSLQVALGKRKTVDETLDKAALQKQKRMIKNRESAARSRERKQAYTTELESLVKHLEIENKQLEEEQAERKKLRLKQLQEFLIPITEQPRPKRKLRRSNSS
MS.gene23905.t1	MsABF23	MDEILKNIFPAAIEAAKQHHQEHHQEEQQSNNNNNNIDDVWTDIVAEGGANHLHHQQHYHHPSSDEGFSACGAGGGDEVTLEDFLVKAGAVPYPHHQYPSSSSAVDDGSHSLQVALGKRKTVDETLDKAALQKQKRMIKNRESAARSRERKQAYTTELESLVKHLEIENKQLEEEQAERKKLRLKQLQEFLIPITEQPRPKRKLRRSNSS
MS.gene028384.t1	MsABF24	MDEILKNIFPAAIEAAKQHHQEHHQEEQQSNNNNNNIDDVWTDIVAEGGANHLHHQQHYHHPSSDEGFSACGAGGGDEVTLEDFLVKAGAVPYPHHQYPSSSSAVDDGSHSLQVALGKRKTVDETLDKAALQKQKRMIKNRESAARSRERKQAYTTELESLVKHLEIENKQLEEEQAERKKLRLKQLQEFLIPITEQPRPKRKLRRSNSS
MS.gene047841.t1	MsABF25	MNFAWDAMSVKTPGSVNLASQSSIYSLTFDELQSTIGGVGKDFGSMNMDELLKNIWNVEETQALTSLTGGGVGEGPNNPNGGSLQKQGSLTLPRTLSQRKVDEVWRDLMKDSGSSMPQRQPTLGEVTLEEFLVRAGVVKEDTPNHAQQIERPNNNEWFSDFSRSNNNTNLLGFQQPNGNNGDMSDNNNLVPKHVPLPPSSINLNHSQRPPPLFPKPTTVAFSSPIHLLNNAQLGNNGRSVVPGVGMHGLSASNVTAPVTSPGSKMSPDLITKRNLDPTLLSPVPYAINRGRKCVPVEKGVERRQKRMIKNRESAARSRARKQAYTVELEAEVAKLKEVNEELQRKQAEFMEMQKSKEDLVRTNKIKYLRRTLTGPW
MS.gene99362.t1	MsABF26	MGIQTMGSKSNGQQSHLQANQLVKQNSWYGLTLDEVNSLLGDLGKPLGSMNLDELLQNVWTAEGNKVVGMESEQASSSSSLQRQASMTLARALSGKTVDDVWREIQLGQKKQYGDDVKVEDSEMSLGGTTLEDFLVQAGLFAGASISPTVGLDAMDTAIPLSFQPNTSLVSSSSISSLSDAKPGRKRDAPDAYEKALERRLRRKIKNRESAARSRARKQAYHNELVTKVTLLEQQNMQLKKEK
MS.gene73966.t1	MsABF27	MISTESDQLIQNPTPDINSSFLYGNNSGSGNNLNETVCNKTINEVWSEINQQKNVIGSMDHNNLQQSILGETTLDNFLAHAKAINIGNQENVHAIGDETQVPFIGVEPNLVMASQPEGLC

		PDFGVANSVYENKLMEIGYSEIPIGATTTHLSSTCSDSKGGAGGSGVGRKHKYSDEMMEKTVERRQKRMAKNRESAARSRAKKQEHINKLQMDKFQLEEKNTELKLIKKVEEQLFSNLTPTYQLRRVSSAKF
MS.gene016887.t1	MsABF28	MGSQSNGQQSHLQANQLVKQNSWYGLTLDEVNSLLGDLGKPLGSMNLDELLQNVWTAEGNKVVGMESEQVSSSSSLQRQASMTLARALSGKTVDDVWREIQLGQKKQYGDDVKVEDREMGLGGTTLEDFLVQAGLFAGASISPTVGLDAMDTAIPQSFQPKTSLVSSSSISSLSDAKPGRKKDASDAYEKALERRLRRKIKNRESAARSRARKQAYHNELVTKVTLLEQQNMQLKKEKEFEQGLQPESSPEPKYRLRRHTLRRLHGVCSGNRSSILRSISACLFPCTSSDEGKGLLETRAQPHKRATLYNRRKMQKLNMAVSLELILKRIPWPINTEVSISLVDQVNNGLNTVTCACKRAFEPNSPKLDVPPLISVNDFFKTELGYFLNGSCLIQFSISCPNKSEFFFLEALGAGAPKTAETAVCDKTAVDSSLGTSGGSSIKTKSKRLALQSAAGPVFGAKYDASAGGSKVVASVGGSSIETESKVTTSVSGRSVETETKAGASDGGSPIETKNKAAVPKKSVDPSMGCVIKDTPDLSVEPGCVTKGAKDKTDLLGLFSQAYIKEIKEAWEDLKGFHEVPEVINLMQPQMDRVFSVGKVVECRAEISCCEKTLSDLKNQLLVLENEAASYVEEPESAIGIGSI
MS.gene063659.t1	MsABF29	MEEVWKDINLSSLNDQNTRPIIMSTRNSTFGGGVILQDFLTRPLTLDPPKSLDYSSNNSSSSVASDQNNNNASFYCPSSTTTPPLVTALSLNSRPDFLYDPLIRHNKHNNSQLLLQQQHQQQHNIGVSNVSACFVNASPYDQNVGVAASSSFTCFGKRFGEAPDISPGERRNKRMIKNRESAARSRARK
MS.gene035959.t1	MsABF30	MISTESDQLIQNPTPDINSSFLYGNNSGSGSGNNLNETVCNKTINEVWSEINQQKNVIGSMDHNNLQQSMLGETTLDNFLAHAKAINIGNQENVHAIGDETQVPFIGVEPNLVMASQPEGLCPDFGVANSVYENKLMEIGYSEIPIGATTTHLSSTCSDSKGGAGGSGVGRKHKYSDEMMEKTIERRQKRMAKNRESAARSRAKKQKVEEQLFSNLTPTYQLRRVSSAKFQEKIASFFLFL
MS.gene37622.t1	MsABF31	MGIQTMGSKSNGQQSHLQANQLVKQNSWYGLTLDEVNSLLGDLGKPLGSMNLDELLQNVWTAEGNKVVGMESEQASSSSSLQRQASMTLARALSGKTVDDVWREIQLGQKKQYGDDVKVEDSEMSLGGTTLEDFLVQAGLFAGASISPTVGLDAMDTAIPLSFQPNTSLVSSSSISSLSDAKPGRKRDAPDAYEKALERRLRRKIKNRESAARSRARKQAYHNELVTKVTLLEQQNMQLK

		KEKVQDLIHFSPT
MS.gene67488.t1	MsABF32	MEEVWKDINLSSLNDQNTRPIIMSTRNSTFGGGVILQDFLTRPLTLDPPKSLDYSSNNSSSSVASDQNNNNASFYCPSSTTTPPLVTALSLNSRPDFLYDPLIRHNKHNNSQLLLQQQHQQQHNIGVSNVSACFVNASPYDQNVGVAASSSFTCFGKRFGEAPDISPGERRNKRMIKNRESAARSRARKQEKIASFFLFL
MS.gene39793.t1	MsABF33	MGSQSNGQQSHLQANQLVKQNSWYGLTLDEVNSLLGDLGKPLGSMNLDELLQNVWTAEGNKVVGMESEQVSSSSSLQRQASMTLARALSGKTVDDVWREIQLGQKKQYGDDVKVEDREMGLGGTTLEDFLVQAGLFAGASISPTVGLDAMDTAIPQSFQPKTSLVSSSSISSLSDAKSGRKRDAPDAYEKALERRLRRKIKNRESAARSRARKQAYHNELVTKVTLLEQQNMQLKKEKEFEQGLQPESSPEPKYRLRRHTLRRLHGVCSGNRSSILRSISACLFPCTSSDEGKGLLETRAQPHKRATLYNRRKMQKLNMAVSLELILKRIPWPINTEVSISLVDQVNNGLNTVTCACKRAFEPNSPKLDVPPLISVNDFFKTELGYFLNGSCLIQFSISCPNKSEFFFLEALGAGAPKTAETAVCDKTAVDSSLGTSGGSSIKTKSKRLALQSAAGPVFGAKYDASAGGSKVVASVGGSSIETESKVTTSVSGRSVETETKASASDGGSSIETKNKAAVPKKSVDPSMGCVIKDTPDLSVEPGCVTKGAKDKTDLLGLFSQAYSINLNQFVEMKFRKAHRAIYFKDALYDLLSALMKKTWIGLDIKSVKEIKEAWEDLKGFHEVPEVINLMQPQMDRVFSVGKVVECRAEISCCEKTLSDLKNQLLVLENEAASYVEEPESAIGIGSI
MS.gene62322.t1	MsABF34	MGSQGGTVSESKTLPLSRSGSLYNLTLDEVQNHLGNLGKPLGSMNLDELLKSVWSVEAGEVSDFGGSDVAAAAGNIQHNQLGLSSQGSLTLSGDLSKKTVDEVWKDMQGKKRGVDRDRKSREKQQTLGEMTLEDFLVKAGVVGESFHNNKDDGGLLRVDSNEDSRHNVSQHGLHWMQYPVHSVQQQQHQYEKHMMPGFAAVHAIQQPFQVAGNQVLDAAISPSSLMGTLSDTQTLGRKRVASGILVEKTVERRQKRMIKNRESAARSRARRQAYTQELELKVSRLEEENERLRRQNEIEKEVPTAPPPEPKNQLRRTNSASF
MS.gene47208.t1	MsABF35	MGSQGGTVSESKTLPLSRSGSLYNLTLDEVQNHLGNLGKPLGSMNLDELLKSVWSVEAGEVSDFGGSDVAAAAGNIQHNQLGLSSQGSLTLSGDLSKKTVDEVWKDMQGKKRGVDRDRKSREKQQTLGEMTLEDFLVKAGVVGESFHNNKDDGGLLRVDSNEDSRHNVSQHGLHWMQYPV

		HSVQQQHQYEKHMMPGFAAVHAIQQPFQVAGNQVLDAAISPSSLMGTLSDTQTLGRKRVASGILVEKTVERRQKRMIKNRESAARSRARRQAYTQELELKVSRLEEENERLRRQNEIEKEVPTAPPPEPKNQLRRTNSASF
MS.gene013906.t1	MsABF36	MGSHGGAIQEQKTGTLAREGSLYNLTFDEVQNQLGNLGKPLGSMNLDELLKSLWTSEAAQGSGLDSGTSDGYMQHGQLASGSSMNPLTLSGDLSKKTIDEVWRDMQQKKSATQDRRTATLGEMTLEDFLMKAGVATESFPSEDNAMSGRVDSQQQQQNTSQHGHWMQYQVPSVQQPQQQHQHQNHQNNMMTGFAGYMTGHVVQQPVLDAGYTEAMVSLSPSSLMATSSDTQTQGRKRVASGVVVEKTVERRQKRMIKNRESAARSRARKQAYTQELEIKVSHLEEENERLKRLHEIERVLPSMPPPDPKHQLRRTSSAPL
MS.gene050328.t1	MsABF37	MVVREGEMNWQQGEVESLQREGEEAIRNDVNNVISSSLGRQSSSIYSLTLDEFQHSLCDSGKNFGSMNMDEFLSSIWNAEENQQQAASNNNNSNNNNLSAAQKGISKQASLPRQNSLSIPAPLCRKTVEQVWSEIHKEQQNHHNINNVAQNTESTPRQPTFGEMTLEDFLVKAGVVREQQSGMPVAIAPPPAAAAVSSHRPQQHYAAVYPNNNSTMAQAASFAIGGGGGNLNVVAPPYQTVAQGGGGVGEPSGSGYVGNGKTRDSIGTGYPPPPPAVCYGGRVVNGGAGSYGVAVAQTMGMGGPVSPVSSDGIGNENSGGQFGIDMNGLRGRKRMVDGPVERVVERRQRRMIKNRESAARSRARKQAYTVELEAELNQLREENSQLKQALAELERRRRQQVTNDVFRGNKRESSNQSSESKRETERLKKEYKLSYVKKTSHGEE
MS.gene068056.t1	MsABF38	MGSHGGAIQEQKTGTLAREGSLYNLTFDEVQNQLGNLGKPLGSMNLDELLKSLWTSEAAQGSGLDSGTTDGYMQHGQLASGSSMNPLTLSGDLSKKTIDEVWRDMQQKKSASQDRRTATLGEMTLEDFLMKAGVATESFPSEDNAMSGRVDSQQQQQNTSQHGHWMQYQVPSVQQPQQQHQHQNHQNNMMTGFAGYMTSHVVQQPVLDAGYTEAMVSLSPSSLMATSSDTQTQGRKRVASGVVVEKTVERRQKRMIKNRESAARSRARKQAYTQELEIKVSHLEEENERLKRLHEIERVLPSMPPPDPKHQLRRTSSAPL
MS.gene44707.t1	MsABF39	MEEVWNWKYMSTRNCTFGGVILQDFHTQALTSDPPKSIDYSSNNLSSFFASDQNNNNASFYCPSSMTPPPLVTDFHFVHQNISAPRVSASVNPSPYDQNVGVAASNSFISFGKRSCEATDISRSERRNKRMIKNRESAARSRARKQAKILSAYTIELEQQVQLLEEENARLRRQQQEDYT

		ILLEQKVQLLQEENARLRKQQQKLREAESVGQQKK
MS.gene41866.t1	MsABF40	MGSHGGAIQEQKTGTLAREGSLYNLTFDEVQNQLGNLGKPLGSMNLDELLKSLWTSEAAQGSGLDSGTSDGYMQHGQLASGSSMNPLTLSGDLSKKTIDEVWRDMQQKKSASQDRRTATLGEMTLEDFLMKAGVATESFPSEDNAMSGRVDSQQQQQNTSQHGHWMQYQVPSVQQPQQQHQHQNHQNNMMTGFAGYMAGHVVQQPVLDAGYTEAMVSLSPSSLIATSSDTQTQGRKRVASGVVVEKTVERRQKRMIKNRESAARSRARKQAYTQELEIKVSHLEEENERLKRLHEIERVLPSMPPPDPKHQLRRTSSAPL
MS.gene41906.t1	MsABF41	MGSHGGAIQEQKTGTLAREGSLYNLTFDEVQNQLGNLGKPLGSMNLDELLKSLWTSEAAQGSGLDSGTSDGYMQHGQLASGSSMNPLTLSGDLSKKTIDEDRRTATLGEMTLEDFLMKAGVATESFPSEDNAMSGRVDSQQQQQNTSQHGHWMQYQVPSVQQPQQQHQHQNHQNNMMTGFAGYMAGHVVQQPVLDAGYTEAMVSLSPSSLIATSSDTQTQGRKRVASGVVVEKTVERRQKRMIKNRESAARSRARKQAYTQELEIKVSHLEEENERLKRLHEIERVLPSMPPPDPKHQLRRTSSAPL
MS.gene77815.t1	MsABF42	TMGSQGGGDGSGRRSQLHSLVRQNSVYSLTLDEVQNQLGDLGKPLSSMNLDELLKNVWTVEVNQSTNTDNEGTTQSSEASLQRQASLALKAAFSKRTVDEVWRDIQQKKDNEEKKSRERQTTLGEMTLEDFLVKAGIVAEASSNKKNTDTTSAADSNVAVSQFPLQGQWLQYPQPQYQHLQQSSMGIYMPSQGIAQPLHMGSGVSMEIPFADSHMALGAPLMGTVSDTQMPGRKRSTPEDMVEKTVERRQKRMIKNRESAARSRARKQVISLFISSVVTRKSLLFDLFLL
MS.gene063953.t1	MsABF43	MGTQTMGSQGGGDGSGRRSQLHSLVRQNSVYSLTLDEVQNQLGDLGKPLSSMNLDELLKNVWTVEVNQSTNTDNEGTTQSSEASLQRQASLALKAAFSKRTVDEVWRDIQQKKDNEEKKSRERQTTLGEMTLEDFLVKAGIVAEASSNKKNTDTTSAADSNVAVSQFPLQGQWLQYPQPQYQHLQQSSMGIYMPSQGIAQPLHMGSGVSMEIPFADSHMALGAPLMGTVSDTQMPGRKRSTPEDMVEKTVERRQKRMIKNRESAARSRARKQAYTNELEIKVSRLEEENEMLRKRKELESMLPCTPIAEPKYQLRRIASCPF
MS.gene016376.t1	MsABF44	MGTQTMGSQGGGDGSGRRSQLHSLVRQNSVYSLTLDEVQNQLGDLGKPLSSMNLDELLKNVWTVEVNQSTNTDNEGTTQSSEASLQRQASLALKAAFSKKTVDEVWRDIQQKKDNEEKKS

		RERQTTLGEMTLEDFLVKAGIVAEASSNKPNTDTTAAADSNVAVSQFPLQGQWLQYPQPQYQHLQQSSMGIYMPSQGIAQPLHMGSGASMEIPFADSHMALGAPLMGTVSDTQMPGRKRSTPEDMVEKTVERRQKRMIKNRESAARSRARKQAYTNELEVKVSRLEEENEMLRKRKIE
MS.gene59798.t1	MsABF45	MGTQTMGSQGGGDGSGRRSQLHSLVRQNSVYSLTLDEVQNQLGDLGKPLSSMNLDELLKNVWTVEVNQSTNTDNEGTTQSSEASLQRQASLALKAAFSKRTVDEVWRDIQQKKDNEEKKSRERQTTLGEMTLEDFLVKAGIVAEASSNKKNTDTTAAADSNVAVSQFPLQGQWLQYPQPQYQHLQQSSMGIYMPSQGIAQPLHMGSGVSMEIPFADSHMALGAPLMGTVSDTQMPGRKRITPEDMVEKTVERRQKRMIKNRESAARSRARKQAYTNELEIKVSRLEEENEMLRKRKELESMLPCTPIAEPKYQLRRIASCPF
MS.gene83996.t1	MsABF46	MGSQGGTVSESKTLPLSRSGSLYNLTLDEVQNHLGNLGKPLGSMNLDELLKSVWSVEAGEVSDFGGSDVAAAAGNIQHNQLGLSSQGSLTLSGDLSKKTVDEVWKDMQGKKRGVDRDRKSREKQQTLGEMTLEDFLVKAGVVGESFHNNKDDGGLLRVDSNEDSRHNVSQHGLHWMQYPVHSVQQQQHQYEKHMMPGFAAVHAIQQPFQVAGNQVLDAAISPSSLMGTTVLSKTPTPSTGTLSDTQTLGRKRVASGILVEKTVERRQKRMIKNRESAARSRARRQAYTQELELKVSRLEEENERLRRQN