

Table S1. The ZF-HD protein sequences of *Arabidopsis*, tomato and tobacco

Gene name	Accession number	Putative protein sequences
NtZF-HD1	Nitab4.5_0003309g0010.1	MQGDKANDNIYRECLRNHAASLGSYATDGCGEFTLDDNNNNNTSPRSASLHCAACGCHRNFHRKVMYGASYSNNSSRDREIVA AELTDYGGGRMSAALTAESPRSGKKRFRTKFTTDQKEKMLAFAEKLGWTL
		QRKDQENETERFCREVGVSRKVFKVWMHNHNNTSSVSTGNASSLTQ
NtZF-HD2	Nitab4.5_0001418g0030.1	MYWDAAAAKCRLTMVGKFFKRKPKMTAIRASFSAKYPLKDHVKIVSFDSLHVFLDFTNEEDYDAIFFKETIIVAGA QMEVFRWTPEFHVFHGYHVMQTKMKPDNHTAKVEGRDETLGIMELDKNEHIGGGNEYGS
		KESEAAPKNTHILEDGLYISDSVDCVPEATHSDSAERV ASPVNCSTATSEIQASAETSCSGSSGLSFASDGIAGGIPSVMDSSSMCSTDMSFRGTYSNHNQKLYGRGWKYGSKSTSNAADWASEKLNQPLDALPIGE HHEDRKSRPPIQVQYSTYRGRQAVTFPENYWESLVPDCKLTLLIGNFFQRKPRMKEIRADFIKNPLKGQVKITHYTSQQVSLDFTNEADYDTVLSKKTLTVAVMQISWWSRDIHHEVVSTLNPQKQEWKAMDKERD VKPGIMEQQKTELDELIGGETEYKIDAPEAVLETDPDILGEVSDVSNLHIVPEVAHPDFRDNDASPVNCDTDTSKMHPSIGITCCQLSGISAPQN MIDGTSPYVMNVNSSKCTYSILSIVTTGLSSNDKDQSKSIRDVAV SHQSELTESDRERHSSEIPSVSSPPRSPRSIGSVIQLMSKLVSVTNDPNSVKRSTSDNSNLTQKSVPLFNSAENAVLLSVDPHKSIIEPKAIEKPLVRSISITTENFPSNQVTASATAEMPMPLLPTLPLLAHVS PAAQLCA DPPTAIDTYVPQSYPNGIVGSHIFGRSEQAGSGSIFPSQALHQHSLAQHRSQNLNSYKVDKNAHLQESNMIA GPTQLQSLTTSVSDTTSIRYMECLKNHAASMGGAIDGCGEFMPSGGEGTPGALKCEACNCHR NFHRKKIINHRQMAGIGSHIEPRNNSNSRNIHKQSPISQQYQHNYSYSPSSVNNSSDYPQLPLPISGQICLPQGLERKEPSLIRPSYSYEMVNHDTVQQWEYFWRDRSRNTSIDHPSLRNENQNFDMFKPLNYRTSDNIPS EFANEFPHLDIINNRLRYDEHGKGRTLMPNSGFQNLNNGSYHLNGHFT
NtZF-HD3	Nitab4.5_0006178g0010.1	MEVPNEEGEMAMPINSAYGHGHMIIHDPAPQNNHIIPSSQIITSKNGPPISSNKKMMKYKECLENHAAAMG GNATDGCGEFMPSGEEGTFEFLTCSVCNCHRNFHRKETEGELVRKVYVGHPhKAFVYPASRAAPHQ MIMSYNNHMG SIPGINQEDGIINGCGV MARPLNYQQLVKKRFRTKFSQE QKEKMLNFAEKIGWKMQQEEAMVQQFCQQVGVKRRLK VWMHNLAKKNSNDINTESQV
NtZF-HD4	Nitab4.5_0000014g0020.1	MDSTYSIPTRNHIPTKTPDSEKDFPPYPQVPLKPLSFTNVTSSKHHQVHNHQPPSAAVTYKECLKNHAASIGGYTV DGCGEFIPTDAIAADPTSLKCDVCGCHRNFHRERDDDFMDFRHHHAQVATPATPTALKPEK PRRRRRFR TKFSQE QKNRMYSFSEKLGWKLQKCD EAMVEEFCNEIGVGKG VFRVWMHNNKSTLGKKGF PKCQQYQTVPYNNKQ
NtZF-HD5	Nitab4.5_0001507g0130.1	MEFDEEHEE QEEEIGNIHQISSAAATVNYQTQGNNSVRGVEEGVSTTVRKSSVRYRECLKNHAVGIGGHA VDGC GDFMPAGEEGTMDALKCAACNCHRN FHRKEVEGEVFHHTPPPHLTHHHQP HHSHPHFSPY TSYRTPHHPSGYLHVTTPSHQRPLALPSTSEDEDMSNPSSSGGGGNGGVGGSSRKRFR TKFTADQKDKMLAFAERL GWRMQQDEALVQQFCAETNVQRHVFKVWMHNNKHTLGKKP
NtZF-HD6	Nitab4.5_0002224g0080.1	MALAGEDKEMRMQGS LGYHSLDQNLDAQPVV PYSGGSTNNKFKITSRARYRECLKNHAASIGGNVTDGC GEFMPCGEEGTLEALKCAACNCHRN FHRKEQHV GADNNNNAGIMVVHPLQLPQLPSPLPSMNH HHQHGRSVWSTMPQPVKMAFRGSGGGGSGATDSSEELNFNTYQQATSVPPQPQPPFVLAKKRFR TKFTQDQKEKMLEFAEKLGWRI PREDDTEVQRFC SQVGVKRVFKVWLHNNKNPSAKKNPQEEP
NtZF-HD7	Nitab4.5_0001122g0170.1	MDFENHQEEEE TEPPRHDSDLNDSNSTHTKMPSP TMELEPLAVVHTWHNNPKPKYKECLKNHAVSIGGHA VDGC GEFM PAGEDGSLDSLKCAACNCHRN FHRKITQPPN AVEPLPFVNYHSSYYRSLPPPCGYL QYHVAPQQRPLALPSTSGGGGYWEDQEDMSNLNNSGGSGSKKRFR TKFSQE QKEKMQELADKL GWRIQREDEELVQQLCNETGVRRQVFKVWMHNNKNTLGKKP
NtZF-HD8	Nitab4.5_0002472g0040.1	MDSTCSIPTPTIPTKTQVPLIKPLSFTNVTSSKHHQVHNHQPPSAVVTYKECLKNHAASIGGHTVDGC GEFI PPSATAADPTSLKCDVCGCHRN FHRREPDDDFMDIRHHHAQVATPATPTALKPENPRRRRRFR TKF SQEQKNKMYSFSEKL GWRLQKCD EAKVDFECNEIGVGKG VFRVWMHNNKSTLGKKDFQ NANNSTRPYPTTNSKR
NtZF-HD9	Nitab4.5_0000136g0410.1	MEQKGQEKEMGIPNSIGYNPSSNTRRNEKAGSGNVILS PIQTLNQHNQHS LQHSQNLNSHQLEERDPLVAATNRAQLRQLSTTSGNGTITTTTTTTTTSSSVVRRYRECLKNHAASMGGHILDGC GEFMPEEEEGALK

		CAACNCHRNFRRETFSEAEQIARPHPPYSTCNPPIHSSSYHYNYSTASVMMTFGRNAESSSEDNLNFSNVGGGQSSKSKKRFRTKFTAQKERMHEFAEKVGSIQKQDEQELQHFCNQVGVKRQVFRIWMH NSKQANKKRQM
NiZF-HD10	Nitab4.5_0000274g0220.1	MDLTNNSTTTTTTLANTTTITTTSAHIKIPAEIETPTQIQKPKPFSFSGVLKRKNLQHHHPVVIYKECLKNHAASLGGHAVDGCGEFMPSPPTANPADPTSLKCAACGCHRNFRREPEEPVVIPPPPIATAALEYQPH HRHHPPPPPLPRGDHSSPNSPPPISSAYYPASAPHMLLALSAGFSGEKNHNPISSPVVNTTNCNGRKRFRTKFTPDQKVKMLEFAERVGWKMQRDEDLVRSFCNQIGIEKGVLVWMHNNKNTFGKKLDQHHL ADININNNGNSTNVVNGFCIVSRNNNSHHHNSTDSEFHHLHHHESSNDNKKISDHIKSVGTANVVVATNGSSSSS
NiZF-HD11	Nitab4.5_0000564g0050.1	MKKVLRKSSNDSSHNSTNSTFTVRTVRYVEQKNHSASVGGYVIDGCREFMGETSGAALTCACGCHRNFRKEVETDVASDYMMHFAPNKSYFNLVTEPVKEAVLLEGLIGQDKVRPVEEWGRKANVKKVS VKSMNVLKPHSRLFFEHHFLFVPD
NiZF-HD12	Nitab4.5_0003247g0060.1	MELPIQEEEMPMPINSTYVGGGEGHGHGHHHDPTVPNNTNHIIPSSFMPSGEEGTIEALICSACNCHRNFRKEMEGEQQLQLPPSSCDYYNLNRGGKKVYLGHSNHHKGLLGPEPFGTIIPSRAAAPHHHQMIM SYNNMGSLPSESEEHEDINGGGGVMMAMAMARPLHHHNQIVKKRFRTKFTQEQQEKMFNFAEKVGWQIQKQEETVVQQFCQELGIKRRVLKVVWMHNNKHSLAKKNSNSTIPQNQV
NiZF-HD13	Nitab4.5_0001759g0020.1	MALAGEDKEMRMQGSGLGYHSLDQGNQHHHQPNNNNLQPQQDNEKSSSGGTGAAPPVVVPYSSGGSTNNKFITSRARYRECLKNHAASIGGNVTDGCGEFMPSGEEGTLEALKCAACNCHRNFRKEQPNVDNN NAGIMVVHPLQLPQLPSPLSMNHHQHGRSVWSTMPPQPVKMAFGGSGGGSGATDSSSEELNFNTYQQATSVPPQPQPPFMLAKKRFRTKFTQDQKEKMLEFAEKLGWIRPREDDTEVQRFCSQVGVKRQVFK VWMHNNKNPSAKKNPQEEP
NiZF-HD14	Nitab4.5_0000948g0160.1	MASNSSSTPTMITYGECLKNHKKKHGHYLFDCREFVKSGEDGTKGSYVCANCGCIRSFRHMNNQPLHRHQAIRLCFFHHCVIPNGMQPIHFHFNETQVSVSATSLPVTIISDPESVSVQENVSCVMTPPMLPLPLF PKDEMGVPVPLPLFPETPSSGTFGLLKGGQDMDMD
NiZF-HD15	Nitab4.5_0000948g0180.1	MATNNKHFLVKYGECKHNYAASAMGYALDGCGEFCPNGIPESLICAACHCHRSFHRKMEMEIPVLSKSHHNHGTSLVIVVPTPSQQQSRIHPRQTYDKNNGAETTEMGGGEIEVVEQINTKGKRINSEQKERVKAF AEKIGWRWTKYNEEVKPFCAEIGITPYFLKNWIDNRRRFGPKKTI
NiZF-HD16	Nitab4.5_0000948g0190.1	MANNMMLRANQAARANNRPMISPAVYGEICIRNRLTGAMTYDTDGCLAFAPGSTQALRCQTCGCSRTFHRRLDTGNLPPPVASHQIYDDTRLVYSTPPVFAAPSSSTIIPPPPLPLPTQPDAPAADAHMENSANANSL AESFRVTAVENTSTGSVNVQCVDHPVAVTRGSVKGKEVMDAEIAKTFTSLPPLPRRQSRKSPAVSGKRKSTISSDVVSEIMKDKVWLLTEELEWLNMKNKEEDKKNNNTNKQLEETNSNVSRKPIVDHTIERWM NNRAEVLKTMNHQFLVIATTLTARRELGDQSSCFGTSNTELENDESSSDSDS
NiZF-HD17	Nitab4.5_0000460g0070.1	MEVPNEEGEMAMPINSTYGHEHMIYHDTAPQNNHIITPPQIVTSKNGPISTSTLETSDNVVPYKKMVKYKECLKNHAAAMGGNATDGCGEFMPSGEEGTFEFLTCSVCNCHRNFRKETEDELIRKVYVGHPHKAF VYPASRAAPYQMIMSYNNHLGSFPYIEQEDGIINGCGVMARPLNYQQLVKKRFRTKFSQEQQEKMMLNFAEKIGWKMQKQEDAMVQQFCQEVGVKRRVLKVVWMHNNKHSLAKKNSNDINLQSQI
NiZF-HD18	Nitab4.5_0005164g0020.1	MEIPSQEEEMPMPINSTYVGGGGHGHGHHHDPTVPNNTNHIIPSSNHAAAMGGNATDGCGEFMPSGEEGTIEALICSACNCHRNFRKEIEGEQQLQLQPPSSCDYYNLNRGGKKVYLGHSNHHKSLLGPEQ YGTIIPSRATAPHHHQMIMSYNNMGSLPSESEEHEDINGGGVMAMAMARPLHHHNQMVKKRFRTKFTQEQQEKMFNFAEKVGWQIQKQEETVVQQFCQELGIKRRVLKVVWMHNNKHNLAKKNSNVTIPQNQV
NiZF-HD19	Nitab4.5_0003597g0010.1	MEFDEEHEDQEEEIANIPQIPTENNYQELGEGGPISQAAATLRKNNVIPRYRECLKNHAVGIGGQAVDGCGEFLPSGEEGTLDALKCAACNCHRNFRKEVEGEILNFHHPTPPPILHHPHHYPIRYHQRPLALPSI SSREDIEEYVSNPSSSGSGSRKRFRTKFTQDQKEKMFAFAEGLGWRIQKENEAAVQQFAETNIRRVQVKVWMRNNKNTLGKKP
NiZF-HD20	Nitab4.5_0005738g0020.1	MVGKFFKRKPKMTAIRASFSAKYPLKGQVKVVSYSLSLVFLDFTNEDDYVAVLFKERIIVAGAQMECAGKLLVDNLLSSKTKMKPDNHTAKEEGRDETLMELDKKEHIGGQNEYGAAPKNTHIEDGLYISDS

		VDCVPEATHSDSEERVASPVNCSTETSEIHASAEATSCSGISGLSFASDGLAERIPSDMDDSSSMCSTESVSFRETYSNHNSQKSYGRGWKYGSKSTSTAADLACATLNQPLDALTIGECHEDRKSKPLIQVQYSTYRGRQ AITFPETTVKALSPILSLIGNFFQRKPRIKEIRADFIANKPLKGQVKITHYTSQQVSLDFTNEADYDTVLSKKT LIVAGAVMQISWWSRDIHHEVVSALNPVLGKQEQAAMDKERGMELQKTERDELIGENEYKTEA AEAVLEKPDILEEVS DVNSLHVVEVAHPDFGSDASPVNCDTGT SKMHP SIGTTCRLSGLSAPQNMIDGTSPYVMNVNSSTCSTYTIPPVTTGLSSNHKDQSKSTSDVADSASKAHSQLLDDLPDARQQVLKKE VAISHRSELTEADREKPSLEMPSVSSPRNPPRSIGSAIQSMSKLVSVKNDLISVKRSISDNFNLTKQSVPLFNSAETA VLLNADPHKALEPKDMENPLVQSVAITSENFLSHQVTAPATAEKPMAVEAPFPALAKRWIST PLLSSITSSIRIKDMHLDREPNMTLGPTQLQPPSTTSVRDITTSIRYGECLKNHAASMGHVAVDGCGEFMPSEGQGTGALKCAACNCHRNHFHKEIVNHRQMAGVGS HIEPRN SSSGYIHNQAPISQQYQHNSVFTL QIHILNYLYRSLARYVFHRAWKE MEFDEEHEDQEDEIANISQIPATTENNYQEFGE GGPISQAAATLRKNNVPSPRYRECLKNHAVGIGGQAVDGCGEFLPAGEEGTLDALKCAACNCHRNFRHKEVEGEILNFHHTTPPILHHPAHHPYRYLQRPLALP SVSSREDIEDYVSNTSSGGGGSGSRKRFRFTKFTQDQKEKMF AFAEGLGWRIQKENDAAVQQFCAETNIRRQVFKVWMHNNKHTLGKKP MEHTGQDKDMGMPNCIGFNSSHLNQESTPFAAAKLPTAPIVSSLPDRTRNEQISHGNTIFSPNQTL DHQHNLTPNSDPDPTIIAAQLRQQSTTSASDRNSSIRYKECLKNHAASLGGHVL DGCGEFMPSGEETPEYLK CAACDCHRNFRHKEDELEQTAGVYRNNSNSHRVHIQTPPSLPVPPQQHHHKYSHNYSRGMPPPVMMNFGGNTGVPAESSSED LNMFHSNAGGQGV IQPCAFSVSKKRFRFTKFTQQQKEKMQEFAEKL EWRIQK QDEQEVQQFCNEVG VKRQVFKVFMHNCKQAIKRKQT MASNSSSTPIRYGECLKNH SKRHGY YLFDGCREFVKSGEDGTKGSYICANCGCIRSFHRMNNLPLHRHQAIRLCFFHHCVIPNGMQPIFHPMTTAGESTQVS VSAASLPVTIISNPESVSVQENVPYVMT PPMPLPLLPLF PKDEMGPVPLPLPLFPETPSSAEQN MASNSKHFLVKQKYECKHNYAASTMGYALDGCREFCPNGAPESLICAPCLCHRSFHRKMEVELPILSNTHHRHGTSLVIVVPPTPTSQQRSRIHPHKYDENNNVAATSPPQGAETTEMGGGEIEVVEQMSIKRKRI NSEQKERVKAFAEKIGWRRWTKYNKEVKTFCAEIGITPYFLKNWIDNNRRRFGPKKTI MANNNMLRANQAARANNRPMISPAVYGE CIRSRLTGAMTYDTDGCLAFAPGGPPGST EALCCQTCGCSRSFHRRLDTSNLLPVASHQIYDDTRLVYSPPVFTAPSSTIIPPPPPPRTPQPDAPAADVNM EFSNANANS LAESFRVTAVENISTGSVNLQCVHSPVSATRGSVKGKEVMDAEIAKTFAKLPLPPRQQRSKSPAVSGKRKSTVSSSDV VSEIMKDKVWLLTEELEWLN MKNKEEDKKNNNKQLEETNSNEARRKPIVDHTIDRLMS NRAEVLKTMNHQFLVIATTLTARRELGDQSPCSGTSNSTESESENDESSSDSDSDS MEHTGQDKDMGMPNSIGFNSSHLNQESTPFAAAKLPTAPIVSSLPDRTRNEQISHGNTIFSPNQTL DHQHNLTPNSDPDPTVIAVQLRQQSTTSASDKNSSVRYKECLKNHAASMGHVL DGCGEFMPSGEETPEY LKCAACDCHRNFRHKEDESEQTAGVHRNNSNSHRIHAQIPPSLPAPPQQQHYHKYTHGYSRGMPPPVMMNFGGNSG VPAESSSED LNMFNSNAGGQGV IQPCTFSASKKRFRFTKFTQQQKEKMQEFAEKL GWRIQ KQDEQEVQQFCNEVG VKRQVFKVFMHNCKQAIKRKQT MDLTNNTSTTTTTPTLTNTTTTTSAHIKTPEAEIETPTIQIKPKPFSFNGVLKRKNL FQHHPV VVIYKECLKNHAASLGGHAVDGCGEFMPSP TANPADPTSLKCAACGCHRNFRHREPEEPVIPPPPIATAALE YQPHHRHHPPPPPPLPRGDHSSPNSPSPPISSA YYPASAPHMLLALSAGFSGEKNHNPISSPVVNTTNSNGRKRFRFTKFTPDQKV KMLEFAERVGWKMQRDEDLVRFCNEIGVEKGVLK VWMHNNKNTFGKKL DQHHLADINNNNGNSTNVVNGFCIVSRNNNSHHHNSTDSAEFHLHHHESSNDNKIIDHIKSVSTANV VVG TNGSSSSS MKKVLRKSSKSSNNSTNSSSFTVRTVRYVEQKNHAASVGGYVVDGCREFM PGATAGAALTCAACGCHRNFRHKEVETVKKAMLLERP WIDQDKVRPVEVWGRKTDVNKVTVKSMNSLKPHSRLFFEFHHFL FVPD
NtZF-HD21	Nitab4.5_0002025g0010.1	
NtZF-HD22	Nitab4.5_0001960g0020.1	
NtZF-HD23	Nitab4.5_0002698g0010.1	
NtZF-HD24	Nitab4.5_0002698g0080.1	
NtZF-HD25	Nitab4.5_0002698g0100.1	
NtZF-HD26	Nitab4.5_0018250g0010.1	
NtZF-HD27	Nitab4.5_0004308g0050.1	
NtZF-HD28	Nitab4.5_0008383g0010.1	

SIZF-HD1	Solyc01g014970	MANMLRANQGARAICKPKDLIVYRDCNHSVLPSVSVVDSCQAFASGGPIGSMESFQCQFCHCHQNVHRWLDVNNHQIAPPPAQQTVTQRDVKPEVSSNTTNANRLGRINAQIFDSLAVSIELAESIMARATENWVN CNNKDVGNKSKKSWDEHVAEEYEKEQPQILANQLELTLNMRSQNGKNKKIKKDEDEKPDGFELYIKTKSKAIKKLQIAQAENNVFGQSYYPN MELPSQDHEDMPIPINSTYGHLIHHDTPPNNTNHIIPPSMNGPPIDAPPVATAADHHVPFKKIVRYKECLKNHAASMGGNATDGCGEFMPSGEEGTIEALICSACNCHRNFRHRKEVEGDQQQLASSCDFHHVNNRVL
SIZF-HD2	Solyc01g102980	GGGSTKKVYLGHNHHKTSLGPEPFGTIIPTRPPHHQMIMSYNMGSLPNSESEEHDIQDHHHIGGIMGMARPLHHVKKRFRFTKFTQEQQDKMLNFAEKVVGWIKQKEEGVVQQFCQEVGVKRRVLKVVWMHNNKHSL AKKNITTNPENQLP
SIZF-HD3	Solyc01g103810	MASNSSSNPNGDITIKYGICLKNHATKFGDYSVDGCREFVKKGDDGTKEAFICANCGCFRDFHRMNSQSLFRLAIHRSRFIHPHVMPHGGGNAPINFHPMARVMSVQYIRRPVFY
SIZF-HD4	Solyc01g103820.1	MASNSSSNSNDDMTIKYGICLKNHATKFGDYSVDGCREFVKKGDDGTKEEFICANCGCFRGFHRMNSQSLFRPPLRSCFIHAHVITHGGGHTG MASNNKKYFLVKYLECRHNYAARSNGYVLDGCGEFCPTGALETLESFICAACHCHRNFRHRKVEVELEDGVESPIISINHPSRGTPLVIIDDPLQYTVKSRAQFCETSKKNNIDVETMKMRDIGEIKVRKLKRKYNASSS
SIZF-HD5	Solyc01g103830	KRMRLNPYQRERIWIFANEIMRWKWTKSNEQVIPFCDEIGIAPKFLKNWINNTKSRTPLAKNGHVRNKK
SIZF-HD6	Solyc01g103840	MASNNKHFLVKYLECRHNYAARSNGYVLDGYGEFCPTGAPETLEFFICAAWHCHQNFHKKVEVEVENKVESPVISINPSHGTC MELTNNNNTTISTITTTTIVKTPEAEIETPTQIQKLKPFPSNGVLKRKSSFNHNHHHPVVVIYRECLKNHAASLGGAHVDGCGEFLPSAANPSDPTSLKCAACGCHRNFRHRREPEEPVIPPPPIATAVLEYQPHHRH
SIZF-HD7	Solyc02g067310	HPPHPPPLQGEHSSPNSPSPPISSAYYPASAPHMLLALSAGFSGEKNQNPTSAPLGHSNGRKRFRFTKFTPDQKVKMQEFAERVGWKMQRDEDLVSNFCNEIGVEKGVLKVWMHNNKNTFGKKSDQPNSGSGDGD NDNDDNHHQNATSA MELNINTNTTAAITTVKTPELAETETPSRIQQPKPFSFNGVLKRKNHHHPVVVYKECLKNHAANLGTHAVDGCGEFLPIAANPADPTSLKCAACGCHRNFRHRREPEEPPIATAAIEYQPHHRHHPPPRGDHGSPN
SIZF-HD8	Solyc02g067320	SPSPPISSAYYPASAPHMLLALSAGFSGEKNQNLPTSTTPMAVANSNGRKRFRFTKFTPDQKIKMLEFAEKVEWKMQKRDEDLVNNFCNEIGVEKGVLKVWMHNNKTTSISGKKLDQPNTDNGHNGHNGNSNYTVN GFCIVDRNNTTHHHDNTDSEFHHHESSMNDDNKKENSSFGANNVVVTNGSSSSS
SIZF-HD9	Solyc02g067330	MRKIQLFENQDDESVTSESSTNSAFTVRIVRYKECQKNHAARVGGHAVDGCREFMPSGEEGTSSAFICAACGCHRNFRHRREVETEVAASHLSSSSSSSCVLF MEHRGQEKDMGLPNPNPMSYNPSQLNQESSSSAANKFLTAPNRTTNEHENTIFSPNQTLQHNITQNSDPDPVRQLSTSSASERNITPVRYKECLKNHAANLGGYVLDGCGEFMPSGEEETLEYLKCAACDCHRNFRH
SIZF-HD10	Solyc02g085160	RKETEDESQTPGVHRNHRIPNQTPPSLPAPVTPQQQHHHKYPHSYPRGHMAPVMMSFSGNTGVAEASSSEDLMNFHGQGQGVQPNCFSASKKRFRFTKFSQQQKDRMLEFAEKLGWRIKQKQDEQEVHQCNEVGVK RQVFKVWMHNSKQATKKKQN
SIZF-HD11	Solyc02g087970	MKKVLRRNDYSRNSTNSSFTMRRVRYVEQQRNHAASVGGYVIDGREYMPGETTSGTLNCAACGCHRNFRHRREVETDVASECTSASSTTK
SIZF-HD12	Solyc03g061620	MTKRHEDDEENDGSLHTSITIRTVRYRECQRNHAAGVGGYAVDGCREFMPSGEEGTPGALSCAACGCHRNFRRREVETEVAASNCSSPS
SIZF-HD13	Solyc03g098060	MQGDKSNDIYRECLRNHAASLGSYATDGCGEFTLDDTNTSPGGSTSLNCAACGCHRNFRHRKFCGGSYSNSSRRDREIIAAHDYRLATTEESPAVSERSGKKRFRFTKFTGDQKEKMLAFAEKLGWTLQRKDEENET

		ERFCREIGVSRKVFKVWMHNNHKNSSSVSSTVTGNNASSLTQ
SIZF-HD14	Solyc03g116070	MMKKRQVVVRRISSGSSTIRNVRYVEQQRNHAANIGGYAVDGCREFMATGDDGTAALTCAACGCHRNFRHREVDGGEVVSESS
SIZF-HD15	Solyc04g014260	MEFEDQQKQRDEEIAAAPRHNDSLDNSDLTTKMPPSPQLELEPLTAVQLWTNNPKYKECLKNHAVGIGGHAVDGCGEFLPAGEDGSIDSLKCAACNCHRNFRKIAPPPIAAAAAGVGGEVPVPFVYHSHNQLPTY RTLPPPCGYLQYHVAPNQRPLALPSTSGGYREDQEDISHPNYSGGSKKRFRTKFSQVQKDKMQELADKLGWRIQREDEELVQQLCNETGITRQVFKVWMHNNKHTLGKKP
SIZF-HD16	Solyc04g074990	MEFDDDDQEEQEIGAVGAENYVTTGNNSGREEGISTSSIGRKSNNVRYRECLKNHAVGIGGHALDGCGEFMPAGEEGTMDALKCAACNCHRNFRHKEAEERLGWRMQKQDEALVQQFCAETNVKRHFVKVWMH NNKHTLGKKP
SIZF-HD17	Solyc04g080490	MALGGGNEEKEMRISGFQNIDL VSPGGAAPDDIVSAAPHNNSTTGSNKLNGTSTVRGRYRECLKNHAANIGGNVTDGCGEFMPSGEEGTLEALKCAACNCHRNFRHKEIPNNVGAGVGGVGGDNNNNAGIMVV HPLQLPQPLPSPIPSLNHHHHHHQHGGRSIWTTMPPQPVKMAFGGSGGSGATDSSSEELNFNTYHHQQATSVPPQQPFMLAKKRFRTKFSQEQKEKMLEFAEKLGWRIPREDDAEVQRFCSQVGVRQVFKVWM HNNKNPSSAKKNIIQEDQP
SIZF-HD18	Solyc05g007580	MELTYSINPTPTPSSTKTPDSEVDTPLIKPLSFTNGNNHSHHNQSPPTAVIYKECLKNHAASIGGHAVDGCGEFMPSPSTPSDPSLKCAACGCHRNFRHREPSDDSSPPAHFIDFRRHIFPPIKRFSPSTPSPLSPSL SPPLPSLFQPQPVTPTGLKSENPNGRKRFRTKFTAQKEKMHFSFEKLGWKLQKCDEAAVDEFCNEIGVGKGVLRVWMHNNKNTFGKDYQISNNSSRDHSFENKNGFNINGTASSNEEDQHRNNNNNDNSTTSNC ELHLHISTNASSSSS
SIZF-HD19	Solyc05g018740	MSNNSSSNPSGDMTIKYGICLKNHATNFGDYSVDGCREFVKRGDDGTKEAYICANCGCLRSFHRMNSHSLYHPPILRSRFLHPIHPHGRENAPIISHPFMSRFVLVQYIRRPVFYNHP
SIZF-HD20	Solyc05g020000	MTNSSSNPSGDMTIKYGIYLNHATNFGDYSVDGCREFVKKGYGGTKEAYICANCGCLRRFHRMNSHSLYPPILRSHFFHLHVHPHGGENAPIISHPFMSQFVSIQYIRRPVFYNHR
SIZF-HD21	Solyc05g051420	MSKYKECLKNHAAGIGGHAVDGCGEFMPSGDIFKCAVCNCHRNFRKDTVHHHPCGYFPHIMPRRSLVLPSTSRGGGFREDQELLEMCPNPNKIIGTLLKKRFRTKFSQECHKDKMLRLAEKLGWKLQRHDEGVV QQLCNEIGIKRHFVKVWLHNNKHTLGKKTNP
SIZF-HD22	Solyc09g089550	MAAPQRDFNIENQEEPISKIVLYNRYRRVPAVIFRKKYWDWNMSVAVCKLTMVGKFFIPKPKMTKIRASFHAKLSLKGVVKIRSYDSYHVDFDFTAEEDYQSVLLKERVVVAGAIMEVFQWTFEFHDQFREAFGVVEL ENTKKDEHIGGGNEYGTEESDSVACVPEVTHSDSEDRVASPIKCETSKLPSSVGISCSEFSGLSSAPYRITGRIPSVTYESSSMCSTELVPFRGTYLNHNNLKSYSREWNYGSKPTSEAADLACETLSQPLYALSIVERHEN QKSRPIEVQHSTYMGYP TLTFPRRYGESLVSDYKLTLLGNFSYKRPKMKEIRADFKAQNPLSGQVKIRNCSSRQVLILFSNEEDYTYVLYKKAHVAGALMQISWSSPDFHHEVKQNIHPDFRLSDAKSVNWN TDTSK LHPSINGLLAPATDEKSMQLQVPAVSQCLSVSPICPPLLLAHSVSVAGRLCADRLTTSGIYVPQSYPKGIVGIPFGSNEQAGSGNTFPRPSQALNQSLAQQHNQLNSYKPNMTVRIAQLQPPSTTSVSDITSSIRYRECL KNHAASMGGHALDGCGEFMPSGEEGTPGALKCAACNCHQNFRHKEIDDYQPMDDVGSHSRFSQPRNNSSSGSIQNQVLISLPTQQYHHHDYSDSCSPRSLVDSLQPYTQPPSPSTSGSVSQQALERIQPSSIRSSYSYEM VNHNTMQNGKQREYFWSOSSRNTSRDHPSVRNENWNFDMDKPLNNRTPDHIPLEFTYPSRCQPQTFTDEFPHLDIINNLLHEEHETGRTLMSNSGSQRLNKG S* MEFEDNNNNNDEEQEEDMNLHEEEEDDDAVYDSPPLSRVLPKASTESHETTGTSTGGGGGFVVHGGGGSRRFRFRECLKNQAVNIGGHAVDGCGEFMPAGIEGTIDALKCAACGCHRNFRKELPYFHHAPPQHQ
AtZF-HD1	AT5G65410.1	PPPPPGFYRLPAPVSYRPPPSQAPPLQLALPPQRESEDPMETSSAEAGGGIRKRRHTKFTAQEKERMLALAERIGWRIQRQDDEVIQRFCQETGVPRQVLKVWLHNNKHTLGKSPSPLHHHQAPPPPPQSSFHHEQ DQP

AtZF-HD2	AT4G24660.1	MNFEDQEEDMEMSGVNPPCGYDSLSGEGATSSGGGGVGRSKGVGAKIRYRECLKNHAVNIGGHAVDGCCEFMPSGEDGTLDALKCAACGCHRNFRHKETESIGGRAHRVPTYYNRPPQPHQPPGYLHLTSPAAPY RPPAASGDEEDTSNPSSSGGTTKRFRTKFTAEEQKEKMLAFAERLGWRIQKHDDVAVEQFCAETGVRRQVLKIWMHNNKNSLGKKP MEIASQEDPIPINTSYGNSGGGHGNMNHSHHANSAPSSLNITTSNPLLVSNSNGLGKNHDHSHHHHVGYNIMVTNIKKEKPVVIKYKECLKNHAATMGGNAIDGCGEFMPSGEEGSIEALTCVCNCHRNFRHRETE
AtZF-HD3	AT2G02540.1	GEEKTFFSPYLNHHQPPQQRKLMFHHKMIKSPLQQMIMPIGVTTAGSNESEDLMEEEGGGSLTFRQPPPPSPYSYGHNQKKRFRTKFTQEQKEKMISFAERVGWKIQRQEESSVVQQLCQEIGIRRRVLKVVMMHN NKQNLSKKSNVSNVLDLSAGNNDITENLASTNP MEIASQEDHDMPIPLNTTFFGGGGSHGMIHHHDHHAANSAPPTHNNNNTTQPPMPLHGNGHGNNYDHHHQDPHHVGYNAIHKPMIKYKECLKNHAAAMGGNATDGCGEFMPSGEDGSIEALTCACNCHRNFR
AtZF-HD4	AT1G14440.1	HRKEVEGELAATAMSPYHQPPHRKMLNLHQKIRSAMPHQMIMPIGVSNRYMHNNSESEDFMEEDGVTASRSLPNLPYNQKKRFRTKFTPEQKEKMLSFAEKVGWKIQRQEDCVVQRFCIEIGVKRRVLKVWM HNNKIHFSSKNNINLEDNDNEKINNLNVDLSGNNDMTKIVP MDMRSEMIERRREDNGNNNGVVISNIISTNDDNCNGNNNTRVSCNSQTLDDHQQSKSPSSFSISAAAKPTVRYRECLKNHAASVGGSVHDGCGEFMPSGEEGTIEALRCAACDCHRNFRHKEMDGVGSSDLISHH
AtZF-HD5	AT1G75240.1	RHHHYHHNQYGGGGRRPPPPNMMLNPLMLPPPNYQPIHHHKYGMSPGGGGMVTPMSVAYGGGGGAESSSEDLNLYGQSSGEGAGAAAGQMAFSMSSSKRFRTKFTTDQKERMMDFAEKLWWRMNKQD EEELKRFCGEIGVKRQVFKVWMHNNKNNAKKPPTPTTL MEVREKKDEKMEMTRRKSSALDHHRLPPYTYSQATANKEKPTTKRNGSDPDPDPLDTNPISISHAPRSYARPQTTS PGKARYRECQKNHAASSGGHVVDGCGEFMSSGEEGTVESLLCAACDCHRSFHRKEIDGLFV
AtZF-HD6	AT2G18350.1	VNFNSFGHSQRPLGSRHVSPIIMMSFGGGGGCAAESSTEDLNKFHQSFSGYGVDQFHHYQPKKFRRTKFNEEQKEKMEFAEKIGWRMTKLEDEVNRF CREIKVKRQVFKVWMHNNKQAAKKDL MELGGKCNAITTTT MISTEVKPHTDPEPEAKPESDPSMALFPIKENQKPKTRVDQGA KYRECQKNHAASTGGHVVDGCCEFMAGGEEGLGALKCAACNCHRSFHRKEVYGHNRNSQDQHQLMITPAFYSSNSSYK
AtZF-HD7	AT3G50890.1	PRVMHPTGEIGRRTSSSED MKKILSHRNQNV DGKSLMMMMMRKKRVRTKINEEQKEKMEFAERL GWRMQKKDEEIDKFCRMVNLRRQVFKVWMHNNKQAMKRNNSE MDVIATTTTIVSDLDSRQPEIEAPIRIQPAKPISFNGKRCHHHHLASEAVAVATYKECLKNHAAGIGGHALDGCGEFMPSPSFNSNDPASLTCAACGCHRNFRHREEDPSSL SAIVPAIEFRPHNRHQLPPPPPHLAGIR
AtZF-HD8	AT5G15210.1	SPDDDDASPPPISSSYMLLALSGGRGGANTAVPMSRKRFRTKFSQYQKEKMFESERV GWRMPKADDVVVKEFCREIGVDKSVFKVWMHNNKISGRSGARRANGGVVVGVDGRSQSVPTNGSFSST MLEVRSMDMTPKSPEPESETPTRIQPAKPISFNGIIRHHHHHHNNNKVTYKECLKNHAAAGGHALDGCGEFMPSPSSTPSDPTSLKCAACGCHRNFRHRETDSSAVPPPSLLPSSTTTAAIEYQPHHRHHPPPPPLAP
AtZF-HD9	AT3G28920.1	PLPRSPNSSPPPISSSYMLLALSGNNKTAPFSDLNFAAAANHLSATPGSRKRFRTKFSSNQKEKMHEFADRIGWKIQKRD EDEVDRFCREIGVDKGVLK VWMHNNKNSFKFSGGGATTVQRNDNGIGGENSDDGV RGLANDGDGGGGRFESDSGGADGGGNVNASSSS MMDMTPTTTTTTTTTPTPKSPEPESETPTRIQPAKPISFNGIIRHHHHHHPLIFTYKECLKNHAAALGGHALDGCGEFMPSPSISSDPTSLKCAACGCHRNFRHRDPDNNNDSSQIPPPSTAVEYQPHHRHHPPPPPPPP
AtZF-HD10	AT5G39760.1	PRSPNSASPPPISSSYMLLSL SGTNNNNNLASFSDLNFSAGNNHHHHHQHTLHGSRKRFRTKFSQFQKEKMHEFAERVGWKMQRDEDDVRDFCRQIGVDKSVLK VWMHNNKNTFNRRDIAGNEIRQIDNGGGNH TPILAGEINNHNNGHHGVGGGGELHQS VSSGGGGGGFSDSGGANGGNVNGSSSS MDLSSKPQQQLNSLPIAGELTVTGEMGV CYKECLKNHAANLGGHALDGCGEFMPSPTATSTDPSSLRCAACGCHRNFRHRDPSENLNFLTAPPISPSGTESPPSRHVSSVPVCSYYSAPPHVILSLSSGFPGPSDQD
AtZF-HD11	AT1G69600.1	PTVVRSENSSRGAMRKRTRTKFTPEQIKMRAFAEKAGWKINGCDEKSVREFCNEVGIERGVLK VWMHNNKYSLN GKIREIEHGLCLNTHSNDGDGSSSS MVLVLYNECLKNHAVSLGGHALDGCGEFTPKSTTILTDPPSLRCDACGCHRNFRHRSPSDGFSQHRSPPSPLQLQLAPVPNLLLSLSSGFGPSDQEVKNKFTVERDVRKTAMIKKHKRTKFTA EQVKVMRGFAERAG
AtZF-HD12	AT5G60480.1	

		WKINGWDEKWVREFCSEVGIERKVLKVWIHNNKYFNNGRSRDTTSSMSLNLKL
AtZF-HD13	AT5G42780.1	MDEIKPKKEENSKRRNRVKPICRETGDHVVHYLPTCKTKPKPTRTHHAPPILDSIFKVTHKPHYECRKNHAADIGTTAYDGCGEFVSSTGEEDSLNCAACGCHRNHFHREELIPENGGVTETVLEVLKISSCQFRIFCSP YGGGKSEGKKKKKEKESYGGDPIIKDRFGGAEEEEGIVKRLKTKFTAETKEMRDYAEKLRWKVRPERQEEVEEFCVEIGVNRKNFRIWMNNHKDKIIIDE
AtZF-HD14	AT1G14687.1	MQSTCVYRECMRNHAAKLSY AIDGCREYSQPSTGDL CVACGCHRSYHRRIDVISSPQINHTRFPTSLRRVKQLARLKWKTAEERNEEEEDDTEETSTEEKMTVQRRRKSKFTAEOREAMKDYAAKLGWTLKDKR ALREEIRVFCEGIGVTRYHFKTWVNNNKKFYH
AtZF-HD15	AT1G74660.1	MMKKRQMVIKQRSRNSNTSSSWTTSSSSSSSEISNVRYVEQCQNHAANIGGYAVDGCREFMAAGVEGTVDALRCAACGCHRNHFHRKEVDTEVVCEYSPPNA
AtZF-HD16	AT3G28917.1	MRKRQVVLRRASPEEPSRSSSTASSLTVRTVRYGECQKNHAAAVGGYAVDGCREFMASRGEETVAALTCAACGCHRSFHRREIETEVCDCNSPPSTGN
AtZF-HD17	AT1G18835.1	MKKRQVVIKQRKSSYTMSSSSNVRYVEQCQNHAANIGGYAVDGCREFMASGGDDALTCACGCHRNHFHRREVDTEVVCEYSPPNANN
OsZHD1	LOC_Os09g29130.1	MDFDHDDGDDEEMPPMPVSSSYETPPQHGLAGGGMAPKPPGEIGSRVKGPSGGGRYRECLKNHAVGIGGHAVDGCGEFMAAGEEGTIDALRCAACNCHRNHFHRKESESLAGEGSPFSPA AVVPY GATPHHQFSPY YRTPAGYLHHHQHHMAAAAAAAAAAAGGYPQRPLALPSTSHSGRDDGDDL SGMVGPMSAVGPLSGMSLGAGPSGSGSGKKRFRTKFTQE QDKMLAFAERVGWRIQKHDEAAVQQFCDEVGVKRHV LKVWMH NNKHTLGKKLP
OsZHD2	LOC_Os08g37400.1	MDFDHDEGDDEEMPPMPLSSGYDAPMQPLGGGGGGVPKPGGGVGGGGGGGGGGGGGARYRECLKNHAVGIGGHAVDGCGEFMASGEEGSIDALRCAACGCHRNHFHRKESESPTGVGAEPSAVSPAISA YGASPHHQFSPYYRTPAGYLHHQQHQMAAAAAAAAAAGGYPQRPLALPSTSHSGRDEDDMSGMVGPMVIGPMVGMSLGSAGPSGSGSGKKRFRTKFTQE QDKMLAFAERL GWRIQKHDEAAVQQFCEEV CVKRHV LKVWMHNNKHTLGKKAP
OsZHD3	LOC_Os12g10630.1	MDLSGAQGELPLPMHAAASPYLGLHHDHHHHHGGGGGGGMNGRHMSPTPPAAAEESKAVVVVSSSATAAARYRECLKNHAAIGGSATDGCGEFMPGGEESLDALRCSACGCHRNHFHRKELDAAAAPLHH HHHQLLGVGAHPRGHGHHHHHLLVAALPPPTRMV MPLSAMHTSESDDAAARPGGGAAARKRFRTKFTA EQKARMLGFAEEVGWRLQKLEDAVVQRFCQEVGVKRRVLKYGSGAPEELKKLDFFWERRGGGGG NPLRNKMKIHLASASTSIRLQLSPTETL
OsZHD4	LOC_Os11g13930.1	MVSILQLQTRTEASPASASAAATRIFAVRRQQQE QEGEEEEFEFQERMDLSGAQGELPIPMHASAAASPFAGMGAHGGAGGGHVVELHRHEHVGNNGQAMAMASPPPTNVAVAAEQEGSPVAGKKRGGMAV VGGGGGVAVKYRECLKNHAAAGGNATDGCGEFMPSGEEGSLEALKCSACGCHRNHFHRKEADDLADSCAAALRAAAGRHHHLLGPALPHHHHKNGGGLLVAGGDPYGAAAYAAARALPPPPPPPHGHHHHHQI IMPLNMIHTSEDEMDVSGGGGGVGRGGGSSSSKKRFRTKFTA EQKARMLFAERVGWRLQKLD DAMVHHFCQEIGV KRRVLKVWMHNNKHN LAKKPLPSSPPPPQIPPM SMPPSPPPQIPPM SMPPSPPPMPM PMPPSPQLKLE
OsZHD5	LOC_Os01g44430.1	MELSEHEEDAGDVGGCSPPTPPHRVLTSAAPETIRCRYHECLRNHAAASGGHVVDGCGEFMPASTEELACAACGCHRSFHRRDPSPRAGAARLPQLHLPASINSRAPALLLPAAAAASKQGLFPGYGTPSGGT GTTTASSSDERLRSPVQPRRRSRTTFTREQKEQMLAFAERVGWRIQRQEEATVEHFCAQVGVRRLQALKVWMHNNKHSFKQKQQQENRQEQQQ
OsZHD6	LOC_Os05g50310.1	MEFRGHDEPVDEMGVAYGRTPSSSSSPAASASAGNGAGAAEVRYHECLRNHAAAMGGHVVDGCREFMMPGDAADALKCAACGCHRSFHRKDDGQQQQLRL LIPSPPTPRVPLLMPPQPQPHPHPQHPYLHP PPFYHHTPSGSGGTTTESSEERGPPSSAAAAQGRKRFRTKFTPEQKEQMLAFAERVGWRMQKQDEALVEQFCAQVGVRRLQVFKVWMHNNKSSIGSSSGGSRQPQEQQSQQQQQQ

OsZHD7	LOC_Os02g47770.1	MEYKRSSHVEEEEEEEEDDEEEDDEEQGHHQYTTAAAQQLHPQVLGSSASSPSSLMDSAAFSRPLLPPNLSLVSPSAAAAAAPGGSYLHAAHHHGQGRRVEAPGGESQHHLQRHHEPARNGVLGGVAGAHAAAS TLALVGGGGGGPRGGEGAAGEAPTWRYPRECLKNHAARMGAHVLGDCGEFMSSPGDGAAALACAACGCHRSFHRREPAVVAPASLSLCPASASASAAAGLVSLSPSATPTGANSSRLMPLLLAPPHMQKRPPVLPV SPASAPAALAESSEELRPPLPSSHPHAHAAAVVAASASAPPGSKKRFRTKFTAQKERMREFAHRVGVRIHKPDAAAVDAFCAQVGVSRRLVKGDDTSTALAAKPPFLRAFAAFFGGQFCLSCF
OsZHD8	LOC_Os04g35500.1	MMDHLSLVPYEGGSAGGGGGGGKYKECMRNHAAAMGGQAFDGCGEYMPASPSLKAACGCHRSFHRRAAGIGGGPVFFRPPPPQPHSHHAALQGFLPSSVPAPAPPPQLALPYHAVPAAAWHHAAAAAAGR AGSETPPRMDDFGPGSAGSGSGGGGIGFRKRFRTKFTPEQKERMREFAEKQGWRINRNDGALDRFCVEIGVKRHVLKVMHNHKNQLASSPTSAAAAAGVMNPGAGIGLGTGLGTGISGDGDGDDDDTDDSP PRAAVSSPSPISV
OsZHD9	LOC_Os09g24820.1	MEAMDVKYKPLVFPNGAIKKAAPAAVAPAVGGGGGGETVYRECLKNHAASLGGHALDGCGEFMPSAANPADPTSLRCAACGCHRNFRRLPEGSPPPPPALLPAPMPPHRGEETPEVRLPGVDGEDSDSDS DGSEYDDERSVSPPPPLAAAVAHQVYYPSAPHMLLSLGSSGQAQRLPPQVMSAAAAAPPGGGGGMPRKRFRTKFTAQKQRMQELSERLQWRLQKRDEAIVDEWCRDIGVGKGVFKVVMHNNKHNYLGHH SARRSASSSSAAAAAPPFNPTSPPPPPPPHATDFNINGTATAATAAAAATIAAGNHQENGASSPQSA
OsZHD10	LOC_Os08g34010.1	MEAVVGKYRPVFPNGGAAAAAGKSKATPASATAAVYRECLKNHAASLGGHAVDGCGEFMPSAADAADPASLKAACGCHRNFRRLPEAPSPPLLALPPPPPPPPPPPPQPPQHLPRTAAVAVAPQLLLH GSHQRREQSPETDRVRGPGHHHDDDAADDDSEDSEMSDYDDDRSASPLQAPPPVLSPGYLSATHMLLSLGSASAPAVAASRPHAAAAAMGPPPPGAATSASRKFRFTKFSPEQKQRMQALSERLQWRLQKRD EAVVDECCREIGVGKGVFKGQLVLPLSTVITSFVLELIWVCMDNDDDDVLIGVLGGVVF
OsZHD11	LOC_Os03g50920.1	MEQQQERPREVYRECMRNHAAKLGTYANDGCCEYTPDDGHPAGLLCAACGCHRNFRHKDFLDGRATAAAGGAGGAGVGVAPMLPAPGGGGPPGYMHMAAMGGAVGGGGVDGGGGSGGRRRTRTKFTEEQ KARMLRFAERLQWRMPKREPGRAPGDDEVARFCREIGVNRQVFKVWMHNNHAGGGGGGGSGGPGAGGGAQTSSSTTRGGGDVGVLSPAMGGDGEDDEEVRGSEMCM
OsZHD12	LOC_Os11g03420.1	MGPQQDRSAAKPYANGSTAAAAAAGRKENNKVVRYRECQRNHAASIGGHAVDGCREFMASGAEGTAAALLCAACGCHRSFHRREVEAAAAECDCSSDTSSGTGRR
OsZHD13	LOC_Os12g03110.1	MGPQQDRSAAKPYANGSTAAAAAAGRKENNKVVRYRECQRNHAASIGGHAVDGCREFMASGADGTAAALLCAACGCHQSFRHREVEAAAAECDCSSDTSSGTGRR
OsZHD14	LOC_Os09g24810.1	MMKRLVVLRRREPAVRFSCCGVRYGECRRNHAASGGHAVDGCREFIAEDGGGNSTSAVGVAALKAACGCHRSFHRRVQVYEVAWDDDCASGDTSSSSPSSSSLSSE
OsZHD15	LOC_Os06g23030.1	MMKRMVILRRCEPPPPQAAAVVAAMGGCCGRVRYGECRRNHAARMGGHAVDGCREFLAEGEETGGALRCAACGCHRSFHRRVVVVQCCACDTAAAAAAGGWEWRDCSPSSSSASSTTAS
NsZF-HD1	mRNA_48369_cds	MEFETQEDQKEIRASPNNYSVLEISNSTNEPKMPSNSDELILDAPLQMRKPKYKECLKNHAVGIGGHAVDGCGEFMPAGEDGSLDALKAACNCHRNFRHFKETQIHHPYPYRTPPCGYFQHVMPQRPLALPSTSGGG GYREDQEEMCNPNNSGTTKFRFRTRFNQEQKEKMLEAENLGWRIQRQDEGVVQQLCNEIGIKRHVFKVWMHNNKLTGKKTLIQSISPSLFPAQERS
NsZF-HD2	mRNA_48370_cds	MEFETQEDQKEIRASPNNYSVLEISNSTNEPKMPSNSDELILDAPLQMRKPKYKECLKNHAVGIGGHAVDGCGEFMPAGEDGSLDALKAACNCHRNFRHFKETQIHHPYPYRTPPCGYFQHVMPQRPLALPSTSGGG GGGGYREDQEEMCNPNNSGTTKFRFRTRFNQEQKEKMLEAENLGWRIQRQDEGVVQQLCNEIGIKRHVFKVWMHNNKLTGKKTLIQSISPSLFPAQERS

		MEFDEEHEEQEEEIGNIHQISSAAANVNFQTQGNNSVRGVEEGVSTTVRKSSVRYRECLKNHAVGIGGHAVDGCRDFMPAGEEGTMDALKCAACNCHRNHRKEVEGEVFHHTPPPHLTHHHQPPHSQHPQ
NsZF-HD3	mRNA_54725_cds	MEVPNEEGEMAMPINSAYGHGHMIIHDPAPQNNHIISSQIITSKNGPPISSNKKMMKYKECLENHAAAMGGNATDGCGEFMPSGEEGINQEDGIINGGCGVMARPLNYQQLVKKRFRTKFSQEKEKMLNFAEKIG
NsZF-HD4	mRNA_60670_cds	WKMQKQEEAMVQQFCQQVGVKRRLLKVWMHNLAKKNSNDINTESQV
		MEIPSQEEEMPMPINSTYVGGGGGHGHGHIIHHDPTVPNNTNHIISSVANSINGPPIEATPVSAHHVYPYKKIVRYKECLKNHAAAMGGNATDGCGEFMPSGEEGTIEALICSACNCHRNHRKEIEGEQQLQLQPP
	mRNA_61886_cds	PSSCDYYNLNRGGKKVYLGSHNHHKSLLGPEQYGTIIPSRATAPHHHQMIMSYNNMGSPLSEEEHEDINGGGGVMAMAMARPLHHHNQMVKKRFRTKFTQEKEKMFNFAEKVGWIKQKEETVVQQFCQEL
NsZF-HD5		GIKRRVLKVWMHNNKHNLAKKNSNV TIPQNV
		MALAGEDKEMRMQGS LGYHSLDQGNQH HHQPNNNNLQPQDNEKSSSGGTGAAPPVVVPYSSGGSTNNKFITSRARYRECLKNHAAASIGGNVTDGCGEFMPSGEEGTLEALKCAACNCHRNHRKEQPNVDNN
	mRNA_63507_cds	NAGIMVVHPLQLPQLPSPLPSMNH HHQHGRSVWSTMPPQPVKMAFGSGGGGSGATDSSSEELNFNTYQQATSVPPQPQPPFMLAKKRFRTKFTQDQKEKMLEFAEKLGW RIPREDDTEVQRFC SQVGKRVFK
NsZF-HD6		VWMHNNKNPSAKKNPQEEP
		MDFENHQEEEETEPPRHDDSLDNSNSTHTKMPSPTEMELEPLAVVHTWHNNPKPYKECLKNHAVSIGGHAVDGCGEFMPAGEDGSLDSLKCAACNCHRNHRKITQPPNAVEPLPFVNYHSSYYRSLPPPCGYL
NsZF-HD7	mRNA_72248_cds	QYHVAPQQRPLALPSTSGGGGYWEDQEDMSNLNNSGGSGSKRFRTKFSQEKEKMQELADKLGWRIQREDEELVQQLCNETGVRRQVFKVWMHNNKNTLGKKP
		RQAVTFPENYWESLVPDCKLTLIGNFFQRKPRMKEIRADFI AKNPLKGQVKITHYTSQQVSLDFTNEADYDTVLSKKTLTVAVMQISWWSRDIHHEVGKQEWKAMDKERDVKPGIMEQQKTDELIGGETEYKIDA
	M	PEAVLETPDILGEVSDVSNSLHIVPEVAHPDFRDNDASPVNCDTDTSKMHP SIGITCCQLSGISAPQN MIDGTSPYVMNVNSSK CSTYSILSIVTTGLSSNDKDQSKSIRDVADSASKAHSQPLDDLPEARQ QMLKKDVA
		VSHQSELTESDRERHSSEIPSVSPPRSPPRSIGSVIQLMSKLKVSVTNDPNSVKRSTSDNSNLTQKSVPLFNSAENAVLLSVDPHKSI EPKAI EKPLVRSISITTENFPSNQVTASATAEMPMPLLPTLPLLAHSVSPAAQLC
		ADPPTAIDTYVPQSYPNGIVGSHIFGRSEQAGSGSIFSPSQALHQHSLAQRHSQLNSYKVDKNAHL DQESNM IAGPTQLQSLTTSVSDTTSSIRYMECLKNHAASMGGH AIDGCGEFMPSGGEGTPGALKCEACNCH
		RNFHRKKIINHRQMAGIGSHIEPRNNSNSRNIHKQSPISQYQHNYSYSPSSVVNSSDSYPQLPLPISGQICLPQGLEKKEPSLIRPSYSYEMVNHD TVQQWEYFWRDRSRNTSIDHPSLRNENQN FDMFKPLNYRTSDNI
NsZF-HD8	RNA_82504_cds	PSEFANEFPHLDIINNRLRYDEHGKGRTLMPNSGFQNL SNGSYHLNGHFT
		TFPENYWESLVPDCKLTLIGNFFQRKPRMKEIRADFI AKNPLKGQVKITHYTSQQVSLDFTNEADYDTVLSKKTLTVAVMQISWWSRDIHHEVGKQEWKAMDKERDVKPGIMEQQKTDELIGGETEYKIDAPEAV
		LETPDILGEVSDVSNSLHIVPEVAHPDFRDNDASPVNCDTDTSKMHP SIGITCCQLSGISAPQN MIDGTSPYVMNVNSSK CSTYSILSIVTTGLSSNDKDQSKSIRDVADSASKAHSQPLDDLPEARQ QMLKKDVAVSHQ
		SELTESDRERHSSEIPSVSPPRSPPRSIGSVIQLMSKLKVSVTNDPNSVKRSTSDNSNLTQKSVPLFNSAENAVLLSVDPHKSI EPKAI EKPLVRSISITTENFPSNQVTASATAEMPMPLLPTLPLLAHSVSPAAQLCADPP
		TAIDTYVPQSYPNGIVGSHIFGRSEQAGSGSIFSPSQALHQHSLAQRHSQLNSYKVDKNAHL DQESNM IAGPTQLQSLTTSVSDTTSSIRYMECLKNHAASMGGH AIDGCGEFMPSGGEGTPGALKCEACNCHRNH
		RKKIINHRQMAGIGSHIEPRNNSNSRNIHKQSPISQYQHNYSYSPSSVVNSSDSYPQLPLPISGQICLPQGLEKKEPSLIRPSYSYEMVNHD TVQQWEYFWRDRSRNTSIDHPSLRNENQN FDMFKPLNYRTSDNIPSEFA
NsZF-HD9	mRNA_82505_cds	NEFPHLDIINNRLRYDEHGKGRTLMPNSGFQNL SNGSYHLNGHFT
		PPIQVQYSTYRGRQAVTFPENYWESLVPDCKLTLIGNFFQRKPRMKEIRADFI AKNPLKGQVKITHYTSQQVSLDFTNEADYDTVLSKKTLTVAVMQISWWSRDIHHEVGKQEWKAMDKERDVKPGIMEQQKTDEL
NsZF-HD10	mRNA_82506_cds	ELIGGETEYKIDAPEAVLETPDILGEVSDVSNSLHIVPEVAHPDFRDNDASPVNCDTDTSKMHP SIGITCCQLSGISAPQN MIDGTSPYVMNVNSSK CSTYSILSIVTTGLSSNDKDQSKSIRDVADSASKAHSQPLDDLPE

		ARQQMLKKDVAVSHQSELTESDRERHSSEIPSVSSPPRSPRSIGSVIQLMSKLKVSVTNDPNSVKRSTSDNSNLTQKSVPLFNSAENAVLLSVDPHKSIEPKAIEKPLVRSISITTENFPSNQVTASATAEMPMPLLPTLPL LAHSVSPAQLCADPPTAIDTYVPQSYPNGIVGSHIFGRSEQAGSGSIFSPSQALHQHSLAQRHSQLNSYKVDKNAHLQDQSNMAGPTQLQSLLTTSVSDTTSSIRYMECLKNHAASMGGAIDGCGEFMPSGGEGT PGALKCEACNCHRNFRKKIINHRQMAGIGSHIEPRNNSNSRNIHKQSPISQQYQHNSYSPSSVNVSSDSYPQLPLPISGQICLPQGLEKKEPSLIRPSYSYEMVNHDTVQQWEYFWRDRSRNTSIDHPSLRNENQNFD MFKPLNYRTSDNIPSEFANEFPHLDIINNRLRYDEHGKGRITLMPNSGFGNLSNGSYHLNGHFT VTFPENYWESLVPDCKLTLIGNFFQRKPRMKEIRADFIKKNPLKGVKITHYTSQQVSLDFTNEADYDTVLSKKTLTVAVMQISWWSRDIIHHEVGKQEWKAMDKERDVKPGIMEQQKTELDELIGGETEYKIDAPEA VLETPDILGEVSDVSNLHIVPEVAHPDFRDNDASPVNCDTDTSKMHPSIGITCCQLSGISAPQNMIDGTSPIYVMNVNSSKSTYSILSIVTTGLSSNDKQSKSIRDVADSASKAHSQPLDDLPEARQQMLKKDVAVSH QSELTESDRERHSSEIPSVSSPPRSPRSIGSVIQLMSKLKVSVTNDPNSVKRSTSDNSNLTQKSVPLFNSAENAVLLSVDPHKSIEPKAIEKPLVRSISITTENFPSNQVTASATAEMPMPLLPTLPLLAHSVSPAQLCADP PTAIDTYVPQSYPNGIVGSHIFGRSEQAGSGSIFSPSQALHQHSLAQRHSQLNSYKVDKNAHLQDQSNMAGPTQLQSLLTTSVSDTTSSIRYMECLKNHAASMGGAIDGCGEFMPSGGEGTGPALKCEACNCHRN FRKKIINHRQMAGIGSHIEPRNNSNSRNIHKQSPISQQYQHNSYSPSSVNVSSDSYPQLPLPISGQICLPQGLEKKEPSLIRPSYSYEMVNHDTVQQWEYFWRDRSRNTSIDHPSLRNENQNFD MFKPLNYRTSDNIPSEFANEFPHLDIINNRLRYDEHGKGRITLMPNSGFGNLSNGSYHLNGHFT
	mRNA_82508_cds	MQGDKANDNIYRECLRNHAASLSGYATDGCGEFTLDDNNNNNTSPRSASLHCAACGCHRNFRKVMYGASYSNNSSRDREIVAELTDYGGGRMSAALTAESPRSGKKRFRTKFTTDQKEKMLAFAEKLGWTL
NsZF-HD11		QRKDQENETERFCREHLRHLFLVPFFIFF
NsZF-HD12	mRNA_82807_cds	MQGDKANDNIYRECLRNHAASLSGYATDGCGEFTLDDNNNNNTSPRSASLHCAACGCHRNFRKVMYGASYSNNSSRDREIVAELTDYGGGRMSAALTAESPRSGKKRFRTKFTTDQKEKMLAFAEKLGWTL
NsZF-HD13	mRNA_82808_cds	QRKDQENETERFCREVGVSRKVFVWMHNNHKNNTSSVSTGNASSLTQ
	mRNA_9947_cds	MDISSNTNTAIAATTVKSTEAEPETPIRIQPAKPIFSNGVLKRHNSLHLPHHHGFNNNHAAAHVVTYKECLKNHAASLGGAHDGCGEFMPSPPTANPVDPTSLKCAACGCHRNFRHREPEEPVLPNQNTIPALEYQPH HRHHPPPPPPHHGGSGGHSSPNSSPPPISSAYYPASAPHMLLALSAGLSGPPAETNPLISPSSNPMSSAHLNPNNGSGRKRFRTKFTQDQKERMLEFAEKVEWKIQKRDEELISDFCSKIGVEKGVLVWMHNNKCKK
NsZF-HD14		DQATAAAAVNAVASTNNLNGNANGFGFISRNNTDAIASEFHHRESSNDNDKNHNNHLLHNNDVSVAHGVTNNGSSSSS
	mRNA_9948_cds	MDISSNTNTAIAATTVKSTEAEPETPIRIQPAKPIFSNGVLKRHNSLHLPHHHGFNNNHAAAHVVTYKECLKNHAASLGGAHDGCGEFMPSPPTANPVDPTSLKCAACGCHRNFRHREPEEPVLPNQNTIPALEYQPH HRHHPPPPPPHHGGSGGHSSPNSSPPPISSAYYPASAPHMLLALSAGLSGPPAETNPLISPSSNPMSSAHLNPNNGSGRKRFRTKFTQDQKERMLEFAEKVEWKIQKRDEELISDFCSKIGVEKGVLVWMHNNKCKK
NsZF-HD15		DQATAAAAVNAVASTNNLNAMEN
		MEFDEEHQEEIEGNIHQISSAAATVNYQTQGNNSVRGVEEGVSTTVRKSSVRYRECLKNHAVGIGGAHDGCGDFMPAGEEGTMDALKCAACNCHRNFRHREVEGEVHFHTPPPHLTHHHPQPHSHHPQFSPY
NoZF-HD1	Ntom0273300.1	TSYRTPHHPSGYLHVTPPSHQRLALPSTSTREDEDMSPSSGGGGNGGVGGSSRKRFRTKFTADQDKMLAFAERLGWRMQKQDEALVQQFAETNVQRHVFKVWMHNNKHTLGKKP
		MEFETQEDQKEIKASPNNYSVLEISNSTNEPKMPSNSDELILDAPLQMRPKPYKECLKNHAVGIGGAHDGCGEFMPAGEDGTLDAKCAACNCHRNFRHREVEGEILNHHPTPPPPILHPPHHPYPRYHQRPLALPSI
NoZF-HD2	Ntom0174840.1	GGGGGYREDQEEELCNPNNSVTKKRFRTRFNQEQKEKMLEAEKLGWRIQRQDEGVVQQLCNEICIKRHVFKVWMHNNKTLGKKTLIQSTNP
		MEFDEEHEDQEEIEANIPQIPTTENNYQELGEGGPISQAAATLRKNNVPIPRYRECLKNHAVGIGGAHDGCGEFLPSGEEGTLDALKCAACNCHRNFRHREVEGEILNHHPTPPPPILHPPHHPYPRYHQRPLALPSI
NoZF-HD3	Ntom0331490.1	SSREDIEEYVSNPSSGGSGSRKRFRTKFTQDQKEKMFADAEGLGWRIQKENEAAVQQFAETNIRRVFKVWMHNNKNTLGKKP

NoZF-HD4	Ntom0261800.1	MELPIQEEEMPMPINSTYVGGGEGHGHGHIIHHDTPVPNNTNHIIPSSVANSINGPPIEATPVSADHHVPYKKIVRYKECLKNHAAAMGGNATDGCGEFMPSGEETIEALICSACNCHRNFRHKEMEGEQQLQLPPS
		SCDYYNLNRGGKKVYLGHSHNHHKGLLGPEPFGTIIPSRAAAPHHHQMIMSYNNMGSLPSESEEHEDINGGGVMAMAMARPLHHHNQIVKKRFRTKFTQEQQEKMFMFAEKVGWQIQQEETVVQQFCQELGIK
		RRVLKVMHNNKHSLAKKNSNSTIPQNQV
NoZF-HD5	Ntom0292910.1	MVVIIAKYGGGGGMVVDNAQPTFPTRTYSHQLEEERDPLVAATNRAQLRQQSTTSNGNTTTTTSSLSVVRRYRECLKNHAASMGGHILDGCGKFMPEEEGALKCAACNCHRNFRHRETSEAEQIARPRPPYS
		TFNPPIHSSSNYHHNYSTASPVMMTFGRNAESSSEDLNLFNSNAGGGQSSKSKKRFRTKFTAQKERMHEFAEKVGWSIQQDEQELQHFCNQVGVKRQVFRIWMHNSKQANKKRQM
		MEVPNEEGEMAMPINSTYGHEHMIYHDTAPQNNHIITPPQIVTSKNGPPISTLTLESDNVVPYKKMVKYKECLKNHAAAMGGNATDGCGEFMPSGEETFEFLTCSVCNCHRNFRHKETEGELIRKVYVGHPHKAF
NoZF-HD6	Ntom0185660.1	VYAASRAAPHQMIMSYNNHLGSFPYIEQEDGIINGGCGVMARPLNYQQLVKKRFRTKFSQEQQEKMLNFAEKIGWKMQQEDAMVQQFCQEVGVKRRVLKVMHNNKHSLAKKNSNDINLQSQI
		MEHTGQDKDMGMPNSIGFNSSHLNQQUESTPFAAAKLPTAPIVSSLPDRTRNEQISHGNTIFSPNQLDQHNLTNQSDPDPTVIAVQLRQQSTTSASDKNSSVRYKECLKNHAASMGGHVLDDGCGEFMPSGEETPEY
		Ntom0175880.1
NoZF-HD7	Ntom0181410.1	LKCAACDCHRNFRHKETEDESQTAGVHRNNSNSHRIHAQIPPSLPAPPQQQHYHKYTHGYSRGPMPVMMNFGGNSGVPAESSSEDLNMFNSNAGGQGVQPCTFSASKKRFRTKFTQQQKEKMQEFAEKLGWRIQ
		KQDEQEVQQFCNEVGVKRQVFKVFMHNCKQAIRKQT
		MDISSNTTIAITTVKTTAEPTIRIQPAKPISFSNGVLKRHNSLHLPHHHGFNKNHHHHHHHAVVVTYKECLKNHAASLGGAHDGCGEFMPSPTANPVDPTSLKCAACGCHRNFRHREPEEPVLPNQNTIPALEY
NoZF-HD8	Ntom0167540.1	QPHRRHHPPPPPHHGASGGHSSPNSPSPPISSAAYYPASAPHMLLALSAGLSSPPAENNLISPSSNMSSANLTNPNGSGRKRFRTKFTQDQKERMLEFAEKVEWKIQKRDEELINDFCISKIGVEKGVLKVMHNN
		KCKKDQATAAAINTVATPNLLNGNNGNGFGLISRNNNTDTIASEFHLHHESSKDNDKDHSHQLHNNDVSVAHGVTNTGSSSSS
		MELTCGSNPTKSTPDSENDTPPLIKPLSFSNGILKNHHFYHHQPPSAAVTYKECLKNHAASIGGHAVDGCGEFMPSPDSTPSNPTSLKCAACGCHRNFRHREPAEDSSPTHFPSHFINFRHHILPPIRRFSPSSSSPPPPF
NoZF-HD9	Ntom0167540.1	QPQPITPKVEHNPSGRKRFRTKFTQQQKEKMHSFSEKLGWKLQKCDEAKVEEFCNEVGVGKGVLRVWMHNNKNTFAKKEELQNGNNNSNGFNHGGSSSNEDHNNCGLHLHISTNGSSSSS
		MQGDKANDNIYRECLRNHAASLGSYATDGCGEFTLDDDDNNNTSPGASLHCAACGCHRNFRHKVVIYGASYSNSSRDREIMAADDYAGGRTAEESPRSGKKRFRTKFTTDQKEKMLAFAEKLGWTLQRKDQEN
		ETERFCREVGVSARKVFKVWMHNNKNTSSISTGNASSLTQ
NoZF-HD10	Ntom0268890.1	MDSTYSIPTRNHIPTKTPDSEKDFPPYPQVPLKPLSFTNVTSSKHHQVHNHQPPSAAVTYKECLKNHAASIGGYTVDGCGEFIPTDAIAADPTSLKCDVCGCHRNFRHRRKDDDFMDFRHHHAQVATPATPTALKPE
		KPRRRRRFRTKFSQEQQKNRMYSFSEKLGWKLQKCDEAMVEEFCNEIGVGKGVFRVWMHNNKSTLGKKGFPKCCQQYQTVPYNNKQ
		MDSTYSIPTRNHIPTKTPDSEKDFPPYPQVPLKPLSFTNVTSSKHHQVHNHQPPSAAVTYKECLKNHAASIGGYTVDGCGEFIPTDAIAADPTSLKCDVCGCHRNFRHRRKDDDFMDFRHHHAQVATPATPTALKPE
NoZF-HD11	Ntom0318250.1	KPRRRRRFRTKFSQEQQKNRMYSFSEKLGWKLQKCDEAMVEEFCNEIGVGKGVFRVWMHNNKSTLGKKGFPKCCQQYQTVPYNNKQ
		MDFENHQVEEEETEPPPSYDDSLNNSNSTHPTKMPSPTPMELEPLAAVHTWHNNKPKYKECLKNHAVSIGGHAVDGCGSGSNKRFRTKFSQEQQEKMQLADKLGWRIQREDEELVQQLCNETGVRRQVFKVWMH
		NKNNTLGKKP
NoZF-HD12	Ntom0008120.1	MMKKRQVVVRTDGSRRNIGSSSIRNIRYVEQCQNHAANIGGYAVDGCREFMASGEDGTTAALTCAACGCHRNFRHREVDGGEVVSECAAAAAA
NoZF-HD13	Ntom0064960.1	
NoZF-HD14	Ntom0064960.1	

		MDLTNNSTTTTTLANTTTTTTSAHIKPEAEIETPTQIQKPKPFSFSGVLKRKNLFQHHHPVVIYKECLKNHAASLGGHAVDGCGEFMPSPATANPADPTSLKCAACGCHRNFRHREPEEPIVIPPPPIATAALEYQPH
	Ntom0227830.1	HRHHPPPPPPPLPRGDHSSPNSPSPPISSAYYPASAPHMLLALSAGFSGEKNHNPISSPVVNTTNCNGRKRFRTKFTPDQKVKMLEFAERVGWKMQRDEDLVRSFCNQIGIEKGVLKVWMHNNKNTFGKKLDQHHL
NoZF-HD15		ADININNNGNSTNVVNGFCIVSRNNNSHHNSTDSAEFHHLHHHESSYDDNKISDHIKSVGTANVVVATNGSSSSS
NoZF-HD16	Ntom0328480.1	MTKRQVILMKDDFSDDDSTNSSFTIRTVRYRECQKNHAASVGGYAVDGCREFMPCGEEGTPGGLTCAACGCHRNFRHREVETEACDCSFPT
NoZF-HD17	Ntom0181400.1	MKKVLRKSSNDSSHNSTNSSTFTVRTVRYVEQCQKNHAASVGGYVVDGCREFMPGETSGAALTCAACGCHRNFRHKEVETDVASDCTSASSITT
	Ntom0241790.1	MASNSSSTPTMTIRYGECLKNHSKKKHGHYLFDGCREFVKSGEDGTKGSYVCANCGCIRSFHRMNNQPLHRHQAIRLCFFHHCVIPNGMQPIFHPFNETQVSVSATSLPVTIISDPESVSVQENVSCVMTPPMLPLLPLF
NoZF-HD18		PKDEMGVPVPVPLPLFPETPSSGTFGLLEGKQDMDMDAAAAAA
