>56

METASLSFPVPNTSFGVNKSMPLGLNQLTPYQIHQIQNQLNHRRSTISNLSPNRIRMKNLTPSTSKTKNLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFETAEKAALAYDQAAFQLRGDIAKLNFPNLIHEDMNPLPSSVDTKLQAICKSLRKTEEICSVSDQTKEYSVYSVSDKTELFLPKAELFLPKREHLETNELSNESPRSDETSLLDESQAEYSSSDKTFLDFSDTEFEEIGSFGLRKFPSVEIDWDAISKLANS

>57

MALNMNAYVDEFMEALEPFMKVTSSSSTSNSSNPKPLTPNFIPNNDQVLPVSNQTGPIGLNQLTPTQILQIQTELHLRQNQSRRRAGSHLLTAKPTSMKKIDVATKPVKLYRGVRQRQWGKWVAEIRLPKNRTRLWLGTFETAQEAALAYDQAAHKIRGDNARLNFPDIVRQGHYKQILSPSINAKIESICNSSDLPLPQIEKQNKTEEVLSGFSKPEKEPEFGEIYGCGYSGSSPESDITLLDFSSDCVKEDESFLMGLHKYPSLEIDWDAIEKLF

>58

MTTSMDFYSNKTFQQSDPFGGELMEALLPFIKSPSNDSSAFAFSLPAPISYGSDLHSFSHHLSPKPVSMKQTGTSAAKPTKLYRGVRQRHWGKWVAEIRLPRNRTRLWLGTFDTAEEAALAYDKAAYKLRGDFARLNFPDLRHNDEYQPLQSSVDAKLEAICQNLAETTQKQVRSTKKSSSRKRSSTVAVKLPEEDYSSAGSSPLLTESYGSGGSSSPLSELTFGDTEEEIQPPWNENALEKYPSYEIDWDSILQCSSLVN

>59

MAAAMNLYTCSRSFQDSGGELMDALVPFIKSVSDSPSSSSAASASAFLHPSAFSLPPLPGYYPDSTFLTQPFSYGSDLQQTGSLIGLNNLSSSQIHQIQSQIHHPLPPTHHNNNNSFSNLLSPKPLLMKQSGVAGSCFAYGSGVPSKPTKLYRGVRQRHWGKWVAEIRLPRNRTRLWLGTFDTAEEAALAYDKAAYKLRGDFARLNFPNLRHNGSHIGGDFGEYKPLHSSVDAKLEAICKSMAETQKQDKSTKSSKKREKKVSSPDLSEKVKAEENSVSIGGSPPVTEFEESTAGSSPLSDLTFADPEEPPQWNETFSLEKYPSYEIDWDSILA

>60

MAAIDMFNSNTDPFQEELMKALQPYTTNTDSSSPTYSNTVFGFNQTTSLGLNQLTPYQIHQIQNQLNQRRNIISPNLAPKPVPMKNMTAQKLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFDTAEEAAMAYDLAAYKLRGEFARLNFPQFRHEDGYYGGGSCFNPLHSSVDAKLQEICQSLRKTEDIDLPCSETELFPPKTEYQESEYGFLRSDENSFSDESHVESSSPESGITTFLDFSDSGFDEIGSFGLEKFPSVEIDWDAISKLSES

>61

MEESNDIFQNNFSPKISEIRASLSQIILAGGPNTLDSIFSLLTPSSVESATTSFNTHNPPPPPQLGSSVYLRQRDIIEKFHLQNRAISTPHPPLFSSTYDHHQTSELMLQAAAGSPAAAFAAALAAGRVTKKKKLYRGVRQRHWGKWVAEIRLPQNRMRVWLGTYDTAEAAAYAYDRAAYKLRGEYARLNFPNLKDPSELLGLGDSSKLIALKNAVDGKIQSICQRVRKERAKKSVKVSKNSSATADSSCLSSPEILSSSPVTTTTTAVTSEDSYWVSPMGLCNSENSSPVSVSVPSEVPATAEEEAMMGVDTDGFLLARMPSFDPELIWEVLAN

>62

MITPIHTQHSLILVYINIYSPPILSKLRTGFILWTNTQKTNKKRNMEDQFPKIETSFMHDKLLSSGIYGFLSSSTPPQLLGVPIFLEGMKSPLLPASSTPSYFVSPHDHELTSSIHPSPVASVPWNFLESFPQSQHPDHHPSKPPNLTLFLKEPKLLELSQSESNMSPYHKYIPNSFYQSDQNRNEWVEINKTLTNYPSKGFGNYWLSTTKTQPMKSKTRKVVQTTTPTKLYRGVRQRHWGKWVAEIRLPRNRTRVWLGTFETAEQAAMAYDTAAYILRGEFAHLNFPDLKHQLKSGSLRCMIASLLESKIQQISSSQVSNSPSPPPPKVGTPEQKNHHMKMESGEDVMMKKQKSHKEVMEGDGVQLSRMPSLDMDLIWDALSFPHSS

>008

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LTVSNGGGRGGDLSAAYIRRKAAEVGAQVDALGATVVVNTGGENRGDYEKIENCRKSGNGSLERVDLNKLPDPENSDGDDDECVKRR

>009

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>010

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>011

MDAGVAVKADVAVKMKRERPFKGIRMRKWGKWVAEIREPNKRSRLWLGSYSTPEAAARAYDTAVFYLRGPTATLNFPELLPCTSAEDMS

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>012

MVKQERKIQTSSTKKEMPLSSSPSSSSSSSSSSSSSSCKNKNKKSKIKKYKGVRMRSWGSWVSEIRAPNQKTRIWLGSYSTAEAAARAYDVALLCLKGPQANLNFPTSSSSHHLLDNLLDENTLLSPKSIQRVAAQAANSFNHFAPTSSAVSSPSDHDHHHDDGMQSLMGSFVDNHVSLMDSTSSWYDDHNGMFLFDNGAPFNYSPQLNSTTMLDEYFYEDADIPLWSFN

>013

MVKQELKIQVTTSSSSLSHSSSSSSSSTSALRHQSCKNKIKKYKGVRMRSWGSWVTEIRAPNQKTRIWLGSYSTAEAAARAYDAALLCLKGPKANLNFPNITTTSPFLMNIDEKTLLSPKSIQKVAAQAANSSSDHFTPPSDENDHDHDDGLDHHPSASSSAASSPPDDDHHNDDDGDLVSLMESFVDYNEHVSLMDPSLYEFGHNEIFFTNGDPFDYSPQLHSSEATMDDFYDDVDIPLWSFS

>014

MVKTLQKTPKRMSSPSSSSSSSSSTSSSSIRMKKYKGVRMRSWGSWVSEIRAPNQKTRIWLGSYSTAEAAARAYDAALLCLKGSSANNLNFPEISTSLYHIINNGDNNNDMSPKSIQRVAAAAAAANTDPSSSSVSTSSPLLSSPSEDLYDVVSMSQYDQQVSLSESSSWYNCFDGDDQFMFINGVSAPYLTTSLSDDFFEEGDIRLWNFC

>029

MNSFSAFSEMFGSDYEPQGGDYCPTLATSCPKKPAGRKKFRETRHPIYRGVRQRNSGKWVSEVREPNKKTRIWLGTFQTAEMAARAHDVAALALRGRSACLNFADSAWRLRIPESTCAKDIQKAAAEAALAFQDETCDTTTTNHGLDMEETMVEAIYTPEQSEGAFYMDEETMFGMPTLLDNMAEGMLLPPPSVQWNHNYDGEGDGDVSLWSY

>031

MNSFSAFSEMFGSDYESSVSSGGDYIPTLASSCPKKPAGRKKFRETRHPIYRGVRRRNSGKWVCEVREPNKKTRIWLGTFQTAEMAARAHDVAALALRGRSACLNFADSAWRLRIPESTCAKDIQKAAAEAALAFQDEMCDATTDHGFDMEETLVEAIYTAEQSENAFYMHDEAMFEMPSLLANMAEGMLLPLPSVQWNHNHEVDGDDDDVSLWSY

>033

MNNDDIILAEMRPKKRAGRRVFKETRHPVYRGIRRRNGDKWVCEVREPTHQRRIWLGTYPTADMAARAHDVAVLALRGRSACLNFADSAWRLPVPESNDPDVIRRVAAEAAEMFRPVDLESGITVLPCAGDDVDLGFGSGSGSGSGSEERNSSSYGFGDYEEVSTTMMRLAEGPLMSPPRSYMEDMTPTNVYTEEEMCYEDMSLWSYRY

>035

MGKQINIESSATHHQDNIVSVITATISSSSVVTSSSDSWSTSKRSLVQDNDSGGKRRKSNVSDDNKNPTSYRGVRMRSWGKWVSEIREPRKKSRIWLGTYPTAEMAARAHDVAALAIKGNSGFLNFPELSGLLPRPVSCSPKDIQAAATKAAEATTWHKPVIDKKLADELSHSELLSTAQSSTSSSFVFSSDTSETSSTDKESNEETVFDLPDLFTDGLMNPNDAFCLCNGTFTWQLYGEEDVGFRFEEPFNWQND

>037

MTESSIISVKQSSPVPEEEDHHHHQQDSHRTNTKKRVRSDPGYRGVRMRTWGKWVSEIREPRKKSRIWLGTFSTPEMAARAHDAAALTIKGTSAVLNFPELATYLPRPASSSPRDVQAAAAVAAAMDFSPSSSSLVVSDPTTVIAPAETQLSSSSYSTCTSSSLSPSSEEAASTAEELSEIVELPSLETSYDESLSEFVYVDSAYPPSSPWYINNCYSFYYHSDENGISMAEPFDSSNFGPLFP

>039

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>041

MAEEYYSLRSERVTQLLVPNSESDSVSDKSKAEQSEKKTKRGRDSGKHPVYRGVRMRNWGKWVSEIREPRKKSRIWLGTFPTPEMAARAHDVAALSIKGTAAILNFPELADSFPRPVSLSPRDIQTAALKAAHMEPTTSFSSSTSSSSSLSSTSSLESLVLVMDLSRTESEELGEIVELPSLGASYDVDSANLGNEFVFYDSVDYCLYPPPWGQSSEDNYGHGISPNFGHGLSWDL

>043

MADSSSDKEKKENNKQPVYRGVRMRSWGKWVSEIREPRKKSRIWLGTFPTAEMAMRAHDVAAMSIKGTSAILNFPELSKLLPRPVSLSPRDVRAAATKAALMDFDTTAFRSDTETSETTTSNKMSESSESNETVSFSSSSWSSVTSIEESTVSDDLDEIVKLPSLGTSLNESNEFVIFDSLEDLVYMPRWLSGTEEEVFTYNNNDSSLNYSSVFESWKHFP

>044

MAVYEQTGTEQPKKRKSRARAGGLTVADRLKKWKEYNEIVEASAVKEGEKPKRKVPAKGSKKGCMKGKGGPDNSHCSFRGVRQRIWGKWVAEIREPKIGTRLWLGTFPTAEKAASAYDEAATAMYGSLARLNFPQSVGSEFTSTSSQSEVCTVENKAVVCGDVCVKHEDTDCESNPFSQILDVREESCGTRPDSCTVGHQDMNSSLNYDLLLEFEQQYWGQVLQEKEKPKQEEEEIQQQQQEQQQQQLQPDLLTVADYGWPWSNDIVNDQTSWDPNECFDINELLGDLNEPGPHQSQDQNHVNSGSYDLHPLHLEPHDGHEFNGLSSLDI

>045

MAVYDQSGDRNRTQIDTSRKRKSRSRGDGTTVAERLKRWKEYNETVEEVSTKKRKVPAKGSKKGCMKGKGGPENSRCSFRGVRQRIWGKWVAEIREPNRGSRLWLGTFPTAQEAASAYDEAAKAMYGPLARLNFPRSDASEVTSTSSQSEVCTVETPGCVHVKTEDPDCESKPFSGGVEPMYCLENGAEEMKRGVKADKHWLSEFEHNYWSDILKEKEKQKEQGIVETCQQQQQDSLSVADYGWPNDVDQSHLDSSDMFDVDELLRDLNGDDVFAGLNQDRYPGNSVANGSYRPESQQSGFDPLQSLNYGIPPFQLEGKDGNGFFDDLSYLDLEN

>046

MEKEDNGSKQSSSASVVSSRRRRRVVEPVEATLQRWEEEGLARARRVQAKGSKKGCMRGKGGPENPVCRFRGVRQRVWGKWVAEIREPVSHRGANSSRSKRLWLGTFATAAEAALAYDRAASVMYGPYARLNFPEDLGGGRKKDEEAESSGGYWLETNKAGNGVIETEGGKDYVVYNEDAIELGHDKTQNPMTDNEIVNPAVKSEEGYSYDRFKLDNGLLYNEPQSSSYHQGGGFDSYFEYFRF

>047

MPRKRKSRGTRDVAEILRKWREYNEQTEADSCIDGGGSKPIRKAPPKRSRKGCMKGKGGPENGICDYTGVRQRTWGKWVAEIREPGRGAKLWLGTFSSSYEAALAYDEASKAIYGQSARLNLPLLPLCQARLLHFLMNLKFVHVRIQMQDLVLVRSD

>048

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>049

MSSIEPKVMMVGANKKQRTVQASSRKGCMRGKGGPDNASCTYKGVRQRTWGKWVAEIREPNRGARLWLGTFDTSREAALAYDSAARKLYGPEAHLNLPESLRSYPKTASSPASQTTPSSNTGGKSSSDSESPCSSNEMSSCGRVTEEISWEHINVDLPVMDDSSIWEEATMSLGFPWVHEGDNDISRFDTCISGGYSNWDSFHSPL

>001

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>002

MEHQTTPKQKTKEKSKGNKTKFVGVRQRPSGKWVAEIKDTTQKIRMWLGTFETAEEAARAYDEAACLLRGSNTRTNFANHFPNNSQLSLKIRNLLHQKQSMKQQQQQQHKPVSSLTDCNINYISTATSLTTTTTTTTTTAIPLNNVYRPDSSVIGQPETEGLQLPYSWPLVSGFNHQIPLAQAGGETHGHLNDHYSTDQHLGLAEIERQISASLYAMNGANSYYDNMNAEYAIFDPTDPIWDLPSLSQLFCPT

>003

MARPQQRFRGVRQRHWGSWVSEIRHPLLKTRIWLGTFETAEDAARAYDEAARLMCGPRARTNFPYNPNAIPTSSSKLLSATLTAKLHKCYMASLQMTKQTQTQTQTQTARSQSADSDGVTANESHLNRGVTETTEIKWEDGNANMQQNFRPLEEDHIEQMIEELLHYGSIELCSVLPTQTL

>004

MVHSRKFRGVRQRQWGSWVSEIRHPLLKRRVWLGTFETAEAAARAYDQAALLMNGQNAKTNFPVVKSEEGSDHVKDVNSPLMSPKSLSELLNAKLRKSCKDLTPSLTCLRLDTDSSHIGVWQKRAGSKTSPTWVMRLELGNVVNESAVDLGLTTMNKQNVEKEEEEEEAIISDEDQLAMEMIEELLNWS

>005

MVHSKKFRGVRQRQWGSWVSEIRHPLLKRRVWLGTFDTAETAARAYDQAAVLMNGQSAKTNFPVIKSNGSNSLEINSALRSPKSLSELLNAKLRKNCKDQTPYLTCLRLDNDSSHIGVWQKRAGSKTSPNWVKLVELGDKVNARPGGDIETNKMKVRNEDVQEDDQMAMQMIEELLNWTCPGSGSIAQV

>063

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>064

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>065

MDEYIDFRPLKYTEHKTSMTKYTKKSSEKLSGGKSLKKVSICYTDPDATDSSSDEDEEDFLFPRRRVKRFVNEITVEPSCNNVVTGVSMKDRKRLSSSSDETQSPASSRQRPNNKVSVSGQIKKFRGVRQRPWGKWAAEIRDPEQRRRIWLGTFETAEEAAVVYDNAAIRLRGPDALTNFSIPPQEEEEEEEPEPVIEEKPVIMTTPTPTTSSSESTEEDLQHLSSPTSVLNHRSEEIQQVQQPFKSAKPEPGVSNAPWWHTGFNTGLGESDDSFPLDTPFLDNYFNESPPEMSIFDQPMDQIFCENDDIFNDMLFLGGETMNIEDELTSSSIKDMGSTFSDFDDSLISDLLVA

>066

MMMDEFMDLRPVKYTEHKTVIRKYTKKSSMERKTSVRDSARLVRVSMTDRDATDSSSDEEEFLFPRRRVKRLINEIRVEPSSSSTGDVSASPTKDRKRINVDSTVQKPSVSGQNQKKYRGVRQRPWGKWAAEIRDPEQRRRIWLGTFATAEEAAIVYDNAAIKLRGPDALTNFTVQPEPEPVQEQEQEPESNMSVSISESMDDSQHLSSPTSVLNYQTYVSEEPIDSLIKPVKQEFLEPEQEPISWHLGEGNTNTNDDSFPLDITFLDNYFNESLPDISIFDQPMSPIQPTENDFFNDLMLFDSNAEEYYSSEIKEIGSSFNDLDDSLISDLLLV

>067

MERRTRRVKFTENRTVTNVAATPSNGSPRLVRITVTDPFATDSSSDDDDNNNVTVVPRVKRYVKEIRFCQGESSSSTAARKGKHKEEESVVVEDDVSTSVKPKKYRGVRQRPWGKFAAEIRDPSSRTRIWLGTFVTAEEAAIAYDRAAIHLKGPKALTNFLTPPTPTPVIDLQTVSACDYGRDSRQSLHSPTSVLRFNVNEETEHEIEAIELSPERKSTVIKEEEESSAGLVFPDPYLLPDLSLAGECFWDTEIAPDLLFLDEETKIQSTLLPNTEVSKQGENETEDFEFGLIDDFESSPWDVDHFFDHHHHSFD

>068

MKSRVRKSKYTVHRKITSTPFDGFPKIVKIIVTDPCATDSSSDEENDNKSVAPRVKRYVDEIRFCDEDDEPKPARKAKKKSPAAAAENGGDLVKSVVKYRGVRQRPWGKFAAEIRDPSSRTRLWLGTFATAEEAAIGYDRAAIRIKGHNAQTNFLTPPPSPTTEVLPETPVIDLETVSGCDSARESQISLCSPTSVLRFSHNDETEYRTEPTEEQNPFFLPDLFRSGDYFWDSEITPDPLFLDEFHQSLLPNINNNNTVCDKDTNLSDSFPLGVIGDFSSWDVDEFFQDHLLDK

>069

MKRIVRISFTDMEATDSSSSEDESPPSSRRRGKKLVKEIVIDHSDPPEVGKTRFKIRIPASLLAARNTTANKKKFRGVRQRPWGKWAAEIRCGRVKGRPERIWLGTFETAEEAALAYDNAAIQLIGPDAPTNFGRPDVDSAVVKKQDSDASGGASEEVV

>070

MKRIIRISFTDAEATDSSSDEDTEERGGASQTRRRGKRLVKEIVIDPSDSADKLDVCKTRFKIRIPAEFLKTAKTEKKYRGVRQRPWGK

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>071

MCGGAIISDFIWSKSESEPSQLGSVSSRKKRKPVSVSEERDGKRERKNLYRGIRQRPWGKWAAEIRDPSKGVRVWLGTFKTADEAARAYDVAAIKIRGRKAKLNFPNTQVEEEADTKPGGNQNELISENQVESLSEDLMALEDYMRFYQIPVADDQSATDIGNLWSYQDSN

>072

MCGGAIISDYAPLVTKAKGRKLTAEELWSELDASAADDFWGFYSTSKLHPTNQVNVKEEAVKKEQATEPGKRRKRKNVYRGIRKRPWGKWAAEIRDPRKGVRVWLGTFNTAEEAAMAYDVAAKQIRGDKAKLNFPDLHHPPPPNYTPPPSSPRSTDQPPAKKVCVVSQSESELSQPSFPVECIGFGNGDEFQNLSYGFEPDYDLKQQISSLESFLELDGNTAEQPSQLDESVSEVDMWMLDDVIASYE

>073

MCGGAVISDYIAPEKIARSSGKSSWRSNGVFDCSIYDFDGNFDELESDEPFVFSSTHKHHASGSASDGKKKQSSRYKGIRRRPWGRWAAEIRDPIKGVRVWLGTFNTAEEAARAYDLEAKRIRGAKAKLNFPNESSGKRKAKAKTVQQVEENHEADLDVAVVSSAPSSSCLDFLWEENNPDTLLIDTQWLEDIIMGDANKKHEPNDSEEANNVDASLLSEELLAFENQTEYFSQMPFTEGNCDSSTSLSSLFDGGNDMGLWS

>074

MCGGAIISDFIPPPRSRRVTSEFIWPDLKKNLKGSKKSSKNRSNFFDFDAEFEADFQGFKDDSSIDCDDDFDVGDVFADVKPFVFTSTPKPAVSAAAEGSVFGKKVTGLDGDAEKSANRKRKNQYRGIRQRPWGKWAAEIRDPREGARIWLGTFKTAEEAARAYDAAARRIRGSKAKVNFPEENMKANSQKRSVKANLQKPVAKPNPNPSPALVQNSNISFENMCFMEEKHQVSNNNNNQFGMTNSVDAGCNGYQYFSSDQGSNSFDCSEFGWSDQAPITPDISSAVINNNNSALFFEEANPAKKLKSMDFETPYNNTEWDASLDFLNEDAVTTQDNGANPMDLWSIDEIHSMIGGVF

>075

MCGGAIISDFIPPPRSLRVTNEFIWPDLKNKVKASKKRSNKRSDFFDLDDDFEADFQGFKDDSAFDCEDDDDVFVNVKPFVFTATTKPVASAFVSTGIYLVGSAYAKKTVESAEQAEKSSKRKRKNQYRGIRQRPWGKWAAEIRDPRKGSREWLGTFDTAEEAARAYDAAARRIRGTKAKVNFPEEKNPSVVSQKRPSAKTNNLQKSVAKPNKSVTLVQQPTHLSQQYCNNSFDNSFGDMSFMEEKPQMYNNQFGLTNSFDAGGNNGYQYFSSDQGSNSFDCSEFGWSDHGPKTPEISSMLVNNNEASFVEETNAAKKLKPNSDESDDLMAYLDNALWDTPLEVEAMLGADAGAVTQEEENPVELWSLDEINFMLEGDF

>076

MAPTVKTAAVKTNEGNGVRYRGVRKRPWGRYAAEIRDPFKKSRVWLGTFDTPEEAARAYDKRAIEFRGAKAKTNFPCYNINAHCLSLTQSLSQSSTVESSFPNLNLGSDSVSSRFPFPKIQVKAGMMVFDERSESDSSSVVMDVVRYEGRRVVLDLDLNFPPPPEN

>077

MTTEKENVTTAVAVKDGGEKSKEVSDKGVKKRKNVTKALAVNDGGEKSKEVRYRGVRRRPWGRYAAEIRDPVKKKRVWLGSFNTGEEAARAYDSAAIRFRGSKATTNFPLIGYYGISSATPVNNNLSETVSDGNANLPLVGDDGNALASPVNNTLSETARDGTLPSDCHDMLSPGVAEAVAGFFLDLPEVIALKEELDRVCPDQFESIDMGLTIGPQTAVEEPETSSAVDCKLRMEPDLDLNASP

>079

MPNITMGLKPDPVAPTNPTHHESNAAKEIRYRGVRKRPWGRYAAEIRDPVKKTRVWLGTFDTAQQAARAYDAAARDFRGVKAKTNFGVIVGSSPTQSSTVVDSPTAARFITPPHLELSLGGGGACRRKIPLVHPVYYYNMATYPKMTTCGVQSESETSSVVDFEGGAGKISPPLDLDLNLAPPAE

>081

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>083

MRKGRGSSVVGPALPVTAGGSVKEPRYRGVRKRPWGRFAAEIRDPLKKSRVWLGTFDSAVDAARAYDTAARNLRGPKAKTNFPIDCSPSSPLQPLTYLHNQNLCSPPVIQNQIDPFMDHRLYGGGNFQEQQQQQIISRPASSSMSSTVKSCSGPRPMEAAAASSSVAKPLHAIKRYPRTPPVAPEDCHSDCDSSSSVIDDGDDIASSSSRRKTPFQFDLNFPPLDGVDLFAGGIDDLHCTDLRL

>089

MEKALRNFTESTHSPDPNPLTKFFTEPTASPVSRNRKLSSKDTTVTIAGAGSSTTRYRGVRRRPWGRYAAEIRDPMSKERRWLGTFDTAEQAACAYDSAARAFRGAKARTNFTYPTAVIMPEPRFSFSNKKSSPSARCPLPSLPLDSSTQNFYGAPAAQRIYNTQSIFLRDASCSSRKTTPYNNSFNGSSSSYSASKTACVSYSENENNESFFPEESSDTGLLQEVVQEFLKKNRGVPPSPPTPPPVTSHHDNSGYFSNLTIYSENMVQETKETLSSKLDRYGNFQANDDGVRAVADGGLSLGSNEWGYQEMLMYGTQLGCTCRRSWG

>091

MAFGNIQELDGEILKNVWANYIGTPQTDTRSIQVPEVSRTWEALPTLDDIPEGSREMLQSLDMSTEDQEWTEILDAIASFPNKTNHDPLTNPTIDSCSLSSRVSCKTRKYRGVRKRPWGKFAAEIRDSTRNGVRVWLGTFQTAEEAAMAYDKAAVRIRGTQKAHTNFQLETVIKAMEMDCNPNYYRMNNSNTSDPLRSSRKIGLRTGKEAVKAYDEVVDGMVENHCALSYCSTKEHSETRGLRGSEETWFDLRKRRRSNEDSMCQEVEMQKTVTGEETVCDVFGLFEFEDLGSDYLETLLSSF

>092

MDPFLIQSPFSGFSPEYSIGSSPDSFSSSSSNNYSLPFNENDSEEMFLYGLIEQSTQQTYIDSDSQDLPIKSVSSRKSEKSYRGVRRRPWGKFAAEIRDSTRNGIRVWLGTFESAEEAALAYDQAAFSMRGSSAILNFSAERVQESLSEIKYTYEDGCSPVVALKRKHSMRRRMTNKKTKDSDFDHRSVKLDNVVVFEDLGEQYLEELLGSSENSGTW

>093

MEYSQSSMYSSPSSWSSSQESLLWNESCFLDQSSEPQAFFCPNYDYSDDFFSFESPEMMIKEEIQNGDVSNSEEEEKVGIDEERSYRGVRKRPWGKFAAEIRDSTRNGIRVWLGTFDKAEEAALAYDQAAFATKGSLATLNFPVEVVRESLKKMENVNLHDGGSPVMALKRKHSLRNRPRGKKRSSSSSSSSSNSSSCSSSSSTSSTSRSSSKQSVVKQESGTLVVFEDLGAEYLEQLLMSSC

>101

MYGQCNIESDYALLESITRHLLGGGGENELRLNESTPSSCFTESWGGLPLKENDSEDMLVYGLLKDAFHFDTSSSDLSCLFDFPAVKVEPTENFTAMEEKPKKAIPVTETAVKAKHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTFETAEDAALAYDIAAFRMRGSRALLNFPLRVNSGEPDPVRITSKRSSSSSSSSSSSTSSSENGKLKRRRKAENLTSEVVQVKCEVGDETRVDELLVS

>103

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>105

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>107

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>108

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>110

MSAMVSALTQVVSARSQTEAEGAHSSSSSAGHKRGWLGIDSAPIPSSFARVDSSHNPIEESMSKAFPEEAREKKRRYRGVRQRPWGKWAAEIRDPHRAARVWLGTFDTAEAAARAYDEAALRFRGNKAKLNFPEDVRILPPPPPLLRSPADTVANKAEEDLINYWSYTKLLQSSGQRSFLERGQEESSNIFEHSPMEQPLPPSSSGPSSSNFPAPSLPNT

>111

MCVLKVANQEDNVGKKAESIRDDDHRTLSEIDQWLYLFAAEDDHHRHSFPTQQPPPSSSSSSLISGFSREMEMSAIVSALTHVVAGNVPQHQQGGGEGSGEGTSNSSSSSGQKRRREVEEGGAKAVKAANTLTVDQYFSGGSSTSKVREASSNMSGPGPTYEYTTTATASSETSSFSGDQPRRRYRGVRQRPWGKWAAEIRDPFKAARVWLGTFDNAESAARAYDEAALRFRGNKAKLNFPENVKLVRPASTEAQPVHQTAAQRPTQSRNSGSTTTLLPIRPASNQSVHSQPLMQSYNLSYSEMARQQQQFQQHHQQSLDLYDQMSFPLRFGHTGGSMMQSTSSSSSHSRPLFSPAAVQPPPESASETGYLQDIQWPSDKTSNNYNNSPSS

>113

MVSALSRVIENPTDPPVKQELDKSDQHQPDQDQPRRRHYRGVRQRPWGKWAAEIRDPKKAARVWLGTFETAEEAALAYDRAALKFKGTKAKLNFPERVQGPTTTTTISHAPRGVSESMNSPPPRPGPPSTTTTSWPMTYNQDILQYAQLLTSNNEVDLSYYTSTLFSQPFSTPSSSSSSSQQTQQQQLQQQQQQREEEEKNYGYNYYNYPRE

>114

MYGKRPFGGDESEEREEDENLFPVFSARSQHDMRVMVSALTQVIGNQQSKSHDNISSIDDNYPSVYNPQDPNQQVAPTHQDQGDLRRRHYRGVRQRPWGKWAAEIRDPKKAARVWLGTFETAESAALAYDEAALKFKGSKAKLNFPERVQLGSNSTYYSSNQIPQMEPQSIPNYNQYYHDASSGDMLSFNLGGGYGSGTGYSMSHDNSTTTAATTSSSSGGSSRQQEEQDYARFWRFGDSSSSPHSGY

>115

MANSGNYGKRPFRGDESDEKKEADDDENIFPFFSARSQYDMRAMVSALTQVIGNQSSSHDNNQHQPVVYNQQDPNPPAPPTQDQGLLRKRHYRGVRQRPWGKWAAEIRDPQKAARVWLGTFETAEAAALAYDNAALKFKGSKAKLNFPERAQLASNTSTTTGPPNYYSSNNQIYYSNPQTNPQTIPYFNQYYYNQYLHQGGNSNDALSYSLAGGETGGSMYNHQTLSTTNSSSSGGSSRQQDDEQDYARYLRFGDSSPPNSGF

>ThERF15

MAQLKSKRVLEENMNFDSLPLDENDSEDMVLFAVLKEALNLGWSPQEGSRNHSKMENLGKNGGFEGKKGGFGEKKEKTDSVGERKHYRGVRRRPWGKFAAEIRESASRRWLGTFDTEEEAAMAYDKAALLMRGSRALLNFPLDMVLSAIARDPKPHNLKRKRLRRTEAPQRAEHLQYQYQIPRVENEQMEEKSESSPESMEFENELMEKISESSPESQLTTESQSSSERVEFEDLGAEFLEELLNSSTEIDDCFGSLYQYSSQSLSCDLQLN

>ThERF39

MKYEYSPEEFCTPRRMKSKKATKGKRASKKGCKMLQAYERFKAGRFTKSSPALRSSAQKTSKYKGVRQRRWGRWAAEIRDPLRGVRVWLGTFNTAEEAAKAYDKAAKKFKGTSAPNNFVWSSFASRRNAGASHKKQIYDAPCTGFNSVVTRSAANAKTKPNTIESCLASSSTSFSCISEEASDVEWVPNQAPIMEASASASASLVDDFGSEDAGCSRMIECSTSCSFSSDFLPDYLDDNAYQCSSEELLVELDNCNALEDASLDLSNMEQQHDIATEDNPPLVDFFIPPISEEQCYSALESSYGDFSSHDLYFLNEFGKVFEMDHAGPVPGLLSFPDSLDLIDEGNNISGLNDLLEEENFIPSLNFDLSSETLSWINV

>ThRAP2.3

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>OsERF15

MLLNPASREVAALDSIRHHLLEEEEETPATAPAPTRRPVYCRSSSFGSLVADQWSESLPFRPNDAEDMVVYGALRDAFSSGWLPDGSFAAVKPESQDSYDGSSIGSFLASSSSEAGTPGEVTSTEATVTPGIREGEGEAVAVASRGKHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTFDSAEEAAVAYDRAAYRMRGSRALLNFPLRIGSEIAAAAAAAAAGNKRPYPDPASSGSSSPSSSSSSSSSSSSGSPKRRKRGEAAAASMAMALVPPPPPPAQAPVQLALPAQPWFAAGPIQQLVS

>OsERF114

MVTALAHVIRAAPDLHLPHHPSSSASAAAHPQQASSFYPTAAAAASSPSDQLAAAAAAEEQGRRRHYRGVRQRPWGKWAAEIRDPKKAARVWLGTFDTAEDAAIAYDEAALRFKGTKAKLNFPERVQGRTDLGFLVTRGIPPAATHGGGYYPSSSPAAGACPPPRQQQTVVPYPDLMRYAQLLQGGVGGSYMPFGGAATMSSSTVSSSSAPQILDFSTQQLIRAGPPSPMPSSGSGSATAAASSTTSASSPGAWPYGGSERKKKDSSS

>OsERF2

MSLSLGFSAGAGVGADRLAAAPALQAAGALPPRVDVSLSLARAANGQPSSYLPLNENDSLDMVLFDVLREASAVAALSSSSSSSPELGARTTAPVVAGHPAGRKGGGGGGGGRGAAARGGAAGGRHYRGVRRRPWGKYAAEIRDPTRHGARLWLGTFGTAEEAAAAYDRAAFRMRGAKALLNFPPAVAGDGARRGAAAAAKQVGMSDVVPRACHVVCYSVLSAHIFYDIFRGVIPIP

>EgERF15

MVPPFPTAELPLNENDSQDMVIYHVLNEAMSQNNSSLPHPNQSGSPSSGGSLEPSRGITKKHYRGVRRRPWGKFAAEIRDSLRHGA

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>PtERF15

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TAEDAALAYDRAAYRMRGSRALLNFPLRVNSGEPDPVRVTSKRSSPEPSSSVDSGSPKRRKKVGGTAGAATVVAKAGLEIGNGVGCQVGTHGEQMLVI

>PtERF5 Potri.001G154200.1

MSTDVSTALEFIKHHLLGDLLSPIATSSSASFCQFSTNTEISTYETTGCCSQASTSDSSTAFPYFLDSPGPDFFVFSSDFSPAQDNKTNIFEFEAKPEIIDLLTPKPLDSTSHLNSQPSSSSSSSNSSNLFEFVKPQIISHPVNNFFYEESKPRVEPTRKPSLKISLPSRKSEWIQFSNTNP

QPVDDNSGVAVEEKKHYRGVRHRPWGKYAAEIRDPNRRGSRVWLGTFDTALEAARAYDRAAFKLRGSKAILNFPLEAGRCDVRANEEGERKRLRECDAEEREDVKRVMRVVKREEPERDVPLTPSCCTAAWDICGDSKGVFNVPPLSPLSPHPSLGFPQLLVI

>OsERF39 LOC\_Os09g26420.4

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>OsERF1 LOC\_Os06g09390.2

MCGGAILSDLIPPPRRVTAGDLWLEKTKKQQQQKKKNKGARRLPLRQEEEDDFEADFEEFEVDSGEWEVESDADEAKPLAAPRSGFAKGGLKNTTVAGADGPAARSAKRKRKNQFRGIRQRPWGKWAAEIRDPRKGVRVWLGTFNSPEEAARAYDAEARRIRGKKAKVNFPDGAPVASQRSHAEPSSMNMPAFSIEEKPAVMSAGNKTMYNTNAYAYPAVEYTLQEPFVQIQNVSFVPAMNAIEDTFVNLSSDQGSNSFGCSDFSQENDIKTPDITSMLAPTMTGVDDSAFLQNNASDAMVPPVMGNASIDLADLEPYMKFLIDGGSDESIDTLLSSDGSQDVASSMDLWSFDDMPVSAEFY

>EgERF71

QCVGAPSSPTSSRRLTSDFLWPDLKRSAGKQSRRPARSEVVDVVDDDFEADFQGFKDESDVEDDFDDEVEVDVKPFAFSAAEPRYSKGSSTTKSVEYNGQAEKSAKRKRKNQYRGIRQRPWGKWAAEIRDPRKGVRVWLGTFNTAEEAARAYDAEARRIRGKKAKVNFPDDSSSASSKRSVKSNVQKLPKTTTNNVQPNLNQNFNYANSSDDDIYSSMGFVEEKPPTNQFYMDALNAQGVSGMNSLSPADSAPLYFNSDQGSNSFECSDFGWGENGPRTPDVSSVLSATLEVDESQFEDANPRKKIRSASDDVSEEENTAAKTFSEELSAFESDMKFFQMPFVDGGWDPSVEALLGGEATQDGGNAVDLWSFDDLAPMMGGVF

>PtERF39

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>PtERF1

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>PtRAP2.3

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>PtRAP2.4

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>TwERF15 ALJ11036.1

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>GaERF71 XP\_017624362.1

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>JcERF109 XP\_012079573.1

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