# Supplementary Information

## Genome-wide characterization and analysis of bHLH transcription factors in *Panax ginseng*

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**Table S1** Amino acid sequences of 169 PGbHLHs.

| bHLH No | Amino acid sequence |
|---|---|
| PG00183 | MIVNQEMYEEGSACFDPIPMKDQTLGDQEQGLSYPQQDAATAAVAAANGAVAAAMELELQQQMGFEIDHNCYNPNNNMEAHLMQHPSLSSWETHHQEMNYNQYHQIQEMHNNNTNRYPQSFMNTDSCSLTETDPYPPTQDFLNLFHLPRCSSSLLPNSSISFTNPTQKLGFHGDFANASGSSVLYDPMFHLNLPPLHPLFREVFDQSLPQKYNFPGTITGSLSGGVEEIERSGEFDNEVLEFSKGMNCLAKEREGKDIKHFATERQRRVHLNDKFNVLKELVPNPTKCNPKPDRASIVGDAIEYIKELQRTVNELKVLVEKKRYSRERFRRHKAEDDSVLEVDSTNMKPHGDPDHPYNGSLLRSSWLQRKSKNTEVDVRIIDDEVTIKMVQQKRINCLLFVSKVLDELQLDLQHVAGGLVGDFYSFLFNSKIYEGSSVYASAIANKLIDLVDRQYVASQPISCYRCMMLPKVVERLHGAFQFLLAIKSTH |
| PG00883 | MSSRRSRSRQSSSGGGSRITDDQINDLVTKLQQLLPQITRDSARSDKVSSARVLQETCNYIRSLHREVDDLSERLSELLANTDTNQAAMIRSLLMQ |
| PG00933 | MDDLVVSSSSSSSLVSLSQESHPPTTLQQRLEHILGSQPAADSWCYAIFWQTSTDHNGRLLLSWGDGHFQGTKTPPPKHPPTNAKLERKKAIRGLFHALLNDNPDTECSIDTDDEGGDVTDAEWFYVTSLARTFPGGEYSEAFSSGTCVWLAGVDQLQLAKCERVREAQIHGIQTFVCIPTCYGVLEMGSNIALKQNWSLVQQANTLFGSDVSGFISDQKVPNTSNNNINVINNNGFLDGSNCFADIGVKMGTGSQEEESINLEAAKQEESEHSVSEFHEFVSAAGAKASVEKRAPKKRGRKPCPGRDMAMNHVEAERQRREKLNNRFYALRSVVPNVSRMDKASLLADAVSYINNLKAKVEELESQIQRESKKARVVVVESAGDTTIDNNSSTTTCINDIRPSSNSNNPVLEVEVKMVGPDALIRVQSQNCNYPGAKLMEALRELELQLHHASMSRVDELMVQDVVIRVSDGLRTEDALKAALLRALDH |
| PG01029 | MWWSPVVAVGSNCRKGFQILRELIPNSDQKRDTASFLLEVIEYVQYLQEKVQKYEGSYQGWSSEPTKLMPWRNSHWRVQSFVGNPQAVKNDSGPGSTFSGRFDENNVTIIPTMHTNPENPVESDLSRDASCKPMDQQPELANKGMVMPMPLQASMAVPVQGDGVFSLPLRRPVSDAQSTECPITGDVLNQQDDLTIEGGTISISSVYSQGLLNTLTQALESAGVDLSQATISVQVDLGKRANRGLNSGIILAKDHVDPSDSQPVGHFSEA |

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|---|---|
| | NNGEDTDQVQKRRKI |
| PG01277 | MHGLGHPRVPTKSQPTTSHTKYTWDKPSAGGTLESIVDQATFFPDYKSAVDGSCGGGDDNVDELVPWFNNHHRSIAVPPSATVTASATMVMDALVPCTLNSNRNEGGGSMHVLDSGIGTRVESCSGAAPFQTGKVARAAVAHEWSSCRDQSVTESATFCSRQVTLDTCEKGFGVGGFTSTSLGSPGNISSGEQCTGDDHDSVCHSRPQKRRDKINQRMKTLQKLVPNSSKTDKASMLDEVIEYLKQLQAQVNMMSRMNMSPMMLPLAMQQQQLQMSMMAPMMGMGMGMGMGSMGIGMGTVMDMNAAMAGRPSITGMPPVLHPSAFMSPLTSWEGAGDRLHTPASVMHDPMSTFLAACQSQPMTMDAYSRMAALFQQLHQNSAPGAKNL |
| PG01478 | MLSRVNSVVWMEARKDEETASWNNNHNNNNGGLENKDEMCSLSAYKSMLEVGEEDEWYLANNNITFSPTFTQADNNLLLQPVDSSSSCSPTPASVFNNFDPSQVTYFLPPKPTNSINLNPLSSNPLENSFDLSYETGFLGNQALNSLCRGNRVLTGFNDLSSHTHMDTSNLTSNPHFSTTQLLQLAGNSGTMSAGFCSSGFQGFELGNGNSLFLNRSKLLKPLENFASIGAQPTLFQKRAALRKNLADSGGNLGLLGNVEGYDGKREVGEASDKKRKTSYGDDLDNVSFDGPGSNYDSDEFTENNKGEDSGKNGGNSSNANSTVTGGNQKGKKKGLPAKNLMAERRRRKKLNDRLYMLRSVVPKISKMDRASILGDAIEYLKELLQKISDLHNELESTPPSSSLTPSTSFYPLTPTPPTLPGRIKEELCPSLLPSPTGQPARVEVRLREGRAVNIHMFCGRKPGLLLSTMRALDNLGLDIQQAVISCFNGFALDIFRAEQCKEGQDVHPDQIKAVLLDSAGFNGMV |
| PG01763 | MANNPPEGYSDDFLEQILAIPTYSGLAGTDGSSSETTPLTASHLASGGGVGIQQPFFPLGLSLDNGQRERGSMYMGSLFPVFEHLQPHSVRHSVPQIHQAFQSQTTTSTAVTVPHPPNMRPRVRARRGQATDPHSIAERLRRERIAERMRALQELVPSCNKSDKAAMLDEILDYVKFLRLQVKVLSMSRLGGAGAVAQLVADIPLQSVEGGISENGNDRPIWENWSNDDTEQEVAKLMEEDVGAAMQFLQSKALCIMPISLAALIYPTNQPDISTLVKPEPPAPSFESY |
| PG01888 | MDPPAIMNHGAFRSGNAAPNNLAEIWPFQFGQSLGQFTENPNREDDPMVLDQRGERKRRQDDDSIIGVSTSSAANGTSDSDIKRLKASGSRDEELESKVETEAINSGKQADQSTNPAEPTKQDYIHVRARRGQATDSHSLAERARREKISERMKILQDLVPGCNMVIGKALVLDEIINYIQSLQQQVEFLSMKLEAVNSRTGPSIEGFPSKDYGQQTF |

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| | DMAGVTFGSQAPREFSRDPSPEWLHMQIGGNFERSA |
| PG02200 | MDQQQQQMNSGLTRYRSAPSSYFANLINSTGYGGDDCDEFLNPRSSSPESDQFFSRFMSSCGSEESNSPNLCDIGRNSLVNEPVQAQFVASMKHEPEVLNPQQQQQQQQQQQMVYLSQSQLDHKPVGSNLGMDSSYNVSNSMGMDRLPQMKMGGSGGSNSNLIRHSSSPAGLFANINIDNGYAVMRGMGNFGAGSGTNAEASFSSGSRLKNQIDFPPGPPSSGIMPHASEIGGKSMGMGSPESESFGESRRNDGGYMTGGFPSTSWDDSTLLSDNFLKGLAENQSGEGGTRTPTVLAHHLSLPTSSAELSAMEKLLQFQDSVPLKIRAKRGCATHPRSIAERVRRTRISERMRKLQELVPNMDKQTNTADMLDLAVDYIKDLQKQVKILSDTRAKCTCPNNQKT |
| PG02335 | MNKVRILFNFNAIESGSWPLPSDPNEPDPSALWLTDPLPVPSVEIKEIPWNSNSKPPQIMFENHSSSTLTENPSTSSVINVHNQHLNQQNGVLHRELNFSGFGFDGISSTNVRNGNLNSHACKPESGEILNFGESKRSSCSGNGNLFSGNSPFGGIVEDNKKKKSPNSRGSHEEGMLSFSSGVILPSSGVVKSSGGGGDSDHSDLEASVVKEVESSRVVDPEKKPRKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVPNVSKMDKASLLGDAISYINELKSKLQESDSEKDELRSQLDSLRKELAKKVSQYPTQATQAAVEQDLKMSNHHGSKLLDLDIDVKIIGWDAMIRFQSTKKNHPAARLMAALKELDLDVHHASVSVVNDLMIQQATVKMVSRFYTQDQLRVALTARVSETR |
| PG02475 | MDPPAIMNRSAFRSGNAAPYNLAEIWPFHFGQNLGEFNDNPNREDDPMVLDQRGERKRSQDDDSAAGASTSCAADDMSDSDSKRLKVSVSRDENIASKAETEANSGKQAEQSRKPSEPPKQDYIHVRARRGQATDSHSLAERARREKISERMKILQDLVPGCNKVIGKALVLDEIINYIQSLQRQVKFLSMKLEAVNSRTNPSIEGFSSKDFGQQTFDMAGLTFGSQAPREFSRGSSPEWLHMQIGGNFERST |
| PG02883 | MEKEYFFNTEFPPQLHFQPSLSALQMPNGFHNPNFDKLMEQYSQFESALSSMVTSPAASNSATDTFAIRELKGKLGTIFNTGEISPEFLQGVSYIGGGNNSPNSSCYNTPTDSPPQLHLPIMSHFVKEDLPNLGNPIPMNSALPALSADPGFAERAAKFSCFGSRSFNGRTSQIGLNNAEFQYRSSSLLMGNGKLPRVSSSPFLKEAGSPMGIQVNKNCVQTQMEMRSGNGSASASGRKFSNLSGSAANSNEASSVSEQNPSGENSLGTPKELNYRKRKGVSRGKAKEAALSQSANAKKEAEGDDNLNVKRSKMTGGGGSVKTEEETKIGAEEDQKQANNDQKTPEPPTDYIHVRARRGQATDSHSLAERVRREKISERMK |

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| | LLQDLVPGCNKVTGKAVMLDEIINYVESLQRQVEFLSMKLATVNPRMCSRLLSKDIIFQPNGTFPNQMCQVNSSSASAYYGHQAQGQQIPQVYKSVEPLLDATLCRNLGMHLDGFGEGLSQFPAFSEDDHCSNGFW |
| PG02930 | MDWYSCNSKKWDFGFGHFGLVEQFWGSLGGNLGSGSMLNSHTLVLDGEKGELVKAPGGVEKKDGVLEVKDVAALKSHSEAERRRRERIKAHLDTLRGLVPCAGKMDKATLLAEVICQVKQLKNSATEASKGVLIPMDADEVRVEPLDESSRDGTYFLASLCCDYNPELLSDVKKALNALQLNIVKAEISTLGKRVKNVFVFTSGRGNGNAEEQQLLLNSVRQALSSIVDKISVCMEYSPRTLLPNKRRRISFFESSSSSS |
| PG03153 | MDPPIINETSFSAANPSSYTLAEIWPFPINGTDSPGTASGGGGGGLGLRMSGFGETTTNPDVSIEESTVTDQSWSRGAGKKRRDVNSEDGSSKLFSANINNANDLNDSSGKRLKVMGSNEEHGGSKAEVEASSGSGNKSTEQVKDYIHVRARRGQATDSHSLAERVNFFKAFPNCNLLVFLFMHPILLHARREKISERMKILQDLVPGCNKVIGKALILDEIINYIQSLQRQVEFLSMKLEAVNSRMDPTIEGFPTKNLGVPTFDATGMIFGSQAPRGEYAQASQPDWLHMQVGSSLERAT |
| PG03239 | MDPPIINETSFSAANPSSYTLAEIWPFSINGTDSPGTAGGGLGLRMSGFGETTTNPDVSIEESTVTDQSWSRGAGKKRRDVNSEDGSPKLVSANINNANDSNDLSGKRLKVMGSNEEHGGSKAEVEASSGSGNKSTEQVKDYIHVRARRGQATDSHSLAERVNFFKAFPTCNLLARREKISERMKILQDLVPGCNKVIGKALILDEIINYIQSLQRQVEFLSMKLEAVNSRMDPTIEGFPTKNLGVPTFDATGMIFGSQAPREYAQALQPDWLHMQVGSSFERAT |
| PG03489 | MAMEDNQILHDQNKLPLGTTLWPNSYPLQDHHHISSSSLNQLPSSSDFIRQRGENHNNHRIQAEQERQEDQEEELGAMKEMMFKIAAMQPVDIDPSTIRKPKRRNVRISDDPQSVAARHRRERISEKIRILQRLVPGGTKMDTASMLEEAGRYIKFLKRQIRQLEDNHQPQCIGVMSNFPVTPNKALVGSTGSFSMEPVAQTTYTAAGHEHNDLKNSNDTRNVRGIGIITTEAHPDQMFTIVLSNNLQSLSRFNDTSDIESKTGGGSKLPMCNKDKFAN |
| PG04363 | MVEKFWVKEEDKALVEGVLGNEAFEYLVWSASNNVLSEFVAPAGDLGLQQGLCKIIEGSNWTYAVFWQVCSSKSGKSALVWGDGHYRESKGGEAEDRKSKGDNKKQVLDKLHACFRGSGEDNFAAKFDSVSDVEMFYLTSMYYSFPFDKPSSPSQSFN |

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| | SNPFELQTIGTNQVYGNSSNGHRSNDSESKLFPQMNQVILGGLNSQALVSNLEQGKDDSLLQADERKPRKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVPNISKMDKASLLGDAISYITDLQSKIRILETEKDEVNNNQKQCAIPEIEFHTTQENAVVRVSCPLDTHPVSGVIKTLREHDVITHDSSVSTTDNGEIVHTFSIRTQGGSAEKLKEELSTALSG |
| PG04535 | MERTDSSGIPMGHVDDDYNLVDFMDEANFEHFIALVRGESADPIVKFCPNYLDCDHINDCSVDNQFVPTRGLPYDQFNPPINTFSDPINPLLFDSLPCDLKEGEEENDTEEYSSATINTTPPPPPPNTNTTTSTKKSTKGDRSRTLISERRRRDRMKEKLYALRALVPNITKMDKASIVGDAALYVQELQMQAKKLRAEIASLESSLTGVDKQGGGLYDNVNNKIQSKNIHPTSKKISQIDVFQVEEKGFYARVVCNKGQGVAASLHRALDSFSSFIVQSSNLATADKNFVLTFTLNVREREMDMNLPNLKLWVAGALLNQGFDF |
| PG04685 | MQPCSREMQAMNSILNHQQQQQSQMANSLHQQDPQQQIIQSHGFDPTSSHDDFLDQMLSSLPSCTWPPSDLSSSAQNPNNKSLPWEPNLNMCPPSFDDQSVMLASKLRHHQISGGGPTSPAAKVLMLQQQLMLSRGLSGGLPSPTGDSGAGDSGLLPLPPSLSSSDDTIDGSSFKSLNPGGDGSVQALYNGFAGSLHASSQTSNQAQHFHHPQGGTMQAQNYRTPVGGMNQAPASGGSGGGAAAQPRQRVRARRGQATDPHSIAERLRRERIADRMKSLQELVPNANKTDKASMLDEIIDYVKFLQLQVKVLSMSRLGGAAAVAPVVADISSEGGGDCIQPNATAAGGAGGVGRPSNGTQTAASSSSNNNDSMTVTEHQVAKLMEEDMGSAMQYLQGKGLCLMPISLATAISTATCHRSPSTRSHLNNTLLPGGPTSPNLSVLSVQSATMGNVIADSSVSKP |
| PG04790 | MADLYGNNGHRSSSLESEEMSSFLHNLLQNSAGTPPYSFFKEKQNSDFADPGGFFPAEAKDSTVNPFCSVGSNSDQITSSRRNLPYNSNDADEFDFGCEEPEEPEVPANSVPPRSSKRTRAAEIHNLSEKRRRSRINEKLKALQNLIPNSNKTDKASMLDEAIEYLKQLQLQVQMLTMRNGLGLNPVYLPETLQPVQLTQRGVNYDEGNVLMTANRRDTVSTDPKFSAQRPLYMSNPAPRIVIPSITNINNSETSYGLEPSIPESI |
| PG05026 | MEEFGGSSSSSSSPVSLLSQKHVPTLQQRLQYILESQPDCWSYVIYWQTSKDSDNGSLLLSWGDGHFRGATKHNTLRKDQTNHTIDGFIDSDVMDAEWFYIMSLTRIFRAGDGSVPGKVLISGAHIWVCGTDQLHVAECERAKEAQVHGFQTFVCIPTCSGVLEMSSDITISENWSLVQQAKSLFGSDLIDLIPKQPNPSNVGSCSYLDMEMFDFDLH |

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| | DQFVAVGPGTPHVEKKNAAKKRGRKPILGQDMPVNHVEAERQRREKLNNRFYALRAAVPNVSRMDKASVLADAVSYINELKVKVDELESQLLEFRALKKSGKAESAGDDTVENPNNTTTTSVDQKMGKSTPLVDVEVKMVGSDAMNIRIQSDNSDYPGTKLMIAIRELELHVHHASMSNVNELIMLQDVVIKVPAADSDGGLRSEEGLRSALLRALMEH |
| PG05306 | MSKCPKWINLITTPRDNQFNPYQSSINDQTPLDYIPITEAEPKECNVARKVQKADREKLRRDRLNEQFMELGNTLDPDRPKNDKASILGDTIQVLKDLSAQVNRLKAEYASLTEESRELTQEKNDLKEEKASLKFDIDNLNLQYQQRYRAMFPWGGVDHSVVMHPPSYPYPVPMPIPPGPIPMHPSLQPYPFFGNQNPALVPNPCSTFVPYLTLNTIIEQQSAHYVSPVVPPSSRSHVSSKQDSRNRSSDQGKSKTDKYEDSNDVATELELKTPGSTADQDSSLGQRKYKKSLRKESSLSDGNSSSRCSSSHTVQASSSDSVVGGGMRAEDTERGQI |
| PG05437 | MGCKIGEIELGMSIDAQVDMEMEMRNWFPEDFSQQALPRELPQPTDQNLLSSSSSSLRSVSIDSPEGAPFLYNITSTSYIPQPPIEPSTLQLAMPPLTPITTNPFQEAIQTLSQIRNAQFPTIESEDAAMTRAILAVISSTSPTSSTSSHQPQQKSSAFKSYISSFSPRSQITSRVIQKQNMLKRAIAFIRNSSLLMRSQEQMQTGNRPMSNQLQHMISERKRREKLNESFQALRSLLPPGSKKDKASVLSSTMEYLNSLKAEVEELTKRNQILEEAQLVVRQNETTIISDGSSSTERLQVRITNIVETTFDARILDLRVILRGESSLLDLAIRVLEFLKTLGNVTVLSVEGDTPSSVSQLVWRLKIEVDGWDNL |
| PG05942 | MFGDSRALFTDSNAIFSSNSNPKGEDMLTKSRMNFDMNNNSSIQDYKQYQNNQTNSGLLRFRSAPSSLLANFDNGVDKSGDSNEDLMAESFKGLDDNKTLPNGFAVNSQLPPHYPRHSSNLELGTQVGAVDNSSSYRMGSSMGMENQAKMVSSLMRQNSSPAGLFSHLNSQTGTVQYRSLFSVKTEVLNISKQFSGYAAMRGGVGNYRLGNGSNGDISPTASRLKSQMSFSSGLPSSLGMLSRISEIEGENIGATGNDDAKNGSGNGDTQFYTSEFPLSSWSDSLHFAENFTGLKRELDDDEKLFSGAQNTDLANRPPLLSHHLSLPKNSSEMTAMDKLLQFQDSVPCKIRAKRGCATHPRSIAERVRRTRISERMRKLQELVPHMDKQTNTADMLDLAVEYIKDLQKQFKVSHNKINSKTWYTF |
| PG06292 | MALESVVFQQDPFTSYGCKDFYAMEDIGGGYFSNFDHEQKKKVHDHGCSFNENTNTNTNNNNNNNNNNNNNNNNWKYNYSPPPSMMQTNSSSPDEVCTGITGHGFF |

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|---|---|
| | TGAYPPPAAAPPPVTPRRKRSIKSTKNKEEVENQRMTHIAVERNRRKQMNDYLAVLRSMMPPSYAQRGDQASIVGGAINYVKELEQLLQLLEARKQVKHDQQSNDTDNDHDSTLFANFFTFPQYSTRPTSHKSSVAPELMDETQSTAADIEVTMVESHANIKILAKRQPKQLFKMVSGFQSIGLLILHLNITTVDHRVLYSFNLKVEDDCQLTTVNEIATAVHEMVIMIQEEAIFC |
| PG06381 | MANNPPEGYSDDFLEQILAIPSYTGLAGADGSSSETTPLTAAAQLNSGAGIQQPFFPLGLSLDNGQRERGSMNMGSLFPVFEHLQPHSVRHTVPQIHQTFQGQTTTSTTVTVPHPPNMRPRVRARRGQATDPHSIAERLRRERIAERMRALQELVPSCNKPHSVRHTVPQIHQLFVAYWPLSISIPIPHPEFTFLYLDYQIMTFQGQTTTSTTVTVPHPPNMRPRVRARRGQATDPHSIAERLRRERIAERMRALQELVPSCNKTDKAAMLDEILDYVKFLRLQVKVLSMSRLGGAGAVAQLVADIPLQSVEGGMSENGNNQPIWENWSNDDTEREVAKLMEEDVGAAMQFLQSKALCIMPISLAALIYPTNQPDISTLVKPEPPAPS |
| PG06438 | MEELLASSSSSSSLVSLTSQEQYPPPLPLPLPLSSTTLQHRLQYLVETQPADHSWSYAIFWQASSNDQLVLSWGDGHLRGTTKNTPVPLKESSKKPVRGLFLHALLNDNPDASIVDSDVTDAQWFYVSSMARTFPGNSSFGGVPWKAFSSGAHIWLSGPDQLGSFECERAQEAQIHGIKTLVCIPTSSGVVEMGSTVPLKENWNLVQQAKSLFGSDLAGLIYKKYVDDPSNNNMNGFEFDRSICFSDINGLFTSLQDQEDSINLLDAKLLDSEHSDSEFQFAAASAAGGVATSIEKRAPKKRGRKPCPGRDTPANHVEAERQRREKLNNRFYALRSVVPNVSRMDKASLLADAVSYINDLKIKVEELESQLQNESKKLKVEAAAAAAGAASTDTADNNNSTTTSVDQATPNSNTTSVPLEIEVKMVGPDAMIRVQSENSNYPGAKLMEALRELELQVHHASMSSVKELMLQDVVIRVPDALRTEDALKAALLRVIITHMRSRSSVPN |
| PG06642 | MSLVSLGRVSEIAPFRGFVGLLGFGSKLQVQKLTMGTEDNGDMRFQQRDGDGTMNRNPLSEKVAEMGMRSGSIFKGSNGAESYFGSGWDPLVSLSQSENFGAHNGFSNPAYPVVMENQVMSTTSHLVHYQSDSGGLGEMVPKLSCFGSGSFSEMVNSFGLSECGQMSYSQNKEGGTGKALLIGTDSQEECRNSEGKVSPNGKKKRRTSESRSPFNPNKNTEVEQQEDPSGDSLEQDDKKQKIEQNVNANLRGKQTSKQAKENSDSGDAVKDNYIHVRAKRGQATNSHSLAERVRRERISERMRLLQELVPGCNKITGKAV |

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| | MLDEIINYVQSLQQQVEFLSMKLATVNPELNIDIDQILSKDILNSRGSNATILGFPG<br>LRPAHPFPQGSLPGIPSTTPPFHSMPQTVWDNELQNLLQMGFDSNNNLGPTEGKT<br>EDLIDKDDCFY |
| PG06701 | MALEQPQPEEEGVADISRKKLALAVKSIQWSYAIFWSISSKQPGVLEWSDGYYN<br>GDIKTRKTVQAVQVDADQLGLHRTDQLRELYESLTDAETNPQSTRPSAALSPED<br>LTDTEWYFLICMSFEFNIGQGVLEWSDGYYNGDIKTRKTVQAVQVDADQLGLH<br>RTDQLRELYESLTDAETNPQSTRPSAALSPEDLTDTEWYFLICMSFEFNIGQGLPG<br>RTLANNETIWLRNAHYADSKVFNRSLLAKTVVCFPYSVGVIELGTTKLVSEDPNI<br>IQHITTSYLETPSTIVSKNYKYVSEATRNEKDTDHVELDQDVLDTNLNPEIEWEE<br>VNTCSMSNNISEGFEPNHQVQKSLMVEGINGGASQVQSWQLMEDEISNGVLNS<br>VSSSDCISQTFVSPEKLVPLPNEEKGNDDRLPDLENCKDAELTSDEIRNDDIQYQS<br>IVSTILKSSHQLILGPFFQSSIKDSSFVRWNNNRLFCCQKSRSGGASQRLLKKVVY<br>EVAKMHSGCLLESRENNGSGGELRKPEADETDANHVLAERRRRAKMHEKFVIL<br>GSMVPSTGKVDKVSLLHDTIEYLKNLKNRVEELESQKEVQDIEARRRMKPRDV<br>VERTSDNYGAKRIRNSKKRVMNKRKASDVNETEAVNRVQPEDNFTDDVTVSKI<br>EKNVLIEVKCPWREDLLLEIIDAISNLQLDSHSVQSSNIDGNLSLTVKSKVKGSTM<br>TSVKMIRQAIQRVTRKC |
| PG06793 | MPLSEFYRMAKGKVEGSQQKATTCSTDFVPDSEIVELVWENGQVMMQGQSSRS<br>RKTPKIPTSNSYNFQTDRFRDKDTASQTTSKPGKYGTIDSIYSDIATSIPSGETGLS<br>QDDDMVPWFNYPIEDTLQQDYCPDFLPELSSVTVNEPSNRNSFASMEKRDRTNQ<br>IVRDSHNVSVHNGLSLGQSNVSKLPSTSSAQLYPWSLPQGKTSVPSGISSVSDIIST<br>NTNNIHHDVSGNLVPAQPPVGLFSHLKMQKQDSELPRSNSSLLNFSHFSRPAAM<br>ARSSIQNASNVSASGSLGTDRMGETDKVVPAICKNPAESRHLDPNCVLPKEMNF<br>HTQPNLVSAYVDLKPLETKPVEESHPGRQSDTVFREDGRKNDKSPNQDHGGNT<br>ANGVPDNEKTAEHVGASSVCSGNSVERASNDPTVNLKRKNCRYTEESEGQSED<br>VEEESVGVKKAAPARGGSGSKRSRAAEVHNLSERRRRDRINEKMRALQELIPNC<br>NKVDKASMLDEAIEYLKTLQLQVQIMSMGAGLYMPPMVAGGWKHIHAAHLPH<br>FSPMSVGMGMGMGMGMGFGMNMLDMNGGVRGCSMIPMPPMQRAHFPSPPIS<br>GSTSFQGMAGANLQVFGHPSQGVPMSVAGAPLVPLSGRPINSATGMSALRMGV |

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| | NMEAPDAAPNLNLKDLTQTTNSQVMHSSEASMSLNKQSSQFQETNQGFDQPAL |
| | VPKNDQGPDGDGSAAVNLTKTNDAVPSREARVYGSKLHRFRYSEDTWNHSPPH |
| PG07133 | MALEQPQPEEEGVADILRKKLALAVKSIQWSYAIFWSNSSKQPGVLEWSDGYY |
| | NGDIKTRKTVQAVQVDADQLGLHRTDQLRELYESLTDAETNPQSTRPSAALSPE |
| | DLTDTEWYFLICMSFEFNIGQGVYYTFFLKLFLIRLPGRTLANNETIWLRNAHYA |
| | DSKVFNRSLLAKTVVCFPYSVGVIELGTTKLVSEDPNIIQHITTSYLETPSTIVSTN |
| | YKYVSEATRNEKDTDYVELDQDVLDTNLNPEIEWEEVNTCSMSNNSSEGFEPNH |
| | QVQKSLLVEGINGGPSQVQSWQYMEDEISNGVLNSVSSSDCISQTFVSPEKLVPL |
| | PNEEKGNDDRLPDLENCKDAELASDEIRNDDIQYQSIVSTILKSSHQLILGPFFQSS |
| | IKNSSFVRWNNNRFFCCQKSRSGGASQRLLKKVVYEVAKMHSGCLLESRENNG |
| | SGGELRKPEADETDANHVLAERRRRAKMHEKFVILGSMVPSTGKVDKMSLLHD |
| | TIEYLKNLKNRVEELESQKEVQDIEARRRMKPRDVVERTSDNYGAKRICNSKKQ |
| | VMNKRKASDVNEMEAVNQVQPEDNFTDDVTVSKIEKNVLIEVKCPWREDLLLE |
| | IIDAISNLQLDSHSVQSSNIDGNLSLTVKSKVKGSTMASVKMIRQAIQRVTRKC |
| PG07157 | MNQCVPSWDLDENSKLNFRSHSNSLSITPDVPTLDYEVAELTWENGQLSMHGL |
| | GHPRVPTKSQPTTSHTKYTWDKPSAGGTLESIVDQATFFPDYKFTVDGSCGGGD |
| | DNVDELVPWFNHHHRSIAVPPSATATASATVVMDALVPCTLNSNRNEGGGSMH |
| | VLDSGIGTRVESCSGAAPFQTGKVAHEWSSCRDQSVTGSATFCSRQVTLDTCEK |
| | EFGVGGFTSTSLGSPGNISSGEQCTGDDHDSVCHSRPQVGHEETKKKANKCSVS |
| | NKRSRAAAVHNQSERKRRDKINQRMKTLQKLVPNSSKTDKASMLNEVIEYLKQ |
| | LQAQVNMMSRMNMSPMMLPLAMQQQLQMSMMAPMMGMGMGMGMGMGM |
| | GSMGMGTVMDMNTAMAGRPSITGMPPVLHPSAFMSPLTSWEGAGDRLHTPAS |
| | VMHDPMSTFLAACQSQPMTMDAYSRMAALFQQLHQNSAPGAKNL |
| PG07173 | MDDPIVSHQSRMSSLDDYDTFTFESTISSESYSVYPSFSPPKSIPIIDSFQSVIHQKP |
| | AAKMLKTNNWNSCSTPKKTIPNQSSSAMIISFDKANSHSNELYGNLNCNIIKPKK |
| | EIMAPYYGNGDFSYTISHGDEVLGFSEANKRVSTFSRTPLQAQDHVLAERKRRE |
| | RLTQRFIALSALVPGLKKMDKASVLGDATKYIKQLQERVKTLEEYLKAGEKDRS |
| | EAVVSVKRSRIHLDEGSDENFDCSLNESNIPEIEVRIWERNVLFRVHSKKIPGFTV |
| | RMLSEIEKLHMTIISSSAMPFANSSLHITITAKMDAEFCVNANDLAKSLQVSTRTH |

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| | MQSS |
| PG07174 | MNHLYDLYELKSSYSHESYSTYPTSNPQSLPLDNMMSNIGIESLKTEYDSSFYSK<br>QMISTSNASTSNSTNFIAFGYPNSVPPLEQHQFYASLNLPKKSKDELVPQEIFKFS<br>HKMQSQLSYNKNYASEFGEEIKRIDSSINRSPLQAQEHVIAERLRREKLNKLFIAL<br>SAHILGLKKPYIWSLKKKLHHLSFVSEYDVLLQLDKASILKDAVEYIKQLQEREK<br>VLEEEACKQSEEPIVTKKKTLMLSEDGDDTHSPQLPPLSDIKARVRGQNVLIRIHC<br>QRPKGSSIVLKFLDELEKIHLTIINCCVIPFDNSLDITITAQIDAKFCITTNYELVEEV<br>RSAFSKLV |
| PG07175 | MEMSVVRWNSQQATADECNFMNHFELNSLGFDALDDELTAEQYLVSSSEETFQ<br>KSSLSPDCYTSFLAMDQENKINHSMTTDISGHGFERPTKQIKTNTWNSKQHNLL<br>AKDHSSSPSSSHLISFANFSSQPTDSRTASCVDLVSPVLVPCKDELLTYEDLTQTY<br>NLDDRNIICSSKGGQGTKRSATTTILSRTPSHAQDHVIAERKRRERLTERFIALSAI<br>VPGLKKLDKASVLGDAIKYMKHLQERVKLLDEQIKKKKPEVSFVSLNSCHLPDY<br>DDHDSSSSDVNSSGCLNKALPEIEARVSEKNVLIRIHCEKQKGFIPKMLSEIEKLH<br>LMVINTNVLPFGDYAIDVTVVAQMDDEFCSTVKDLVRNIRSALH |
| PG07247 | MELELQQQMGFEIDHNCYNPNNNMEAHLMQHPSLSSWETHHQEMNYNQYHQI<br>QEMHNNNTNRYPQSFMNTDSCSLTETDPYPPTQDFLNLFHLPRCSSSLLQNSSISF<br>TNPTQKLGFHGDFANASGSSVLYDPMFHLNLPPLPPLFREVFDQSLPQKYNFPGT<br>ITGSLSGGVEEIERSGEFDNEVWEFSKGMNCLAKEREGKDTKHFATERQRRVHL<br>NDKFNVLKELVPNPTKCNPKPDRASIVGDAIEYIKELQRTVNELKVLVEKKRYSR<br>ERFRRHKAEDDSVLEVEITNMKPHGDPDQPYNGSLLRSSWLQRKSKNTEVDVRI<br>IDDEVTIKMVQQKRINCLLFVSKVLDELQLDLQHVAGGLVGDFYSFLFNSKIYEG<br>SSVYASAIANKLIDVVDRQYVASQPSNSY |
| PG07364 | MEEFGGSSSSSSSPVSALSQKHVPTLQQRLQYIVESQPDCWSYVIYWQTSKDSDN<br>GSLLLSWGDGHFRCATKHNTFRKDQTNHTIDGSIDGDVMDAEWFYVMSLTRIF<br>RAGDGSVPGKVLSSGAHIWVCATDQLHVAECERAKEAQLHGFQTFVCIPTCSGV<br>LEMSSDITISENWSLVQQAKSLFGSDLIDLIPKQPNPSNIGSCSYLDMEIFDFDLHD<br>QFVAVGPGTPHVEKKNAAKKRGRKPILGQDMPVNHVEAERQRREKLNNRFYA<br>LRAAVPNVSRMDKASVLADAVSYINELKVKVDELESQLLEFRASKKSGKAESA |

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| | GDDTVENPNSTTTTSVDQKMAESTPLVDVEVKMVGSDAMNIRIQSDNSDYPGT<br>KLMIAIRELELHVHHASMSNVNELIMLQDVVIKVPAAAADSDGGLRSEEGLRSA<br>LLRAMEH |
| PG07462 | MFSLNQTDELVFQIHPSIPEQQQEEALVTQDLTLPDQAYGACTVPTTNANNTKR<br>HRKKSLLNTATGDNNNIIDESGKKVMHREIERLRRQEMGKLYGSLRNLIPLEFIK<br>GKRSISDHMHQAVNYINHLQGSIKELDMKRNKLIKNMPVKSVISPAGRSGSSSN<br>NCFRENNSIVTVSPCWCGVEILISIGLMMEEGFHLSRAMEILVNEEGLNVISYAST<br>RANQRLLHTIQSQLRTFATDPTCIDMSALQQKLNDVKLPMHEIDELGANRMPIY<br>VPGHDLVIFRKAKSSLASPSITHII |
| PG07481 | MGGTMWSEEDKAMAAAVLGTRAFDYLISSSVSAECSLMAVGNDENLQNKLSD<br>LVDCPNFSNFSWNYAIFWQISRSKSGDLVLGWGDGSCRELREGEESEVSQILNLR<br>FEDENQQRMRKRVLQKLHSLFGGSDEECYAFGLDRVTDTEMFFLVSMYFSFPR<br>GEGAPGKCFGSGKHVWLSDALKSSTDYCFRSFLAKSAGIQTFVLIPTDVGVVEL<br>GSMRSIPESLELVQSITSSFSSFLSASKPKLMAAAPVVSEDGNTQFSNLDVVEGPR<br>ITKIFGQDFNSTRSQFREKLAVRKAEERPWDACSNGNRSPFPNARNGLNGSNWA<br>QFNNVKQGDTVETYSPQTPANNLHELLNGGAREEFRFNNFKTQKPAQMQIDFT<br>GAMTRPAVISRPASGESEHSDVEVACKDGQMGLLADAKRPRKRGRKPANGREE<br>PLNHVEAERQRREKLNQRFYALRAVVPNISKMDKASLLGDAIAYITELQKKVKD<br>LESGREKIGSTSREASSSDANPNSEYKNQVSNIEVEAAAHDEVTVRVTCPLDSHP<br>VSRVIEAFREAQVTVTESKLTAGNDTVFHTFVIKSEGPEQLTKEKLVAAFSREAS<br>SLQPLSSVG |
| PG07666 | AALPGSFSGVDYSLDHHPHQQFMKPHTGETSGDNSNQMVDYMLNNPPQQHISS<br>GFCNSTSFDKLSFADASLPGSFSGVDYSLDHHPHQQFMKPHTGETSGDNSNQMV<br>DYMLNNPPQQHISSGFCNSTSFDKLSFADVMQFADFGPKLALNQSKTSEEEHGID<br>PVYFLKFPVLNEKLQDDHDHQALMVPQDNQDKARMMEGEGEKEDETRVSEGT<br>SVQLQFLVEDAQKSPVAEGKNKRKRPRTTKTSEEVESQRMTHIAVERNRRKQM<br>NEHLRVLRSLMPGSYVQRGDQASIIGGAIEFVRELEQLLQCLESQKRRRIYGDAP<br>RPMGDNSSNAMQQVQPPFVVSDDPVKLVEFETGLREEIAENKSFLADVEVRVLG<br>FDAMIKILCRRRPGQLIKIIAALEDLELNILHTNITTIEQTVLYSFNVKVKWHI |

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| PG07762 | MEQQQQQQEVNSGLTRYRSAPSSYFADLMNFTGYGGVGEDCDRFLRASSPDSDRFFSRFMSSCGAEESKSSNFGEIGQNLLVTEPVQSQFMPPMKHEPDVINPQQQQVVYTTQSQSDHKPVVPKLGVDNSYNVASSMKMEGGSNSNLVRHSSSPAGLFAQINVDTGYGVMRRGMGNFGTGSVVANAEASFSSASRLKNQMDFPPGPPSSSGIMPCATEIVGSPESGSFGESHRNDGSYTTGGFPSTSWDDSGLLPDNFLKGLEENDGKAFSNLNSLENQSGEGGTRTPTVLAHHLSLPTSSAELSNMENLLQCQDSVPLRIRAKRGCATHPRSIAERVRRTRISERMRKLQVLVPNMDKQTNTADMLDLAVDYIKGLQKQVKTLSDNRAKCTCSNNQQTQPDEA |
| PG08342 | MGGMMWTDEDKAMAAAVLGPQAFDYLMSSSVSVECSLTAVGNDENLQNKLSDLVDRPNLWNFSWNYAIFWQISRSKSGDLVLGWGDGSCRDLKEGEESEVARVLNLRLEDETQQRMRKRVLQKLHSLFGGSDEECYAFGLDRVTDTEMFFLASMYFSFPRGEGAPGKCFGSGKHVWLSATLKSSSDYCFRSFLAKSAGIQTFVLIPTDAGVLELGSVRSIPESFELVQSIKSSFSSVSKPKPASAAPLVSEKEDGNAQFSNLGMVERPRITKIFGQDFNSNASQFREKLAVRKAEERPWDGYSNGKRPPFPNIRNAHHGSNLSQFNNVNQAGSVEIYSPRTPPKNLHELVSGGALEQLRFNNLKTQKQAQMQIDFTGATSRPSVISRPLSGESERSDVEAAYKEELTGLADDKRPRKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVPNISKMDKASLLGDAIAYITELQKKVKDLESGREKIGCTSREASSSDANPNSEYHNQVSNIEIEAAHDEVTVRVTCPLDSHPVSRVIEAFREAQVTVTESKLAAGNETVFHTFVIKSEGPEQLTKEKLIAAFSREANSLQPLLSVG |
| PG08366 | MERIRRIVGLKGWNYCVFWKLSEDKRFLELMDCCCAGTENNMENNNNDCGEDVELLFPVSSVISCRDVMFQHPRTKSCDLLSQLPSSIPLDSGIHAQTLISDQPRWLINFSNSCHSHLLEEPVETRVLIPVSVGLIELFVVYKQVSEDQRMIDFITSQFKISNIEQQTMTTNSSFSVLKAGSSTIVNENDEKELFQPPVSPATMLQNLNLQYDISEDQIPPLHDNSPMNFFQQFNHAAENGINNLLESANEVPDSMPLNPFKCSAQGFDQEDVDTLFQKSMLINSTTTNATAVNNNVEPLASRKRQNEDRDSMNRSDSLSDCSDQNDDEDNIKCRRRNGNKGPQSKNLVAERNRRKKLNERLYNLRSLVPKITKLDRASILGDAIEYVMELQQQVRDLQNELERNIDLDDEGTAADDKHNSTLQSEVLHGNGNGNEVKNIGPKYQHGNGTPHMGASSGIGTESTNGNVQQMEPQVEVIQLNGKEFFVKVFC |

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| | EHKPDGFVKLMEALNSLGLEVTNANVTRVLSLVLNVFKVEVCMYVNLKLIYMH |
| | MLYIFMTKGKIHSYILVQKSNI |
| PG08551 | MYDPEHRESTYNQIGFTESLFCAREDDERETKHLQALEQGTNEQSPPLMAPPIWS |
| | FWIGGAILGESGWEFGKWVNVEFAHFGVGWGERGAREGSWKDGVLEVKDVA |
| | ALKSHSEAERKRRERINAHLDTLRGLVPSGYASWSYAICLDDIRITNLWYPTSKT |
| | LAENVALEFAKEKGLDVVVVNPETVMGHEVTSLYKSLSPEKLTPRDSTRVCNAI |
| | ALLQLLDNSYGWINPVVFKSYVEMRQAESTRIREKYLDRILYLTSELPVQVIVEK |
| | AEKSDIPDIDKKKYLVPADLNVGQFVYVVRKRIKLSAENAIFIFVKNMLPLIAAL |
| | MSGIYDEHKDEDGFLYVTYSGENTFGALGICPVYISPHLMFLVKIGAGKYIVRSF |
| | AGRSCGYHRDSVPLDCVGDSTASSYDRSRGVRVDTIETLFRWIALEIRPHRF |
| PG08659 | MERGKLFKGITIPPTWNSSHFGIEIQTNELNEQIPNCFFNPNWDNSMDQSDPFESA |
| | LSSIVSSPANSNAGIPNNGENFVLRELIGRLGGICNSGEISPHSYIGGNNSTNTSCY |
| | NTPLNSPPKLNLSIENQIRGNLQIPGNQLPFSTDPGFAERAARFSCFGGKNESKFPP |
| | KTEFSGSQIGLQENREGFLQKGIEVSDKKFHRFSRSSTPEKDSMEESSVSEQIPGG |
| | EIVKKSQSDGNGRKRKSIPRGKGKEIPSAPSAKESMVVAENEESNSKRSKENEGN |
| | DSGKVTGEGNQKQNKDSAKPPEPPKDYIHVRARRGQATDSHSLAERVRREKISE |
| | RMKFLQDLVPGCNKVIGKAVMLDEIINYVQSLQQQVEFLSMKLSTVNPRMDLN |
| | MEALLSKDIFQSRVSLPHNIFPADSSAQAFPYAYQSQQGPNLHSNMPNGTKNPFS |
| | INPLTAAILRNTAGMQMPSVGGFHEAAASQVPTFWEDDLQSFVQMGFGQNQHE |
| | ILHGSNSTSSHMKVEI |
| PG09058 | MSVENNMQTTYLLPELIFQEDSHEFVDTNFAAGGAASLEDIFSILEALEGVSSDEL |
| | NLLTPVLDHHDETTSFLGPKLEAAGVNQQQEESTSHATTTTKLATQKSTSSAPV |
| | DLEELETELEEEEEAAAKNCSPKTKRQKHSKAAAKGEEELDGQQKISHIAVERN |
| | RRKQMNDNLSVLRSIMPSFYVKRGDQASIVGGVVDYITELQQVLQSLEAKKQR |
| | KLIYNEVLSPRRQQQLVSSPRLTSLPISPRKPPISPRIVVPISSLPTSPTTPQPTSPYM |
| | NHHQTSLLHYQLPYLSPTNSMLNSSLEPSLSSSSSSSCSTSNSIDHANELVAHSKS |
| | AVADVEVKFCGPNVLLKTISPKIPGQVLNIISALEDLSLEILNVSLKTIDELTMLNS |
| | FTIKVLQSLEAKKQRKLIYNEVLSPRRQQQLVSSPRLTSLPISPRKPPISPRIVVPISS |
| | LPTSPTTPQPTSPYMNHHQTSLLNYQLPYLSPTKSMLNSSLEPSLSSSSSSSSSSC |

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| | STSNSIDHANELVAHSKSAVADVEVKFCGPNVLLKTISPKIPGQVLNIISALEDLSLEILNVSLKTIDELTMLNSFTIKESKTQSDKLTSGLP |
| PG09196 | MEYNGHDFLEELLALRTDPWELATNIPTESNVFDTTNSHNVDNFLENPFAKIPQNPCFEDFSSIPFDPQALNCSSFSEFCAPFGDEAVDSSNNKLDTPPLLIPCGEEYSLLSIMDDLEVQAANACKIEPAQSAEVPIFNMGMCLERKTKAKKLVGQPSKNLMAERRRRKRLNDRLSMLRSVVPKISKMDRTSILGDTIDYMKELLERINNLQEEIEVGSNNHHKLSLTSIFRDVKPNEVLARNSPKFDVERRNIDTRIEICCAGKPGLLLSTVTTLEALGLEIQQCVISCFNDFGMQASCSEEMEQRGSISSEDIKQALFRNAGYGGRVIMDAIGEERRSFWSKSGKKLEKEKVEVSGYARRGRPVVHCTPRRGGGPDSVVSCSVATSAGAQFVGLE |
| PG09666 | MEDLISSSSSSSFLCHGGASPTIQQRLQFIVQSRPEWWMYYIFWQTSKDSTTDRLVLSWGDGHFRGTKDFMLKAASSNIGLGQQDQQQQQHPKFGFELERRKVAKGIQSLFSETLPGIDGVVEADFPDSEWFFMVSVTRSFAAGDDNIVGRTFSSGSYVWLAGDHELQFHNCDRAKEAYLHGIKTLVCISTPCGIIELGSSYTIKEDWGLVHLAKSLFSPDNNMTISNMTSPAALAHAPQQNPTRSLSFFDINAVSGDQNKTSGEEEGNTKNNKLAKIGRSSSDSGNSDFESNLAPDSAMNMRLKKRGRKAASTGRELAQNHVEAERLRREKLNHRFYALRSVVPNVSRMDKASLLADAVTYINELKVKVEDLEGKLREEMKKPKSISDVVYDTQSTSTTNVYHTAARSSMSYGPMNMEVDVKILGSQAMIRVQGPDVNYPAARLMDALRMLEFRIHHASVSSVKEIMLQDVVIKVPDGLTSEEALKTALLRTLQI |
| PG10212 | MALARIARSGLRRSGATGSYASQKDMPYEGVSTRKYSLPSVENDKSCGSLSYLSNIKRADHVSFGSRGIKVTPQYQFAQAERVVEESDSEYENQKYPSLEATKPGENPRVVVLGTGWVACRLLKGLDTKIYDVVCISPRNHMVFTPLLASTCVGTLEFRSVAELVSRIQFALAQDPNSYFYLATCTDVDTDKHEVYCETVGDVGLPHEHYPFKVAYDKLVIATGSEPLTFGIKGVKEHAYFLRERRRDRINEKMRALQELIPNSNKVDKALMLDEAIEYLKTLQLQVQIMSMGAGFFICLQWWLEVGKLVCFGADLAIGIGDLGSVEG |
| PG10233 | MATEALSSTEMLDFIIYDTISATPYSCNDSSDTNFLLEKHEYFADSLNGASLVTPQRSSVGPETADRRQNLAVQGRKKRRRRPKVCKNKEEAETQRMTHITVERNRRKQ |

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| | MNEHLAVLRSLMPESYVQRGDQASIVGGAIDFVKELEHILQSLEAQKFQLLEEEGRRFEGIERATLLSAGCSSATPFAQFFAQPQYYMSSCSTQSTPNKFYNYRCSKNGGIAEIEVTLVETHANIRVLSPKRLRQLSKLVAAFHNLYLTILHLNVTTLDPLVLYSISTKVIILCMSSYLYTYIDDVYIKLFVCCTVIHANFYG |
| PG10428 | MKCQQDHHLQQHNFFNGNDQLNIFSIPAGQAQKFQPLINCESGFGGFLNRAVKPDPGMENGWPDYGKFDGDNHLGYGACGYGNVIEDEGIKEKKIKGCAEDGDSKITTEHNNKKSTTNSNDCTNRETSTDTWKENSKITEVQKPDYIHVRARRGQATDSHSLAERVRREKISERMKYLQDLVPGCNKITGKAGMLDEIINYVQSLQRQVEFLSMKLAAVNPSLLDFNIDNFFTKEMFPACTSDFPTIGSSSERANPAYFQFNPLQQVVTCCGLDLGINPPDMALTRTISAPVSITETFVDSSCFNTKAMVQGPESKAMVQGPELRSCDGLVNYQVEMVSSISKTYKA |
| PG11005 | MVSPENNSNWVFDYGLLDDIPVPGGDLPPLEPGFQWPTNAFPASTGPSAEFVDPFVTSDGIKEYGSRKRIKSGSCSASDSKACREKMRRDRLNDRFQELSSILEPGRPPKMDKAVILSDAVRMVNQLRDEAKKLKESHEVLQDKINELKAEKNELRDEKQKLKAEKEKLEHQMKTVHTQSGFLPSAVPAPFAGPGQVFGGKMVPFMGYPGVPMWQFTPPATVDTTQDHIEPHVSSTCIVPPDIKSSKAGHKHCA |
| PG11234 | MANNPGDGTADDLLEQILGFPAYAGTDSNLAGNGAAAPMMLQLNSGDGSGQLSGGAGVGGGFHFPLGLSLEQGKGGFLKMDEASGSGNRFREDVDSRISSSVKTGFHGQPMHNTLPAMPHPPAIRPRVRARRGQATDPHSIAERLRRERIAERIRALQELVPNVNKTDRAAMLDEIVDYVKFLRLQVKVLSMSRLGGAGAVAPLVTDIPISSVEEEGSSEGGRNQPAWEKWSSDGTERQVAKLMEENVGAAMQLLQSKALCIMPISLASAIYNTQPPDATSHVNPEMNPPS |
| PG11323 | MGKGLSNNNTYDYDQGCRKSSLLQNRGEYCSNEGGGFQLISENDHPPEAKKARLLENKLPSSSNINFQQPSNCNLSANYVDDQEQDSEAIAQMKEMIYRAAAFRPVNLGEEEVVEKPRRKNVKVSSDPQTVAARQRRERIGEKIRVLQRLVPGGTKMDTASMLDEAASYLKFLRSQVKALETLGQGQNNKLDSFVNSSSFPFNHSFPMQTPPFFPSETLIMIPSTLH |
| PG11934 | MAMETVFLPQDPFYYACKEFYSLGCDYFIPQENKDITGNISSNNLEQSLHGIWESYSSSIVRQNVQEWDPNSSPEAAYSGGQLLREGSPVMEASPVLTTTGRRKRRRSR |

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| | SSKNKEEMESQRMTHIAVERNRRKQMNEYLAVIRSLMPSSYVQRGDQASIIGGAINFVKELEQQLQTLEAQNRTTQEKINNGCSLSPVFADFFPFPQYSMRTSTPSTRILGIRNDQRMVENRPVALGDIEVTMVESHANLKILSKKRPKQLMKIVAGLQCMWLTILHINVTTVDEMVFYTISLKLEEGCQLNTVDEIADAVNHLLGRIQEEDVLS |
| PG11966 | MSIIGDLEVEAAAATCCKMETIQSPEIPIFNMGIWSEKKSTQVKKLNGQGQPSKNLMAERRRRKRLNERLSMLRSVVPKISKMDRTSILGDTIDYMKELLERINNLQEEIEVKPNDLQQLISLKSIFKDVKPNEGGLLRNSPKFDVERRNMDTRIEICCAGKPGLLLSTVTTLEALGLDIQQCVISCFNDFGMQASCSEEMEQRGIITSADIKQALFRNAGYGGRCL |
| PG11971 | MNHCVPDFDIEEEDSIPSSSALNRSKMSSVAEEEDIMELLWQNGQLVAHSQSQRSLKKSHVGGASEQREIRSEEETATAHQLFMQEDEMASWLHYPLEDSSFDRDFYGDLLYSAPVAAAVSAPHRQPVAVAPRPPVPPQRRLESSIEFQSTQRRYQNFSFFSRPKGKIDSGPSSSNKTGKESTVVDSNDTPFTKALESRVSCVADNAAQVSSRNVVCSVTGTATDTSPSSPGGSGASVSAASAEPAHKLTTTTIGAMAAMTEDRKRKGREAGDSECQSEDVDFESAHAKKQVCGSTKTKRSRAAEIHNLSERRRRDRINEKMKALQELIPRCNKSDKASMLDEAIEYLKSLQMQVQMMSMGYGMVPVMFPGVQQYMPPMGLGMGMGMSMDMGMNRPMVPFPSVLPGSALQNPGAAPHLTPRFPIPGFHMPSISLPDPPRIQETSHSDLMLNSLAPQNSNQARMSNFPDPYQQYLGLHQAQNQVVQPSPSKPNGSREGGNPDNHQSG |
| PG12035 | MERLALGGDIEYQLYWETNRFYQAEELDSLVLDETLSGYYDSSSPEGAQSSAAAASKNIVSERNRRKKLLDRLYALRAVVPNITKMDKASIIKDAINYIQELHEQERKIQAEISELESKKNNFLHDFDQDQTPFMANSRLKKKKIEQQHSYDSEGSRISSSPIQVIELRVSYAGEKTVVVSLACSKRTDTIIKLCEVFESLKLKIITANITTFSGTLLKTVFIEVPLFSSLCLYASFMRAVGMTYY |
| PG12278 | MEDLISSSSSSSFLCHGGASPTIQQRLQFIVQSRPEWWMYYIFWQTSKDSTTDRLVLSWGDGHFRGTKDFMLKAASSNIGLGQQDQQQQQHPKFGFELERRKVAKGIQSLFSEALPGIDGVVEADFPDSEWFFMVSVTRSFAAGDDNIVGRTFSSGSYVWLAGDHELQFHNCDRAKEAYLHGIKTLVCISTPCGIIELGSSYTIKEDWGLVHLAKSLFSPDNTMTISNMTSPAALAHAPQQNPTRSLSFFDINAVSGDQNKASGEEEGNTKN |

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| | DKLAKIGRSSSDSGNSDFESNLAPDSAMNMRLKKRGRKAASSGRELAQNHVEA |
| | ERLRREKLNHRFYALRSVVPNVSRMDKASLLADAVTYINELKVKVEDLEGKLR |
| | EEMKKPKSISDVVVYDSQSTSTTNVYHTAARSSMGYGPMNMEVDVKILGSQAM |
| | IRVQGPDVNYPAARLMDALRMLEFRIHHASVSSVKEIMLQDVVIKVPDGLTSEE |
| | ALKTALLRTLQI |
| PG12599 | MEDRVPKVAQNLKWTTVREKYLGFGFFCYFCEGDVNMASPDKIEPEKRDDDSK |
| | NYHAPNNSSDWRFSSSNLTYTSMGLIPTENPIAVCKGDLIESSLCSSASMVDSFCP |
| | NIWDQPTNSQNMGFCDVNVQNNASSSSTLGFRKGSLGPPRNDLERALDMGWTP |
| | PNSMLKGSMLLPTSSRMLPQSLSQFPTDSGFIDRAARFSCFSGGNFGDMVNPFSI |
| | AESMSPYSRVAAPMQGAQEIFAGSRLNLTSGGHSHENEMSMVEGSKDVSMSIEH |
| | GASGQSPLNNEGNSEIFVRSRDEAKQGFHESGNDSGEPEFSSGGGQAEPSLLEGT |
| | GGGTSARGHGLKKRKRIGQDTELDQVRIASNPPEAIKQNSEIQQKGDQNPTSTAN |
| | MPGGGKHCKQGSQASDSLKEEYIHVRARRGQATNSHSLAERVRREKISERMKFL |
| | QDLVPGCSKVTGKAVMLDEIINYVQSLQRQVEFLSMKLATVNPRLDFNIEGLLA |
| | KDIIQSRAGPSSALGFHPDMSLPYAPLHPSQPGLIQTGLPGMGTSSDALRRTISSH |
| | LTAMSGGYKEPTSQAPNVWEDELHNIVQMGLNSSISLDGQDLDGSLPPGHMKA |
| | EL |
| PG12618 | MYTVGGSEAISRDMDNMLFSSNFKYPSQTEFAKSKEMMHSDLYDYNHRQLHQ |
| | QQQPPPQQPLRQQPLRQQPQNSNLARYRSAPSSFFASLLNDGVDGSNYSNGESM |
| | NPELMFPRFNSGEGDSHDLKFGANLKQEMAESVDDYSVSASDMVYAAPAPNLN |
| | PVTSAIPSVENSFRGLNSSMGMENLNQSKKSSGGNCSNLIRQSSSPAGFLSNLVD |
| | EIGFGATNDMGNFRACNQTNMEVSSTTSRLNNHMNFSSGQSSHSRFIPQITENGN |
| | ENVGTSSQQNGHLGSGQNRDHSNRHYLPTIPNDSSFTSLKRNRDGEMKMFSNLN |
| | GLDTQNGDSKHFNSGLLHQLSLPSTSAEMATIENFLQFQQDTVVPCKMRAKRGF |
| | ATHPRSIAERVRRTRISERMKKLQELFPNMDKQANTADMLDLAVEFIKDLQQEV |
| | QTLNETRARQLLQHDLLLSAKIIRRWGRWKVITKEDDLDFEIQGKFMRIYNKSA |
| | WPEVWVVDFLGFVSDKFGWLILPQKNYVIRQQVLKELSVS |
| PG13088 | MEDLISSTSPSSFLCHGGASPTIQQRLQFIVQSRPEWWMYYIFWQTSKDSTTDRL |
| | VLSWGDGHFRGTKDFMRGSSNNGQQDSIQQQQQSKLGFELERKKVAKGIQSLF |

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| | SDTLPGIDGAVVDADFPDSEWFFMVSVTRSFAAGDDNIVGRTFISGSYLWLSGDHELQFHNCDRAKEAYLHGVKTIVCISTPCGIIELGSSYTIKEDWGLVHLAKSVFSPECNSNYMMSMMSTARPPALAHAQNHTRNLSFFDINVVSRDQRNKTCGDLEENTEKVQAKIGRSSSDSGNSDFESPLDQSTVNTRFNKRGRKAAASRRELAQNHVEAERLRREKLNHRFYALRSVVPNVSRMDKASLLADAVTYINQLKAKVEDLEGKLHEEMKKPISTISPDHHVVYDSTATQSTCTTTVYHTAAAGFIQMEVDVKMLGSQAMIHVQSPDINYPAARLMDAFRLLEFRVSHASVSSTVKDVMLQDVVIKVPAGFTSEEALKSAILGTLHNII |
| PG13708 | MFSIPAAQAQQFQPLISNDSGFSGLVNRAVKPDPGMDNGWPDYGKFGGDDHLGYGYGNVNGIELNYAISRTTSCPPEVAVTIAEAAGADTEQREEILPEKMSSPVTEDEGIKEKKIKGGAEEGDSKITTEQNKNCNKRETSNDTSKDNSKISEVQKSDYIHVRARRGQATDSHSLAERVRREKISERMKYLQDLVPGCNKITGKAGMLDEIINYVQSLQRQVEFLSMKLAAVNPRLDFNIDNLFTKEVKTQISQIAIKNNYIQIFVTNSVFQHQQMFPACTSNFPTIGLSPEMANPAYFQFNPLQQAITCCGLDLGVNPPDMALRRTISAPVSISETFVDSSSFNVISSTLFVPSFVIILYF |
| PG14023 | MNHCVPDFDIEEEDSIPSSSALNRSKNSLVAEEEDIMELLWQNGQLVAHSQSQRSLIKSHVGGASELREIRSEEETATAHQLFMQEDEMASWLHYPLEDSSFDRDFYGDLLYSTPVAAAVSAPHRQAVAVAPRPPVPPQRRLESSIESQSTQRRYQNFSFFSRPKGRIDSGPSSSNKTGKESIVVDSNDTPFTKALESRVSCVADNAAQVSSRNVVCSVTATATNTSPSSPGGSGASVSAASAEPAHKLTTTTIGATAAMTEDRKRKGREADDSECQSEDVDFESAHAKKQVCGSTSTKRSRAAEVHNLSERRRRDRINEKMKALQELIPRCNKSDKASMLDEAIEYLKSLQMQIQMMSMGYGMVPVMFPGIQQYMPPMGLSMGMGMSMDMGMNRPMVPFPSVLPGSALQNPGAAPHLTPRFPIPGFHMPPISLPDPSRIQATSQSDLMLNSLAPQNSNQARMSNFPDPYQQYLGLHQAQNQVVQPSPSKPNGSREGGNPDNHQSG |
| PG14197 | MDSRLPAAGPIINTCNLGQENRSDSFRYCIANTESLSFEEEEEEGLGEGEEVKPRQHFKIPSLEDKMPFTQMLKSVESPSPFLPSFIQPQSFQVLLRLQHQIQRAWDQSHTHYSYLPPETTSPINHGAVEPENCLTHDILDESETNNPHPSVSQEQPSFPTAAVQSSLDAVSGPLVKNVTDKEKRKRREREGRRGKPKRMIHIAVERNRKRQMNDHLNSLR |

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| | SLMPPSYAQGVLSVTDPV |
| PG14512 | MSNRRSRSRQSTAGASGISDDQIADLVSKLQQLIPEIRNRRRNSDKVSASKVLQETCNYIRNLHREVDDLSDRLSELLDSTDTDSDQAAIIRSLLM |
| PG14815 | MVEFGGSSSSPVSLSQEHVPTLQQRLQYIVESQPHCWSYVIYWQTSKDSENGCLLLSWGDGHFRGPTKHTTLPKDQTKHTIDGSIDGDVMDAEWFFVMSLTRIFRAGDGSAPGKAFSSGAHIWVCGTDQLHVAECERAKEAQLHGFQTFVCIPTCSGVLEMSSDITISENLSLVQQTKCLFGSDLIGLIPKQPNLSNVGSCSYIDMEIPDFDLHDQFVAVRPATPHVEKKNAAKKRGRKPILGQDIQVNHVEAERQRREKLNNLFYALRAAVPNVSRMDKASVLADAISYINELKAKVDDLDSQLLEFRASKKSGKAESAGADTVENPNSTTTTSVDQKMTESTPSVDVEVKMVGSDAMTIRIQSDNAIYPGEKLMKAIRELELHVHHASMSNVNELIMLQDIVIRVPAADGGLRSEEGLRSALLRAMEQ |
| PG15082 | MFGDSRALFTDSNAIFSSNSNPKGEDMLTKSRMNFDMNNNSSIQDYKQYQNNQTNSGLLRFRSAPSSLLANFDNGVDKSGDSNENLMAESFKGLDDNKSLPNGFAVNSQLPPHYPRYSSNLGLETQVGAVDNSSSYRMGSSMGMENQAKMVSSLMRQNSSPAGLFSHLNSQTGYAAMRGGVGNYRLGNGSNGDISPTASRLKSQMSFSSGLPSSLGMLSRISEIEGENIGATGNDDAKNGSGNGDTQFYTSEFPLSSWSDSLHFAENFTGLKRELDDDEKLFSGAQNTDLANRPPLLSHHLSLPKTSSEMAAMDKLLQFQDSVPCKIRAKRGCATHPRSIAERVRRTRISERMRKLQELVPHMDKQTNTADMLDLAVEYIKDLQKQFKTLSDNRANCKCSVTV |
| PG15345 | MSSRRSRSGQSSGASRISDDQIADLVSKLQQLIPEIRNRRRPDKVSASKVLQETCNYIRNLHREVDDLSDRLSELLNSTDSDSAQAAIIRSLLM |
| PG15509 | MLPCSNGIAWLEGEEDKGISWAVRDNSEGDTCKNLGMNAASLTSFKSMLETDWFANNTMNPSQNILTNHHPDFNNGNLLLQAMDSSSSCSPAPAFTLDPSQSHYPFFPPKSSFSSLFNVPFDNSFDLDCELNFLTNSNSPVLPNPELSSGSDFAATRFLPIYDNNDNSIGGGFSPIGYDGFQGSSSGNALFSNSAKILRPLEVLPPVGAQTTLFRKRVALRQGSGEVDKLGNWGNREDLCKKMKRSFSEDDDEIDILGSFYYDSDELYSRNVNDNNNTNDGGIGNNSNANSSVTVEDQKGKKKGLPAKNLMAERRRRKKLNDRLYMLRSVVPKISKMDRASILGDAIDYLKELLQRINDLHNELEATPPGSLITPTSSFHPLTPTPSTLPHRVKEELCPSALPSPKNPSARVEVRAREGRAVNIHMFCARRPGLLLST |

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| | LRALDSLGLDIQQAVISCFNGFALDIFRAEQCREGQDVLPEQIKAVLLDSAGFLGAM |
| PG16018 | MATEALSSTEMLDFIIYDTISATPYSCNDSSDTNFLLEKHEYFAASLDGASLVTPRRSSVRPETADRRQNLAVQGRKKRRRRPKVCKNKEEAETQRMTHITVERNRRKQMNEHLAVLRSLMPESYVQRGDQASIVGGAIDFVKELEHILQSLEAQKFQLLQEEGRRFEGIETAALLSAGCSSATPFAQFFAQPQYYMSSCSTQSTPNKFYNYRCSNNGGIAEIEVTLVETHANIRVLSPKRLRQLSKLVAAFHNLYLTILHLNVTTLDPLVLYSISTKVIILCMSSYLYTYIDDVYIKLFVCCTVIHANFYG |
| PG16210 | MDSVRVFLNEDWDSLSKMFSSDEEADLALQFLQHFGTNPSNLFDENLFYSYENFNTNFYPSQEISTNYSTSANVLWLNEETGNDTLENADNSTALGLKRKFEEPQQHETVKVLKTKSESVENPKKKSQIVKDKPKNKRNAQPKKKQKLIENVNNDEESSSSCSLEDDSNVSQELIGGEGLKSSQKARSGRGAATYPQSLYARKRRERINERLKILQNLVPNGTKVDISTMLEEAVHYVKFLQTQIKLLSSDDMWMYAPIAYNGMDMGLYQKISPTL |
| PG16376 | MLPRSNGGVWMEGEEDDAVLWAARNSNEGETGKDLGMSGSSLNSFKSMLETEWFGNNTLNPSQSILSNQHPEFNNSNLLLQAMDSSSSCSPSQAFTLDPSQSHSPFFPPKSCFSSLFNAPFDNSFDLACEPTFLTNSNSPVLMSFNGISSMPNLELGSNSDFAANRLLPISENNCNNPIGGGFNPIGFDGFEGSSTGNALFSNRAKVLMPLENLAPVGAQPTLYQKRTVLRQGSSEADKLGNWGMREDFDKKRKRNINEDNDEIDEESIDISGSFNYDSDEPYTGNMNNNDNSGGGIGNNLNANSSVTVGDQKGKKKGLPAKNLMAERRRRKKLNDRLYMLRSVVPKISKMDRASILGDAIDYLKELLQRINDLHNELEATPPGSMITPTSSFHPLTPTPPTLPHRVKEELCPSAIPSPKNPSARVEVRAREGRAVSIHMFCARRPGLLLSTMRTLDNLGLDIQQAVISCFNGFALDVFRAEQCREGQEVLPEQIKAILLDSAGFDGSV |
| PG16383 | MDIDFYKSAPEDQIEMLMMMQMDKLPDFLGAYNNHVVSEIPAMEYSNTQGSGSSTNTDTNNNSNNIGGLPQVVESSSTFMHQPSTCISFTGSQPVEESAELSFLMSSSNPGRWRNGGEINIPSQAQKRSSMAAMREMIFRIAAMQPIHIDPESVKPPKRRNVKISKDPQSVAARHRRERISERIRILQRLVPGGTKMDTASMLDEAIHYVKFLKNQVQSLERSAVNRHATTAAGIGFPVPMSSGSFIPMQQAIKGYQLSSAQNVQHYLDA |

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| PG16916 | MSGGGGENNMHTLLANFFDTSELDAETIYLGAASPDNIFSILEALESSEFEPITSMTHETSHLDPKEGEPEAEGAKRLVSQKSSSSSLSSSAPLEESKTELEAAAANDSSPKTKRQKLSIGAAGEEDDGQQKISHITVERNRRKQMNDNLVVLRSLMPSFYVKRGDQASIVGGVVDYISELQQVLQSLEAKKQRKVYSEVVLSPRLVVSSPRLTSSPLSPRKPPPSPRLVPTSSSLPISPRTPTPITIPYKHHRLHQLSPTMPAAAAAASSLEPSPSSPSIDHTSCGNELLANSKSAIADVEVKFSGPNVLLKTTSPRIPGQAVKIISALEEHLSLEILNVSVNTIGQTMLNSFTIKVTN |
| PG17327 | MDNLGWECSPVVTNVESSWSNQQHQIAERFIATDSNCSGFGTGVKIFIPIQRLHKIIDHEPSDHVDHSNSKKESQMVRHLVPPLDSIKVATTLNISQHQEATRLAANTMLAKSGAGTSWGEALIRPHMMGDPLSGLMANFGMPQDGNKAAAVSTTTASLESLDCLLSATNSNTDTSVEDDGINSILFSDHSKNLWNNFGSNNISSGSDSGINNNSSRIKYHNQYCSRWMNESVPNSTTKRRNEGDSWNKGGGFQLISENPPQIVKKARLEKRPSSSNISFQQPSNSSIINTCVEEPDSEAIAQMKEMIYRAAAFRPVNLGEEAVEKPKRKNVRISSDPQTVAARQRRERISEKIRVLQRMVPGGNKMDTASMLDEAANYLKFLRSQVKALEALGHKIDFVNCPISTPLNPNHPFPNSVIPFNRSIFPMQTTHFSLPKP |
| PG17916 | MSDAYLQADAGGSSIMFPEVMPWTLPPPVHHGFNPIRDQDPFLLPPPPPCAPYGGGFFNRRSFGYDVGPSSDHLRLLSDKVLGQVIQPGSSPFGLQAELGKLTAQEIMDAKALAASKSHSEAERRRRERINNHLAKLRSLLPSNTKTDKASLLAEVIQHVKELKRQTSIIAESSPVPTEMDELTVDNEAAEDGRFVIKASLCCEDRTDLLPDLIKTLKALRLRTLKAEITTLGGRVKNVLFITADDQELSGGDQQHPPPPQQYSISSIQEALKAVLEKSSGDESSSGSVKRQRTNISISYT |
| PG18500 | MEPSQYSLLEELLGPSRENWTKFPSAQVNNNNDADELFPGGWSYESLDFTTSNSSLPEVLVTNSQVESPSFACSFNEIYPFVNGYSSKNNGNFGVYNFEEMNSSSSKEQACLDHIPVFDMGTSEDRRRKIRKVEGQPSKNLXHPSKNLMAERRRRKRLNDRLSMLRSVVPKVSKMDRTSILGDTIDYMKELLEKIHKLQGKDHNEADGNNQINSMGNLKELNMKEATDHAKNSSKFDVERRDKSTGIEISCAEKPGLLLSTVNTIEALGLDIQQCVISCFNDFSLQASCSEAAEHRAVVSCEDLKQALHMNACYGGRCL |
| PG18520 | MAMDALSSNELLFNFIIHDTINSSTPLYTCNEDSNFLLENAQKPQEYIAAGSVINA |

TSSMTPRTSSVEPEPKERLPNLAVQGRKKRRRRPKVCKNKEEAEAQRMTHITVE

RNRRKQMNEHLAVLRSLMPESYIQRGDQASIVGGAIDFVKELEHLLQSLEAQKF

QQLQEGGRGSSMNNGSTTTTTDGTTAELIPNPFAQFFEYPQYSCSHMSNKFICSK

SNGAVADIEVTLIDTHANIRVLSRRRLRQLSKMVSSFQTVYLNILHLNVTTLDPL

VLYSISAKYNNSSKILQMKMTTECKNLAGFRQGII

PG18523 MNLWSTTTTTTDDNASMLDAFMASDLTSFWPPPPVPQQSSSTSTSAAAVFSQES

LQHRLQSLIEGAKESWTYAIFWQSSVADYSSSQTLLGWGDGYYKGEDKEKQLL

KRKSTSATEQDHRKKVLRELNSLISGNQASPDDAVDEEVTDTEWFFLVSMTQSF

VNGTGLPGQAFFNSSPVWVTGIERLASSHCERARQGQTFGLQTIVCIPSNNGVVE

LGSTELIFQSSGLMNKVRILFNFNAIESGSWPLPSEPNEPDPSALWLTDPLPVPSVE

IKEIPLNSNSKPPQIMFENHSSSTLTENPSTSSVINVHNQHLNQQNGVLPRELNFSG

FGFDGISSTNVRNGNLNSHACKPESGEILNFGESKRSSCSGNGNLFSGNSPFGGIV

EDNKKKKSPNSRGSHEEGMLSFTSGVILPSSGVVKSSGGGGGDSDHSDLEASVV

KEVESSRVVDPEKKPRKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAV

VPNVSKMDKASLLGDAISYINELKSKLQTSDSEKDELRSQLDSLRKELSNKESRY

PTQAAVEQDLKMSNHHGSKLLDLDIDVKIIGWDAMIRFQSTKKNHPAARLMAA

LKDLDLDVHHASVSVVNDLMIQQATVKMVSRFYTQDQLRVALTARVSETR

PG18773 MADLYGNNGHRSSSLESEEMSSFLHNLLQNSAGTPPYSFFKEKQNSDFADPGGF

FPAEAKESTVNPFCSVGADSDQITSSRRNLPYNSNDADEFDFGCEEPEEPEVPANS

VPPRSSKRTRAAEIHNLSEKRRRSRINEKLKALQNLIPNSNKTDKASMLDEAIEYL

KQLQLQVQMLTMRNGLGLNPVYLPETLEPVQLTQRGVNYDEGIVLMNANRRD

TVSTDPKFSAQRPLYMSDPAPRIVIPSITNINKSETSYGLEPSILESI

PG18879 MEPSQYNLLEELLGPSRENWTKFPSAQVNNNNDDELFPGGWSYESLDFTKSNSS

LPEVLVTNSQVESPSFACSFNEIYPFVNGYSSKNNGNFGVYNFEEMNSSSSKEQA

CLDHIPVFDMGTSEDRRRKIRKVEGQPSKNLMAERRRRKRLNDRLSMLRSVVPK

VSKVIDYTLYHLSSFTQQTSRYFN

PG18931 MERTYSSGIPMGHVDDDYNLVDFMDEANFEHFIALVRGESDDPIVKFCPNYLDC

DHINDCCVDNQFVPTRGLPYDQFNPPINTFSDPILLDSLPCDLKEGEEEENDTEEY

SSATINTTTPPPPNTNSNTTTSTKKSTKGDRSRTLISERRRRDRMKEKLYALRALV

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|  | PNITKMDKASIVGDAALYVQELQMQAKKLRAEIASLESSLTGVDKQQGGGLYDNANNKSIHPTSKKISQIDVFQVEEKGFYVRLVCNKGRGVAASLHKALDSFSSFIVQSSNLATADKNFVLTFTLNVRKLSSFTNSSFCFEDYCMKLIIYTMEIKQVREREMDMNLPNLKLWVAGALLNQGFDF |
| PG19462 | MGGMMWTDEDKAMAAAVLGPQAFDYLMSSSVSVECSLTAVGNDENLQNKLSDLVDRPNLWNFSWNYAIFWQISRSKSGDLVLGWGDGSCRDLKEGEESEVARVLNLRLEDETQQRMRKRVLQKLHSLFGGSDEECYAFGLDRVTDTEMFFLASMYFSFPRGEGAPGKCFGSGKHVWLSATLKSSSDYCFRSFLAKSAGIQTFVLIPTDVGVLEMGSVRSIPESLELVQSIKSLFSSVSKPKPASAAPLVSEKEDGNAQFSNLGMVERPRITKIFGQDFNSNGSQFREKLAVRKAEERPWDAYSNGNRPPFPNIRNAHHGSNLSQFNNVKQAGTVEIYSPRTPPKNLHELVSGEAPEQLRFNNLKTQKQAQMQIDFTGATSRPSVISRPLSGEAERSDVEAAFKEELTGLADDKRPRKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVPNISKMDKASLLGDAIAYITELQKKVKDLESGREKIGCTSREASSSDANPNSEYHNQVSNIEIEAAHDEVTVRVTCPLDSHPVSRVIEAFREAQVTVTESKLAAGNETVFHTFVIKSEGPEQLTKEKLIAAFSREANSLQPLLSVGFCKNKLNANEVCTIRAFQQVGDDSNPN |
| PG19765 | MGSLSTFKSMVEVGEEVEEWYLAATNNITFSPNFTEADNINNLLLQPVDSSSSCSPSSTSLFDNLDPSHVNYFLPQKPTNPLLLNPLSNNPLENNFDLSCETGFLENQALNSLSRGKGILTEFSNLSSQAHMDLHFSTTHLLQLAENSGAISAGFDSTGFQGFEPGDGNSLFFNRSKLLKRLENFPSVGAQSTLFQKRAALRKNLADSVCNFGLLGNVGGFDRREVGEVSEKKRKNTHGDDLDNLSFDGSGLNYDSDEFTENNMVEERGKNGGNSSNANSNVTGGDQKGLPAKNLMAERRRRKKLNDRLYMLRSVVPKISKMDRASILGDAIEYLKELLQKINDLHTELESTPTSS |
| PG20047 | MVSPENNSNWVFDYGLLDYIPVPGGDLPPLEPGFQWPTNAFPASTGPSAEFVDPFGTSDGIKEYGSRKRIKSGSCSASDSKAGREKMRRDRLNDRFQELSSILEPGRPPKMDKAVILSDAVRMVNQLRDEAKKLKESHEVLQDKINELKAEKNELRDEKQKLKAEKEKLEHQMKTVHTQSGFLPSAVPAPFAGPGQVFGGKMVPFMGYPGVPMWQFTPPATVDTTQDHFEPHVSSTCVVPPDIKSSKAGHKHCA |
| PG20127 | MELEAIVFQERLGYSCSNKDLYNLSGGDWSSHHDLDLKETQEKLGSLDIVENQA |

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| | ENCLYNSPFSQEELPHLEQWICHSGIEPEMVNPQEFQPSETSTVMTGKCKRRRSK<br>SKKKMENIENQRMQHIAVERNRRKLMNEYLSVLRSLMPDSYVQKVDQASIVGG<br>AINYVKKLEQQLQYLSGQSPLNQDFESDHTDSSSTFTEFFAFSQYTISSSKRDNST<br>AILEDSMADIEVIMVESHANIKIRSQKRPKQLLKLVKGLESLRLTILHLNVTTSDQ<br>IVLYSLGVKVEGDCKLYSIEEIATAVNQMLAEASSFIYT |
| PG20810 | MALEEAIVFQDLFSYNNSRDLYNLLGGNIWSSDFDLIQAEEILNSSLDIVENQAEN<br>FPYSSPVSQLMPHLEQWGCNSFIEPEIISPNGGQEFPLSETSTTMPCRPKRRRSRSK<br>KNMEDIENQRMTHIAVERNRRKQMNEYLSLLRSLMPKSYVQRIDQASIVGGAIN<br>YVKELEHQLQLLSGQNFEGGTSSSSPFTEFFSFPQYSTGSSSGGNLIATTDDPWAK<br>ENKIAAMADIEVTMVESHANLKIRSKTRPKQLIKMVNGLQSLRLTILHLSVTTVD<br>QVALYSLCVKVEDDCNLNSGEEIAKSINQMLAMIQEVSYYIGG |
| PG21026 | MEELVVSSSSTSNSPSDSLPHQEQQHAPLFTLQQRLQYIVESQPAESWAYVIFWQ<br>TDNGRLLLSWGDGHFRATTKPIIFPSRDQINNMDVVVDGDFTEAEWFYVMSLAR<br>TFPAEDGSIPAKALSSGAHIWLSGGHQLQLSECKRAKDAQAHGIQTLVCIPTSSG<br>VLEMGSSTVIKENLSLVQQVKSLFGSELIGFISNHPNPSSSNAEWSSYLNMELSDS<br>ELLPQFESANDINNNIPVAVDKKKKTAKKRGRKPALHCSQQDIINPNNHVEAER<br>QRRERLNSRFYELRSVVPHVTRMDKASVLADALSYINEMKAKVDELESQLVQL<br>KEESKTRSSAKLECDTTNNSVDQPKPNSSPPSPAAAAGVTLEVDIKIVGAVARIRI<br>QWKNAEYPGAKLMCAVRELELQVQQVNMSTINDFMIQDVVVRVPDGFTTEDG<br>LRDAIVTALQKKK |
| PG21048 | MTDQGSGLLWENQPWAFSSSDNSGGGGCHEKSGEKLPDSSTSNSQTPSGNEPVT<br>EGGEKRSSDEDEGKKNGKEIIEGKGGGESSDHEMHIWTERERRKKMRTMFSNL<br>HALLPQLPPKADKSTIVDEAVTYIKTLETTLKKLQTQKLQSLHGVATMKYDLSS<br>LVTPPKPPMDTREAFIADQVSSNINNMQAMITTATNSSRIPGFPPIFQSCIANNVIL<br>NIVGGLDAQFCVFAPKKPGLLTAITYVLEKYKLEVVSASVWSENYKSMYTIQTH<br>ACREGLIEAFPAEALYKMAARDIDFFINSESTN |
| PG21441 | MANNPPEGYSDDFLEQILAIPTYSGLAGTDGSSSETTPLTASHLASGGGVGIQQPF<br>FPLGLSLDNGQRERGSMYMGSLFPVFEHLQPHSVRHSVPQIHQAFQSQTTTSTAV<br>TVPHPPNMRPRVRARRGQATDPHSIAERLRRERIAERMRALQELVPSCNKSDKA |

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| | AMLDEILDYVKFLRLQVKVLSMSRLGGAGAVAQLVADIPLQSVEGGISENGNDRPIWENWSNDDTGQEVAKLMEEDVGAAMQFLQSKALCIMPISLAALIYPTNQPDISTLVKPEPPAPS |
| PG21758 | MTDDGGGLLWKNQSWANFLNSDNSGAGGVDEKSGKKLLDSSTSNNQIPSENEAAVVAGGKKGSSSDLEGNKKNNKNGKGIIINEGKGGTGGGGGGGGGSDQSSDHEIHIWTERERRKKMRFMFSNLHALLPQLPPKVIPVCLFIDPADKSTIVDEAVNYIKTLQHTLQKLQKQKLERLHGVATVNYGGLPSLVTPPKLAMDTREAFLADQISSNTNSIPITSTNSSISSPQFPPIFQSWNSKNLILNVCGLDAQFCVCSPKKLGLLTGICFVLEKYKLEVVSAQVSSDNCKSMYMIHTHACCLDFLEVVPVEEIYKQAAGEIIFFINSK |
| PG22215 | MDGIYHGENKQLPSSSSGNTRAQTLFEEYQKSVFIVDNRSAPGFAFKNSLPYIEFKELELQTLASTKTQLQFYQEARIKTAIFMGCKTGEIELGMSIDTQADFEMKMRNCFPEDFSQLQSIPIQQLPQPTDQNPPSSSSSSLRSLSIDSPSSTMPNFLFNDNNISTNPYPLEPSVKPVQTLSQIRNNIQFPTLLQSEEDDAMTRAILAVISSSSSPSSSTNSSQKPQQNSSAFKSYRSVLAPTSRVAQKQNMLKRAIAFVTSTSNTLMRNQEQTQNGNRPASNQLHHMISERRRREKLNESFQALRSLLPPGSKKDKASVLSSTKEYVNSLKAEVEELRRKNQILEAQLLQNDDQELGQMITGTDSSTTDQRVVDVRITNIINAETTSSEAARILDLRVIVRSGGEYYCSMLDLAIRVLEFLKQLRNVITLISVEADTPMLLETTSVNRLVLRLKIEGDEWDDTTFQEAVRRVVADLAQ |
| PG22741 | MSEETINVGKMSRGRNGHLDDNTQGFKSKNLDAERRRREKLSARILELRSLVPIITNAIYMQNADENMNKATTITDAVRDLSDKLFEMEARIEQELKTESSEIDAEQEMKKWGIEAEVKVNQIDANKLWMKMVFAKKRGAFTKLVEAMTVLGFILDDTSVTTSNGAVLVTSCVVGKDGGMLAADQISELLLEIIRAI |
| PG22897 | MDNGIEIRRRMDQMEMMTMMMQLDKLSGHNYQDIYEFPEMKFSGGSSSSVESTPPTTFHSSFMGSPVQEPMTQFLEPTFSTPQLRSSSELLQKTNVNSEEAMREMIFRIAAMQPIQIEPESVKPPQRRNVKISKDPQSVAARHRRERISEKIRILQRLVPGGTKMDTASMLDEAVHYVKFLKKQVQSLERAGPNRAMGVGYPATMATAVPTGFLWIKDS |
| PG23736 | MDPPAIMNHGAFRSGNAAPNNLAEIWPFQFGQSLGQFTENPNREDDPMVLDQRGERKRRQDDDSSIIGVSTGRDANGTSDRDIKRLKASGSRDEELESKVETEAINSG |

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| | KQADQSTKPSEPTKQDYIHVRARRGQATDSHSLAERARREKISERMKILQDLVPGCNKVIGKALVLDEIINYIQSLQQQVEFLSMKLEAVNSRTGPSIEGFPSKDYGQQTFDMAGVTFGSQAPREFSRDSSPEWLHMQIGGNFERSA |
| PG23826 | MEISHIRGFTELGMEDPYSNIQWPMNSFDELSALSLAAAFGENLHHSFYQPLYDIKPSPPEVSCTITERPMKQLKTNSWSSERTDHTSNTQATYSNYTNQFGNVKPKDEVLPSKSTTTLPTDLMTSQGSFENQNYVFKASQGAKRISTGAQLSQAQDHIMAERKRREKLSQRFIALSALVPGLKKMDKASVLGDAIKYLKQLQERVKTFEEQTRKKSTESVVFVKKYELLADDDKSSSGEQFSGNPVNEPQPEIEARFSDKDVLIRIHCEKKKGVLEITIAEIEKFQLLIINSTALTFGTSSLDITIIALMDEKFTMTAKDLVKNLRTALKQLIGYVI |
| PG24302 | MEQAPQLLLNIHIARKKCMMEDFGGSSSSSSSPVSLSQEHVPTLQQRLQYIVESQPHCWSYVIYWQTSKDSDNGILLLSWGDGHFRGPTKHSTLPKDQINHTIDGSIDGDVMDAEWFYAMSLTRIFRAGDGSAPGKALSSGAHIWVCGTDQLHVVECERAKEAQLHGFQTFVCIPTCSGVLEMSSDITISENWSLVQQAKCLFGSDLIGLIPKQPNPSNVGSCSYLDMEIPDFDLHDQFVAVGPVTPQVEKKNPAKKRGRKPILGQDMPVNHVEAERQRREKLNNRFYALRAAVPNVSRMDKASVLADAVSYINELKVKVDDLESQLLEFRASNKSGKAESAGADTVENPNSTTTTYVHQKMAEPSPLVDVEVKMLGSDAMNIRIQSDNSDYPGAKLMKAIRELELHVHHASMSNVNDLIMLQDIVIRVPAADGGLRSEEGLRSALLRAMEH |
| PG24323 | MADFTSEIQSLKPSFSFLDFDPNMELLMNQFTNQNPASTGMGFSIDNFFTTQQVPDEFPGNLAENFPGIFHVDEKNIILNSAPPHGNGNEFHQCKKRLAIQELDSTSSSGISSPQTSDNGNKGKNSSGRGKRMKSSEKEEEKPKGVVHVRARRGQATDSHSLAERVRRGKINERLKCLQDIVPGCRKTMGMAVMLDEIINYVRSLQNQVDFLSMKLTAASTFHDFNSDTDALEALQRGKAFEAQKMQRVMRRGYEELASTTQLGPLDFPFGTYPSISYNT |
| PG25084 | MSKCPKWINLITTPWVNQFNPYQSSINDQSPLDYIPITEPKECNVARKVQKADREKLRRDRLNEQFMELGNTLDPDRPKNDKASILGDTIQVLKDLSAQVNRLKAEYASLTEESRELTQEKNDLKEEKASLKSDIDNLNLQYQQRYRAMFPWGGVDHSVVMHPPSYPYPVPMPIPPGPIPMHPSLQPYAFFGNQNPALVPNPCSTFVPYLTLNTIIEQQ |

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| | SAHYVSPVVPPSSRSHVSSKQDSRNRSSDQGKSKTDKYEDSNDVATELELKTPGSTADQDSSLGQRKSKKSLRKESSLSDGNSSSRCSSSHTVQASSSDSVVGGGMRAEDTERGQI |
| PG25232 | MEQQQQQEEEEEVNSGLTRYRSAPSSYFADLMNFTGYGGVGEDCERFLRASSPDSDRFFSRFMSSCGAEESKSSNFGEIGQNLLVTEPVQSQFMPPMKREPDVINPQQQQVVYTTQSQLDHKPVVPKLGVDNSYNVASSMKMEGGSNSNLVRHSSSPAGLFAQINVDTGYGVMRRGMGNFGTGSVVANAEASFSSASRLKNQMDFPPGPLSSSGIMPRATEIVGSPESGSFGESHRNDGSYTTGGFPSTSWDDSALLPDNFLKGLEENDGKAFSNLNSLENQTGEGGTRTPTVLAHHLSLPTSSVELSNMENLLQCQDSVPLRIRAKRGCATHPRSIAERVRRTRISERMRKLQVLVPNMDKQTNTADMLDLAVDYIKGLQKQVKTLSDNRAKCTCSNNHQTQPDEA |
| PG25335 | MGTEDNGDMRFQHRDGDDMLNCPPSMMNTNPLSDKVVGMAMGSDSMFKASNGAVPYFSSGWDPLVSLSQSENFGPHSGFSNAAYPVVLENQVISSTSHLAHYQPDSGLGELMPKLSCFGSGSFSEMVNSFGLPECGRMNYSQNKEGGTGKALITGTHSEEESQNSEDKSSPNGKKKRRASESHPPFNSNKNAEVPQQHDPSGDNLEQDEKKHKIEQNINANLRGKQTSKQTKENSDSGDAAKDNYIHVRAKRGQATNSHSLAERVRRERISERMRLLQELVPGCNKITGKAVMLDEIINYVQSLQQQVEFLSMKLATVNPELNVDIERLLSKDVLNLRSSNAAVLGFPGLSPTHPFPQGSLPGIPTTTQPFHTIPQSIWDNNELHNLLQMGFDSNNHLGPIDGKTETLISKSIYSSFLKRQAPIYILIKKMRNSAKKHFDCLCYELYL |
| PG25345 | MSSEYTVPKWNVRHQRQEGKVEGEIERPNRRSSHVHHHQKPPTPLVHMSNYQVAELTWENGQLAMHELGGILPLPSSAPKATWGRTGDTLESIVHQATYHSQNNINLPQTTNPHLPHKSSVVASSSGKWGENSSHREINPPGFAKKRVRSEYSQCGRNFSSSVQECVDRSACASASATFCRDNDTTMMTWASFESPRSLKTKSADEDSACHDGSIQENPDEERETKGETVRSHSTRRSRAAAVHNQSERRRRDRINQKMKALQKLVPNASKTDKASMLDEVIVYLKQLQAQVQMMNVRNMPQMMMPLGMQQQLQMSLLARMGMGVGLGMNMGMLDMSALARASPQSLSPLIHPNPATTATPSFIPPPFLVPPMIQRHIQSQASANQCATNTSVPFTDPYCTFLAQSMNMELYNKMAAEVYQQQVNQAAQATSGASKSNHKKKKRKKKKKKKKKKKKRLDLQQNELFLLGFSTSIDTQNI |

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| | KGSIIPIEEATILKMGNHNYQGAKSRRGDSRELKCLGDKAPD |
| PG25389 | MALEEAIVFQDLFSYNNSRDLYNLLGGNTWSSDFDLIHAEEKLNSDLDIVENQAENFPYSSPVSQLMPHLEQWGCNSFIKPEIISPNGGQEFPPSETSTTMPCRPKRRRSRSKKNMEDIENQRMTHIAVERNRRKQMNEYLSLLRSLMPKSYVQRVDQASIVGGAINYVKELEHQLQLLSGQNFEGGTSSSLPFAEFFSFPQYSTGSSSGGNLIAITDDPWAKENKIAAMADIEVTMVESHANLKIRSKTRPKQLIKMVNGLQSLRLTILHLSVTTVDQVALYSLCVKVEDDCNLNSGEEIAKSINQMLAMIQDHPIYG |
| PG25512 | MYTVGGSEAISRDMDNLLFSSNFKYPSQTEFAKSKEMMHSDLYDYNHSQLHQQQQQPPPPLPPPRQQPQNSNLARYRSAPSSIFASLLNDGVDGSNYSNGESMNPELMFPRFNSGESDSHDLKFGANLKQEMAESVDDYSVSASDMVYAAPAANLNPVTSAIPSVENSFRGLNSSMGMENLNQSKKSSGGNCSNLIRQSSSPAGFLSNLVDEIGFGATNDMGNFRACSQTNMEVSSTTSRLNNHMNFSSGQSSHSRFMPQITENGNENVGTSSQQNGHLGSGQNRDHSNRHYLPTIPNDSSFTSLKRNRDGEMKMFSNLNGLDTQNGDSKHFNSGLLHQLSLPSTSAEMATIENFLQFQQDTVVPCKMRAKRGFATHPRSIAERVRRTRISERMKKLQELFPNMDKQANTADMLDLAVEFIKDLQQEVQTLNETQARCTCSSKIKQTSPTA |
| PG25659 | MTDYRVPTAAMNLWSTTTTDDNTSMMDAFMSADLTSFWPPPTPPPPPPPQSSSTSTSTAAAAVFNQESLQHRLQSLIEGAKESWTYAIFWQWQSASGDIDYLSSQSSLLGWGDGYYKGEDKEKQLKRKPTSAAEQAHRRKVLRELNSLISGSQSFPDDAVDEEVTDTEWFFLVSMTQSFVNGAGLPGQAFFNSSPVWVTRAERLLSSPCERARQAQTFGLQTMVCIPSNNGVVELGSTELIYQSSDLMNKVRILFNFNSIDSGYWPVPSEPNESDPSALWLTDPSPLPNVEIKEIPMNSAKPPQIGFENHSFSTLTENPSTSSVINVQNQHSKQSQQQNGNITRELNFSGFGFDGISSTVRKGNSNSHVCKPESGEKLNFGESKRSCSGNGTLFAGHSQFVGIVEDSKKKRSSSSRGSYHEEGGILSFSSGMILPSSGIVKSSGGGGDSDHSDLEPSVVKEAIVSQVVDPERKPRKRGRKPANGREEPLNHVEAERQRREKLNQKFYALRVVVPNVSKMDKASLLGDAIVFINELKAKLQTSDSEKDELRSQLESLKKELASKESQYSSQMAADKDLKISNDHGNKFINLDIDVKIIGWDAMIRIQCSKKNHPAARLMAALEEMDLEVSHASISVVNDLMIQQATVKMGSRFYTQEQLRVALAAKVSETR |

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| PG25699 | MLPRSNGGVWMEGEEDDAVLWTARNSNEGETGKALGMNGSSLNSFKSMLETEWFGNNTLNPSQSILTNQHPEFNNSNLLLQAMDSSSSCSPSQAFTLDPSQSHSPFFPPKSCFSSLFNAPFDNSFDLACEPTFLTNSNSPVLMSFNGISSMPNLELGSNSDFAANRLLPISENNCNNPIGGGFNPIGFDGFEGSSAGNALFSNRAKVLMRLENLPPVGAQPTLYQKRTVLRQGSSEADKLGNWGMREDFDNKRKRNINEDNDEIDEESIDISGSFNYDSDEPYTGNMNNNDNSGGGIGNNLNANSSVTVGDQKGKKKGLPAKNLMAERRRRKKLNDRLYMLRSVVPKISKMDRASILGDAIDYLKELLQRINDLHNELEATPPGSMITPTSSFHPLTPTPPTLPHRVKEELCPSAIPSPKNPSARVEVRAREGRAVSIHMFCARRPGLLLSTMRTLDNLGLDIQQAVISCFNGFALDVFRAEQCREGQEVLPEQIKAILLDSAGFDGAV |
| PG26053 | MEISSIKWNSEQIGEECNFMNHLEMNSSLKFDGLDDFRNEQYLMSLPEEGTNFPKSLSPESYSYTSFLTTTDHQEPNNNHKNNIEIYERPSKQIKTNPWKSIPINHVSANASSSSSSSSHLISFANFTAQPTDSHTRCGDVVIFPVVVPKDEIVSCEDHLNQAYKSESYGSLDYKISYSSELGGVGTTKRSSTRSPLHAQDHVIAERKRRERLTERFIALSAIVPDLKKLDKASVLGDAIKYLKHLQERVKLLEEQIKKTKSEETINSSKLFACDDSSSCNENSGGCFNKTLPEIEARVSEKNVLIRIHFEKQKGFIPKMLSEIEKHHLTVINSSVLPFGGCTLDITIVAQVISTYSSELGGVGPTKRSSIRAPLHAQDHVIAERKRRERLTERFIALSAIVPDLKKLDKASVLGDAIKYLKHLQERVKLLEEQIKKTKSEETINSSKLFACDDSSSCNENSGGCFNKTLPEIEARVSEKNVLIRIHFEKQKGFIPKMLSEIEKHHLTVINSSVLPFGGCTLDITIVAQVISTYPNLVTFGQLLLIVDCNYFIILILVNLLYSSKKPLQFLQMDDEFCLTLNGLVRNLRTALQ |
| PG26263 | MVQTHKHGYTSTLLANSAKCGGRLSKKKTGWDFWWVFFHWKPSISTARWGWTKSKKSGSSVELMEISHIRGFAELGMEDPYSNIQWPMNSFDELSALSLAAAFGENLHHSFYQPMYDIKPSPPEVSFTVTERPMKQLKTNSWSSERTDHTSNTQATYSNYTNQFGNVKPKDEVLPSKSTTTLPTDLMTSQGSFENQNYVFKASQGAKRISTGAQLSQAQDHIMAERKRREKLSQRFIALSALVPGLKKMDKASVLGDAIKYLKQLQERVKTLEEQTRKKSTESVGSSVELMEISHIRGFAELGMEDPYSNIQWPMNSFDELSALSLAAAFGENLHHSFYQPMYDIKPSPPEVSFTVTERPMKQLKTNSWSSERTDHTSNTQATYSNYTNQFGNVKPKDEVLPSKSTTTLPTDLMTSQGSFENQNYVFKASQG |

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| | AKRISTGAQLSQAQDHIMAERKRREKLSQRFIALSALVPGLKKMDKASVLGDAIKYLKQLQERVKTLEEQTRKKSTESVVFVKKYELLADDDKSSSGEQFSGNPVNEPQPEIEARFSDKDVLIRIHCEKKKGVLEKTIAEIEKFQLLIMNSTALTFGTSSLDITIIALGMEDPYSNIQWPMNSFDELSALSLAAAFGENLHHSFYQPMYDIKPSPPEVSFTVTERPMKQLKTNSWSSERTDHTSNTQATYSNYTNQFGNVKPKDEVLPSKSTTTLPTDLMTSQGSFENQNYVFKASQGAKRISTGAQLSQAQDHIMAERKRREKLSQRFIALSALVPGLKKMDKASVLGDAIKYLKQLQERVKTLEEQTRKKSTESVVFVKKYELLADDDKSSSGEQFSGNPVNEPQPEIEARFSDKDVLIRIHCEKKKGVLEKTIAEIEKFQLLIMNSTALTFGTSSLDITIIALMDEKFTMTAKDLVKNLRAALKHFCPYMTCVL |
| PG26507 | MHELGMILPTAQTKTTLDGSGETLESIVNQATSHSQNINLAKTDHHQNHPGSTSSVVKSYNVKCGENLSHLEMAPGFANKRVRSDYSDQEHADRSACASASATFCRDNDTTMMTWAFLESPRSLKTEFVVEDSACHDGSENRDKEHETKGETIRSYTTRRSRDSDVHNRSERRRRDRINQRMKALQKLVPNANKTDKASVLDEVIAYLKQLQAQVQMTSVRNMPQIMMPLGMQQQLQMMSARNMPQMMMPLGMQQQLQMSLLARMGMGFGLGMNTGMLDMSTLPQIAIHPNPATAPAPPTFIQPPFVVPPMIQSHISSQSVPSQGATNTCVPFNDPYCAFLAQVSLKHATVLIYSICLCMISNLKAEDVL |
| PG26994 | MLDGSIDLSSLVLDETLSGYYDSSSPEGAQSSAAAASKNIVSERNRRKKLLDRLYALRAVVPNITKMDKASIIKDAINYIQELHEQERRIQAEISELESKKNNFLHDFDQDQTPFMANSRLKKKKIEQQHSYDSGGSRISSSPIQVIEVQALFP |
| PG27139 | MEMMTMMMQLDKLSAGHNYHDIYHEFPEMKFSGGSSSSVESTPPTFHTSFMGSPVQEPMTQFLEPTFSTPQLKSSSELFLQKTNVNSEEAMREMIFRIAAMQPIQIEPESVKPPQRRNVKISKDPQSVAARHRRERISEKIRILQRLVPGGTKMDTASMLDEAVHYVKFLKKQVQSLELAGPNRAMGVGYPATMAAAVNMNYYSPLARANCQPAQMVGSMQMLR |
| PG27219 | MVRTVKSHHVEEEGDDDEFVSRTTDGSFQQGEAKSGDRKANTNRSKHSETEQRRRSKINERQILRELIPENDQKRDKASFLLEVIQYIQFLQEKVQMYEGTYQGWSSEPSKLIPWRNNCGPVESFIDQSQLVRNGSAQEGDIAVTPAVLTNAQNSIDSDFSGEAAYKATDHGAATQTIPLNIPLPTSLFEGVTTQPPQGSFSDAEHLASQSHSPLWHA |

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| | RPCTAECAAPSYTANEPVELKIENGGAISSACSQGLLNSLTHALESSGVDLSQTSISVQLDIGKLTNTGMTSMPFGTKDHENLSPSNQEMSHYGVGSSGEDSDQAHKRLRTEQS |
| PG27746 | MFSLNQTDELVFQIHPSIPEQQQEEEALVTQDLTLLDQAYGACTVPTTNANSTKRHRKKSLLNTATCDNNNIIDESGKKVMHREIERLRRQEMGKLYGSLRNLIPLEFIKGKRSISDHMHQAVNYINHLQGSIKELDMKRNKLIKNMPVKSVISPAGRSGSSSNNCFRENNSIVTVSPCWCGVEILISIGLMMEEGFHLSRVMEILVNEEGLNVISYASTRANQRLLHTIQSQLQWIAVWLFKCTSVFREKIFNITAR |
| PG27847 | MSSRRSRSRQSSSGGGSRITDDQINDLVTKLQQLLPQITRDSTRSDKVSSARVLQETCNYIRSLHREVDDLSERLSELLANTDTNQAAMIRSLLMQ |
| PG27901 | MQPENRPESSDFQKFISRNDDFGSYGIPATMSSSDWNVSGSGSGSGSGGGIIMKDDLVAVEDNTAVARALKASNNHKEAEKRRRQRINSHLDSLRTLLPCNSKVATNTDKATLLAKVVQRLKELKQQSSDIMQLQSFPSESDDIIVVSSNDDQTLFIKASFCCEDRSDLIPDLVETLKSLRLSPLRAEMVTFGGRIRNVLIVSGDKHQSDEVVEFLREALRSLVQRSSSDSRLKRQRRII |
| PG28173 | MGEKFWVKEEDKALVECVLGNEAFEYLVWSASNNVLSEFVAPAGDLGLQQGLCKIIEGSNWTYAVFWQVCSSKSGKSALVWGGGHYRESKGGEAEDRKSKGDNKKQVLDKLHACFRGSGEDNFAAKFDLVSDVEMFYLTSMFYSFPFDKASSPSQSFNSSRLIWVSELKSSLEHYQSRSFLAKLARLETVVFVPLKSGVVELDPFELQTIGTNQVYGNSSNGHWSNDSESKLFPQMNQVILGGLNSQALVSNLEQGKDDSLLQADERKPRKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVPNISKMDKASLLGDAISYITDLQSKIRILETEKDEVNNNQKQCAIPEIEFHTTQENAVVRVSCPLDAHPVSGVIKTLREHDVITHDSSVSTTDNGEIVHTFSIRTQGGSAEKLKEELSTALSECMQI |
| PG28660 | MSDAYLQADAGGSSIMFPEVMPWTLPPPVHHGFNPIRDQDPFLLPPPPPCAPYGGGFFNRRSFGYDVGPSSDHLRLLSDTVLGQVIQPGSSPYGLQAELGKLTAQEIMDAKALAASKSHSEAERRRRERINNHLAKLRSLLPSNTKTDKASLLAEVIQHVKELKRQTSIIAESSPVPTEMDELTVDNEADEDGRFVIKASLCCEDRTDLLPDLIKTLKALRLRTLKAEITTLGGRVKNVLFITADDQELSGGDQQHPSPPQQYSISSIQEALKAVLE |

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| | KSNGDESSSGSVKRQRTNISISYT |
| PG29408 | MEMIRSVVGMKGWNYCVFWKLSEDKRFLELMDCCCAGTENNMENNNNNCGEDVELLFPVSSEPVETRVLIPVSVGLIELFVYKQVSEDQRMIDFITSQFKISNIEQQSMTTNSSFSVLKAGSSTIVNENYEKELFQPPVSPATMLQNLNLQYDISEDQIPPLHDNSPMNFFQQFNHAAENGINNLLESANEVPDGMPLNPFKCSAQGFDQEDVDTLFQKSMLINSTTTNATAVNNVEPLASRKRQNDDRDSMNRSDSLSDCSDQNDDEDNINDAKCRRRNGNKGPQSKNLVAERNRRKKLNERLYNLRSLVPKITKLDRASILGDAIEYVMELQQQVRDLQNELERNIDLDDEGTAADDNHTSTLQSEVLHGNGNGNGNGNGNGNGNEVKNIGPKSQHGNGNGNGTPHMGASSGIGTENTNDKVQQMEPQVEVIQLNGKEFFVKVFCEHKPGGFVKLMEALNFLGLEVTNANVTRVLSLVLNVFKVEVKRL |
| PG29620 | MNSSLQFDGLDDFTNEQYLMSLPEEGTNFPKSLSPESYSYTSFLTTTTTDHQEPNNNHKNNIEIYERPSKQIKTNPWKSIIPINHVSANASSSSSSSSSHLISFANFTSQPTDSHTRCGDVVISPVVVPKDEIVSCEDHLNQAYKSESYGSLDYKISYSSELGGVGTTKRSSTRSPLHAQDHVIAERKRRERLTERFIALSAIVPDLKKLDKASVLGDAIKYLKHLQERVKFLEEQIKKKKSEETVNSSKLFACHDSSSCNENSGGCFNKTLPEIEARVSEKNVLIRIHCEKQKGFIPKMLSEIEKHHLTVINSSVLPFGGCTLDITIVAQMDDEFCSTLNGLVRNLQTALQ |
| PG29658 | MEFSNSFDGFSENFGFLGIMRGGSSLVLDTERGEIVRALVKPAQKGVKAEKALAALRNHSEAERRRRERINAHLATLRSLIPGTNKSSCLDIQMDKASLLAQVINHLKEMRRSAAEATESILIPMDIDEVRVEQLEDGSDGDSYSIKASLCCEYKHEVLSDLRQALEALHLKTVKAEIATLGSRMINLFVLTGCKEGNIKDTEGSQLLAGSVRQALRSVLDKFYASEEFSTNATLSNKRRRGISGETEKTLELTNMLSARKWPSLDDAVIHGEEQLPWITKQVDQTALEFGNQVDEWLKQSSYFDSSP |
| PG29796 | MGYMRGRARNLFSTEIWRARARELYSIFMRGRAGLNFALLMEYDVVVVEKILVETVVLVTGAAAPHITLHLALRRELAVCTVPASRCGASFKAVSRAAAWTLCLRHLHLPQGILEICLGKTSNDITANRRKNSEEEEEEKKKSEREKKKGRKARELEKGIGETLDNQKDNYHLLQARIMLGVLELCLHEVFSKLQFGAATRPNSSFFAPQRSLVALFSRRSALSAPQRRTTVYTVAPQRELAEWFDRDMDMASQDKFEQEKRNEDSLRIP |

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| | DISSDWRFSSTNLENTSMGLIPNENPMAPTSSQKLAFCDISVQNNTSSSSTLVFRKASLGPPRTGMDGTLVMGWTPPNSMLNGNTLLQTSSRMLPQCLSHFPTGSGFIERATRSMSTYSRGGSPMQGPQDVLSGIRLKSIAWEHSQENEMNMIEGSKDVSKSTEHGTSGGSPLSNERKSKSFLRSHDEAKQGFRDSSNSDEAEFSSGGGQEEPSVLEGKGQRIAAKGHGSKKRKRIAQDTELDQVRGASNPPEATKDNSEIQQKRDHNPASTTNRLTGKHQSQASESLKEEYIHVRARRGQATNSHSLAERVRREKISERMKFLQDLVPGCSKVTGKAVMLDEIINYVQSLQPQVEFLSMKLATVNPRLDFNIEGLLAQDILQSQPGPSSALGFHSDMSMSYHPLHASRPGLIQVGLPSLGTSSDALRRTINSHLTAMNGGYNESTAQVPNVWEDDLNNIVRMGLSSDTPLDSQEAY |
| PG30366 | MLPSLNGIAWLEGEEDEGISWAARDNSEGDTCKNLGMSAASLTSFESMLETDWFANNTMNPSQNILTNHHPDFNNGNMLLQTMDSSSSCSPAPAFTLDPPQSHYPFFPPKSSFSSLFNVPFDNSFDLDCEPNFLTNSNSPVLPNPELSSGSDFPATRFLPIYDNNDNSIGGVFSPIGYDGFQGSSSGNALFSNRAKILRPLEVLPPVGAQPTLFQKRVALRQRSGEADKLGNWGNREDLCKKMKRNFSEDDEIDISGSFYYDSDELYSRNVNDNNNTNDGGIGNKSNANSSVTVEDLKGKKKGLPAKNLMAERRRRKKLNDRLYMLRSVVPKISKMDRASIVGDAIDYLKELLQRINDLHNELEATPPDSLITPTSSFHPLTPTPPTLPHRVKEELCPSALPSPKNPSARVEVRATEGGRAVNIHMFCARWPGLLLSTLRALDSLGLDIQQAVISCFNGFALDIFRAEQCREGQDVLPEQIKAVLLDSAGFHGAM |
| PG30998 | MSSRRSRSGQSSGASRISDDQIADLVSKLQQLIPEIRNRRRSDKVSASKVLQETCNYIRNLHREVDDLSDRLSELLNSTDSDSAQAAIIRSLLM |
| PG30999 | MSSRRSRSGQSSGASRISDDQIADLVSKLQQLIPEIRNRRRSDKVSASKVLQETCNYIRNLHREVDDLSDRLSELLNSTDSDSAQAAIIRSLLM |
| PG32606 | MSNRRSRSRQSTAGASGISDDQIADLVSKLQQLIPEIRNRRRNSDKVSASKVLQETCNYIRNLHREVDDLSDRLSELLDSTDTDSDQAAIIRSLLM |
| PG32671 | MAMDALSSNELLFNFIIHDTINSSTPLYTCNEDTNFLLENAQKPQEYFAASSVINASSSMTTRTSSVEPEPKERLPNLAVQGRKKRRRRPKVCKNKEEAEAQRMTHITVERNRRKQMNEHLAVLRSLMPESYVQRGDQASIVGGAIDFVKELEHLLQSLEAQKFQQLQEGGRGSSMNNGSTTTTTDGTTAELIPNPFAQFFEYPQYSCSHMSNKFICSK |

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| | SNGAVADIEVTLIDTHANIRVLSRGRLRQLSRMVSGFQTVYLNILHLNVTTLDPLVLYSISAKVQ |
| PG32830 | MKTQTKFQIWKLKDPAIKVLEISEKMLSRVNSVVWMEARKDEEKASWNNNHNNNNGGLENKEEMSSLSAYKSMVEVSEEDEWYLANNNITFSPNFTEADNNLLLQPVDSSSSCSPTPASVFSNFDPSQVNYFLPPKPTNSINLNPLSTNPLENSFDLSYETGFLGNQALNSLFRGNRVLTGFNDLSSHTHMDTSNLTSNPHFSTTQLLQLAGNSGTMSAGFCSSGFQGFELGNGNSLFLNRSKLLKPLENFASIGAQPTLFQKRAALRKNLADSGGNLGLLGNVEGYDGKREVGEVSEKKRKTSYGDDLDNVSFDGLGSNYDSDEFTENNKVEESGKNGGNSSNANSTVTGGNQKGKKKGLPAKNLMAERRRRKKLNDRLYMLRSVVPKISKMDRASILGDAIEYLKELLQKISDLHNELESTPPSSSLTPSSSFYPLTPTPPTLPGRIKEELCPSLLRSPTGQPARVEVRLREGRAVNIHMFCGRKPGLLLSTMRALDNLGLDIQQAVISCFNGFALDIFRAEQCKEGQDVHPDQIKAILLDSAGFHGMV |
| PG32841 | MDIDLLKSAPEDQIEMLMMMQMDKLSDFCGGVDSNDVVSEMPPMEFTPGKSTSTNKIGHLPQIIDQNSPTFINLPSTISFTGSPPVQEPAELPFLSSSNMGRWRNNGEDQFPTQAQKRNSMAAMREMIFRIAAMQPIQNDPESVKPQKRRNVKISKDPQSVAARHRRERISERIRILQRLVPGGTKMDTASMLDEAIHYVKFLKNQVQSLERAAVNRPVAAAGIGFPVPMCSGSFFPMEQATKGYHQSSSAAQNVQQGVPNFR |
| PG32851 | MEDRVPKVAQNLKWTTVREKYLGFGFFCYFCEGDMNMASPDKIEPEKRDDDSKNYHAPNNSSDWRFSSSNLTYTSMGLIPTENPIAVCKGDLIESSLCSSASMVDSFCPNIWDQPTNSQNMGFCDVNVQNNASSSSTLGFRKGSLGPPRNDLERALDMGWTPPNSMLKGSMLLPTSSRMLPQSLSQFPTDSGFIDRAARFSCFSGGNFGDMVNPFSIPESMSPYSRVAAPMQGAQEIFAGSRLNSTSGGHSHENEMSMVEGSKDVSMSIEHGASGQSPLNNEGNSEIFVGSRDEAKQGFHESGNDSGEPEFSSGGGQAEPSILEGTGGGTSARGHGLKKRKRIGQKDTELDQVRIASNPPEAIKQNSEIQQKGDQNPTSTANMPGGKHCKQGSQASDSLKEEYIHVRARRGQATNSHSLAERVRREKISERMKFLQDLVPGCSKVTGKAVMLDEIINYVQSLQRQVEFLSMKLATVNPRLDFNIEGLLAKDIIQSRAGPSSALGFHPGMSLPYAPLHPSQPGLIQAGLPGMGTSSDALRRTISSHLTAMSGGYKEPTSQAPNVWEDELHNIVQMGLNSSISLDGQDLDGSLPPGHMKA |

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| | EL |
| PG32981 | MEYKGHDFLEELLSLRIDDPWELATNNIPKGVNDFYYTNVDTFLENPFPQNYCFDEFPKFPFDRQTFNCSPEFYTPFGDEALSAPEVTDSSTNKLDTSQMFQEDCSFMSIVGDLEVEASATCCKMETIQSPEIPIFNMGIWSEKKTTQVKKLNGQGQPSKNLMAERRRRKRLNERLSMLRSVVPKISKMDRTSILGDTIDYMKELLERINNLQEEIEVKPYDLQQLISLKSIFKDVKPNEGDLLRNSPKFDVERRNMDTRIEICCAGKPGLLLSTVTTLEALGLDIQQCVISCFNDFAMQASCSEEMEQRGIISSADIKQALFRNAGYGGRCL |
| PG33143 | MDWYSCNSKKSDFGFGHFGLVEQFWGSLGGNLGSGSMLNSHTLVLDGEKGELVKAPGGVEKKDGVLEVKDVAALKSHSEAERRRRERINAHLDTLRGLVPCAGKMDKATLLAEVICQVKQLKNSATEASRGVLIPMDADEVRVEPLDESSRDGTYFLASLCCDYNPELLSDVKKALNALQLNIVKAEISTLGKRVKNVFVFTSGRGNGNAEEQQLLLNSVRQALSSIVDKISIFAKNGAEQV |
| PG33184 | MSIENNMQTTYLLPELIFQEDSHEFVDTNFAAGSAASPEDIFSILEALEGVSSDQLNSLTPVLDHHDETTSFFGPKLEAAGVNQQQEESTSHATTTTKLATQKSTSSALVDLEELETELEEEEEAAAKNCSPKTKRRKLSKAAAKGEEELDGQQKISHIAVERNRRKQMNDNLSVLRSLMPSFYVKRGDQASIVGGVVDYITELQQVLQSLEAKKQRKLIYNEVLSPRRQQQLVSSPRLTSLPISPRKPPISPRLVVPISSLPTSPTTPQPTSPYMNQHQTSLLHYQLPYLSPTNSMLNSSLEPSLSSSSSSSSCSTSNSIDHANELVAHSKSAVADVEVKFCGPNVLLKTISPKIPGQVLNIISALEDLSLEILNVSLKTIDELTMLNSFTIKVTSK |
| PG33513 | MGGTMWSEEDKAMAAAVLGTRAFDYLISSSVSAECSLMAVGNDENLQNKLSDLVDCPNFSNFSWNYAIFWQISRSKSGDLVLGWGDGSCRELREGEESEVSQILNLRFEDEKQQRMRKRVLQKLHALFGGSDEECYAFGLDRVTDTEMFFLVSMYFSFPRGEGAPGKCFGSGKHVWLSDALKSSTDYCFRSFLAKSAGIQTIVLIPTDVGVVELGSVRSIPESLDLVQSITSSFSSFLSVSKPKLMAAAPVVSEKEDGNTQFSNLDVVEGPRITKIFGQNFNSTRSQFREKLAVRKAEERPWDACSNGNRSPFPNARNGLNGSNWAQFNNVKQGNTVETYSPQTPANNLHELLNGGAREEFRFNNFKTQKPAQMQIDFTGAMTRPPVICRPASGESEHSDVEVACKDGQMGLADAKRPRKRGRKPANGREE |

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| | PLNHVEAERQRREKLNQRFYALRAVVPNISKMDKASLLGDAIAYITELQKKVKDLESGREKIGSTSREASSNSEYKNQVSNIEVEAAHDEVTVRVTCPLDSHPVSRVIEAFRETQVTVTESKLTAGNDTVFHTFVIKSEGPEELTKEKLVAAFSREANSLQPLSSVG |
| PG33622 | MALARIARSGLRRSGATGNYASQKDMPYEGVSTRKYSLPSVENDKSCGSLSYLSNIKRADHVSFWSRGINVTPHYQFAHAERVVEESDSEYENQKYPSLEATKPGKKPRVVVLGIGWVACRFLKGLDTKIYDVVCISQRNHMVFTPLLTSTCVGTLEFRSVAEPVYCETVGDAGLPHEHYRFKVAYDKLIIATGFEPLTFGIKGVKEHAYFLRERRRDRINEKMRALQELIPNCNKVDKASMLDEEIEYLKTLQLQVQIMSMGAGLYMPPMVAGGWKVRQFWSGSDNWDRRSRIGGGMIGVWRERNGGGRGRIMGTRRRMTLGYCSSNIMHKIKELISVLDQRKDESIECTFKGVAKYFQEVFSELVQHGHRHLVMMKKKFGKSPNISVPKSRFMDSSVFFAGDSSVKLLMDAIFGNLMFICLLLLGTRVLPKASVVSLRETVSTTCLTILGIKFSCYVYGRQGTKL |
| PG33853 | MDNLGWECSPVVTNVESSWSNQQHQIAERFIATDSNCSGFGTGVKIFIPIQRLHKIIDHEPSDHVDHSNSKTESQMVRHLVPPLDSIKVATTLNILQHQEATRLAANTMLAKSGAGTSWGEALRRPHMMVDPLSGLMADFGMPQDGNKAAAVSTTTASLESLDCLLSATNSNTDTSVEDDGINSVLFSDHSKNLWNNFGSNNISSGDSGMNNNSSRIKYHNQYCSRWMNEIDKSVPNSTTKRRNEGDSWNKGGGFQLISENPPQIIKKARLEKRPSSSNISFKQPSNSSITNACVEEPDSEAIAQMKDMIYRAAALRPVNLGEEAVEMPKRKNVRISSDPQTVAARQRRERISEKIRVLQRMVPGGNKMDTASMLDEAANYLKFLRSQVKALESLGHKLDFVNCPINTPLNPNHPFPNSVIPFNHSIFPMQTTHFSLPKP |
| PG34217 | MVLSYYSNRGPLQYHHNQELTQPELLPPELLNFHDNYLLSDTCIDPLFDQKNFFYSENTLTPPSPPPPPPPPQLFESYPYPKRVKTQEDFYYSDIINYNYDYDVFVPNPPLLPEFFPELVLPLPEFQASSTILPQVYSCGSISNVEQGTSNVKKASGGSLSAQSIAARHRRRKITEKTQELGKLIPGGQKMNTAEMFQAASKYIKFLQAQVGILELMGSTDDQENKEALHSPELQALVTSPLVQEKLYSAEKCLVPRKFVETLAEKRQLQSNPQLIKDIIQLL |
| PG34234 | MVRTVKSHHVEEEGDDDEFVSRTTDGSFQQGEAKSGDRKANTNRSKHSETEQR |

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| | RRSKINERQILRELIPENDQKRDKASFLLEVIQYIQFLQEKVQMYEGTYQGWSSE |
| | PSKLVPWRNSCGPVESFIDQSQLVRNGSAQEGNIAVTPAVLTNAQNSIDSDFSGE |
| | AAYKATDHGAATQTIPLNIPLPTSLFEGVTTQPPQGSFPDAEHLASQSHSPLWHA |
| | RPCTAECAAPSYTANEPVEPKIENGGDISSACSQGLLNALTHALESSGVDLSQTSI |
| | SVQLDIGKLTNTGMTSMPFGTKDHENLSPSNQEISHYGVGSSGEDSDQAHKRLR |
| | TEQS |
| PG35448 | MDQSDPFESALSSIVSSPANSNPGIPNNGENFVLRELIGRLGGICNSGEISPHSYIG |
| | GNNSTNTSCYNTPLNSPPKLNLSIENQIRGNLKIPGNQLPFSTDPGFAERAAKFSC |
| | FGGKNESKFPPKTEFAGSQMGLQENRDGFLQEGIEVSDKKFHRFSRSSTPEKDSM |
| | EESSVSEQIPGGEIVKKSQSDGNGRKRKSIPRGKGKEIPSAPSAKESMVVAENEES |
| | NSKRSKENEGNGSGKVTGEGNQKQNKDSAKPPEPPKDYIHVRARRGQATDSHS |
| | LAERVRREKISERMKFLQDLVPGCNKVTGKAVMLDEIINYVQSLQQQVEFLSMK |
| | LSTVNPRMDLNMEALLSKDIFQSRVSLPHNIFPADSSAQAFPYAYQSQQGPNLHS |
| | NMPNGTKNPLSMNPLTAAILRNTGMQMPSVDGFHEAAASQVPTFWEDDLQSFV |
| | QMGFGQNQHEILHGSNSTSSHMKVEI |
| PG35697 | MDPPAIMNRGAFRSGNAAPYNLAEIWPFHFGQNLGEFNDNPNRGDDPMVLDQR |
| | GERKRSQDDDSAAGASTSCAAIDMSDSDSKRLKVSGSRDENLASKAETEANSGK |
| | QAEQSTKPSEPPKQDYIHVRARRGQATDSHSLAERARREKISERMKILQDLVPGC |
| | NKVIGKALVLDEIINYIQSLQRQVEFLSMKLEAVNSRTNPSIEGFPSKDFGQQTFD |
| | MAGLTFGSQAPREFSRGSSPEWLHMQIGGNFERST |
| PG36060 | MNALPEMLHCMNTATNIAGRTDMSVFERQRARMKWEEDQQQQQQQLSFFSGN |
| | ELNMFSIPAAQAQQFQPLIGNDSGFSGLVNRAVKPDPGMDNGWPDNGKFGVDD |
| | HLGYGYGNIIEDEGIKEKKIKGGAEEGDSKIRTEQNKNCNKRETSNDTSKDNSKI |
| | SEVQKPDYIHVRARRGQATDSHSLAERVRREKISERMKYLQDLVPGCNKITGKA |
| | GMLDEIINYVQSLQRQVEFLSMKLAAVNPRLDFNIDNLFTKEVKTQISQVAIKNN |
| | YIQIFVTNSVFQHQQMFPACTSNFPTIGLSPEMANPAYFQFNPLQQAVTCCGLDL |
| | GVNPPDMALTRTISAPVSIPETFVDSSGFNFNLYYTKYSPLQLGTLIYKTSITRNFN |
| | KEDQQHIHLSYLQSFKVEV |
| PG36640 | MANNPGDGTADDFLEQILGFPAYAGTDSNLAGNGAAAPMMLKLNSGDGSGQL |

SGGAGVGGGFHFPLGLSLEQGKGGFLKMDEASGSGNRFREDVDSRISSSVKTGF
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PG37017 MSDAYLQAAAAGGNSRMFPEVLPWTLPPPDFNPVHFPTNPIRDHDPFLLPPPSPS
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EIMDAKALAASKSHSEAERRRRERINNHLAKLRSLLPSTTKTDKASLLAEVIQHL
KELKRQTSIIAESSPVPTEMDELTVDNESDEEGRFVIKASLCCEDRPDLLPDLIKTL
KALRLRTLKAEITTLGGRVKNVLFITGDHDQELNSGDDDDDDDEQQQQHYSIS
SIQEALKAVMDKTNGDESSSGSVKRQRTNINIL

PG37191 MEPTSTATEVRSASCNQKTEEVGVESLQFGEEIQTLMSVPPETGSSFTALLELPTN
QAVKLLHSPEKLSGEVWSNGPIEHPKPYHFTPMFPSNTALVDRASKFSVFATTEN
SPEPNSIPLNYVKQEPVESDSRRNSSPGLSDSVVPNNDQKSSKRKEREKKVKGPV
KRSKNTENENSKDREKLPYVHVRARRGQATDSHSLAERARREKINARMKLLQE
LVPGCNKVRCCFKLY

PG37222 MEKEGNTFPPTWNSTQFGMEIQNSELNSTSEQIPNCFFNPNWENPIDQSDPFESAL
SSIVSSPTTSHPGISGENIVLRELIGRLGSICNSGEISPHSFIGGNGNHSTNTSCYTTP
LNSPPKLNLSMMDHQIRGMGNQLPFSTDPGFAERAAKFSCFGGINGQTGENESE
FPHKLSRVSSCQSFKVAGSQVGFQENKEGFLQEGIQASDKKFSRFSRSSTPEKAK
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YQSQQGSNIHNNIPNGTETPFPMNSLNAAIRRNTVLQLPSVDGFNEAAASQVSAF
WEDDLQSVVQMGFGQNQPESFHGSNAATNMKVEL

PG37235 MEEFGGSSSSSCSPVSLSKELMSTLQQRLQYIVESQPHCWSYVIFWQTSNDDSDN
GRRLVLSWGDGHFRGPTKHILPIDQINHTIDGSIDGDFMDAEWFYVMSLTRIFRA
GDGSAAGKASSSGAHIWLCGTDQLRFSECERAKEAQVHGFHTFVCFPTCSGVLE
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| | DRLVAVGPSTPHVEKKNAGNKRGRKPIAGQDMPVNHVEAERQRREKLNNRFYELRAAVPTVSRMDKASVLADAVSYINELKLKVDELESQLLEFRVLKKSESGGADTVENPNSSTTTTTTRTSADEKMPESKGLTLEVEVKKVGSEAMNIRIQSDNADYPGEKLMKAIRELELHVHHASMSNVNGSIMLQDVVIMVPEEEADGDGVLRSEDELRSALLRAMNR |
| PG37305 | MDPNPNIGFWIFAIRQIYLRKLVGFGVPGDVGNFRASNRTNTEASSKTSRLSSYMTFSSGPSSCSSVMPPITENGNDNVGTSSQQNGHLGCGQNGEQPSGGYLPNSPNDSTSNNLKRNGDSEVKMFSNLNGFDSQNGDSKHYSSGLVHQLSSPSTSVEMATIENFRPFQQGSTPCKIRAKRGFATHPRSIAERVRRTRISERMKKLQDLFPNMDKQANTADMLDLAVESIKDIQKEVQTLNEIRAKCTCSSKRIQTSPTARPALCKDY |
| PG37445 | MEKEGNTFPPTWNSTLFGMEIQNSELNSTSEQIPNCFFNPNWENPIDQSDPFESALSSIVSSPTTSHPGISGENIVLRELIGRLGSICNSGEISPHSFIGGNGNHSTNTSCYTTPLNSPPKLNLSMMDHQIRGMGNQLPFSTDPGFAERAAKFSCFGGINGQTGENESEFPHKLSRVSSCQSFKVAGSQVGFQENKEGFLQEGIQASDKKFSRFSRSSTPEKAKLGDSMEESSVSEQIPGGEIGIKGKSDANANAKKRKSIPRGKAKEIPSAPCSKDAKAAAENEESDTKRSKSNEGNSNGKDEAKENGIQKQRKDNSKPIEPPKDYIHVRARRGQATDSHSLAERVRREKISERMKFLQDLVPGCNKVTGKAVMLDEIINYVQSLQRQVEFLSMKLSTVNPRMDFNVEALLLKDIFQSRGTLPHNIYAVDTSTQAFPYTYQSQQGSNIHNNIPNGTETPFPMNSLNAAIRRNTVLQLHSVDGFNEAAASQVSAFWEDDLQSVVQMGFGQNLPESFHETKPKKKRMKKKHQKPRLAAVCDVVTWLRNQKTFCKIPSGLEN |
| PG37838 | MKSVKGHQEEEEEDYEDFGSKKDATTSTNSKDGKNSDKANATRSKHSVTEQRRRSKINERFQILRELIPNSDQKRDTASFLLEVIEYIQYLQEKVQKYEGSYQGWSSEPTKLMPWRNSHWRVQSFVGNPQAVKNDSGPGSTFSGRFDENNVTIIPTMHTNPENPVESDLSRDASCKPMDQQPELANKGMVMPMPLQASMAVPVQSDGVFSLPLRRPVSDAQSTECPITGDVLNQQDDLTIEGGTISISSVYSQGLLNTLTQALEGAGVDLSQATISVQVDLGKRANRGLNSGITLAKDHVDPSDSQPVGHFSEADNGEDTDQVQKRRKI |
| PG37858 | MLRAEAEIMELLWQNGEVVTHSQTQRSLKKSHLAVGGASAEQREIRSEEETAA |

NHQLFVQEDEMASWLQYPLDDSSFDRDFYADLLGPAAPSAPVATAVPQQPPQA
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PG37971 MTDYRVPTAAMNLWSTTTTDDNTSMMDAFMSADLTSFWPSPTPPPPPPQSSSTS
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FGLQTMVCIPSNNGVVELGSTELIYQSSDLMNKVRILFNFNSIDSGYWPVXWSVP
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SGIVKSSGGGGDSDHSDLEPSVVKEAIVSQVVDPERKPRKRGRKPANGREEPLN
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DAMIRIQCSKKNHPAARLMTALEEMDLEVSHASISVVNDLMIQQATVKMGSRF
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PG38201 MIVNPEMFEEGSSCFDSTPMQYQTLAEDGLSLNIVPNCNPNFPMEEQVLSYSQQ
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EMNYGHYSQIQDVHNDSNSHHQSFINSTETPYPQTPDLLNLFHLPRCSSSLLPDST
ISFTNLPGPDTGSNSSVLYDPMFHLNLPPPPPMFREMFQSFPNGYNLPPTQTGSLF
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AALKKLVPNPSKPDRASTVGDAIDYIKELQRTVNEFQVLVEKKRYSRERLIRRHK
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KLVQKKRINCLLFVSKVLDELQLDLQHVAGGLVGDFYSFLFNTKINEGSSVYAS
AIASKLIDVVDRQYVASQPANGYMYDASYGWINCTFPSTSSY

PG38302 MSLVSLGSFCMYPAGEFGSICSNLMLFGHLYLPILEYLKRVSEIAPFRGFVGLLGF
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VPGCNKITGKAVMLDEIINYVQSLQQQVEFLSMKLATVNPELNIDIDQILSKDILN
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PG38503 MEDFGGSSSSSSSPVSLSQEHVPTLQQRLQYIVESQPHCWSYVIYWQTSKDPDNG
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DGSAPGKALSSGAHIWVCGTDQLHVVECERAKEAQLHGFQTFVCIPTCSGVLEM
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AVPNVSRMDKASVLADAVSYINELKAKVDELESQLLEFRASKKSGKAESAGTD
TVENPNSSTTTYVDQKMAESTPLVDVEVKMVGSDAMNIRIQSDNSDYPCAKLM
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PG38504 MEDFGGSSSSSSSPVSLSQEHVPTLQQRLQYIVESQPHCWSYVIYWQTSKDPDNG
ILLLSWGDGHFRGPTKHSTLPKDQINHTIDGSIDGDVMDAEWFYVMSLTRIFRAG
DGSAPGKALSSGAHIWVCGTDQLHVVECERAKEAQLHGFQTFVCIPTCSGVLEM
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VAVGSVTPQVEKKNPAKKRGRKPILGQDMTVNHVEAERQRREKLNSRFYALRA
AVPNVSRMDKASVLADAVSYINELKAKVDELESQLLEFRASKKSGKAESAGTD
TVENPNSSTTTYVDQKMAESTPLVDVEVKMVGSDAMNIRIQSDNSDYPCAKLM
KAIRELELHVHHASMSNVNELIMLQDVVIRVPAADGGLRSEEGLRSALLRAMEH

PG38698 MAVKKMNHNASERDRRKKINSLFSTLGSLLPASDQTKKKLSIPNTVSRVLKYIPE

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| | LQKQVERLVGKKEELSSKISKQGQQLIHLQQQRIPNSLYTVSASLMMGGDVMIQISDAVPTTTTRIDFINP |
| PG39433 | MDQFNNNAFGQSTEAPIQSVPELNQRPNSTRLHSDSRLEAGPKECDVARKVQKADREKLRRDRLNEQFMELGNTLDPDRPKNNKASILGDTIQVLKDLTAQVNRLKAEYASLTEESRELTQEKNDLKEEKASFKSDIDNLNLQYQQRYRAMFPWGGMDHSVVMHPPSYPYPVPMPIPPGPIPMHPSLQPCPFFGNQNPALVPNPCSTFVPYLTPNTIIERQSAHYVSPVVPPSSRSRVSSKQDSRNRSSNQGESKTDKYEDSNDVATELELKTPGSTADQDSSLGKRKSKKSPRKESSLSAGNSSSRCSSSHTVQGSSSDSVVVGGMRAEDTERGQI |
| PG39516 | MQPENRPESSDFHKFMISGNDDFGSYGIPAMTGSGGGIIMKDDLVAVEDNTAVARALKASNNHKEAEKRRRQRINSHLDSLRTLLPCNSKVATNTDKATLLAKVVQRLKELKQQSSDIMQLQSFPSESDDIIVVSSNDDQTLFIKASFCCEDRSDLIPDLVETLKSLRLSPLRAEMVTFGGRIRNVLIVSGDKHQSDEVVEFLREALRSLVQRSSSDSRLKRQRRII |
| PG39699 | MEKEYFFNAEFPPQLHFHPSLSALEMPNGFHNPNFDKLMEQYSQFESALSSMVTSPAASNSAADTFAIRELKGKLGTIFNTGEISPEFLQGASYIGGGDNSPNSSCYNTPTDSPPQLHLPIMSHFVKENLPNLGNPIPTNSALPALSADPGFAERAAKFSCFGSRSFNGRTSQIGLNNAEFQYRSSSLLMGNGKLPRVSSSFSLKEAGSPMGIQVNKNSVQTQMEMRSGNGSASASGRKFSNLSGSAANSNEASSVSEQNPSGENSLGTPKELNYRKRKGVSRGKAKEAALSQSANAKKEAEGDDNLNVKRSKMTGGGGSVKTEEETKIGAEEDQKQANNDQKTPEPPTDYIHVRARRGQATDSHSLAERVRREKISERMKLLQDLVPGCNKVTGKAVMLDEIINYVESLQRQVEFLSMKLATVNPRIDSRLLSKDIIFQPNGTFPNQMWQVNFSSASAYYGHQAQGQQIPQVHKSVEHATLCRNLGMHLDGFGEGLSQFPAFSEDEHCSNGFW |
| PG39922 | MVTSPAPSNSATDAFAIRELIGKLGTICNAGEIAPELMPRTTYNNSPNTSSCYNTPLGSPPKLQVPIMNHLVKENLPNLGNPMPMNSALPALSTDPGFADRAAKFSCFGSRSFKGRTSPIGMNNTEFQYRSSGLLMGNGNLTRVASSPSLKAAGSPMGIQQNKNSVQTQMEMRSSNGTVSASDRKFSNLSGSVANSTEESSVSGQNPSGENGLRTPNELSSRKRKVVSRGKAKETAVKEGEGDDDSSVKRSKMTGCSGNNNGGVKTEEETN |

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| | RGASDEDQKQANNNQKPPEPPKDYIHVRARRGQATDSHSLAERVRREKIGERMKLLQDLVPGCNKVTGKALMLDEIINYVQSLQRQVEFLSMKLATVNPRLDVNMDSLLSKDTFQSNGTMPHQIYPVDATASASAYYGNQGLRNPQVHKSVEPLDATLCRNLCMPLDGFGEGLPQFPAFSEEDDLQSIVQMGFVDKRLCESVKHAVSMKLSIVGNFQVNCHYLNPEFHAL |
| PG40693 | MDDLVVSSSSSSSLVSLSQESHPPTTLQQRLEHILGSQPAADSWCYAIFWQTSTDHNGRLLLSWGDGHFQGTKTPPPKHPPTNAKLERKKAIRGLFHALLNDNPDTECSIDTDDEDGDVTDAEWFYVTSLARTFPGGEYSEAFSSGTCVWLDGVDQLQLAKCERVREAQIHGIQTFVCIPTCYGVLEMGSNIALKQNWSLVQQANTLFGSDVSGFIPEKEPNTSNNNINVINNNGFLDGSNFFADIGVKVGTGSQEEESINLEAAKQEESEHSVSVFHEFVTAGGAQASVEKRAPKKRGRKPWRDMAMNHVEAERQRREKLNNRFYALRSVVPNVSRMDKASLLADAVSYINNLKAKVEELESQVQRESKKARIVVVEAAGDTTIDNNSSTTTCINDIPNSNNPVLEVEVKMVGPDALIRVQSQNCNYPGAKLMEALRELELQLHHASMSRVAELMVQDVVIRVSDGLRTEDALKAALLRALDH |
| PG40733 | MDMSHARCFPELELQGMDDCNNFFHLLQNDCTTNTNTTTTTTKTQQLVTASTGNYQHQRPLFCEGSFIKTDSQQLYSSSGEWVMKPKKEEVVLYNDDQLFLSFPSFNWNTPAGRHITSTKSRAPHHTTKDHIMVERRRREKIRQRLIALSAILPGLKKMDKASVLENATKYLKQLEERVKALEQQIKKKKSFESVVVVKKSQICNDDDDDNNSHDHELSAGDHDQGLPEIEARISDKSVLIKIHCQKQTSFLQKLLAQVEKLHLTILNISSLPFGNYAMDITISAQMDAEFCLSQKDLIRVLVRSAFVQTMEHECITNFMTMFVYKNYNSEIIIIIP |
| PG40819 | MELEAIVFQERLGYSCSNKNLYNLSGGDWSSHHDLDLKETQEKLGSLDIVENQAENCLYNSPFSHEELPHLEQWICHSGIEPEMVNPQEFQPSETSTVMNGKCKRRRSKSKKKMEDIENQRMQHIAVERNRRKLMNEYLSVLRSLMPDSYVQKVDQASIVGGAINYVKELEQQLQYLSGQSPLNQDFLSDHTGSSSTFAEFFAFPQYAISSSKRDNSTAILEDSMADIEVIMVESHANIKIRSQKRPKQLLKLVKGLESLRLTILHLNVTTSDQIVLYSLSVKVEADCKLYSIEEIATAVNQMLARI |
| PG40879 | MEELLASSSSSSSLVSLTEQYPPPLPLPLSSTTLQHRLQYLVETQPADHSWSYAIFWQASSNDQLVLSWGDGHLRGTTKNTPVPLKESSKKPVRGLFLHALLNDNPDASI |

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| | VDSDVTDAQWFYVSSMARTFPGNSSFGGVPWKAFSSGAHIWLSGPDQLGSFECERAQEAQIHGIKTLVCIPTSSGVVEMGSTVPLKENWNLVQQAKSLFESDLAGLIHKNYVDDPSNNNMNGFEFDRSICFSDINGLFTSLQDQEDSINLLDAKLLDSEHSDSEFQFAAASAAGGGAASTEKRAPKKRGRKPCPGRDTPANHVEAERQRREKLNNRFYALRSVVPNVSRMDKASLLADAVSYINDLKIKVEELESQLQKESKKLKVEAAAAAAGAASTDTADNNNSTTTSVDQATPNGNTTTSVPLDIEVKMVGPDAMIRVQSENSNHPGAKLMEALRELELQVHHASMSSVKELMLQDVVIRVPDALRTEDALKAALLKVLDH |
| PG40902 | MDIDFFKSAPEDQIEMLMMMQMDKLPDFFGAYNNHVVSEVPAMEYSNTQGSGSSTNTDTNNNSNNIGGLPQVVESSSTFMHQPSTCISFTGSQSVEESAELSFLTSSSNPGRWRNGGEINIPSQAQKRSSMAAMREMIFRIAAMQPIHIDPETVKPPKRRNVKISKDPQSVAARHRRERISERIRILQRLVPGGTKMDTASMLDEAIHYVKFLKNQVQSLERSAVNRHATTAAGIGFPVPMSSGSFIPMQQAIKGYQLSSAQNVQHYLDA |
| PG40922 | MARYVNSTKRIRVTAMANNPGDGPVDDFLEQILGFPAYAGAEPNLTGNEAAAAAPMMLQLNSGDGSGHLGGGSGAGGGFHFPLGLSLEHGKGGEFLKMDEVASGSGKRFREDVDSRVSSPANMGFHGQPMHNTLPAIPHPPTIRPRVRARRGLATDPHSIAERLRRERIAERIRALQELVPSVSKTDRAAMLDEIVDYVKFLRLQVKVLSMSRLGGAGAVAPLVTDIPISPVEKEGSEGGRNQPAWEKWSNDGTERHVAKLMEENVGAAMQFLQSKALCIMPISLASAIYHTQTSDTTTLVNPETKF |
| PG41655 | MNPLYDQYELKSSYSHESYSAYPTSNPQSLPLDNMMSNIGIERFKTEYDSSFYSKQMISTSNASTSNSTNFIAFGYPNSVPPLEQHQFYASLNLPKKSKDELVPQEIFNFSHKMQSQLSYNKNYASEFDEEIKRIDSSINRSPLQAQDHVIAERLRREKLNKLFIALSAHIPGLKKLDKASILKDAVEYIKQLQEREKVLEEEACKQSEEPIVTKKKTLMLSEDGDDTHSSQLPPLSDIKARVLGQNVLIRIHCQRPKGSSIVLKFLDELEKLHLTIINCCVIPFDNSLDITITAQIDAKFCITTNYELVEEVRSAFSKLV |
| PG41742 | MEYLGWECSPNESSWWSNQQCEIGDLSESNCCGYKTEDDILNPIQQLLIHKRTSVGDDYPINSEKLVNQMVQHLAVPPILDSIIVASTINYSRQHEQRQLEAIRLASANNMMPVSESGAACTSWESEADLCNSNSPNSVKMMPDFGIMPQDMIKAAAVFSTFTTTASMDSLDCLLSATNSNTDNTISAHQDDGINSILFSQSHCKNSVLSGDSGKGDD |

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| | HKHLYHEIRPNSSSNKRSNNNIDQCQFFQGGEYCSNKGGGFQLISGNDHPPEAKKARLLENKLPSSSNINFQQPSNCNLSANYVDDQEQDSEAIAQMKEMIYRAAAFRPVNLGEEEVVEKPRRKNVKVSSDPQTVAARQRRERIGEKIRVLQRLVPGGTKMDTASMLDEAASYLKFLRSQVKALETLGHGHNNKLDSFVNSSPFPFNHSFPMQTPHFSLPKP |
| PG41771 | MGTEDNGDMRFQHRDGDDMLNCPPSVMNTNPLSDKVVGMAMSSDSMFKASNGAVPYFSSGWDPLVSLSQSENFGPHSGFSNAAYPVVPENQVISSTSHLAHYQPDSGLGEMMPKLSCFGSGSFSEMVNSFGLAECGRMNYSQNKEGGTGKALITGTHSEEESQNSEDKSSPNGKKKRRASESHPPFNSNKNAEVPQQHDPSGDNLEQDEKKHKIEQNINANLRGKQTSKQTKENSDSGDAAKDNYIHVRAKRGQATNSHSLAERVRRERISERMRLLQELVPGCNKITGKAVMLDEIINYVQSLQQQVEFLSMKLATVNPELNVDIERILSKNVLNLQSCNAAVLGFPGLSPTHPFPQGSLPGIPTTTQPFHTIPQSIWDNNELHDLLQMGFESNNNLGPIDGKTETLIIKSMCEALRGIPIIKFAIELWKLLFSYSSFLQRQAPIYILIKKMWNSAKN |

**Table S2** Gene and protein features of 169 PGbHLHs.

| bHLH No | Gene length | cDNA length | Protein length | Mw | p*I* | Exon No. |
|---|---|---|---|---|---|---|
| PG00183 | 3069 | 1499 | 490 | 55802.87 | 5.63 | 5 |
| PG00883 | 611 | 289 | 96 | 10808.07 | 9.17 | 2 |
| PG00933 | 1472 | 1472 | 490 | 53916.34 | 5.41 | 1 |
| PG01029 | 7993 | 1143 | 285 | 31332.03 | 4.99 | 6 |
| PG01277 | 3726 | 1163 | 388 | 41482.21 | 6.49 | 4 |
| PG01478 | 4574 | 2073 | 526 | 57404.12 | 5.79 | 5 |
| PG01763 | 4616 | 1093 | 289 | 31576.69 | 5.29 | 9 |
| PG01888 | 4001 | 759 | 254 | 28200.21 | 5.16 | 6 |
| PG02200 | 3477 | 2259 | 404 | 43983.83 | 6.19 | 6 |
| PG02335 | 1274 | 1274 | 424 | 46838.49 | 7.81 | 1 |
| PG02475 | 4487 | 756 | 253 | 28214.27 | 6.15 | 6 |
| PG02883 | 2974 | 2291 | 517 | 56364.97 | 7.11 | 9 |

| | | | | | | |
|---|---|---|---|---|---|---|
| PG02930 | 3450 | 1635 | 260 | 28570.65 | 8.46 | 2 |
| PG03153 | 4190 | 900 | 301 | 32655.55 | 5.92 | 6 |
| PG03239 | 4159 | 852 | 285 | 30990.61 | 5.70 | 6 |
| PG03489 | 4764 | 835 | 279 | 31581.47 | 7.20 | 5 |
| PG04363 | 3019 | 1164 | 388 | 43208.12 | 5.61 | 3 |
| PG04535 | 1241 | 974 | 325 | 36354.88 | 5.11 | 4 |
| PG04685 | 5466 | 2014 | 462 | 48348.80 | 6.38 | 8 |
| PG04790 | 3617 | 1249 | 266 | 29676.94 | 5.16 | 5 |
| PG05026 | 1313 | 1313 | 437 | 48425.70 | 5.49 | 1 |
| PG05306 | 2384 | 1423 | 337 | 37803.11 | 6.34 | 6 |
| PG05437 | 1768 | 1124 | 375 | 41951.70 | 5.54 | 4 |
| PG05942 | 2326 | 1228 | 425 | 47002.23 | 8.34 | 5 |
| PG06292 | 2078 | 1026 | 342 | 38711.22 | 5.95 | 3 |
| PG06381 | 8074 | 1849 | 388 | 43098.08 | 6.88 | 12 |
| PG06438 | 2077 | 1522 | 507 | 55445.27 | 5.48 | 2 |
| PG06642 | 3656 | 1383 | 443 | 48608.18 | 5.56 | 10 |
| PG06701 | 6585 | 2538 | 724 | 81905.76 | 5.13 | 8 |
| PG06793 | 5109 | 2705 | 751 | 81580.00 | 6.35 | 10 |
| PG07133 | 4663 | 2280 | 652 | 73922.18 | 5.31 | 8 |
| PG07157 | 4592 | 1389 | 464 | 50170.78 | 6.49 | 6 |
| PG07173 | 1632 | 1011 | 337 | 38000.11 | 8.51 | 3 |
| PG07174 | 1582 | 1035 | 345 | 39603.26 | 6.61 | 3 |
| PG07175 | 2240 | 1479 | 374 | 42018.39 | 5.88 | 5 |
| PG07247 | 1855 | 1285 | 410 | 47276.98 | 5.70 | 3 |
| PG07364 | 1316 | 1316 | 438 | 48334.37 | 5.35 | 1 |
| PG07462 | 2397 | 893 | 298 | 33526.50 | 8.55 | 4 |
| PG07481 | 1811 | 1811 | 603 | 66674.64 | 5.75 | 1 |
| PG07666 | 3698 | 1323 | 430 | 48633.53 | 5.53 | 3 |
| PG07762 | 2469 | 1209 | 404 | 43980.71 | 5.73 | 6 |

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|---|---|---|---|---|---|---|
| PG08342 | 1802 | 1802 | 600 | 66595.79 | 6.43 | 1 |
| PG08366 | 2778 | 1583 | 565 | 63938.11 | 5.14 | 7 |
| PG08551 | 7542 | 1285 | 432 | 49007.90 | 5.89 | 14 |
| PG08659 | 3014 | 2213 | 512 | 56362.82 | 6.63 | 9 |
| PG09058 | 5573 | 1796 | 599 | 65397.08 | 5.89 | 4 |
| PG09196 | 7068 | 1346 | 397 | 44259.22 | 5.28 | 6 |
| PG09666 | 1490 | 1490 | 496 | 55255.41 | 6.69 | 1 |
| PG10212 | 11768 | 2186 | 328 | 36533.80 | 6.34 | 12 |
| PG10233 | 2006 | 937 | 312 | 35471.53 | 8.34 | 2 |
| PG10428 | 4788 | 1005 | 347 | 38602.34 | 5.72 | 6 |
| PG11005 | 2751 | 869 | 254 | 28136.99 | 6.67 | 6 |
| PG11234 | 7687 | 870 | 291 | 30916.85 | 5.73 | 6 |
| PG11323 | 1346 | 682 | 227 | 25464.58 | 7.69 | 2 |
| PG11934 | 2366 | 1364 | 324 | 36898.94 | 6.04 | 3 |
| PG11966 | 1004 | 680 | 227 | 25518.63 | 8.39 | 4 |
| PG11971 | 5006 | 2206 | 506 | 55359.93 | 5.99 | 9 |
| PG12035 | 1233 | 737 | 246 | 28012.97 | 6.36 | 4 |
| PG12278 | 1493 | 1493 | 497 | 55224.39 | 6.52 | 1 |
| PG12599 | 4797 | 2857 | 600 | 65072.57 | 5.61 | 9 |
| PG12618 | 3304 | 1877 | 525 | 59320.20 | 6.91 | 9 |
| PG13088 | 1502 | 1502 | 500 | 55885.02 | 6.50 | 1 |
| PG13708 | 1497 | 1085 | 362 | 40063.18 | 5.32 | 4 |
| PG14023 | 5356 | 2259 | 506 | 55299.80 | 5.85 | 9 |
| PG14197 | 1532 | 717 | 239 | 27119.37 | 6.01 | 3 |
| PG14512 | 665 | 289 | 96 | 10846.05 | 6.56 | 2 |
| PG14815 | 1292 | 1292 | 430 | 47429.70 | 5.64 | 1 |
| PG15082 | 3076 | 1205 | 403 | 44242.12 | 7.06 | 7 |
| PG15345 | 950 | 283 | 94 | 10570.84 | 9.09 | 2 |
| PG15509 | 4719 | 2259 | 495 | 54370.99 | 5.36 | 4 |

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|---|---|---|---|---|---|---|
| PG16018 | 2006 | 937 | 312 | 35455.53 | 8.54 | 2 |
| PG16210 | 1444 | 826 | 276 | 31506.16 | 5.46 | 5 |
| PG16376 | 3613 | 1526 | 509 | 55685.26 | 5.14 | 4 |
| PG16383 | 812 | 812 | 270 | 29967.94 | 7.89 | 1 |
| PG16916 | 1514 | 1081 | 360 | 38636.59 | 6.03 | 2 |
| PG17327 | 1316 | 1316 | 438 | 48426.40 | 8.45 | 1 |
| PG17916 | 1880 | 904 | 301 | 32933.34 | 6.19 | 2 |
| PG18500 | 1315 | 956 | 319 | 35837.33 | 5.62 | 4 |
| PG18520 | 1566 | 915 | 309 | 34811.68 | 9.15 | 3 |
| PG18523 | 1955 | 1955 | 651 | 71652.88 | 5.91 | 1 |
| PG18773 | 3362 | 1173 | 266 | 29720.08 | 5.02 | 5 |
| PG18879 | 563 | 563 | 187 | 21595.00 | 6.75 | 1 |
| PG18931 | 1260 | 1053 | 351 | 39608.70 | 5.16 | 3 |
| PG19462 | 3117 | 1882 | 627 | 69680.32 | 6.29 | 2 |
| PG19765 | 1803 | 1068 | 356 | 39180.47 | 5.15 | 3 |
| PG20047 | 2722 | 864 | 254 | 28116.90 | 7.06 | 6 |
| PG20127 | 2205 | 939 | 313 | 35722.36 | 5.39 | 3 |
| PG20810 | 2718 | 1117 | 321 | 36138.86 | 5.12 | 4 |
| PG21026 | 1346 | 1346 | 448 | 49772.20 | 5.77 | 1 |
| PG21048 | 2982 | 915 | 305 | 33518.77 | 5.62 | 3 |
| PG21441 | 4267 | 1522 | 285 | 30978.08 | 5.52 | 7 |
| PG21758 | 3209 | 986 | 329 | 35546.44 | 7.57 | 4 |
| PG22215 | 2552 | 1433 | 479 | 53762.51 | 5.73 | 7 |
| PG22741 | 999 | 588 | 197 | 22055.33 | 5.28 | 6 |
| PG22897 | 3297 | 657 | 219 | 24892.65 | 9.15 | 3 |
| PG23736 | 4112 | 762 | 255 | 28456.51 | 5.54 | 6 |
| PG23826 | 3088 | 1114 | 338 | 38135.40 | 7.03 | 6 |
| PG24302 | 1900 | 1357 | 452 | 49977.66 | 5.74 | 2 |
| PG24323 | 1726 | 837 | 280 | 31275.08 | 6.61 | 6 |

| | | | | | | |
|---|---|---|---|---|---|---|
| PG25084 | 3372 | 1417 | 335 | 37440.72 | 6.61 | 6 |
| PG25232 | 2362 | 1218 | 407 | 44562.41 | 5.52 | 6 |
| PG25335 | 3515 | 1967 | 448 | 49588.56 | 6.44 | 10 |
| PG25345 | 5536 | 1556 | 521 | 58280.24 | 9.76 | 10 |
| PG25389 | 3247 | 1111 | 319 | 35969.73 | 5.47 | 4 |
| PG25512 | 3127 | 2035 | 451 | 49940.16 | 6.19 | 6 |
| PG25659 | 2012 | 2012 | 670 | 73916.62 | 5.86 | 1 |
| PG25699 | 3541 | 1526 | 509 | 55737.34 | 5.19 | 4 |
| PG26053 | 4995 | 1780 | 594 | 66820.21 | 7.03 | 5 |
| PG26263 | 6951 | 2778 | 929 | 104842.95 | 8.93 | 12 |
| PG26507 | 1695 | 1109 | 370 | 41129.97 | 7.67 | 4 |
| PG26994 | 652 | 463 | 154 | 17343.50 | 6.31 | 2 |
| PG27139 | 674 | 674 | 224 | 25265.22 | 9.18 | 1 |
| PG27219 | 6240 | 1394 | 332 | 36365.79 | 5.06 | 8 |
| PG27746 | 1297 | 774 | 258 | 29429.86 | 8.89 | 3 |
| PG27847 | 612 | 289 | 96 | 10838.09 | 9.17 | 2 |
| PG27901 | 1167 | 721 | 240 | 26701.07 | 8.44 | 2 |
| PG28173 | 3570 | 1526 | 435 | 48585.57 | 5.70 | 3 |
| PG28660 | 1812 | 904 | 301 | 32983.26 | 5.85 | 2 |
| PG29408 | 2979 | 1469 | 491 | 54841.11 | 4.81 | 7 |
| PG29620 | 1430 | 1056 | 352 | 39351.18 | 6.36 | 3 |
| PG29658 | 3497 | 922 | 308 | 34279.80 | 5.67 | 5 |
| PG29796 | 20274 | 2227 | 747 | 82897.45 | 8.97 | 17 |
| PG30366 | 4132 | 2034 | 495 | 54541.12 | 5.15 | 4 |
| PG30998 | 1177 | 283 | 94 | 10560.80 | 9.09 | 2 |
| PG30999 | 1183 | 283 | 94 | 10560.80 | 9.09 | 2 |
| PG32606 | 777 | 289 | 96 | 10846.05 | 6.56 | 2 |
| PG32671 | 1502 | 852 | 284 | 31920.18 | 8.63 | 3 |
| PG32830 | 4467 | 2062 | 551 | 60685.13 | 6.50 | 5 |

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|---|---|---|---|---|---|---|
| PG32841 | 1039 | 790 | 263 | 29309.51 | 8.90 | 2 |
| PG32851 | 4795 | 2829 | 600 | 64988.51 | 5.69 | 11 |
| PG32981 | 1290 | 998 | 333 | 38108.36 | 4.82 | 4 |
| PG33143 | 3474 | 1231 | 242 | 26295.97 | 6.45 | 3 |
| PG33184 | 1746 | 1180 | 398 | 43645.18 | 5.33 | 2 |
| PG33513 | 1796 | 1796 | 598 | 66307.42 | 6.06 | 1 |
| PG33622 | 5467 | 1525 | 467 | 52808.29 | 9.58 | 10 |
| PG33853 | 1322 | 1322 | 440 | 48735.80 | 7.71 | 1 |
| PG34217 | 1369 | 850 | 283 | 32166.62 | 5.34 | 2 |
| PG34234 | 6288 | 1383 | 332 | 36327.73 | 5.06 | 8 |
| PG35448 | 2902 | 1822 | 465 | 50902.75 | 6.82 | 8 |
| PG35697 | 4534 | 756 | 253 | 28024.07 | 5.90 | 6 |
| PG36060 | 4409 | 1197 | 400 | 45241.04 | 6.41 | 6 |
| PG36640 | 7402 | 697 | 233 | 24791.28 | 8.95 | 5 |
| PG37017 | 2118 | 925 | 308 | 34032.15 | 5.26 | 2 |
| PG37191 | 895 | 702 | 234 | 26237.53 | 9.11 | 3 |
| PG37222 | 3243 | 2280 | 531 | 58262.62 | 6.02 | 8 |
| PG37235 | 1328 | 1328 | 442 | 49024.07 | 5.23 | 1 |
| PG37305 | 2808 | 1221 | 268 | 29454.89 | 9.37 | 8 |
| PG37445 | 4452 | 1979 | 560 | 61870.21 | 8.55 | 9 |
| PG37838 | 7354 | 1284 | 329 | 36445.25 | 5.14 | 7 |
| PG37858 | 3775 | 1132 | 411 | 44757.30 | 6.09 | 5 |
| PG37971 | 2021 | 2021 | 673 | 74435.28 | 5.95 | 1 |
| PG38201 | 2876 | 1424 | 475 | 53925.21 | 5.19 | 4 |
| PG38302 | 7141 | 1850 | 598 | 66133.43 | 6.32 | 14 |
| PG38503 | 1301 | 1301 | 433 | 47791.97 | 5.56 | 1 |
| PG38504 | 1301 | 1301 | 433 | 47791.97 | 5.56 | 1 |
| PG38698 | 512 | 379 | 126 | 14162.51 | 10.16 | 2 |
| PG39433 | 4662 | 1405 | 337 | 37460.57 | 7.67 | 6 |

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|---|---|---|---|---|---|---|
| PG39516 | 1447 | 682 | 227 | 25446.89 | 8.44 | 2 |
| PG39699 | 2868 | 2281 | 514 | 56054.37 | 6.88 | 7 |
| PG39922 | 3897 | 1498 | 501 | 54326.05 | 8.60 | 8 |
| PG40693 | 1454 | 1454 | 484 | 53464.81 | 5.24 | 1 |
| PG40733 | 2544 | 1010 | 337 | 38736.24 | 6.89 | 4 |
| PG40819 | 2394 | 921 | 307 | 35035.73 | 5.66 | 3 |
| PG40879 | 1484 | 1484 | 494 | 53870.32 | 5.32 | 1 |
| PG40902 | 812 | 812 | 270 | 29945.83 | 7.90 | 1 |
| PG40922 | 8207 | 916 | 307 | 32985.48 | 7.15 | 8 |
| PG41655 | 1607 | 963 | 321 | 36685.69 | 5.96 | 3 |
| PG41742 | 1322 | 1322 | 440 | 48885.49 | 5.57 | 1 |
| PG41771 | 3591 | 2007 | 459 | 50744.02 | 6.25 | 9 |

**Table S3** Pfam results of 169 PGbHLHs.

| | Alignment start | Alignment end | hmm acc | hmm name | Type | Bit score | E-value |
|---|---|---|---|---|---|---|---|
| PG00183 | 259 | 309 | PF00010.24 | HLH | Domain | 48.4 | 6.20E-13 |
| PG00883 | 22 | 64 | PF00010.24 | HLH | Domain | 30.2 | 3.00E-07 |
| PG00933 | 312 | 357 | PF00010.24 | HLH | Domain | 39.9 | 2.70E-10 |
| PG00933 | 27 | 208 | PF14215.4 | bHLH-MYC_N | Family | 138.4 | 2.50E-40 |
| PG01029 | 14 | 48 | PF00010.24 | HLH | Domain | 22 | 0.0001 |
| PG01277 | 206 | 248 | PF00010.24 | HLH | Domain | 39.9 | 2.70E-10 |
| PG01478 | 341 | 384 | PF00010.24 | HLH | Domain | 36.8 | 2.50E-09 |
| PG01763 | 134 | 178 | PF00010.24 | HLH | Domain | 30 | 3.40E-07 |
| PG01888 | 137 | 184 | PF00010.24 | HLH | Domain | 30.2 | 3.00E-07 |
| PG02200 | 338 | 383 | PF00010.24 | HLH | Domain | 38 | 1.10E-09 |
| PG02335 | 241 | 286 | PF00010.24 | HLH | Domain | 40.2 | 2.10E-10 |
| PG02475 | 136 | 183 | PF00010.24 | HLH | Domain | 33.3 | 3.20E-08 |
| PG02883 | 364 | 411 | PF00010.24 | HLH | Domain | 26.3 | 4.70E-06 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| PG02930 | 75 | 121 | PF00010.24 | HLH | Domain | 36.1 | 4.20E-09 |
| PG03153 | 190 | 230 | PF00010.24 | HLH | Domain | 23.9 | 2.80E-05 |
| PG03239 | 176 | 215 | PF00010.24 | HLH | Domain | 23.1 | 4.70E-05 |
| PG03489 | 118 | 157 | PF00010.24 | HLH | Domain | 26.2 | 5.10E-06 |
| PG04363 | 242 | 288 | PF00010.24 | HLH | Domain | 41.1 | 1.20E-10 |
| PG04363 | 48 | 156 | PF14215.4 | bHLH-MYC_N | Family | 89.9 | 1.90E-25 |
| PG04535 | 147 | 190 | PF00010.24 | HLH | Domain | 33.2 | 3.50E-08 |
| PG04685 | 261 | 306 | PF00010.24 | HLH | Domain | 37.4 | 1.70E-09 |
| PG04790 | 125 | 170 | PF00010.24 | HLH | Domain | 49.8 | 2.20E-13 |
| PG05026 | 253 | 298 | PF00010.24 | HLH | Domain | 40.5 | 1.80E-10 |
| PG05026 | 26 | 185 | PF14215.4 | bHLH-MYC_N | Family | 143.9 | 5.10E-42 |
| PG05306 | 49 | 98 | PF00010.24 | HLH | Domain | 30.5 | 2.30E-07 |
| PG05437 | 216 | 260 | PF00010.24 | HLH | Domain | 40.8 | 1.40E-10 |
| PG05942 | 362 | 407 | PF00010.24 | HLH | Domain | 38.8 | 5.90E-10 |
| PG06292 | 140 | 191 | PF00010.24 | HLH | Domain | 47.1 | 1.50E-12 |
| PG06381 | 237 | 281 | PF00010.24 | HLH | Domain | 30.7 | 2.10E-07 |
| PG06438 | 315 | 360 | PF00010.24 | HLH | Domain | 40.2 | 2.20E-10 |
| PG06438 | 38 | 213 | PF14215.4 | bHLH-MYC_N | Family | 149.7 | 8.20E-44 |
| PG06642 | 285 | 333 | PF00010.24 | HLH | Domain | 30 | 3.30E-07 |
| PG06701 | 526 | 571 | PF00010.24 | HLH | Domain | 34.2 | 1.60E-08 |
| PG06701 | 18 | 130 | PF14215.4 | bHLH-MYC_N | Family | 85.1 | 6.00E-24 |
| PG06701 | 128 | 278 | PF14215.4 | bHLH-MYC_N | Family | 125.3 | 2.70E-36 |
| PG06793 | 463 | 509 | PF00010.24 | HLH | Domain | 50.7 | 1.20E-13 |
| PG07133 | 454 | 499 | PF00010.24 | HLH | Domain | 33.4 | 2.90E-08 |
| PG07133 | 17 | 206 | PF14215.4 | bHLH-MYC_N | Family | 153 | 8.40E-45 |
| PG07157 | 277 | 323 | PF00010.24 | HLH | Domain | 50.8 | 1.10E-13 |
| PG07173 | 156 | 203 | PF00010.24 | HLH | Domain | 41.3 | 1.00E-10 |
| PG07174 | 147 | 218 | PF00010.24 | HLH | Domain | 34.6 | 1.30E-08 |
| PG07175 | 198 | 244 | PF00010.24 | HLH | Domain | 41.9 | 6.40E-11 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| PG07247 | 204 | 255 | PF00010.24 | HLH | Domain | 49.8 | 2.20E-13 |
| PG07364 | 253 | 298 | PF00010.24 | HLH | Domain | 40.5 | 1.80E-10 |
| PG07364 | 26 | 185 | PF14215.4 | bHLH-MYC_N | Family | 142.3 | 1.50E-41 |
| PG07462 | 77 | 129 | PF00010.24 | HLH | Domain | 36.5 | 3.20E-09 |
| PG07481 | 433 | 479 | PF00010.24 | HLH | Domain | 39.7 | 3.20E-10 |
| PG07481 | 46 | 234 | PF14215.4 | bHLH-MYC_N | Family | 188.8 | 8.70E-56 |
| PG07666 | 252 | 303 | PF00010.24 | HLH | Domain | 37.6 | 1.40E-09 |
| PG07762 | 333 | 378 | PF00010.24 | HLH | Domain | 35.1 | 8.70E-09 |
| PG08342 | 431 | 477 | PF00010.24 | HLH | Domain | 39.7 | 3.20E-10 |
| PG08342 | 46 | 234 | PF14215.4 | bHLH-MYC_N | Family | 189.3 | 5.80E-56 |
| PG08366 | 348 | 391 | PF00010.24 | HLH | Domain | 39.1 | 5.00E-10 |
| PG08366 | 2 | 158 | PF14215.4 | bHLH-MYC_N | Family | 81.3 | 8.80E-23 |
| PG08551 | 109 | 135 | PF00010.24 | HLH | Domain | 28.6 | 9.10E-07 |
| PG08659 | 321 | 368 | PF00010.24 | HLH | Domain | 25.4 | 9.30E-06 |
| PG09058 | 154 | 205 | PF00010.24 | HLH | Domain | 40.1 | 2.30E-10 |
| PG09196 | 161 | 204 | PF00010.24 | HLH | Domain | 36.6 | 3.00E-09 |
| PG09666 | 320 | 366 | PF00010.24 | HLH | Domain | 37.1 | 2.00E-09 |
| PG09666 | 24 | 218 | PF14215.4 | bHLH-MYC_N | Family | 153.3 | 6.60E-45 |
| PG10212 | 245 | 284 | PF00010.24 | HLH | Domain | 35.7 | 5.50E-09 |
| PG10233 | 95 | 146 | PF00010.24 | HLH | Domain | 41.6 | 8.00E-11 |
| PG10428 | 159 | 206 | PF00010.24 | HLH | Domain | 30.9 | 1.70E-07 |
| PG11005 | 81 | 127 | PF00010.24 | HLH | Domain | 40.7 | 1.50E-10 |
| PG11234 | 139 | 183 | PF00010.24 | HLH | Domain | 29.9 | 3.70E-07 |
| PG11323 | 133 | 173 | PF00010.24 | HLH | Domain | 23 | 5.20E-05 |
| PG11934 | 120 | 171 | PF00010.24 | HLH | Domain | 37.9 | 1.10E-09 |
| PG11966 | 56 | 99 | PF00010.24 | HLH | Domain | 36.6 | 2.80E-09 |
| PG11971 | 307 | 352 | PF00010.24 | HLH | Domain | 49.3 | 3.30E-13 |
| PG12035 | 60 | 102 | PF00010.24 | HLH | Domain | 32.3 | 6.30E-08 |
| PG12278 | 320 | 366 | PF00010.24 | HLH | Domain | 37.1 | 2.00E-09 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| PG12278 | 24 | 218 | PF14215.4 | bHLH-MYC_N | Family | 153.4 | 6.00E-45 |
| PG12599 | 415 | 463 | PF00010.24 | HLH | Domain | 26.2 | 5.30E-06 |
| PG12618 | 383 | 428 | PF00010.24 | HLH | Domain | 30.4 | 2.50E-07 |
| PG13088 | 319 | 365 | PF00010.24 | HLH | Domain | 38.4 | 8.00E-10 |
| PG13088 | 24 | 216 | PF14215.4 | bHLH-MYC_N | Family | 154.8 | 2.40E-45 |
| PG13708 | 172 | 219 | PF00010.24 | HLH | Domain | 30.9 | 1.80E-07 |
| PG14023 | 306 | 352 | PF00010.24 | HLH | Domain | 50.7 | 1.10E-13 |
| PG14197 | 198 | 227 | PF00010.24 | HLH | Domain | 24.8 | 1.40E-05 |
| PG14512 | 21 | 63 | PF00010.24 | HLH | Domain | 23.1 | 4.70E-05 |
| PG14815 | 248 | 294 | PF00010.24 | HLH | Domain | 39.4 | 3.90E-10 |
| PG14815 | 22 | 181 | PF14215.4 | bHLH-MYC_N | Family | 137.2 | 5.90E-40 |
| PG15082 | 339 | 384 | PF00010.24 | HLH | Domain | 38.9 | 5.50E-10 |
| PG15345 | 20 | 61 | PF00010.24 | HLH | Domain | 22.6 | 6.80E-05 |
| PG15509 | 310 | 353 | PF00010.24 | HLH | Domain | 36.7 | 2.70E-09 |
| PG16018 | 95 | 146 | PF00010.24 | HLH | Domain | 41.6 | 8.00E-11 |
| PG16210 | 202 | 242 | PF00010.24 | HLH | Domain | 32.8 | 4.40E-08 |
| PG16376 | 324 | 367 | PF00010.24 | HLH | Domain | 36.7 | 2.80E-09 |
| PG16383 | 174 | 213 | PF00010.24 | HLH | Domain | 25.6 | 8.20E-06 |
| PG16916 | 131 | 182 | PF00010.24 | HLH | Domain | 39.5 | 3.50E-10 |
| PG17327 | 343 | 383 | PF00010.24 | HLH | Domain | 23.4 | 4.00E-05 |
| PG17916 | 117 | 163 | PF00010.24 | HLH | Domain | 45.1 | 6.30E-12 |
| PG18500 | 148 | 191 | PF00010.24 | HLH | Domain | 37.4 | 1.70E-09 |
| PG18520 | 102 | 153 | PF00010.24 | HLH | Domain | 40.7 | 1.50E-10 |
| PG18523 | 471 | 516 | PF00010.24 | HLH | Domain | 39.5 | 3.70E-10 |
| PG18523 | 55 | 237 | PF14215.4 | bHLH-MYC_N | Family | 193.2 | 3.80E-57 |
| PG18773 | 125 | 170 | PF00010.24 | HLH | Domain | 49.8 | 2.20E-13 |
| PG18879 | 140 | 165 | PF00010.24 | HLH | Domain | 26.4 | 4.50E-06 |
| PG18931 | 146 | 189 | PF00010.24 | HLH | Domain | 32.8 | 4.70E-08 |
| PG19462 | 431 | 477 | PF00010.24 | HLH | Domain | 39.6 | 3.30E-10 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| PG19462 | 46 | 234 | PF14215.4 | bHLH-MYC_N | Family | 188.6 | 9.60E-56 |
| PG19765 | 295 | 338 | PF00010.24 | HLH | Domain | 37.6 | 1.50E-09 |
| PG20047 | 82 | 127 | PF00010.24 | HLH | Domain | 39.5 | 3.80E-10 |
| PG20127 | 120 | 171 | PF00010.24 | HLH | Domain | 42.8 | 3.40E-11 |
| PG20810 | 122 | 173 | PF00010.24 | HLH | Domain | 47 | 1.60E-12 |
| PG21026 | 268 | 313 | PF00010.24 | HLH | Domain | 41.3 | 1.00E-10 |
| PG21026 | 32 | 188 | PF14215.4 | bHLH-MYC_N | Family | 138.6 | 2.20E-40 |
| PG21048 | 89 | 135 | PF00010.24 | HLH | Domain | 38.3 | 8.90E-10 |
| PG21441 | 134 | 178 | PF00010.24 | HLH | Domain | 30 | 3.30E-07 |
| PG21758 | 111 | 164 | PF00010.24 | HLH | Domain | 27.7 | 1.70E-06 |
| PG22215 | 287 | 331 | PF00010.24 | HLH | Domain | 38.9 | 5.60E-10 |
| PG22741 | 30 | 79 | PF00010.24 | HLH | Domain | 26 | 5.90E-06 |
| PG22897 | 142 | 181 | PF00010.24 | HLH | Domain | 26.2 | 5.10E-06 |
| PG23736 | 138 | 185 | PF00010.24 | HLH | Domain | 33.2 | 3.30E-08 |
| PG23826 | 156 | 203 | PF00010.24 | HLH | Domain | 41.1 | 1.20E-10 |
| PG24302 | 271 | 316 | PF00010.24 | HLH | Domain | 40.4 | 1.90E-10 |
| PG24302 | 44 | 203 | PF14215.4 | bHLH-MYC_N | Family | 135.8 | 1.60E-39 |
| PG24323 | 159 | 206 | PF00010.24 | HLH | Domain | 26.3 | 4.80E-06 |
| PG25084 | 47 | 96 | PF00010.24 | HLH | Domain | 30.5 | 2.30E-07 |
| PG25232 | 336 | 381 | PF00010.24 | HLH | Domain | 35.1 | 8.80E-09 |
| PG25335 | 257 | 305 | PF00010.24 | HLH | Domain | 30 | 3.30E-07 |
| PG25345 | 243 | 289 | PF00010.24 | HLH | Domain | 47.8 | 9.20E-13 |
| PG25389 | 122 | 173 | PF00010.24 | HLH | Domain | 47.7 | 9.90E-13 |
| PG25512 | 380 | 425 | PF00010.24 | HLH | Domain | 30.7 | 2.00E-07 |
| PG25659 | 490 | 535 | PF00010.24 | HLH | Domain | 33 | 4.00E-08 |
| PG25659 | 69 | 255 | PF14215.4 | bHLH-MYC_N | Family | 190 | 3.50E-56 |
| PG25699 | 324 | 367 | PF00010.24 | HLH | Domain | 36.7 | 2.80E-09 |
| PG26053 | 202 | 248 | PF00010.24 | HLH | Domain | 41.6 | 8.30E-11 |
| PG26053 | 380 | 426 | PF00010.24 | HLH | Domain | 41.6 | 8.30E-11 |

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|---|---|---|---|---|---|---|---|
| PG26263 | 219 | 266 | PF00010.24 | HLH | Domain | 39.4 | 3.90E-10 |
| PG26263 | 446 | 493 | PF00010.24 | HLH | Domain | 39.4 | 3.90E-10 |
| PG26263 | 744 | 791 | PF00010.24 | HLH | Domain | 39.4 | 3.90E-10 |
| PG26507 | 167 | 212 | PF00010.24 | HLH | Domain | 48.3 | 6.30E-13 |
| PG26994 | 41 | 83 | PF00010.24 | HLH | Domain | 33.5 | 2.70E-08 |
| PG27139 | 131 | 170 | PF00010.24 | HLH | Domain | 26.2 | 5.30E-06 |
| PG27219 | 44 | 92 | PF00010.24 | HLH | Domain | 40.7 | 1.60E-10 |
| PG27746 | 78 | 130 | PF00010.24 | HLH | Domain | 36.8 | 2.50E-09 |
| PG27847 | 22 | 64 | PF00010.24 | HLH | Domain | 29.8 | 3.80E-07 |
| PG27901 | 74 | 124 | PF00010.24 | HLH | Domain | 43.1 | 2.70E-11 |
| PG28173 | 285 | 331 | PF00010.24 | HLH | Domain | 40.8 | 1.40E-10 |
| PG28173 | 48 | 202 | PF14215.4 | bHLH-MYC_N | Family | 128 | 3.90E-37 |
| PG28660 | 117 | 163 | PF00010.24 | HLH | Domain | 45.1 | 6.30E-12 |
| PG29408 | 291 | 334 | PF00010.24 | HLH | Domain | 39.3 | 4.10E-10 |
| PG29408 | 3 | 44 | PF14215.4 | bHLH-MYC_N | Family | 30.9 | 2.60E-07 |
| PG29620 | 181 | 227 | PF00010.24 | HLH | Domain | 42.6 | 4.10E-11 |
| PG29658 | 57 | 110 | PF00010.24 | HLH | Domain | 37.1 | 2.10E-09 |
| PG29796 | 574 | 622 | PF00010.24 | HLH | Domain | 25.8 | 7.00E-06 |
| PG30366 | 309 | 352 | PF00010.24 | HLH | Domain | 34.8 | 1.10E-08 |
| PG30998 | 20 | 61 | PF00010.24 | HLH | Domain | 25.5 | 8.80E-06 |
| PG30999 | 20 | 61 | PF00010.24 | HLH | Domain | 25.5 | 8.80E-06 |
| PG32606 | 21 | 63 | PF00010.24 | HLH | Domain | 23.1 | 4.70E-05 |
| PG32671 | 102 | 153 | PF00010.24 | HLH | Domain | 41.8 | 6.90E-11 |
| PG32830 | 366 | 409 | PF00010.24 | HLH | Domain | 36.7 | 2.60E-09 |
| PG32841 | 164 | 203 | PF00010.24 | HLH | Domain | 25.6 | 7.90E-06 |
| PG32851 | 415 | 463 | PF00010.24 | HLH | Domain | 26.2 | 5.30E-06 |
| PG32981 | 162 | 205 | PF00010.24 | HLH | Domain | 35.8 | 5.20E-09 |
| PG33143 | 75 | 121 | PF00010.24 | HLH | Domain | 39.6 | 3.40E-10 |
| PG33184 | 154 | 205 | PF00010.24 | HLH | Domain | 41.2 | 1.10E-10 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| PG33513 | 434 | 480 | PF00010.24 | HLH | Domain | 39.7 | 3.10E-10 |
| PG33513 | 46 | 234 | PF14215.4 | bHLH-MYC_N | Family | 190.5 | 2.40E-56 |
| PG33622 | 215 | 254 | PF00010.24 | HLH | Domain | 31.7 | 1.00E-07 |
| PG33853 | 345 | 385 | PF00010.24 | HLH | Domain | 23.3 | 4.00E-05 |
| PG34217 | 164 | 208 | PF00010.24 | HLH | Domain | 25.1 | 1.10E-05 |
| PG34234 | 44 | 92 | PF00010.24 | HLH | Domain | 40.7 | 1.60E-10 |
| PG35448 | 275 | 322 | PF00010.24 | HLH | Domain | 25.9 | 6.20E-06 |
| PG35697 | 136 | 183 | PF00010.24 | HLH | Domain | 33.3 | 3.20E-08 |
| PG36060 | 181 | 228 | PF00010.24 | HLH | Domain | 30.7 | 2.10E-07 |
| PG36640 | 139 | 183 | PF00010.24 | HLH | Domain | 30.3 | 2.60E-07 |
| PG37017 | 121 | 167 | PF00010.24 | HLH | Domain | 44.8 | 8.20E-12 |
| PG37191 | 198 | 224 | PF00010.24 | HLH | Domain | 22.9 | 5.80E-05 |
| PG37222 | 342 | 389 | PF00010.24 | HLH | Domain | 26.6 | 3.80E-06 |
| PG37235 | 254 | 299 | PF00010.24 | HLH | Domain | 43.1 | 2.70E-11 |
| PG37235 | 25 | 185 | PF14215.4 | bHLH-MYC_N | Family | 136.3 | 1.10E-39 |
| PG37305 | 189 | 234 | PF00010.24 | HLH | Domain | 26.1 | 5.50E-06 |
| PG37445 | 340 | 387 | PF00010.24 | HLH | Domain | 25.6 | 8.00E-06 |
| PG37838 | 43 | 92 | PF00010.24 | HLH | Domain | 52.8 | 2.50E-14 |
| PG37858 | 329 | 375 | PF00010.24 | HLH | Domain | 51.1 | 8.50E-14 |
| PG37971 | 493 | 538 | PF00010.24 | HLH | Domain | 33 | 4.00E-08 |
| PG37971 | 68 | 254 | PF14215.4 | bHLH-MYC_N | Family | 189.2 | 6.40E-56 |
| PG38201 | 252 | 299 | PF00010.24 | HLH | Domain | 44.9 | 7.40E-12 |
| PG38302 | 317 | 365 | PF00010.24 | HLH | Domain | 29.5 | 4.90E-07 |
| PG38302 | 460 | 508 | PF00010.24 | HLH | Domain | 29.5 | 4.90E-07 |
| PG38503 | 252 | 297 | PF00010.24 | HLH | Domain | 41.4 | 9.50E-11 |
| PG38503 | 25 | 184 | PF14215.4 | bHLH-MYC_N | Family | 136.8 | 7.80E-40 |
| PG38504 | 252 | 297 | PF00010.24 | HLH | Domain | 41.4 | 9.50E-11 |
| PG38504 | 25 | 184 | PF14215.4 | bHLH-MYC_N | Family | 136.8 | 7.80E-40 |
| PG38698 | 4 | 57 | PF00010.24 | HLH | Domain | 48.1 | 7.50E-13 |

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|---|---|---|---|---|---|---|---|
| PG39433 | 49 | 98 | PF00010.24 | HLH | Domain | 31.6 | 1.00E-07 |
| PG39516 | 61 | 111 | PF00010.24 | HLH | Domain | 43.3 | 2.40E-11 |
| PG39699 | 364 | 411 | PF00010.24 | HLH | Domain | 26.3 | 4.70E-06 |
| PG39922 | 308 | 355 | PF00010.24 | HLH | Domain | 25.1 | 1.10E-05 |
| PG40693 | 309 | 354 | PF00010.24 | HLH | Domain | 39.9 | 2.70E-10 |
| PG40693 | 27 | 208 | PF14215.4 | bHLH-MYC_N | Family | 139.2 | 1.40E-40 |
| PG40733 | 131 | 176 | PF00010.24 | HLH | Domain | 40.1 | 2.40E-10 |
| PG40819 | 120 | 171 | PF00010.24 | HLH | Domain | 43 | 3.00E-11 |
| PG40879 | 311 | 356 | PF00010.24 | HLH | Domain | 40.3 | 2.10E-10 |
| PG40879 | 34 | 209 | PF14215.4 | bHLH-MYC_N | Family | 149.8 | 7.80E-44 |
| PG40902 | 174 | 213 | PF00010.24 | HLH | Domain | 25.6 | 8.20E-06 |
| PG40922 | 158 | 202 | PF00010.24 | HLH | Domain | 30.5 | 2.30E-07 |
| PG41655 | 147 | 194 | PF00010.24 | HLH | Domain | 49.1 | 3.80E-13 |
| PG41742 | 355 | 395 | PF00010.24 | HLH | Domain | 21.6 | 0.00014 |
| PG41771 | 257 | 305 | PF00010.24 | HLH | Domain | 30 | 3.40E-07 |

**Table S4** Amino acid sequences and features of 20 conserved motifs in *P. ginseng* bHLH protein**s.**

| Motif No. | Sequence | E-value | Sites | Width |
|---|---|---|---|---|
| 1 | ERRRREKJNERLYAL | 3.5e-1092 | 150 | 15 |
| 2 | KKMDKASMLDEAINYIKELQQQVQFLEMK | 1.7e-1788 | 145 | 29 |
| 3 | IRIQCPKRPGLLLKLMKALEELELDILHA | 2.4e-543 | 73 | 29 |
| 4 | PKDYIHVRARRGQATDSHSJA | 1.4e-478 | 37 | 21 |
| 5 | HGIQTFVCIPTCSGVLELGSTITISENWSLVQQAKSLFGSD | 9.4e-435 | 24 | 41 |
| 6 | PVVEKKRAPRKRGRKPANGREEPLNHVEA | 3E-257 | 18 | 29 |
| 7 | DAAVDGDVTDAEWFYLVSMTRSFPAGDGS | 7E-265 | 24 | 29 |
| 8 | ESWSYAIFWQTSKDS | 6E-182 | 26 | 15 |
| 9 | KAFSSGAHVWLSGTDQLQSAECERAKEAQ | 2E-238 | 20 | 29 |
| 10 | LVLSWGDGHFRGTTKHET | 6E-157 | 24 | 18 |

| | | | | |
|---|---|---|---|---|
| 11 | RSLVPN | 1E-151 | 149 | 6 |
| 12 | ATPPGSSITPTSSFHPLTPTPPTLPHRVKEELCPSALPSPKNPSARVEVR | 1E-148 | 9 | 50 |
| 13 | AVADVEVKMVGSDAM | 3E-145 | 32 | 15 |
| 14 | VQGGKKKRRRPKSKKNKEEIENQRMTHIA | 1E-129 | 11 | 29 |
| 15 | LATVNPRLDFNIEGLLSKDI | 1E-115 | 18 | 20 |
| 16 | PTLQQRLQYIVESQP | 1E-94 | 17 | 15 |
| 17 | VISCFNGFALDIFRAEQCREG | 1.1E-89 | 10 | 21 |
| 18 | MKEMIFRIAAMQPVNJGPESVKPPKRRNV | 2.4E-97 | 9 | 29 |
| 19 | YFSSGWDPLVSLSQSENFGAHNGFSNPAYPVVTENQVISTTSHLAHYQPD | 7.4E-89 | 6 | 50 |
| 20 | SVVNEJMLQDVVIKV | 1.4E-83 | 18 | 15 |

**Table S5** FPKM values of all genes among 21 RNA-Seq databases (see excel).

**Table S6** Pearson's correlation coefficient between the PGbHLH expression of MeJA-up-regulated PGbHLHs and ginsenoside contents in different tissues of *P. ginseng* main roots.

| | Rg1 | | Re | | Rf | | Rb1 | | Rc | | Rb2 | | Rd |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | cor | p-value | cor | p-value | cor | p-value | cor | p-value | cor | p-value | cor | p-value | cor |
| PG40693 | 0.8789 | 0.00181 | 0.9731 | 0.00001 | 0.9209 | 0.00042 | 0.9465 | 0.00011 | 0.9825 | 0.00000 | 0.9749 | 0.00001 | 0.967 |
| PG00933 | −0.2360 | 0.54107 | −0.1832 | 0.63712 | −0.2341 | 0.54444 | −0.2240 | 0.56228 | −0.1849 | 0.63385 | −0.1940 | 0.61692 | −0.201 |
| PG05026 | −0.2323 | 0.54762 | −0.1452 | 0.70938 | −0.1963 | 0.61265 | −0.1999 | 0.60612 | −0.1311 | 0.73677 | −0.1499 | 0.70031 | −0.133 |
| PG07364 | −0.4042 | 0.28058 | −0.3951 | 0.29263 | −0.4807 | 0.19026 | −0.4427 | 0.23278 | −0.4034 | 0.28160 | −0.4221 | 0.25776 | −0.448 |
| PG26994 | 0.8646 | 0.00263 | 0.9112 | 0.00063 | 0.9787 | 0.00000 | 0.9232 | 0.00038 | 0.8997 | 0.00095 | 0.9280 | 0.00031 | 0.923 |
| PG19462 | 0.8203 | 0.00676 | 0.8947 | 0.00112 | 0.8492 | 0.00377 | 0.8797 | 0.00176 | 0.8850 | 0.00151 | 0.8901 | 0.00130 | 0.850 |
| PG38698 | −0.0641 | 0.86987 | −0.3208 | 0.39992 | −0.2208 | 0.56806 | −0.2197 | 0.57004 | −0.3009 | 0.43147 | −0.3088 | 0.41884 | −0.249 |
| PG29620 | 0.8629 | 0.00274 | 0.8789 | 0.00180 | 0.7424 | 0.02197 | 0.8562 | 0.00322 | 0.8620 | 0.00280 | 0.8477 | 0.00390 | 0.774 |
| PG06701 | 0.7917 | 0.01100 | 0.8762 | 0.00195 | 0.8961 | 0.00107 | 0.8556 | 0.00326 | 0.8494 | 0.00376 | 0.8773 | 0.00188 | 0.840 |
| PG21048 | −0.4947 | 0.17578 | −0.4681 | 0.20379 | −0.4903 | 0.18029 | −0.5125 | 0.15833 | −0.4758 | 0.19544 | −0.4821 | 0.18872 | −0.484 |
| PG07133 | −0.4365 | 0.24017 | −0.2298 | 0.55202 | −0.2220 | 0.56585 | −0.3042 | 0.42620 | −0.2187 | 0.57179 | −0.2125 | 0.58305 | −0.186 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PG08342 | -0.6483 | 0.05896 | -0.4856 | 0.18509 | -0.5330 | 0.13948 | -0.5619 | 0.11539 | -0.4771 | 0.19405 | -0.4856 | 0.18511 | -0.479 |
| PG07173 | 0.6911 | 0.03923 | 0.8371 | 0.00488 | 0.8227 | 0.00646 | 0.8061 | 0.00870 | 0.8868 | 0.00143 | 0.8650 | 0.00260 | 0.930 |
| PG24302 | 0.5206 | 0.15074 | 0.5417 | 0.13195 | 0.6355 | 0.06587 | 0.5424 | 0.13134 | 0.4926 | 0.17791 | 0.5434 | 0.13053 | 0.498 |

**Table S7** Pearson's correlation coefficient between the expression levels of selected PGbHLHs and those of ginsenoside biosynthesis enzymes in 21 RNA-Seq databases.

| | PG40693 | | PG26994 | | PG19462 | | PG29620 | | PG06701 | | PG07173 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Enzymes | cor | p-value | cor | p-value | cor | p-value | cor | p-value | cor | p-value | cor |
| ACTT | 0.97195 | 0 | 0.00885 | 0.96964 | 0.81585 | 0.00001 | 0.15715 | 0.49631 | 0.13416 | 0.56206 | 0.53612 |
| HMGS1 | 0.94998 | 0 | -0.0587 | 0.80048 | 0.84341 | 0 | 0.07329 | 0.75223 | 0.08253 | 0.7221 | 0.61502 |
| HMGS2 | 0.98674 | 0 | -0.11352 | 0.62416 | 0.80975 | 0.00001 | 0.12092 | 0.60158 | 0.09006 | 0.69785 | 0.50336 |
| HMGS3 | -0.23623 | 0.30258 | -0.12242 | 0.59705 | 0.02626 | 0.91006 | 0.3599 | 0.10904 | -0.47818 | 0.02833 | 0.02635 |
| HMGR1 | 0.98177 | 0 | -0.07759 | 0.73816 | 0.77024 | 0.00004 | 0.18006 | 0.43478 | 0.18458 | 0.42316 | 0.46923 |
| HMGR2 | 0.96428 | 0 | -0.1434 | 0.53518 | 0.69248 | 0.0005 | 0.13482 | 0.56012 | 0.14438 | 0.53237 | 0.38929 |
| HMGR3 | -0.10042 | 0.66495 | -0.34859 | 0.12146 | 0.03204 | 0.89033 | 0.07063 | 0.76094 | -0.68678 | 0.00058 | -0.20234 |
| HMGR4 | 0.16326 | 0.4795 | 0.11185 | 0.6293 | 0.22142 | 0.33476 | 0.22955 | 0.31684 | -0.12314 | 0.59487 | 0.38087 |
| HMGR5 | 0.27818 | 0.22209 | -0.30959 | 0.17204 | 0.00072 | 0.99754 | 0.10251 | 0.65838 | -0.27479 | 0.228 | -0.03736 |
| HMGR6 | 0.32625 | 0.14892 | -0.09463 | 0.68327 | 0.11497 | 0.61971 | 0.05749 | 0.80449 | -0.08019 | 0.72971 | 0.14219 |
| HMGR7 | -0.07738 | 0.73885 | -0.19173 | 0.40508 | -0.2709 | 0.23493 | -0.12857 | 0.57861 | -0.17027 | 0.46056 | -0.22363 |
| HMGR8 | -0.0538 | 0.81683 | -0.21223 | 0.3557 | -0.28342 | 0.21313 | -0.1401 | 0.54471 | -0.1916 | 0.40539 | -0.20238 |
| MVK1 | 0.74464 | 0.00011 | 0.2162 | 0.34656 | 0.71127 | 0.0003 | 0.29595 | 0.19272 | 0.36856 | 0.10018 | 0.69869 |
| MVK2 | 0.2362 | 0.30264 | 0.05523 | 0.81206 | 0.26224 | 0.25081 | 0.44781 | 0.04178 | 0.10686 | 0.64477 | 0.29937 |
| PMK1 | 0.65996 | 0.00113 | -0.22775 | 0.32076 | 0.4919 | 0.02351 | 0.45751 | 0.03704 | -0.10141 | 0.66184 | 0.06441 |
| PMK2 | -0.15954 | 0.48971 | 0.18814 | 0.41411 | -0.14311 | 0.536 | 0.04851 | 0.83458 | 0.11645 | 0.61519 | -0.12736 |
| PMK3 | -0.24927 | 0.27586 | -0.18984 | 0.4098 | -0.1759 | 0.44564 | 0.44626 | 0.04258 | -0.23495 | 0.30527 | -0.36513 |
| PMK4 | -0.27949 | 0.21982 | -0.29372 | 0.19624 | -0.21009 | 0.36069 | 0.18986 | 0.40976 | -0.39553 | 0.07594 | -0.41617 |
| MVD1 | 0.03262 | 0.88837 | 0.14634 | 0.52676 | 0.27586 | 0.22612 | -0.22748 | 0.32135 | -0.03751 | 0.87176 | 0.40505 |
| MVD2 | 0.26388 | 0.24774 | -0.07724 | 0.7393 | 0.14436 | 0.53243 | -0.22497 | 0.32685 | -0.07765 | 0.73795 | 0.21392 |
| IDI1 | 0.2519 | 0.27066 | 0.24695 | 0.28051 | 0.09634 | 0.67784 | -0.17373 | 0.45138 | 0.21593 | 0.34719 | 0.14077 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| IDI2 | -0.02055 | 0.92955 | 0.25809 | 0.25866 | -0.03663 | 0.87476 | -0.2503 | 0.27381 | 0.13498 | 0.55964 | 0.18486 |
| FPS1 | 0.8692 | 0 | 0.01391 | 0.95227 | 0.65472 | 0.00128 | 0.03034 | 0.89614 | 0.18175 | 0.43042 | 0.54114 |
| FPS2 | 0.75974 | 0.00006 | -0.05511 | 0.81247 | 0.71045 | 0.00031 | 0.00947 | 0.96752 | -0.00872 | 0.97008 | 0.67014 |
| SS1 | 0.90737 | 0 | -0.02738 | 0.90621 | 0.59652 | 0.00431 | 0.04692 | 0.83994 | 0.30423 | 0.17997 | 0.4101 |
| SS2 | 0.87853 | 0 | 0.04652 | 0.84131 | 0.55005 | 0.00978 | 0.16584 | 0.47248 | 0.35361 | 0.11583 | 0.39222 |
| SS3 | 0.89479 | 0 | -0.25293 | 0.26864 | 0.62061 | 0.00268 | 0.16397 | 0.47757 | -0.02091 | 0.92832 | 0.25051 |
| SS4 | 0.18525 | 0.42144 | -0.31523 | 0.16396 | 0.05349 | 0.81789 | 0.38723 | 0.08287 | -0.27658 | 0.22487 | -0.25905 |
| SE1 | 0.66523 | 0.001 | 0.01771 | 0.93928 | 0.62012 | 0.00271 | 0.29615 | 0.19241 | 0.10595 | 0.6476 | 0.27367 |
| SE2 | 0.3157 | 0.16329 | -0.13139 | 0.57024 | 0.37699 | 0.09207 | 0.35647 | 0.11271 | -0.10054 | 0.66456 | 0.14262 |
| SE3 | 0.94664 | 0 | -0.12218 | 0.59778 | 0.7058 | 0.00035 | 0.23238 | 0.31074 | 0.1059 | 0.64777 | 0.38891 |
| SE4 | -0.16915 | 0.46357 | -0.38165 | 0.08779 | -0.14093 | 0.5423 | -0.18869 | 0.4127 | -0.35158 | 0.11808 | -0.39188 |
| β.AS2 | -0.0665 | 0.77456 | -0.18403 | 0.42457 | -0.18445 | 0.42348 | -0.10927 | 0.63729 | -0.13995 | 0.54513 | -0.1965 |
| β.AS3 | -0.28337 | 0.21322 | -0.16366 | 0.4784 | -0.08849 | 0.70287 | 0.44837 | 0.0415 | -0.30006 | 0.18633 | -0.37799 |
| β.AS4 | -0.13088 | 0.57174 | 0.52524 | 0.01448 | 0.04125 | 0.8591 | 0.63782 | 0.00187 | 0.27979 | 0.21932 | 0.15806 |
| β.AS5 | -0.17172 | 0.45671 | 0.06166 | 0.79062 | -0.09817 | 0.67203 | 0.23073 | 0.31429 | 0.0686 | 0.76765 | -0.1063 |
| DDS1 | 0.97618 | 0 | -0.10974 | 0.63583 | 0.71541 | 0.00027 | 0.15306 | 0.50773 | 0.15462 | 0.50337 | 0.40681 |
| DDS2 | 0.94813 | 0 | -0.04218 | 0.85595 | 0.69126 | 0.00052 | 0.18274 | 0.42785 | 0.25938 | 0.2562 | 0.44514 |
| DDS3 | -0.14553 | 0.52906 | -0.34132 | 0.12996 | -0.17728 | 0.44202 | -0.09342 | 0.6871 | -0.3522 | 0.1174 | -0.3636 |
| LAS1 | -0.13135 | 0.57037 | -0.24132 | 0.29197 | -0.10918 | 0.63758 | -0.08195 | 0.72397 | -0.30266 | 0.18235 | -0.3226 |
| LAS2 | -0.22772 | 0.32083 | 0.1766 | 0.44382 | -0.18893 | 0.4121 | 0.12247 | 0.5969 | 0.27452 | 0.22848 | -0.06436 |
| CAS1 | 0.34467 | 0.126 | -0.18214 | 0.4294 | 0.27711 | 0.22394 | 0.53625 | 0.01221 | -0.17614 | 0.44501 | 0.01263 |
| CAS2 | -0.25929 | 0.25637 | 0.00955 | 0.96722 | -0.17351 | 0.45196 | 0.5573 | 0.00868 | 0.01057 | 0.96372 | -0.27017 |
| CAS3 | 0.0026 | 0.99109 | 0.00645 | 0.97785 | 0.02668 | 0.9086 | 0.6314 | 0.00214 | -0.13455 | 0.56091 | -0.03565 |
| PPDS1 | 0.97672 | 0 | -0.1214 | 0.60014 | 0.75154 | 0.00009 | 0.17944 | 0.4364 | 0.07953 | 0.73185 | 0.4016 |
| PPDS2 | 0.97221 | 0 | -0.11372 | 0.62354 | 0.76157 | 0.00006 | 0.19012 | 0.4091 | 0.08197 | 0.72392 | 0.41394 |
| PPTS1 | -0.05173 | 0.82378 | 0.04543 | 0.84498 | -0.00952 | 0.96735 | 0.65588 | 0.00125 | -0.0818 | 0.72447 | -0.25819 |
| PPTS2 | -0.29353 | 0.19656 | 0.09737 | 0.67458 | -0.11023 | 0.6343 | 0.35561 | 0.11364 | -0.09131 | 0.69385 | -0.13278 |
| OAS1 | -0.00183 | 0.99371 | -0.08806 | 0.70425 | 0.49585 | 0.02226 | 0.14777 | 0.52267 | -0.45975 | 0.036 | 0.47696 |
| OAS2 | 0.83095 | 0 | -0.16554 | 0.47329 | 0.78587 | 0.00002 | 0.19379 | 0.39995 | -0.10028 | 0.6654 | 0.42056 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| OAS3 | -0.11002 | 0.63495 | 0.0976 | 0.67383 | 0.18404 | 0.42453 | 0.74747 | 0.0001 | -0.07939 | 0.7323 | 0.02493 |
| DXS1 | 0.98679 | 0 | -0.14204 | 0.53909 | 0.72148 | 0.00022 | 0.14101 | 0.54208 | 0.09959 | 0.66756 | 0.37968 |
| DXS2 | 0.11461 | 0.62081 | 0.5811 | 0.00573 | -0.10505 | 0.65041 | -0.13913 | 0.54753 | 0.72876 | 0.00018 | 0.19008 |
| DXS3 | -0.11963 | 0.60552 | -0.05621 | 0.80877 | -0.42126 | 0.05719 | -0.2513 | 0.27183 | 0.40679 | 0.06724 | -0.09203 |
| DXS4 | -0.22256 | 0.3322 | -0.11959 | 0.60564 | 0.20277 | 0.37805 | 0.05723 | 0.80538 | -0.47828 | 0.0283 | 0.11993 |
| DXS5 | -0.18648 | 0.41831 | -0.10646 | 0.64602 | 0.11923 | 0.6067 | -0.13347 | 0.56409 | -0.40747 | 0.06674 | 0.16894 |
| DXS6 | -0.20908 | 0.36306 | 0.1989 | 0.38739 | -0.16657 | 0.4705 | 0.42693 | 0.05359 | -0.15262 | 0.50897 | -0.04648 |
| DXS7 | -0.18324 | 0.42658 | -0.10829 | 0.64034 | -0.01762 | 0.93958 | 0.33954 | 0.13211 | -0.37901 | 0.09019 | -0.25502 |
| DXS8 | -0.09905 | 0.66928 | -0.06697 | 0.77303 | -0.2513 | 0.27184 | 0.00612 | 0.979 | 0.29943 | 0.18729 | -0.12889 |
| DXS9 | -0.19552 | 0.39567 | 0.09503 | 0.68199 | -0.11485 | 0.62009 | 0.12845 | 0.57898 | 0.31809 | 0.15996 | 0.04593 |
| DXR1 | 0.6009 | 0.00397 | 0.15243 | 0.5095 | 0.25455 | 0.26549 | 0.0009 | 0.99689 | 0.42617 | 0.05406 | 0.23479 |
| DXR2 | 0.77856 | 0.00003 | 0.1296 | 0.57555 | 0.42663 | 0.05377 | 0.03806 | 0.86991 | 0.4953 | 0.02243 | 0.36911 |
| DXR3 | 0.43579 | 0.04829 | -0.17668 | 0.44361 | 0.58453 | 0.00539 | 0.46206 | 0.03496 | -0.20314 | 0.37714 | 0.08741 |
| DXR4 | -0.09532 | 0.68107 | 0.19505 | 0.39685 | 0.44288 | 0.04436 | 0.04002 | 0.86324 | -0.28567 | 0.20937 | 0.30592 |
| IspD1 | 0.0145 | 0.95026 | -0.07803 | 0.73671 | -0.19793 | 0.38976 | 0.37207 | 0.09673 | -0.01776 | 0.93908 | -0.40962 |
| IspD2 | -0.08174 | 0.72466 | 0.08678 | 0.70838 | -0.40109 | 0.07155 | -0.03674 | 0.87436 | 0.19069 | 0.40767 | -0.22365 |
| IspE1 | 0.26585 | 0.2441 | -0.25419 | 0.26618 | 0.08768 | 0.70549 | 0.1037 | 0.65463 | 0.1765 | 0.44406 | -0.16957 |
| IspE2 | -0.08078 | 0.72777 | 0.14573 | 0.52848 | -0.18488 | 0.42238 | -0.35547 | 0.11379 | 0.27694 | 0.22424 | 0.14221 |
| IspF1 | 0.5638 | 0.00777 | 0.27159 | 0.23369 | 0.53915 | 0.01166 | -0.15281 | 0.50844 | 0.3521 | 0.11751 | 0.71463 |
| IspF2 | 0.54933 | 0.0099 | 0.25879 | 0.25732 | 0.50236 | 0.0203 | -0.15446 | 0.5038 | 0.40539 | 0.06828 | 0.61515 |
| IspF3 | -0.04166 | 0.85769 | 0.34923 | 0.12074 | 0.11732 | 0.61252 | -0.30988 | 0.17162 | 0.24328 | 0.28793 | 0.41224 |
| IspF4 | -0.05563 | 0.81071 | 0.25842 | 0.25803 | -0.2384 | 0.29801 | -0.26381 | 0.24787 | 0.55649 | 0.00879 | 0.05019 |
| IspF5 | -0.11702 | 0.61344 | 0.10533 | 0.64953 | -0.21591 | 0.34723 | -0.32713 | 0.14776 | 0.50223 | 0.02033 | 0.08142 |
| IspG.gcpE1 | 0.37411 | 0.09477 | 0.081 | 0.72707 | 0.08728 | 0.70677 | 0.01189 | 0.95921 | 0.77043 | 0.00004 | 0.25393 |
| IspG.gcpE2 | 0.43695 | 0.04764 | 0.22622 | 0.3241 | 0.1715 | 0.45728 | 0.04673 | 0.8406 | 0.77402 | 0.00004 | 0.30298 |
| IspG.gcpE3 | 0.43962 | 0.04614 | 0.00114 | 0.9961 | 0.22864 | 0.31881 | 0.22654 | 0.32341 | 0.54202 | 0.01114 | 0.19201 |
| IspG.gcpE4 | -0.1796 | 0.43599 | 0.36568 | 0.10306 | -0.35153 | 0.11814 | 0.27886 | 0.22092 | 0.64182 | 0.00171 | -0.10302 |
| IspH1 | 0.89373 | 0 | 0.13214 | 0.56802 | 0.64542 | 0.00158 | 0.16597 | 0.47213 | 0.45318 | 0.0391 | 0.44205 |
| IspH2 | 0.47659 | 0.02894 | -0.1087 | 0.63905 | 0.29299 | 0.19742 | 0.32747 | 0.14732 | 0.14087 | 0.54248 | -0.00082 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| IspH3 | −0.2056 | 0.37128 | −0.19032 | 0.4086 | −0.06266 | 0.7873 | 0.32577 | 0.14955 | −0.25234 | 0.2698 | −0.36504 |
| IspH4 | −0.21637 | 0.34617 | 0.09805 | 0.67243 | −0.28032 | 0.21841 | 0.35159 | 0.11808 | 0.4376 | 0.04727 | −0.20231 |
| IspH5 | −0.15231 | 0.50983 | 0.13356 | 0.56382 | 0.06221 | 0.7888 | −0.25132 | 0.27179 | −0.02392 | 0.91804 | 0.05592 |

**Table S8** Abbreviations.

| Abbreviation | Full name |
|---|---|
| 2,4-D | 2,4-Dichlorophenoxy acetic acid |
| AACT | Acetyl-CoA C-acetyltransferase |
| ATbHLH | *Arabidopsis thaliana* basic-helix-loop-helix type transcription factor |
| bHLH | Basic-helix-loop-helix type transcription factor |
| Bl | Bitter leaf |
| Bt | Bitter fruit |
| CAS | Cycloartenol synthase |
| CBF | C-REPEAT/DRE binding factor |
| CDP-ME | Methylerythritol cytidyl diphosphate; |
| CDP-MEP | 4-Diphosphocytidyl-2-*C*-methyl-D-erythritol-2-phosphate; |
| CDS | Coding sequence |
| DDS | Dammarenediol synthase |
| DEG | Differentially expressed gene |
| DMAPP | Dimethylallyl diphosphate |
| DXR | 1-Deoxy-D-xylulose-5-phosphate reductoisomerase |
| DXS | 1-Deoxy-D-xylulose-5-phosphate synthas |
| EST | Expression sequences tags |
| FDR | False discovery rate |
| FPP | Farnesyl diphosphate |
| FPS | Farnesyl diphosphate synthase |
| FRKM | Frangments per kilobase of exon per million mapped reads |
| GT | Glycosyltransferase |
| HMBPP | (*E*)-4-Hydroxy-3-methyl-but-2-enyl pyrophosphate |

| | |
|---|---|
| HMGCoA | 3-Hydroxy-3-methylglutaryl-CoA |
| HMGR | 3-Hydroxy-3-methylglutaryl-CoA reductase |
| HMGS | 3-Hydroxy-3-methylglutaryl- CoA synthase |
| ICE | Inducer of CBF expression genes |
| IDI | Isopentenyl-diphosphate delta-isomerase |
| IPP | Isopentenyl diphosphate |
| IspD | CDP-ME Synthetase; |
| IspE | 4-Diphosphocytidyl-2-C-methyl-D-erythritol kinase; |
| IspF | 2-C-Methyl-D-erythritol 2,4-cyclodiphosphate synthase; |
| IspG | (E)-4-Hydroxy-3-methylbut-2-enyl-diphosphate synthase; |
| IspH | 4-Hydroxy-3-methylbut-2-en-1-yl diphosphate reductase; |
| JA | Jasmonate acid |
| JTT | The Jones, Taylor, and Thornton model |
| KT | Kinetin |
| LAS | Lanosterol synthase |
| LTR | Long terminal repeat |
| MEcPP | 2-C-Methyl-D-erythritol-2,4-cyclodiphosphate; |
| MeJA | Methyl jasmonate |
| MEP | 2-C-Methyl-D-erythritol 4-phosphate |
| MS media | Murashige and Skoog media |
| MVA | Mevalonic acid |
| MVD | Mevalonate diphosphate decarboxylase |
| MVK | Mevalonate kinase |
| MVP | Mevalonate phosphate |
| MVPP | Diphosphomevalonate |
| OAS | Oleanolic acid synthase |
| ORF | Open reading frame |
| PCR | Polymerase chain reaction |
| PGbHLH | *Panax Ginseng* basic-Helix-Loop-Helix type transcription factor |

| | |
|---|---|
| PMK | Phosphomevalonate kinase |
| PPD | Protopanaxadiol |
| PPDS | Protopanaxadiol synthase |
| PPT | Protopanaxatriol |
| PPTS | Protopanaxatriol synthase |
| SE | Squalene epoxidase |
| SQS | Squalene synthase |
| SS | Squalene synthase |
| TSAR | Triterpene Saponin biosythesis activating regulator |
| TSARL | Triterpene Saponin biosythesis activating regulator-like |
| *β*-AS | *β*-Amyrin synthase |

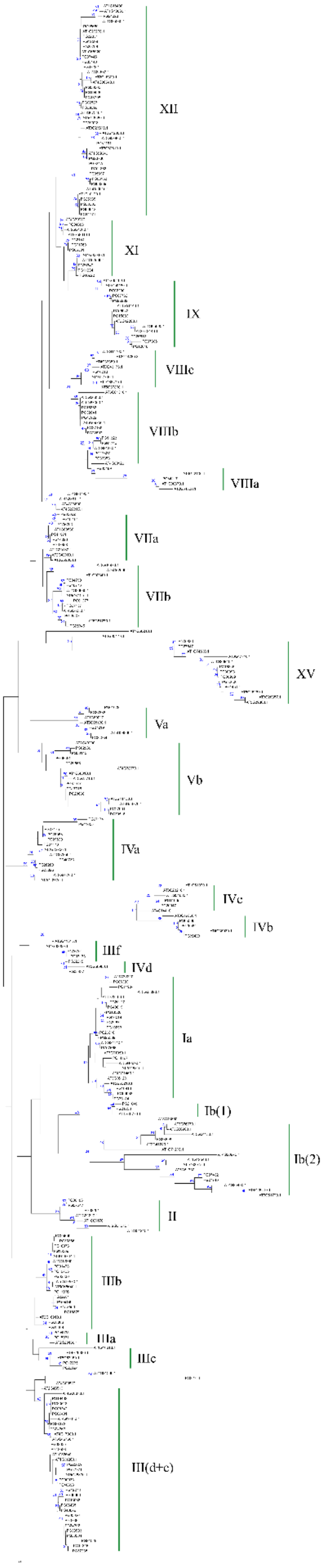

**Figure S1** Unrooted phylogenetic tree **of** 296 proteins from *P. ginseng* and *A. thaliana* and their respective bHLH subfamilies. Only the bHLH domains were used for phylogenetic tree construction. The JTT model was selected as the best-fitting amino acid substitution model with an estimated proportion of invariable sites (I) and an estimated g-distribution parameter (G). The phylogenetic tree was constructed using the neighbour-joining method with 1000 bootstrap replicates and Poisson correction distance. Roman numerals correspond to the bHLH subfamily.

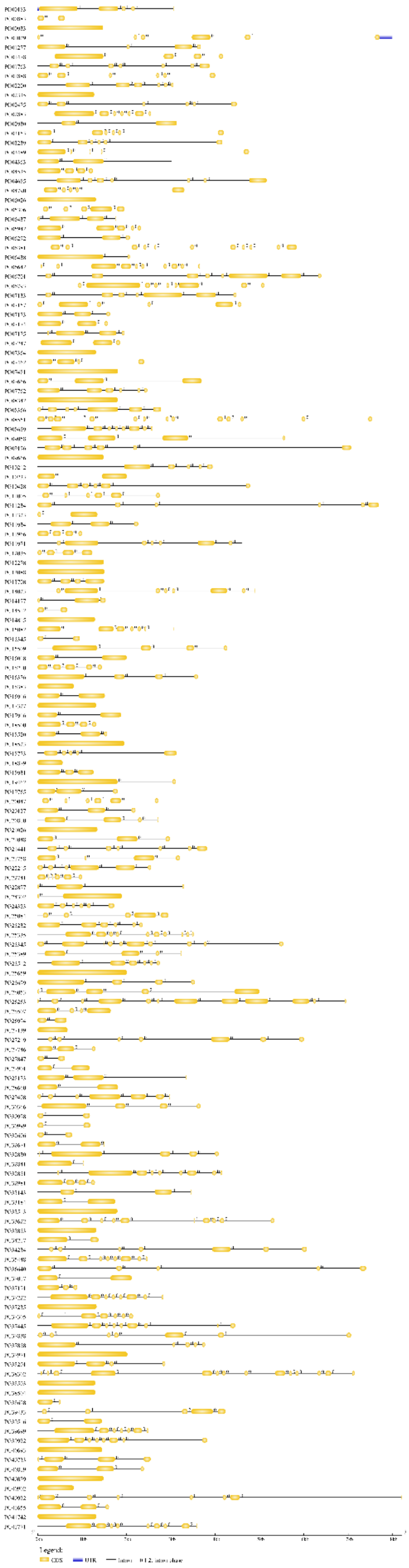

**Figure S2** The structural features of 169 PGbHLHs. The exons and UTRs are represented by yellow and blue round-cornered rectangles, respectively, with black connecting lines as the introns. The numbers above the rectangles correspond to the intron phase.

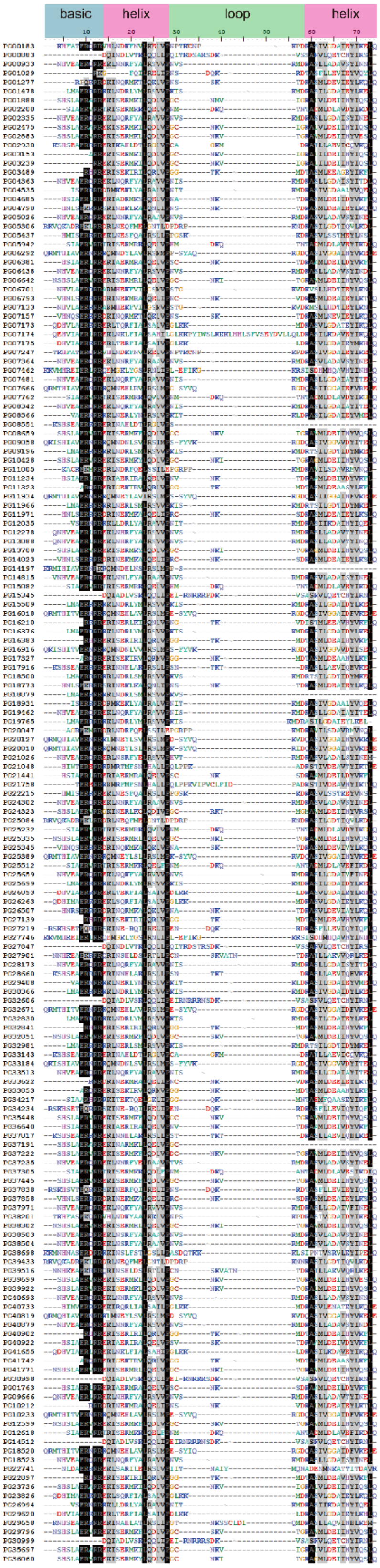

**Figure S3** Multiple alignment of the key domain of 169 PGbHLHs. Alignment of the bHLH domain of 169 PGbHLHs. The shaded boxes above indicate the positions of the DNA-binding basic region, the two α-helixes, and the variable loop region.

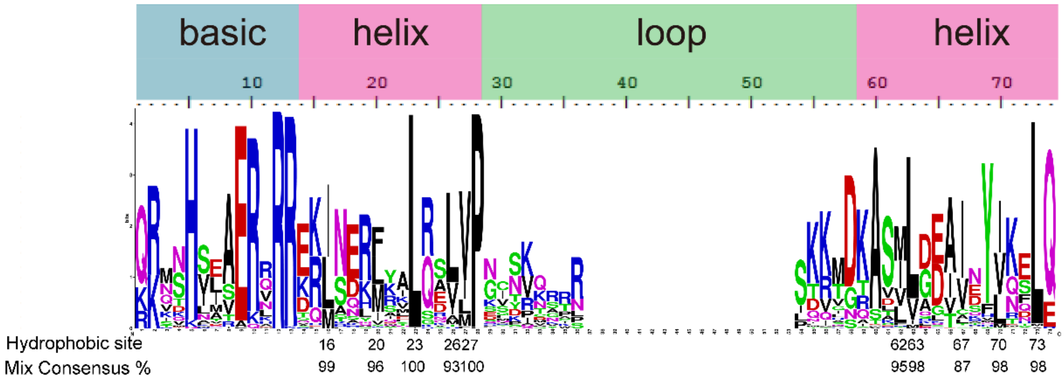

**Figure S4** The conserved hydrophobic amino acids residues in the two-helices region of the PGbHLH bHLH domain. The overall height of each stack represents the conservation of the sequence at that position. The numbering of the amino acid follows.

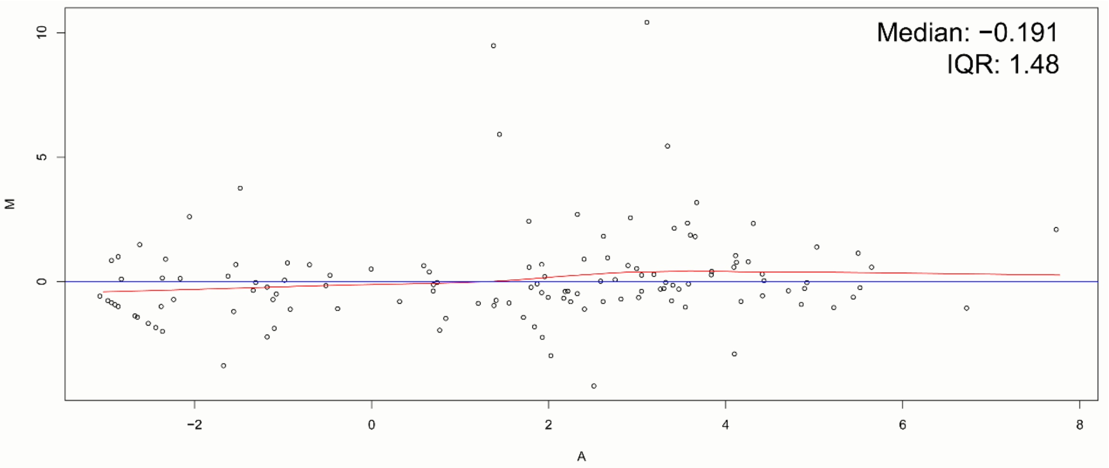

**Figure S5** MA-plot of 169 PGbHLHs for methyl jasmonate treatment analysis