Supplementary file 2

The core proteins found to be non-human homolog genome given in the FASTA format

>CORE_REP|Org39_Gene1249#

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CEENEEESYVIKSDVDENLIYGDNANAMIENIVELNASSGTVAVVGDIFDVDTKELKNGKILMIASITDYTSSISCKLFLTDTNKDGVLESVKKGAY
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KFMEFVGDSVLVAHNAEFDTGFISQKCREQGLLYNNKKVDTLMLARVMLPNLKRHRLNVVAKELGIPLLNHHRAVDDAEATALIFNKFLQML
TEKGAKTLSDVNNILGKIDYTKLSTNHITLIAKNSIGIKNLYKIISDAHVNHFFRAPRILRSVLNEYKEGLIIGSACEAGVVFQAVKKNVSDEEMKKII
DLYDYIEVMPIDNNRFMIDKGEVKDEEELRELNRKLIDTAKKFDKIPVATGDVHFLDKHEAILRKVLKYSQGFKVDEEETYLHFRTTDEMLEEFSY
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NYQPTIHKYTEELFGEGYVVYRAGTIGTVAEKTAFGYARKYVEENNISVPNAEVLRLSNGCTGVKRTSGQHPGGVMVIPDYKDVYDFTPIQYPAN
DTSCGVITTHFDYHSISGRILKLDILGHDGPTIIRMLEDMTGINITEIPLDDKETMSLFTSTEALGVTPEEINCPIGCLAVPEFGTKFVRQMLLDTKP
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IKYMFPKAHAVAYVMTSFRIAYCKVHYPEAFYATYFTTKVEDFDADLIVKGLDAIKSKINEIESLGNDATTKEKGMLTVLEVALEMYARGIKLLPV
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>CORE_REP|Org3_Gene1735#

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VVVQTVSVLSCGRKIEGNVAFLGGPLYFLSELREAFKRVLDLKDENIIFPENAQLYIAIGAGLLSVDEDNIQLKSLIEKLDSIKNIEDGEVNLLEPLFK
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>CORE_REP|Org93_Gene205#

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EEELINTIFEQKVILKKPLFIQNEEEREKISGTERGTIVHLVMEVLDLKNVSSVNDIKSQIRGFVSKGIITEKQASIVNPYKIYKFFASNIGKRMLNAEII
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>CORE_REP|Org96_Gene2569#

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TFNGIEDGTFPCGTAAYEKRGIAVDVPEWIIDNCIQCNQCSFICPHSCIRPVLVTEEELANAPEGFEAKKALGKGLEGLKYRMQLSPLDCTGCGN
CADICPAKEKALVMKPIDTQLDTELDNWAFAVNPDEVAPKGDVMPANTVKGSQFRQPLMEFSGACAGCGETAYIKVVTQLYGDRMMIANA
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>CORE_REP|Org2_Gene1357#

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GSKHHENHDITKYDENISFVKEKLEKLEKEKISIRNNIEELNAKVSGYLSIEKMKTKELEDVKGKLGGIPSSQLLKKLDEEQRKLALLKSNIQEWEKE
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>CORE_REP|Org89_Gene2722#

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>CORE_REP|Org56_Gene2169#

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VEVELELNEDEEELSLELWLNRPDKADVIIVSPTGEESKSVGISNYNKVTGLFDLEGTEYSITYIYPTTFSGQQFTNVTLKNAKRGVWKIRLVGVYII
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>CORE_REP|Org44_Gene3420#

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>CORE_REP|Org18_Gene2344#

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>CORE_REP|Org42_Gene786#

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>CORE_REP|Org43_Gene2572#

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>CORE_REP|Org18_Gene1463#

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VNENNHIKEVKMISRTLYFGQKRSRVRIIKDLSVQRESERLKKALIKQRQYDQMKMEFYANISHELKTPLNNIYSSVQLIENLYKKGKIIDFQDILK
EHIKITKQNMFRLLRLIDNIINISQVKSDIYKIKAVNFDIIDITERIVTSISSYAKSKGIDLIFDTDEETVMVGLDPESIERIILNILSNAIKFTLEGGEILVG
IYKKDETVEIIIKDTGVGIDKEKLNDIFNRFKQIENSGISNEFGSGIGLCLTKSLIEIQNGKIYIDSKVGEGTNVKVIFPIKEVVEEVYDNSNYNDNIEK
FEIEFFDIYK

>CORE_REP|Org57_Gene2421#

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```

SRVPNLLHIVIDNRNVERILSQIIINVALYYLYNYIVSKNIKKTALELHDTNEELTKKTESLKEKNKKLIYETEKIEELKGILMKRESRLQSTLDVAVNSI
VVFSKDGEITYANKSFRNTFGDYKEQDKLTDKIKNFNDLIESIHYVFVHEKNAEKLISTSDNKVYQAIFAPLIIASQTEGVLCVLEDKTKKKEYERKLI
EANKRSKDFLESIGDGIVVLEGNNKIYVNNACREIFKNNLESIDFSLVCKSEESIEKRYVIDGEVKYVEMSFSQYTNAGTNKTIIVIRDTTSRKISQIK
LEESQSSYSRFIDILPDGICLLKEDLSINYANKSFLDMLAFTNIDDIKDSNIKLLMNANTEEKMKFTDNMAKVLNENRSILLLEYELINSYDDIVEVE
LSALPFAIYNTRYIMLIIKDLVHKKYSEQAEKELLERFKTDKIKTEFFANMSHELKTPLNVISSSNQLVDSFYRNEKIKDYNNNIKSHVDLVRQSSYR
LQRLINNIIDLTKMESGFYTLKLAKYNIVSVIEDLFMNIEEYALRKDIKILFDTDLEEINVYIDKVEIERIMLNLLSNCIKFTDNGGWIYVSIHYKIDKVI
ISVKDTGVGIPQDKLELIFEEFSQVDKTLSRNTEGSGIGLAIVKNLVSLHGGDIEVVSEVNKGTEFLISLPMKGFSSEHYTEDKRIYNIQEKIKIEFSDI
YY

>CORE_REP|Org36_Gene1812#

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KIYKKEQATRAKNNFFIKDNLVALREIALRKTAERVNKEVQMTRLSKGDVTVIPTSDTLLACISPSPSSAKVIRTASRISDSTFAKWIALYVETPNTA
RLPFDEQKQLQNNLKLAKKLGGEIIVLHGENIIEQILRIAKLRNVTKIVIGRNHSSNKRFSKRFKKDIVDKLIDEVDYIDIHIIPYKFASDVKYKPKKDK
SSIKSKFKISKVDFIKLIFITLMISILAYAVQSMGFIRENILLIYMLGVVLVSMWTKGYSTGIISSVFNIVLLNYFFTAPLYTLSIADSNYIVTLVVFSIVGI
ITSTLTSKIQHEAETAAKREENTKMIYQIIKGFLRLSNKDDIVNKGIELLSLSLSRDVICYLNVDKHNKSKLYKKNTNNKDKNDLDSEDEKAVASWV
LSNSTVAGNDTDTLPGSKGYYIPIVGMNLTLGVVGISCIDSKLDTEDISLIETIIAQMAIALDREILSEAKENTNLEIERERLRSNLLRAVSHDLRTPL
AGISGAVSTIIKNKGTIGQDIIDELLSGVYEDTQWLIRLVENLLSMTKIDEGKLEVKKHSELVEEIISEALQKIKKRIENALIDINIPEQILFVPMDAKLI
EQVLINLIDNSLKYSKEDCKIEINVYEKDDYVWFEVSDNGPGISKELKKHIFDRFFTGEEGAKDSRKGVGLGLSICKSIIQAHKGEIMVENNKDKG
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>CORE_REP|Org10_Gene150#

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DNMVIHKEQRVQRGLNYAIVDEVDSILIDEARTPLIISGPGDKSTHLYSDANTFVLTLKPDDYELEEKDKAVSLTASGIQKAEVYFNVDNITDISHT
ELYHHINQALRAHVIMKKDVDYVAKDGEIVIVDEFTGRLMFGRRYSEGLHQAIEAKEGLKIQRESKTLATVTFQNYFRMYKKLSGMTGTAKTEE
EEFKAIYKMDVFQVPTNKLMIREDLPDCVYKSEIGKFNAVAQEIIERHKVNQPILVGTVSIEKSELLSQILKKKGIKHEVLNAKHHDKEAEIIAQAG
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TERHESRRIDNQLRGRAGRQGDPGSSRFYIGLDDDLMRLFGSDRISGIVDKIGLEEDMPIEHRILSKSIEGAQKKVEGKNFGIRKHVLQYDDVM
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ERMREVERVILLQAVDNHWIDHIDAMDQLRQGIGLRAVGQQDPVIAYKMEGFDMFDEMNKHIKEDTVRYLFNITIETPVERKAVVDVENLS
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>CORE_REP|Org89_Gene1229#

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KEIKNDFPQDPKEQLMLAIEAVFRSWNNPRAIVYRKLNDIAHNLGTAVNIQSMVFGNMGETSGTGVAFTRNPATGENKLFGEFLMNAQGE
DVVAGIRTPQNISTLADVMPAVFDEFVKITHILEGHYKDMQDIEFTIENERLYILQTRNGKRTAAAAINVAVDLVEAGIIDEKEAIMRIEPNQLD
QLLHPKFEDNALKEAKVIAKGLPASPGAASGKVYFNADDVVKANEKGEKVVLVRLETSPEDIEGMVKAEGILTARGGMTSHAAVVARGMGKC
CVAGCGEIKVDEFNKEIRALDDVVIKEGEYISIDGSTGNVYLGDVKKTEVSLTGNFEKLMNWVDKHKCMMVRTNADNPRDARAAIEFGAEGI
GLCRTEHMFFDEARLPAVREMILSNTVEQREKALEKILPMQREDFVELFKVMDGKPVNIRLLDPPLHEFLPHDDETIEELSKSMGIKVSDIKKRIV
DLDEFNPMLGHRGCRLAITYPEICVMQSKAIIQGAIEAIKAGVKVSPEIMVPLVGEVNELKIIRKMIVETVDAIIKEEGVEVPYTVGTMIEIPRACL
TADEIAQEADFFSFGTNDLTQMAFGYSRDDAGKFLGQYVDEEILEKDPFQVLDQNGVGKLVKMGAKLGREVKPELKLGICGEHGGEPSSVEF
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>CORE_REP|Org86_Gene2727#

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VVPNNVEENNEQDKVEIKATEIEDLQLGKDNSENDMLLNEIKNSKVKHESKSNDIESKFIDKLNSLNNESVSQTIHNEYKKLCGLEELHSVEGYG
FGKEIIKDFACATVVLEFLKRRNRDLIEGAMRLTIIGEFGPENFKEFVDYVIKNKTEISEDTWNKAQNLIKDNYSELENHEIASKRTRRNKDIDIEEY
IYMIKNADKDICFRSSISIEDDAEEGTKEEVDSNNQDIGDVVEDKDTTDKEYDSNKEDIIEPENKKSKKKAKLFGFIKKDNEEVEQEEENLNDISPD
IILDKPVENHQVKSEEIEQNELKEIKQEEPSQHIEEERSVKIEKPINNNLDEKVSSNNESKLEKESKNLEDKKAKEIKEEKLENEKSVVIPIKKKENSN
KKSKNSSKDKYRENKKEMKNYVSDKEDSLDDEEVVSKKSRLKETIIAVVIVVIVGVGYFITVGNNKKNDKENIPKSSTQQQANNKLTEEEKKAQA
EKEKKEAEEKAKAEKEAQEKAQAEKEAQEKAQAEKKAKEMEAYKDGKGVYYTVYAGSLKVEKTAKETAKEYEAKGISSTIIQENGYYKIKIGDYS
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>CORE_REP|Org21_Gene666#

MNLYTSLTIRYLKQNKRRTIVTIIGIILSTALICGIGNIFESFMDYQMRETIKNDGSFHVTFYDVNRKNVEYVTKSAEIEKHAFTKQLGYSKLENSEN
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YNGIATAIAYFNPMNNYNDTINVSVAVRNPKDVYKISNKISKNIYSNKDKEAVSDMIKYNEHLLRLQGASKYSNINSSIKSIIIAVTILVIICTIATVY
NSFSISINERKKQFGILNSIGATSSQIKRLVFIEGIIISLIGIPIGLISGTVAIDLLFKIINKYFTESVVTKMSLQIVYNPIIIIVSIIIVLLTIFISILLPAISASNIS
PLNVIKNTGEYKVGKIKSSRLIKMIFKTEGVLAYKNIRRNRKKFIITLFSLMVSIIIFISFSGFTLLLLRGEEIRNSQRKYDLYLTAKNTARSVEDTISELE
DIDGIKNFELATGQYVSIRVSENKINKSKEDLIRKYYQKYKIGDSYEYDFSNNELIFPGDFAVKNKINNLVQGSFNKERAIEENGVILVRKSAFEEN
GKKGVVELTNYKVGDTVNCEYLDENALSKKVKVKILAITDEERLGLGYQNMGLQFITYDEVAKNLNLKLSKSLIFIDSGGSIKTKKEMEALANKN
NFNFYDESASNESEKQDLKVIKIFVYGFIVVISLVSVTNILNTVSTSINLRKRELAVIQSIGVTPKGFRKMIYLESFIYGILSLLFGIPISIGIILIMNKLISG
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>CORE_REP|Org75_Gene74#

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HSNMTKVLSHKYMTQKKGMFIGILFSLSLGGIIFLCSSYSIQLTKNNNELTMKADDGLNSDYQITMQTTDFDVGIPKDKISRLNNVEGISKVYPV
RYLFGAMQIKEEQLFWKNFFKPLEKDYRIKTFFDGICTKQNEGGYLLKTNIYGYNNGMLEGLNSYIIDGEINTHDMVKNNKVIVRLPMDGTGM
YDAVDINPGDTIKVKVPKTMKPTDEIVKFKEENKNDYTTKEFVVAATVKRVMANNIYFIGDYGMDIVMTNGQMKNNFDIENYNSVSIKKTED
SNSEELSENIKSVVSDVKRCIVTDYTIAIEKNNTYLNQKLLFIYGIVFVLLAISLFHIINTVSYLIFSRRHEFGILRAMGITDNKFLLMMIREGFLYGFYA
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>CORE_REP|Org15_Gene1307#

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SLICGLSSLFSNFYILLIGRVIQAIGGGGIMPIATAEFGTTFPENKRGMALGLVGATYGIANILGSSIGSTILSIFGTQNWKWLFFVNLPICLIILIGGV
FCIKNNKSESKEKIDKLGTLMLVCIIVSLLYGLMNIDFFNFKNSIQDISVYPYLLTFIVLIPIFIFIENRAKDPILSFEYFLNPRILIILILSLIVGIGMMGM
VFVPQYAENALKINAGSGGYFVAILGLFAGVAAPLSGRLIDKFGAKKILLLGFSVSMIGSLYLVLIALKTNTVFSVCLSLMFMGLGMGFTMGTPL
NYMMLSNTRLEESNSALATLSLIRSIGTSISPAIMIGFIAHAGLSVQDNIMDLVGKPSTPKIVQLEELENMIDDLKSDPEMAKNLKNVSIPNMND
TSNINMDMTGGKLPKYLLDKVQSADTTNITNITKEISTTMFDEKVPSIISKIQKNVQKGIDGTQSGINGIEEGESKLNSGIKGVQTGIDNMVKAR
AGINQGIDGVKKGIAGIDKGIKGMEQGLKKQDKAIDELTTAYNKIPTTEKIPTNNENNSNEQNQDNASNSESDATNNDSTENKNNNSNDNKP
NLNEQKESLNAQIQKLKKTRNELNAKLQKNKAQKNELSKKLKSMESQKKELQSKLNNSINQKKDMEKSLDTMQQQKKSLQAVLEKTQEVKTE
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>CORE_REP|Org24_Gene1978#

MKIILKYIFTNIKERKIRTAVMLLSIVLSTVLLFVSFSIGLSYESAQRKMAKGMYGTATISVQSKNPDILTNLEDIPDLNAIKSKVGVLESSAIYNKGG
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SGYTRVLIESEEEMTENLVNKLSEELSTEKYMVSNTINETKIISDARQKTMPFFLISFFALTLSIFIIYSSYKVITLERLPFIGTFRSIGANEKTVTRILML
ESILYGSIGGLIAIPIGVVVLNLMLHGLGSSLEQGISIPVVISPIGVIISVIVAIIVSSFSAYIPVKKASHLPIKNIVLGTVEEKNVSNRSILFIGSIMFILSILL
PRISPENTLYLAGGFSLLGLIVATIVLIPLITDIMSIVFEFVYKNILGNEGKLAARNMKNNKNIIQNITLLFISISAVIAISVVGNFVKTYITDVFRDAEL
QGFADGKMNEEFIEDVRHMDGIKKILPLYVMNNEISGNGVTLSRLEGTDNIKLYNSMFGINYTNFEIKKQVIEAFNDKRSVILNEDTLKKVGLSI
GDTITLSNDKYDFSYKIVGSFKSRANDVEAVIPSHYAVSDFDKTNYGFLVYTAVNPDAVMIQIRYLFGDTYNWSRTVEEFNNDSLNTISSFLSPM
NKMTYFIFLLATVGIINNLLINYIQKRRSIAMYKSIGLSNKQNIKVTLIEGFTSGLLGAVIGIVISILEIQTIFIVAGPKISMKPDLDFKTFIIVGLLGIIVTL
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>CORE_REP|Org77_Gene300#

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MSIVYADDTAIKLMNFQPLKGNLPTNKNEIAISEKYLQEFGLDKDIGDSIKLNYYDDITNKEVQCDFIIIGFLENYYQDNAKQYYTVVSNDYFKNI
ASTPLQNKSNTFDESIPDTVDVLVKLSEENTEKDSASIKTQLKKIALSLGIKKYNIYLNDNYIESNLIDGEQIITVLVVGIVVLFSSVFVIYSIFYISVVNS
VQMYAKLKSLGMTSFQLKKIISLQGNILSIIFIPLGVIASCIIAYIIQPLAWQMRADLFIILILSLVMFLTVRISLFKPTRIISKISAIEAMQYTETKFRKK
VKNFSYINIKNLALKNIESNRKKNLIALISLSISGVLFISIANLANSIDFKKQLSQQFVYNEDYIISIKSDNLYKHITEIQQNNPLTDSLKNEIKSIHGVKK
LIESKSIKSNIIEPCVKDRDEKQFITLIKGITPELSKSLEEYIVSGKIDYTHLDSDSLIINKYRTKSYRLNLKVGDTVTFNIFSGNDIIKKKMKIMGIIDNS
NTGGMFFASDKTLESLTPYNTNLDFSILIDKKHSKEIEEKLLSIIQKNSNLMLYSYEDDYRMITRAFQYIIIASYIFVGLISCFGILNMTNTLINSVLIRK

KEFALLQAVGMTRKQLQNMLYREGLNISIKAICISSILGYFGSNLLCTFIKDVIRLDFINFKFSIFTILIFSFVLIGIQVLVTELLVRNIEKNHLQNAYVL
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>CORE_REP|Org8_Gene2663#

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GVAFKMIQALTPKEEFKTSMYNYLEIVTLATICDIVPLIDENRIIVKNGLKSMKEGKNIGLRELIKVCGVESDKIGSSHIGFAIGPRINASGRLGYSYL
GVELFTTQSQEEAVEIASILEEKNNERQMIEAKMYHEAEEMLKSNSRYNDDKVLVLAKEGWQHGIIGIVASKLTEKYYKPTILLGIENGEATGSA
RSIKGFNIFEALIKCKDLMTKFGGHEQAAGLSLDSDNVEILANEINKFADYNLTEDDMIENVNVEFELQENVINLNLVEELHKLEPFGLNNPNPR
FIVRNYILKDLKVIGKNQQHLKLSIEKEKSYECIGFNMSHLKSMYKVGDKVDVLFQLDENNYMGNRKVQFLLKDIRLARPKSASNDKLSLKLMSK
IIPKDTQSLYNISVSDFELFDGNTDINIFDYFEKDTLIISNSINGFYRAMSDISLIDLDFNINYNIIEDVSKNTDKLELIFSPNIDKIDLKRYNNIILYDYLY
NKGEYSYIYENKREESEIIKYYNKTDLLYLKNVVSNIVPSRDEFITIYKQALIKKEIDLDMVNIRETFNVIPLKFFTILNVFRELNLLDFNLNYEKNSVLI
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>CORE_REP|Org51_Gene1251#

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YGLLNAGTLPVDSPLKGNMFDDVMKLGVSGQGSGLIATTIAYYMSKIFGIAGGWLISIFALILSVMFIFNISIKDLVSNAKSKSKASKDSNLTFKD
KIANMKKSAIDMMTDEVDDTTINKKPGFFKGLMSKGRNNEDEDEDEYFEEENSDGVDDKTIKIVGFNKAEDEYLEILEGTQSMPELDVLKELQ
KATNENPVVDTKPEKKVDIAKPNLNIEKTQPMSIVAEPVNEDYSNYKKPSIELLNKVNKKSDENGKKKVLKNASLLEKTLSDFGVEAKINQVTVG
PTITRYEIQPSPGVKVSKIVNLTDDIALSLAAKSIRIEAPIPGKSAIGIEVPNEEAQMVGVREVLESEEFNNFNSPLAMGLGKDVAGKIIIGDIGKMP
HLLIAGSTGSGKSVCVNTLISSILYKANPDEVKLLLIDPKVVELANYNGIPHLLIPVVTDPKKAANALNWAVTEMNRRYKLFADAQVKDVTSYNE
KAEEKLPKIVIIIDELADLMMASANDVEDYICRLAQMARAAGMHLIVATQRPSVDVITGVIKANIPSRIAFAVSSQTDSRTILDMGGAEKLLGKG
DMLFYPLGAAKPVRLQGAFISESESEKVIDFVKSQVKDGIKYEEDIIETISKVNTSKGSDEDEFLSEAIEFVVESGQASASMLQRRFKIGFNRAARLI
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>CORE_REP|Org42_Gene617#

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IDKLSESMFIDSDYNNGQIEDSVLNYRKFKYILYKGMLNLIDHSASSRQKGIKFYNDFTDEEIDNMILDEIYKSQGNLEKNNIEFNTIQKRLRELSG
RNVLTVAFTGSGKTAADYRKTFKRKFFLVPNKISAESFYRKNIFQNKNDLNTRNSNDYIGLLHGDINLYSENEDNGEHDFVLTLRDIDLSINFCKP
CVIATVDQLLLSMFKFPGYEKIFAAVKNASITVDEVHLLEPKMFLILIYFMQFACKYLDVDFHLMTATLPKSYKEQMINKGIIFQEESNENVTDKG
EIAFIESNKEENICEGKDVKVSFIKEKEIKSIVEGALENKQKILIIKNTIDSVNRTYEFLKENLSDKYSGVDIDVLHSRFKFKDKKEKYSKILNGKGDIWI
STQSVEISLDLDFNIIISDLATMDSLIQRMGRCNRNNKYEYGNFYILPSEDKIYDNKLKNTTKSILNNVIKTNSIFTMGIRKTILDDYYDNSVVKKYF
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>CORE_REP|Org62_Gene2561#

MINTTKIAKNNLKQNKSKSILIIITIILSTLMLSSIGIYIVNAGAYQKENTIKYSGNYQGILANVDEKQADILSNHADVELTGEMNGVGVEKLEDDS
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NMSQEDFNIYVKFNDKSNLSIEQIKEKLDKIANDIGLDTINTAVNENYINALKPDMETIMGGVFVGLVIVLSSILVIYNIFYISIVTKVQEFGKLRAI
GATKKQIKNIVFKEGFILAGISIPIGIILGYVLANIIIKSFMNIDAKSSQLPVILLVAVISFISVVLSLLKPMKVASKVSIVDAVRYSGNKISNKNKRKGY
KNINLNRLSHANLERNKKRTYMTLASLILSGTIFITVSTALESFDAEKMAREHFPYDIEVRLSGYEMNSDKNPKNNLNILQMDNPLSKDFFNQIK
NIEGIKRIESARSVKIGMEDYDVEFKYDLLQSINENDVKSLSKNLIDGKINLERLQTGDEIVITHVDTAKEMGVKAGDKIRLTLYDGDKKIKKEFKV
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SIVTRKKELGMLQAIGLTNKQLVKMLNSEAISYTSGMMIGSILFGGILGYIAVMVLKKTGLSYATYSLPIVPILLMIVCILIAQFITTYLIGRSFNKESL
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>CORE_REP|Org52_Gene2634#

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YYENDAREGKITESEAQELIEALWIKLSEWVWTISANTANYFAGYNQFQNLTVGGKKRNGTDGTNDISYMCLKATESVKTHQPGLSVRVSQG
APDNFVMAVAKLVKQGTGFPAIHSDSAGAQMLLQDGYDAEDARDWSNCGCVVPHFRKTGQWTSAVNINFAAALEYAMNEGKSRLTGEK
MGLDTKNITEFTSFEELKDEFLKQLAYLVKSSVIGTTVAQQIHKEMVPRPFLSTCVDGCLDKGVDLSKGGAKYNIGPVLTGIGLGVVSNSLAAIKK
LVFEDKVTTLEELTKALNNDWEGYEELRKLALDVPKYGNDNDYVDSLAIEVSDFYYTETRKYKDIFGSKFNSAFMGISNYVPTGKIVGATPCGRK

ATKPLTEGVSPFVGTDTTSPLAAMKSASKINHDVHTGGTLLNLRLNQDLVETERGLRNLTSMIKSYFALGGFHVQFNTISNDTLLKAQENPEEY
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>CORE_REP|Org15_Gene2474#

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KKDGEKEEYEKVGFVQTPQSFYNPDLFQFNLHSEGRIPNEQDYFYRDIQLARNRTNSVIYGGSNTVISREALEEVDGFYTYSITEDFATGILIQSK
GYRCYAIPDVHASGLSPTDLKSLIKQRERWARGCIQTGRRLNILFRRGLGFWQKISYISSITYWYASIKRFVYIMAPILFSVFNVIVVKCTLLQVLIF
WLPMYILSSLSLKIFSQNIRNTRWTNIYETIMFQSLMPAVILETFAISKNKFSVTNKNKLEENRMYKFLQGIPYFIYMVLSIIGILKMFVAIFKMSS
MTYSVVLFWLIGNLFNLVMATLFISGRQQLRKSERYTAEIDFKLKQNSYVLSSKTIDISENGFAFLLENPEYISPEEEFEIEFREKSGNEMYIANMK
AKIVNVVELNSKWKYAAYITHIEDSEIDNWMCIVHDRIPTLPMTISNQLGFFDDLQINVKKRIEKTRTLSRRSPRVNMNFQMDIKNIGKLRIVNF
NYQYVLLTFENKNIYPKEIALEINEGIVLECDLCEGKIDERGILYKVNNIDSIMQNFFLRDEMMDWILQNKTIIVSKPGEKKEKSIDEFEPMEYI

>CORE_REP|Org86_Gene2672#

MLSDAKNNRYGLSIIAVISILVITISCLIYGSRLNKTLGEETNQYLSEIANQSVNVLKKQINGDIKLLESISIFIEGEESFEVDNILSILKRQAINSSFKRM
GVILPNGTAYTTDGYIEDFSKRDYFLKSMQGEVVITGKLKDVIEDDKNTNSNINVYSVPIYKDNEVKGVIFATHSTKLYEKILSVPTFNGKGYSYIT
RSNGDIVLNPSSKNANSTKENLFSYIGRSDSISKSSINNMKSNIKNFKSGSLSYSMFGKGYYLSYAPIGINDWYLFSEVPKTAISEKSYAIIKLTLSAC
VVLIIIFTALTIYILFIHKKSKEKLEEFAFKDNVTGIGNSNKFNLEGGKFLSSHEKKNLVLIYFDIDKFKLVNDRFGYEEGDRVLKEIAEIIKNIFKEQSVF
SRISNDNFAIIFEKKNNRESIIEICELIRKKLSMIKTSLGVELNLIPSIGVYFVEEGETNISTCLDKAMIAKTTVKRKYLKVYEIYAENLKETLIEERDIEQ
EMHDALKNEQFKVYLQPKVDLSTTKIVGAEALVRWQHPKKGLISPGVFIPIFEKNGFITELDMFVFTQVCKNFKRWENENFPTFPISINLSRVHL
ENPGFISELERITKEYEVEPNLIEIELTESAIFDNTKILFKIMQTLKSVGFKISMDDFGSGYSSLNMLKDMPIDVLKLDRQFFITVGNAKKSQIVVSSI
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>CORE_REP|Org17_Gene3372#

MKLVLAEKPSVAKTIASFLGAKTRQDGYFEGNDYIITYAVGHLVSLYDMKDYDKDKYSGSWKMNNFPFIPEDKFKFKIDSSKTKQFNTVKKLLN
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IGRVILPTVKLVYDRDMEILNFVPKTYYEIEGHFKAETGEYKGKYIKGKESKFDTLEDANKIIASIASKTGKILDKKVTMSKEYAPKLFSLTSLQGYITS
KYSNFTSDKVLNVCQSLYEGNGKGGYITYPRTDSIFLEESLASKASQTLDKLKVGLEYENKIKFSKTKRVFDSSKVDSHSAIIPTYIIPKNLSKDEQLV
YDAIKDRFIANFMPPAEYENTEIKTEVDNCTFLTKGKVLKSKGYLEVYNKEEKNDLLPLVNKDDVVDVLEIKPLTKQTTPPKPYTEDTLLKAMKNC
GKNVPEEDTTVLSGYSIGTSATRADVLKKINQVGYVKKKGKSYSITDLGKNLVEIFPVKDLFDVDYTGKLEKSLSDIQKGKYTRKEYLTNIISFIYQN
VNIIKQDASKNINTEEYTFDSKTKKFTKTKEKKQKKDTTNAEKEVAISKDSNNKKESKNGDENQPLGKCPVCQGDVLEFDKGFACKNHKECKFV
IWKNDKYLSLYKKKVNKTMVKNILKKGETKVKSLTAKNGNKFDALLKYNKNPDTGYFNWKIEFDN

>CORE_REP|Org48_Gene1471#

MKKREKVFDGLVFKHILILLILLVLIDLTSTIIYASNSMEITSRNMIETSKRELENYLEINISLLKALSKDDRFSDSETSLIEKGKLLRPYQKEYNLFMIGI
TDTKGNTSSTYREKVGSIKDRPSFEKAIKTKQVVVSDIEVSNVTGDKVFIIYVPIIKNNEMIGTIFASFYFQDVNNLISRSNLDDSIKFLMIDKNYTII
SHPNKKYVNDKSKILDLEGNIIGTTKSEILKNINEKCQGKFLYWDNWRLYNVKYTNIKWTNWTLVSKCNIFKNFQSLIVNFMIKLYFYIVIFMILW
KLSNAKLIEQLKKLAYYDSLSGIKNKEKFRKDSMYILKNYYQDNFYLVQLDVNKFKYINEMFGYAEGNKILIHISQVLNNNTNKYEICARMDNDH
FILLIACSTEDELLNRLSKINKEICNLSTTNSSKYKIVMSSGIYKINKKDDIKKIDLLIDRANIAAKSKKEKYEHSYSFFNEETRNRLYKEKRLEDNMNK
ALEKGEFIVYYQPKYSLNDVNEIEGAEALIRWNSPEFGFISPIDFVPLFEKNGFIVNIDMFVFEEVCKTLNKWINKGYTPVPISVNMSRVHLYRDN
FIENITDLISKYNISPEFIELELTESVVFDNLNILIDIMKKIKEIGFLISMDDFGSGYSSLNLLKDLSFDILKLDRGFLIETTDTKRGKIIISKIVEMAKAIDI
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>CORE_REP|Org80_Gene31#

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DINFESSSKDRNIVFESATGKSAKGINNLTINKSVNENLNFGEYGSVLGSLGQSLSDNGLKASVLGNSDIIENGQLIKNRNLCLTAMDEYGRIPNG
NVDTINKKDLSMPYGISTDYDKLIVETKEAYKNNDVVFVELGDTYRLDLYKPNLNEKTYENMKNKIEKNIDVYLKNIFSMVGENDTIYIASAFPSD
LDYKNKRRLSPIVKLNGVGKGLLSSSTTRREGIVTNLDVGVEILDNFNIKNQNMVGRKYELINRDDNKEFLMDEYQKIVSISSIRSTILNGFVSIVF
LSWIVAMIAILFRKHISKKYKETTFFILKELLKIGIVMPLSFMITPIMNFKTPLAISLGIIIITLTIYLISKVLIKNDLKNMLFFTGLTIVIMVIDAGFGSYL
MKSNVMSYDCIIGARYYGVGNEYQGVAIGSAIFTFAILLTYKNIPKWSVIVFSLLILITSASPIMGANVGSAISECVAFLLFILLIYNVKIDFKKIVLLGI

AVLFVLGAFVAIDMILGSNSHLGMFVKEIYFNGPGEIIQTFSRKIEMNLKLAQTSAWVNILLTGIGVILALMINQIRYFKQLMDEYPIVFKGFIASI
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>CORE_REP|Org58_Gene1413#

MSIKIGLIGNPNCGKTTMFNGLTGSSQYVGNWPGVTVEKKGGKLKGNKDVEIVDLPGIYSLSPYTLEEVVTRNFMLDDKPDAVINIVDASNIER
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TPYIDVETRWLAIKLFERDENVIQKLDISKTILNSIEEITRNCEDELDDDSESIITANRYEFISSIISSIIKKNRKGKETVSDKIDKIVTNRILALPIFALIM
WGVYYIAVSSLGTIATDWTNDVLFGEIIQGNVSNFLASLNVAEWLQGLVVDGLIGGVGAVLGFVPQIMLLFLLLSILEDCGYMSRVAFIMDRIF
RKFGLSGKSFIPMLISSGCGVPGVMSTRTIENDRDRKMTIMLTTFIPCGAKIPIIALFAGALFGGASWVAPSMYFLGIAMIIICGIILKKTSLFAGEP
SPFVMELPQYHIPSAKGVLIHMWDRGKAFIIKAGTIIFVACGVIWFLQSFNWSLQMVDAGDSILASLGNIVAPIFAPLGFGNWQSSVATVTGL
VAKENVVGTFGVLFGISDATEQDPTLLASVANMFTVASAFAFMAFNMLCAPCFAAIGAIKREMGSWKWTWITLGFQTLTAYIIALLINQVGSL
VLGTGGSIAGAIISIFIAVAVVFVVLTYSNKNMKKEKMGKLSYMKN

>CORE_REP|Org94_Gene2800#

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KRLGVKNVYLIGGTNTLDINVEKQLKAENISFERISGNNRYQTSLKLAEKLSKEKEISNIVVVNGEKGLADAVSVGSVAAQENMPIILSDTINGIKD
TEKFIKEKNIKKSYIVGGIYSVSNSVEQSLPNSKRIAGNNRNETNAKVIEEFYKNTDLKNVYITKDGMKKQSDLIDSLAVGVLAAKNNSPVVLVGN
KLDFTQNDVLNTKIIKNVVQVGGLGNENAVESIIDSQEETTYTVKNTDELNVAIKKSDANDIIKFKPEKEKNITESFKVETDKSISVEFEGTYTQTISI
NMPNGSITNLGDVNGTIKIMDVRSSTLVNKGEINYLDIYDNNGCRVENERDGDIWLVTISNESRDVHIENDGDINKISNSCSSVTIKNSGNIDTL
SGSKEIAISGKKPKVDDTDKDDERASGINIKVEPCSIPKRDYVKVRIVTEPKNSNYKIYYKVVSKKPTSRYVGDKIKVSEWDDAPSAGTSFEVEAR
NGFYIEAVEINTSTNKISKWGRSDSTDDGFKSIEVAKGLSANVFIDGDKVELTTTRANSGCEIYYRIMSSKPTAMNVGSSITLSSWEKISSSSLELE
SSEVSEKYIELVELEKSTNLVTRWGSTEKINIPNSSI

>CORE_REP|Org78_Gene1320#

MDNLKKKKITSRQKKIILMIVENSKKNIPITISEIAGTLELSSRTVLRDMSGIEKWFDENDFNFVKKPGVGLILEENIENQNFIIELLEEEKIEKEYSKE
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DKAIEILSENRLLNLMDRCIIIKVEATLTKKLSDLDVNLADSAYIGLVVHISLALQRIKNGENITMDKEFLKELSITEEFKLAKEIVKGMETDFNMDIP
VDEVGYITMHIRGAKQRSSSNHKALNLDDIEIMEITNKMIDLAEDEFKISLKNDERLFKDLANHLGPSINRLNMGLEIRNPLLDEIKSKYSYAYDG
VEKISRIIKDKLNINSIPESEIGYIAMHFASAIEKNLMMNTNINIVVACPTGIGTSRFLSTKIENKFPNLNILETISAINIDEEYLKGKDVDLIVSTVELN
TSLNYICVGPFMSLDDEQIIKEKIKSIAQNKLINLNTKNDTKSKNKVYEQITESMNIGKDILQFLEEIRFEKFESKDLSELIEDSSKIFAKSSEDIMSIKE
SLKERLKISIPYIEESKILLLHCMSERIDIMKLSIIKLENRIVLDSNEEIDNVVFMLLPKNSPSYQRQIMSEISGSLIDNIIFTNKINKFSIEEMTLEVKDIV
FNFYTNRLKAFIDE

>CORE_REP|Org18_Gene1493#

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IVARDFICFGNPDAVIVVCDATCLERNLNLVFQVMELTDKVILCINLIDEARKKGITIDKKLLEDSLGIPVILTAARNGSGMDELLDTLNDVSFDKY
KLNNKPVRYNENIENVVKSIQPELDNIIPGINSRWLGLRLIDGDESIFESMSNYIDKDSIDAINEVKKKIPDNINKQKIRDEFTKINYDYAKKLSDEC
CSNVAKKSTDREEKVDKILTSKIFGLPIMLLLLGTILWITIEGANYPSTLLSNLLLGFEPSISGILNSINCPSWLNDMLVLGLYRTLAWVISVMLPPM
AIFFPLFTLLEDFGYLPRVAFNLDHLFKKACAHGKQCLTMCMGFGCNAAGVIGCRIIDSPRERLIAILTNNFVPCNGRFPTLIAISTIFFSSVITNSF
VSSVATALCITLLIILGVIITLLVSYTLSKTLLKGVPSTFTLELPPYRVPQIGRTLYTSIIDRTIFVLGRAVMVAIPAGVITWIFANIYIGDLSILSHVANFL
DPLAKLIGLDGFILLAFILGFPANEIVVPILLMAYLATGSMIELDSFSALGQVLREHGWTYLTALNVMLFSLLHWPCATTLLTIKKETGSLKWTALG
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>CORE_REP|Org40_Gene2650#

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DANKFERQFDLLLSIIDDGIICTNNDGIIQFYNHIARKILSINANEMIDSFVGDCIKDINFQNILTNKTPFFEKLIKINHIDINLEIKHIQLNVFDGFILK
MTKFSQLEKKQAKLRAQLVNSGNISKYTFDDILGSSIQTINTKKIANKMAQSNSSILIIGESGTGKELFAQSIHSASRRKDGPFVAVNCSTFQENLL
QSELFGYDEGAFTGAKKGGKIGLFELANNGTIFLDEIGEMDLNSQSKLLRVIQEKQVRRIGSNNVIDIDVRIIAATNRNLKELVSKNMFRRDLYFR
LNVLPLKIHPLRERAADIFEIFGSLKYDIPCNFILSEEVKEIFKMYRWEGNVRELRNLGEYFCYLGKDIIEICDLPEYILDTIDSNYSRTVCNKVSDNIK
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INRSNKLNS

>CORE_REP|Org65_Gene2693#

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SEYLTGTQGKDPGYDPLPFLIEEAHKRGMEFHAWFNPYRITMADESIDKLPANHPAKKNPSWVVKHGNKYYYDPGLPEVRKYIVDSIAEVVQ

NYDIDGVHFDDYFYPGVSFNDTATYQKYGKGQNKDDWRRENVNTLLRDVKASIKSIKPNVVFGVSPAGIWRNKSSDPTGSDTSGNESYVGTY
ADTRAWIKQGLIDYVVPQLYWPIGLKAADYSKLVAWWANEVKGTNVDLYIGQGIYKQGQSSYGGQNIAKEIVQQVTLNRKYSEIKGSMYFSA
KDIANSTSIQKDLKSLYSSSEEPVTPPSNVKVEKLRGDERYDTAVAISKKGWATNSDTVVLVNGYSIVDGITSTPLATSNDAPILLVNKDNIPTSTK
NELKRLNPSKVILIGGNNSIGDKVESEIKDTLSNVSINRVGGSDRYSTSLMIAKELVKTNPVEKLYITSGTGEADSLSIASKAGEEKQPIVLVSKDNV
SDEVYNWISDLKVKDAYFIGGNLSISDSVINKLDKVITNDVSKNRIAGENREETNGKVIQKFYPNAEYSSMFVSKSNQLVDALTSGPLAAKLKSP
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>CORE_REP|Org15_Gene2127#

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ASGFAEEGTEEGTDLENQLIEISNTYDMKILGPNCMGLLNCIDKVNLWAGGSKWDLDTKKPGIGIVGQSGFITAEIVSSDYFNISYGFSTGNGNI
VTLEDAVDFLVDDNYASVIAIYLEGLKNPQKFIDALKRAAQKRKPVIILKSGRSEKGAISAASHTGNLAGSSKAFESIFEKYGVISVENLEQFMCLA
QAFSVLDGNLPTNSNFAAINFSGGENTICADLAEENGVELAEISSETKEEMKKYLPGFATPKNPLDATTALFHEKDMIVGLLHTFEKDSSVGFT
MVGANIRDEENEMHETLCQAVSEAREQGLKKPVFAVPTLEGNRYLDYRNRLEYNQVPIMSSVGTTFTCFNKMAKFIDYDYSKRTLEFKAVKKR
ESNNVVALSELDSKIEMKKYGVPVPGQGNAKSIDELDEILKYIKYPVVLKINSSEILHKSDVGGVKIGIKNRDEAVDAYNEILTNVKKAKPDANID
GILVQEMVESGIEIIIGITNDDQFGPMLLVGLGGVFVEVFKDTTLYPLPINHDEAIMMLKKLKSFKLLNGYRGSEPCDIDALADMMVKLGKYAYE
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>CORE_REP|Org95_Gene1329#

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PGEIVKNPLVYWKKIVHPEDWNRFYKSNTEIGKNQMDYHTVEFRAKNRSGEYIWLRCRGQLMRDEFGEPSIFAGIMTQLGKQNKIDSLTQLL
NYHEFMSVFEDKISNPMIEKLCIVLLDIDDFKNVNEMYDRDFGDNIIKTLAQSVQSILPDNAELYKLDGDEMGILVDNVEENEILTLYNQIQNMI
IHLQLWRKYGLNITISAGCVIYPKHGDTVKELYKCASYSLQYAKEHGKNRLVFFSQEILKNKMYSLEMMRDLKASINDDFRGFSLRFQPQVDTES
HKIIGVEVLLRWTNDKCKAISPLEFIPILEENDMINIVGAWVLRMALRTFRKWIDYYPFFKVSVNVSAVQILEDTFIEDIVKIIDDENFPYQNLVLEL
TESHTVQNMSILQFKFKALQDLGIYIAMDDFGTGYSSLEVLKFSPIDIVKIDRVFVKDILKSKFDATFIHFIVAICHDVGIKVCLEGVETQEEYDLVK
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>CORE_REP|Org82_Gene846#

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TAVFNLASSFGKITKNDDLKLDVKLYSEMKNWSDDNIIYIGKPENTAEEILDILSIKEQTLLSSNCIIKQVDSPYNKNKKMMVVIGSNEDDLIKASN
LLIENRLSNQVLSSSVLVNKETNIKINREQKLNLGHLTLKDLGYSDFLLEGAFNQQALFDVKIPTGKVLDDGSKIILNLRYSDNLDFEKSLVTVSIND
VIVGSKKLDRSHSNNDKLELKIPKDIDNKNYYQVKLTFNLSIKNSNCVTRESNNPWAYVSNNSYLALSTKENETLSFENYPYPFVRDDEFNDLTVI
MPDYSGSQAMTWMFRLGVTLGTNINSHNGNINVIRGKEFSDKYKDTNIVVFGVPHNNSVIKMLNNNLNIKFDKNYSNFISNDKISFIDDYGK
NISTIQLIKSPYNNQKNIMVISSMNEKNLYLGMDYLLNKSKVNDLKGDTLIIDEYGEVEDLAYNLKPKKEVKDSSWNMSINKTTKVFLMISFITIIV
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>CORE_REP|Org18_Gene2588#

MLDLYKDVQYVKGIGPKKADKLNKLGIFTLKDLLYYFPRQFEDRNNLKKIAQLEDGEKVTIKAVISSINTFSPKEGMTLTKIDVKDETGSAKLVFFN
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NIHSPSSKESLKIALYRIVFEELLILQLGLFVFKSGRNKEDGIKFETSKDLKKIISALPFKLTKAQNRALDEIIQDMNLEKIMNRLVQGDVGSGKTVV
ALLALANCVLNGYQGALMAPTEILAGQHYISLTESLKDFGINVGLLIGSLTKKQKDTVLEQIKNNEIDILIGTHALIEDKVEFNNIGLVITDEQHRFG
VMQRSKLSLKGANPDILVMTATPIPRTLALILYGDLDISIIDELPPGRQPIETIAIEKSKRDRAYNNLVRREVESGRQVYIVCPLVEESEAIEAKSAVE
LVEELRAEYFHDLRLGLLHGKMKSSEKDEVMRLFKNKEIDILVSTTVIEVGVNVPNATLMIIENAERFGLAQLHQLRGRVGRGSHKSYCVLIYDS
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EISLN

>CORE_REP|Org49_Gene2710#

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MKSFLEIIDEGIASIDKLGKFIYCNKVFSNLIGIDQNEIISNNFMDLFSDKVVKKIFFQEDEVNDEVVNLNNKKLIINKVNVYENNERIKSIISIKDISAI
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SFTGAIKGGKMGIFERAHTGTIFLDEIGDISLDVQQRLLRVLQEKEVMRMGGSKIIPIDVRIIAATNKDLKKKIKEGSFREDLYYRINVLHIEIPRLRE
RKEDISLISKYFLDEINSNKCFTEESMKALKLYEWPGNVRELKNLVYYIDTIVEEDRVDYEHLPEQFRFEKNNTLVNENFDSIILDFKQSNFFEESICI
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>CORE_REP|Org63_Gene2679#

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LSLHKWNLEEIPMVIVIQIMTPLFVYFVAEEIGVSGILAVVMAGIAHGIEKEHLQNTTTKLRIISDNTWYVLEYVLNGFVFTLLGFLLPSIYTGLSSK
NENMALELTFISTLIVLILFIIRFIWVYLWHNSFIKTKKNPLNNFFVGFLGFKDEEVVKESISKCKYSLIVATCGVHGTFTLATALSIPFYLADKDVFP
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QQGLLAVLKLLEDGKISDRAFKLYRFYITKSRKSVQKSIFKIVKLKISMWIINRKVKKEVKEKITKIVSENKEIIKEFHHAYALSTKTAISFINKNTDEN
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>CORE_REP|Org18_Gene2819#

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SGADRHETNANVIKTFYPDKELSAMLVAKSDIIVDSITAGPLAAKLKAPILITPKTYVSAYHSTNLSEKTAETVYQIGDGMKDSVINSIASSLSKHN
APTEPDNSGSAAGKTVVIDPGHGGSDSGATSGLNGGAQEKKYTLNTALATTEYLRSKGINVVMTRDTDKTMALGERTALSNTIKPDLFTSIHY
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>CORE_REP|Org82_Gene2537#

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>CORE_REP|Org18_Gene2241#

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AVYVPFGLMYIFMVSIPVGKSEFPMRLSALAVGAVIIMIAQFVMNRNRMKNVGDKELISICDELLEKISLLKNTINDDSSIIKSSMRKIDSCNYRI
NSISKNLKMVIFDNRKDDFYISIRGIDIMNILFSLERISLILERYKKDSKEFEDEDIKNILEESSINSKSDVLVVATKEINYIKMCLENKDTITDKEILGFR
DYVIAQDTKNINLKEIYSVLENLYEFLVDYKKVKSRDEKKAERKSKIPHEFKRLSIYKKNFNLNSIRFSYAVKIALATAVAGFIMDYFHLRDGRWIM
LTVFSLTQPYAENCIQRSRKRIEGTFIGAVIFIVLFSIIKDSTLRSLIVLLAGYINSYVVDYRKLMVCVTVSALGSAVVMGDPNVLTISRISYVALGAII
ALIVNKFILPYDAKTGYQHVIEMYKGIVKNIIDEVNKSIENVADVYYIKNLLLIPSLIEDRLMLINAIYKDKHQEDFLENQKLLISNMYNLYINVNKN
KIKDEDVEKILRDTNYISNYNVDKYDEGRSVILESIVNTKSLGDKIICLNLLQTLNGVKEMYRISNITKVSIKEAA


>CORE_REP|Org36_Gene176#

MKKSVALVNDSRKDLIDFLENNLKLVFGDSININRYFINEINDNDIINDDVILVMSVERLDKIINNILDKKKVIVVRRTFREDKIYNLLSLPQGTNVLI
VNDSDETTLETISLFYKIGVTNIRPIPYMNDNNYKNIKIAITPGVPEKVPSFISDIFDLGHRYIDISTFIEIINLLQIDSKEIQSNLVKYSEEIISLDTGIKD
KYKELFLKIEELDTILNLSKDGILFTSKDGEINTYNSKVKDILDINEDIYGKYIEDIFVDSLKVLLSEKEILDKVVVFNKKYINVNKKNIYNRDEKMGTY
YSLQEITYIKKLEQNLTKKLREKGQIAKYTFKDIKTNSPKMFECIDLAKKVSKSDLSILIRGESGTGKELIAQSIHNNSNRKNQPFIAVNCAAVPENL
LESQLFGYDKGTFTGGLKDGKQGLFELANNGTIFLDEIGDMPLELQTKLLRVLQEKQIMPVGSHNVINIDVRIISATNKNLEQMIDNSQFREDLY
YRLNTIPINIPPLRERKEDILIIMEDLINKKLIITPEAKKLIQNYMWKGNIRELQNVTSYLNIMCEDIVLEKDLPPNLRSSDNKNTSLKLKYSKNDILNI
LEILILNKESDVGIGRGLILKALLDKNLQITEGKIKKIFEYLKKEELIICSSGRYGSKITQKGEDFYNKLKYKGL

>CORE_REP|Org14_Gene669#

MILLQKKIGIIASDIELKERIEELYREDVENGTIIIDILNLDLMENQGRILVEKGAQAIIGRGGGYSLVIDTVNVPVIPMNMKSTDLLRAIEIAKKYSK
KVVLILGDNEVSFDYVGWRNVISTEITEEWFESKYEIRSKVVKYIDQKDEVVIVGGGLACSFARQYGIDSVFATASDESIREAVEYCKKLLDTLGEE
KFNNEVLRNILDGIKDGVIAIDSNGSIILYNESAKNMLKVERKCALNKYILDVFPKMEWMLDCLHEKEAVEDRKIRNINNLIVNTRTTLIKVDNST
YGVLGIIQDITKLQNLERKIRFDLNQKGLYARYTFDDFLFKDKLTKEFIEEAKKIGKSDYTTLLYGESGSGKEIIAHSIHNISKRKDRPFVAINCATIAE
NLLESELFGYEEGAFTGARKGGKRGLFELAHGGTLFLDEINSLSFNIQTKLLRVIEERQIMRIGSDYIIPLDIRIIAATNESLTEKIVMGTFRADLFYRL
SSLEINIPPLRDRREDIIPLFNNFVNEVLKDDGLNGINSIDENFVLTKDEIDKLYNYSWPGNVRELKTIAQKYVVTGKIKLRQDRNFKTKQSLSNSE
VDKFNSETTASAEVQDESINISKINDGKISIDIKEVNKYVEEKIISMLFAQGLSKNEVAQVLGISRTSLWKKYNKNI
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>CORE_REP|Org18_Gene1724#

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NHLMSGKVDAVVGDEPVLRYYINNYGLSNKYSVLSNPIYTKKAVLAVPKQYEELVSILNKGIFKLQKNGVYKDLKKKWYSTYNEVDDILYERGIV
PSIYLFIGIILISIYVFYSYTYLLKIEIKRKTEQVIENKKTLEATFNSITDIIMLVDENNNIVESNKVLYDFMGEMSYKIADLISMIKGVIENTFSENTNKT
SEIEIHNKILKINTFPVEYKKNNTEYIVVLIKDITNDKIVEAKLLRENKMISIGQLASGVAHEIRNPLGIIRNNCYLLKDNVTMEEVNDCVKSIESNVD
RASNIITNLLNFARISDDNLEHINIRNFIENIVKLQYKMLQLKNVEIKIDCEHNLICYINGESLKHVFINLISNSIDAIHQDGKIIIYCYEKNHCLFIDFK
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>CORE_REP|Org33_Gene2805#

MLKLGEKIIYELSDGFELSGISRYSKEYKKLHITNLGNIIISKSDEVNEDTGVKYIYSFSDNKEKLEAVLEDSQIIVYGNNLPFYIKSENSSKNVTANLT
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DSVVPSDLNERVKDNQKIGNLPKDCEIVFCKISGNIDGFDYKNTNMLLVKYQDQLIFINKKSKKTIVKSAKDNCSKLNLGEDIILYDNKNVFNLHI
NDKNREIMQIDDLKDIENEIVGYTLKHAPFFIQEDFDSLTILKSFQKEIISIKNSDIKDIVINKELENENSNFVETEIKFNNQKVLLNLSKSMVQKLM
QDVFIYAKQPLLKENSIEVIYKNWSKAMNDMIIFNFFGNIYYMKSEFDKILEKELNDEIRIEVINSLYKQIQEQRNNLDLLSAYMPRILENQEIDLF
EKYNTKLDVQVFKQIKNLLSDLSYNISSYLNEVEKSLDNIIFVISGEDKKKYNYRMLKESESASLDVFLKQAISRLNHLVENMYPYYVDETSREMFK
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>CORE_REP|Org48_Gene1112#

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VIGDIYDRGPRPDIIVDKLIEHHCVDIQWGNHDILWMGAASGEKTCIANALRISARYANLDIVEDIYGINLLPLATFAIEMYKDDPCKEFIPKIND
QSVTTTEKSLMAKMHKAISIIQFKLEGEVIRRRPEFEMEHRLLLNMINYDEGTITLKGKTYKLKDTYLPTIDKKDPYKLTIEEKNVIDKLVSSFRGSE
KLQKHVSFLFSKGSIYLKANSNLLIHGCVPLNEDGSFMSMNIMGKEYKGKALMDRMESLAREGFFFKDKAEEKLYGMDIMWYLWTGKCSSLF
GKDDMTTFERYFIAEKETHKENKNPYFKLRENEMACKKLFEEFDLELDESHIINGHVPVESKNGESPIKANGKILVIDGGFSRAYQKTTGIAGYTLI
YNSRTLQLVSHEPFNSAEEAIANESDILSTTVVVEHKAKRKMVRDTDEGVKIQEEIEDLKLLLMAYKKGLIKEM

>CORE_REP|Org94_Gene2636#

MKKYEIFIFMSIIVLCFISFPHKVFGQEENCLEDFERWVQENKNNKEEIVYTLSCDMVIDEEFRFYIPYDSNFTIDTNKYKILIKNHGRFIIDDNELNI
IGEGGKEGVIHIENGGSISIGINNIIATDGTALYVEEGGDLHIKSSYESVEKIKANGKDAIGIYTENDIRILNKDIEVNGEHAIGVYSKGDVEIEETSIK
AYSSNNESGLLKDNNKLAQSIISESKKVYIIDDYNELIPSIAEDSGYNIVKCCHRGIGVFSDEIKVSKDDKIENIKFPKYMVLETSSGNRLDIDVEWD
FTDYYEKLEKGENFNITGKFKTEMLNKEKIIINDDVVPILNVSVIDKKPIDNLELEFQNTKNGYVAVLFYDMPYSASKVFVEYSSDGINWISEEQE
DIRDQAILFFEDFKLRCFRVKVVGGLKEGYSNIVFKPGFIMGGGDNQETPDDERENDDIDGDRGGGGRDDPDRDEDDNNQDGNNGNENN
DSNNNQNNNNENNNNENNNNENNNNENDNSDEKQPNTPKDDVESSTDSNENKNPHDIPKDGNKENNSDKEKGFYNKNSITENDDNYDL
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>CORE_REP|Org86_Gene2665#

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LIVSTDASGREIPQGMEKYYEPVQGNGLVLSIDEVIQHYTEKAVQKAYELNNAKKVTAIAMNPKTGDILALASKPDYDPNDSRTPIYPYYQEELE
KYNDKDKIKGYYQMWRNPAVSDTYEPGSTFKLITSSSALEEGVIKDGEKFTCTGSVTVGGRKIKCWRHYRPHGTQEFKQAVQNSCNPVFVELG
SRLGVGKMYDYIEAFGLMDKTGIDLPGEAKGILYNEKNVGPVELATISFGQSISVTPIQLITAISSIANGGDLMQPRVVKSYTDNKGNITETVKPK
KVRSVISKETSKKMLEIAESVVTEGGGKIAYIPGYRLGGKTGTAQKVIDGKYAPGKYICSFVGIAPCDDPQIVVLAIVDEPTGVSAFGSTTAGPIVK
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>CORE_REP|Org15_Gene2337#

MSVTEKIPSIDHKIFKILIMCSKKEFVSINSIANELNVTTRSVRTYIKQLNKDLGNDIAIIKYIKGQGYKLEIKDEQILNKIIDINRKNVFSLNSKEDRVE
FILNYLTELDGFITLDSLADEMCVGRTTLVNDFQYVEKVLASYNLNLIKKQNTGMKLNGNELDIRLFILNQLYKNSRKDFNNSKYFKGIKKEEIINL
EEKLLTLFKKNNFYVTDEMLREVINYIVVLVYRVKETKKVKDYDVKFDLLKSYDEYFIAREIKHIISEMFECILNDEEIIYLTIPLVSGNAPASECALNS
SRINKNIDELMESIFNQIYVDMGIFINEDELRVGLGYHLSFTLNRLLFNIKLKNVLLEEIKQNYILPFKLAQIAGKVIEKKYNLEVSEDEIGYIAIHFSG
YLERNSSRFYSIKKIAIICSTGLGTAKLLKIRVEKLIGNNPKIDTLSSFNLRNINLDEYDIVFTTIDLDTSNINTIVLKINTIFDENKLREQLKTVLCLREG
NIDTTNSTNLLINNLLDEDKFMILNEKTILDSLEKMMDNLMDLGCIDDKFRKNIFNREEKSPTVFDKGLLFPHSVNEKSDKFLMAVGILEEPIKYA
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>CORE_REP|Org36_Gene886#

MENKFLPISKQDMIDRGWEELDFVLVTGDAYVDHHSFGTAIISRVLESAGYKVGIIAQPDWRTTDDFMKLGKPRLAFLVNAGNMDSMVNHY
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NDGYDPKYIRHIDGTCYISDTLEEIYDKYILIPSYKEICEDKMKYVEAFKIQYDEQDPFRGNIIVQPHGSKYLVQNKPEKPLSREELDEVYGLPYQKT
YHPVYEKFGGIPAIEEVKFSIVSSRGCFGSCSFCAITFHQGRAVQSRSEKSIIDEAIGITNLDDFKGYIHDVGGPTANFRRPACKKQITKGACKNRQ
CLSPSPCKNLDADHSEYLHLLRAVRKLPKIKKVFVRSGIRYDYVMADKNNKFLRELIEHHVSGQLKVAPEHISEEVLKYMQKPAGKTYDKFRQKF
FAINEELGKKQYLIPYLMSSHPGSTLNSAIELAEYLRDTHYQPEQVQDFYPTPGTLSTTMFYTGIDPLTMKPVYVPKSKRDKAMQRALLQYRAP
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>CORE_REP|Org77_Gene1152#

MKKSLKQYLVLALTLVLVFACGVPESSAASKHVIIVNSRKNTLGYFVNNKLVKEFRVATGEKGSETPTGKTKVVNKIKNRPYYKGNIPGGSPRNP
LGDRWMGLALKGTYGDTYGIHGNNNESSIGKHISGGCIRMHNKDVRWLFDQVPVGSDVIIDYSNDSYVKIAAKYKINLNQTGWKTENGKKY
YVKSDGTYQKNSWLKVNGKMYYFDASGVMQTGWKTINNKKYYLGTDGARVSGWKIIDGKTYYFNSDGVMQTGWQEKNGKKYYLGADGL
SVTGWQEIDGNKYYFDKTGIMQIGWQQIEGKSYYLDKDGKMLTGAQKIDGKDYTFNEDGTINPTWDTIIGANRFDTAKKISSVGNWNADSS
DTVILVNGNAIADGITATPLASSYDSTILLTNTDNLPNETVEEMKLLAPKTVILIGGENAISSKLEQEIKTIFNAETKRIAGQDRYQTATRIAEELGSR
EEIKTAYIVSGNGEADALSVASKAGEEKQPIILVNKDGITEESYKWLTERKLENAYFIGGPSAISDSVIARMNDITTEDISGNRIYGDSRVDTNAKV
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>CORE_REP|Org45_Gene309#

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NVANNVMSLVGSKFYKWKFDIEVNPLLLGIGFIVGLEVSLTMFAGSILSNFGIAPLIGYFTDMAKDGAMVWNNPAMPLNQMDVGAISSSYVK
YIGAGMMLCGGIIGAIKLIPTIIASIKETLKAKSSTGEGEEGSSIQMILLLGGVVIGFLAAFLISGGNIVMAIIGAIISLLLSLLFVIVAGRLTGTIGTSNL
PVSGMTIASLVIVTLVFVIMGWTDLEANKSLLLFGSFIVVAIAIAGGYTQSQKVTYIIGGSKNEMQRYFTIASIVGVIVVVGVILLLSDQLRATGDN
VQFALPQANLMSTLTSGIMSGSLPWVMIIVGVFMAIVLYALNLPIMTIAIGFYLPIATTSIILVGALIRLFVELVSKTEKEKEVKVSNGISLSSGLVA
GGSIIGLIGIILQVTGVVTPKVPSGFAATNSMAIALLVVLVVLTALPIILSKVKNNEQE

>CORE_REP|Org76_Gene171#

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YILYNNTYIKLEDLANSLYVSKFTILNDIKRIKPILSKYNLILVSKPYYGVKVEGKEIDIRRCISNNMINRNFENYIIGITDREIELFNNVDLIELQRVVLS
EINKFNINFLDFNLKNFIIHLAITISRILDGYCLDNVLDVVLTDFQSNTTVENIFNYIESKYTIIISKADRVYLYNHFITKSSLLDNVSNRVDTKIIEYVEEI
LEVINNQYTFDLRNDSVLFDDLVLHFKSILNSKSYNLNKVNPLINTIKSNYPLAFEITLNAIEKVFKNSIYSLTEDEIGYVSLHIGAGIERFFQNNIKCK
NVVLVCGSGYGSSRLLEVQLNKVFHDKINILQCLSFNQFLASELSDVDIIISTIPLNHDSIPIVLVDLKLLKKDIENISKSITNNSHIYSNLLDNFFDKN
LFIVNPKIKDKDELIKLMCNKLTQSEIVFPSFAESVFYRESLSSTNIDDFLAIPHPMELSSIRTKICISILNEPIYWSEDSTVKLIMMLAINKDDYIKINSI
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>CORE_REP|Org66_Gene2171#

MKIIDLLDEKSIKLNLNSKTKSEAIEELVDLVANSGNLNDKENYKKAILAREEMSTTGIGEGVAIPHAKNSSVTKACIAAAVSKEGIDYESFDGSLS
NLFFMIAAPDGANNTHLEVLSRLSTILMDEDFRNKLINSSSEKEFKEIIDKKEREKFSEEYQDEKVAEKNIIDTKENDANKYPKVLAVTACPTGIAH
TFMAAESLNKMAENKGVSIKVETNGSAGVKNKLTKDEIENATCIIVAADKNVEMARFNGKKVIKTKVADGIHKAEELIDKAVNGDAPIYHGGD
GSHNESNEESESGFRKIYKHLMNGVSNMLPFVIGGGILIAIAFLLDDYTINPSNFGSNTPIAAFFKGIGDKAFGFMLPVLAGYIAYSISDRPAFVV
GFVGGALAGDGGSGFLGALLAGFIAGYLVEGLKKIFSVLPASLEGIKPVLLYPLLGTLLMGIIMTFLVIPPVTAINNAMVGFLNGLGGTSKIFLGLV
LGGMMAVDMGGPVNKAAYVFGVASLESGQFEIMAAVMAGGMVPPLAIALATTFFKNRFTKEERDSGKVNYVMGLSFVTEGAIPFAAGDPL
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>CORE_REP|Org9_Gene1067#

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YLLNDDFYLKNLFTEVRYIIVDSLESSSNAEVDFITEALDNTLQSYIYFDYSRDYSVFNNVDIDYINEKIISKIKSKEENIKKKEIRIEDLYLLPANIELNQ
SSQLYNEMLDLISEKVISLIEEDVSPRDIAIISPINNSILEHQIRDSLIEKNIDVFSTKKDKKAVDYPYGNALVVATCIFYGYLDFIKEDEYLSFLETLLEI
NRIKAFKIFNETRHLSIDDIDEHSQYREILQYIEEKKKSDIKIHEFLTQFYIDKMLNLKEGKKNVGLCKKIIAESESFSESLSLLGMKKEKIFVEALKSTI
NDYYSVVDIEELKSKDKIVITTPYSYISSNIDRSIQIWVDIGSNAWNMKIEKDISNLIVLRKSFEEKKIYTNEMEEYYKKYYLYNTVYNLLLNAKKIYA
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>CORE_REP|Org54_Gene2682#

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VGTTSDIKAVVEKYNVDEIIFSIANIEKRRKKEIIDICKNTNCKIKTIPGIYEIIDGKVDIKQIREVEIEDLLGREPIKTNLREISNYIEGKVILITGGGGSIGSELCRQIAGFNPKELIIVDNYENNAYSIQQELLRKYKNKLDLKTVIASIREEKRMDEIFNKYKPEVVFHAAAHKHVPLMESSPGEAIKNNIFGTLNIAGLSSKYRAKKFVLISTDKAVNPTNIMGATKRAAEMIIQTMNAESQTEFVAVRFGNVLGSNGSVIPLFKKQIEDGGPVTVTHPDIIRYFMTIPEAVGLVIQAGAMAKGGEIFVLDMGEPVRILDLAKNLIKFSGFEPDVDIKIEFSGLRPGEKLYEELLMSEEGLLDTEHKKIFIGRPIDVDREKITKYLKLLREITNNEEVEKIDGIMRELVPTYIKPEDANIKEIATTREK

>CORE_REP|Org51_Gene2854#

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>CORE_REP|Org28_Gene980#

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>CORE_REP|Org52_Gene1227#

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>CORE_REP|Org44_Gene3221#

MDSLLYVIEKDKHTNEELREILKSNKNIRFVSLMGVDLGGNATDEKIPVELFLDDIDKFLESAIQTDGSSVELYNIATLNNAKVDLMPDKSCHWYVDYNMEYIDEEVGLPVGTLKIPAFLIHDNKKVCSRGVLQKADKYFKKSMYEIFREYPHVINNIGIDSVDDIEEIMLTAATELEFWVNTPEDKADLEKLYVSQSLKEQYWKRTHGIIRTCLEKSLIILQKLGVSPEMAHKEVGGIQSSISIDGRTNHAMEQLEVSWKFSTPLQAADNELLVRDVIEDVFTSHGLEVTFKAKPIHGVAGSGGHTHVGVSAKLKDGSIKNLFAPKDLKEDYLSELGYGALMGLLYNYEVLNPIVTASNDGFNRLVPGFEAPVCIVTSLGHSYEIPSRNRSVLVGLIRDMKNPKTVRFELRSPSPLSNTYLVIAGCYQTMLDGIKAAAKSGLSTKELEKELSKNVGEESFYLEKDRAYRDENDVFEHYSLEERNARFGIPPATVYENMKNLEIYASKLKSLKQGDVFTDSIIESFKIGAIDKWQKKLKTRIIEEGIQKIRSIVKIHTKENMDALDEVVWNSISDLKFNIMKDTLTRESLFTRVREAVENKDYQAASDLQIELKRSMEEIQQLYMQYKKNIY

>CORE_REP|Org18_Gene2400#

MVIYLKRSLIEDLKRNINKIEYDMLTKFYLNLTDLNYILDYHKDLLNTKLEDNSRVYTLYLISLINYIKKDREASYNYLIESLKYIKKLSLKDDSDIISKIYIYLTLSAISIRKYDKVNNFYFSAKKIIRQNHLNELLVLLNMSLCVEISALYQTKTDVIALVEEVSFFKTLKNKALVSRANYIFGRVYLYLFNNFIKSMEYLIECLKLAQENNLYSIEAFCKCIISLCYLESGNNVEAIKYINNVLDVAHSNNSISVTERVSIKIDLIWAYLKEDMNKEAEVILLKTIKLMKVVEGVYKDYLYSFIFLYSAEIELKKDNCSFEKVNTYLILSKNIYKSFGDVFIYNSKLDYIYKLYGDLYIKFGNIDEGISCYIKGLNLVKKSSLNLRKISIFYGLIANGYELKKDFKLAIEYYKSMDWYSDRWEKNNSYKTSQAIHKQYELRQKQESLRLLVDDNKKLENDILKDGLTKLYNRRYLEQQLDLFNGTRDKNMVAILVDIDCFKSYNDNYGHLAGDKVIVKVTDIIRSVFIDITEHIIRYGGEEILILVDSIESIGVEEIDNIELYIKRVFKLLEFEGIEHIYSKIKNYITISAGVSIKRCHSRKDVEILIEDADKNLYKSKKAGRNQYIII

>CORE_REP|Org13_Gene2746#

MLSNKKRSMAIVMAGATVMSAAAPIFADNTVTENVDKNYTVSAKDSAKLIEEVRKALEVKFEDTKAGANVNDRVYDIKVDNVNLTNATQLQNKINSLTEGQSLKVTIQDKGHQVLGGKVVDYKIENYKTAQEIVDAVNAYNATLAEDSDNKLTATIKSTNTVEVKRAKDSANVITLNVGDQHLDFSKVITSEEGTFEGYEKSYSDIDSKELHTITVKNADLQDISAEELFDGIRLTTLGREIVNKVKNGYALTFENEAILTQEQEDSDDKDKPEKSSFDIVLSKANEKSETISVSSKNHKLVRDLHKVLTDVKDGKELKVEVLSGDSRFTTAVEVSKERFKDGEAEAIILVGEDAIVDGLASAPLASQKNAPILLSKKDSLPSEIEAEILRVLGSNLSSKKIYIVGGESKVSKETEEKLSKLGVSKVERVSGEDRFETSLEIAKQLKDTFKTAFVVGGNGEADAMSISARAAQFGAPII

VTGNELDANAEKLLKGKELEIVGGENSVSKEVEDKLVDIDLNNKVERLAGENRKDTNAKVINKYYAGATKAYVAKDGYVGGNGQLVDALTAA
PLAASSKAPIVLTTEELSKSQEEVVELRLKNATKLVQIGEGIAKNAIEKIAEKINLFTKN

>CORE_REP|Org96_Gene2374#

MITKKHAIIVKSLSNKDGYMTSNELAIKLDVSTKTIKRYIADLNSVLSKYDLVIASSRGIGYKLSGSKNNIARAVKEANKYIDGFLDDSEESRMSNII
CMLINRNYMSIEAMAEELNLSIAAINKLSSKLKRKLEKYDLVIKSKPYYGSYIHGEEINIRQLITDYAIKLDEKSKVKVFLDDISENDIHCIESILEKHLR
EKDTIISDKDFNLLLSKIIVSVFRSKRGHSNNINLMDTSYRFHNYYFIENLMKEISDKIGFKLIEDEVIYISNYSGVIAYKGTQGRKNTSEIEERISTVIS
SALQDIFLISGSDYTKDDEFMVAISDHIKRFLNRARANVKSNNPLLHQIKEKFPIAFNLAVFLSNKLETEFNLKLDEDELGYIAIHFAASNERMKKN
TSKKICIVCHYGIGTGQLISEKLKQNISDLSVVGVYPVRYLDMAISQDVDLIVSTVELKGYEKPVLYIENIFDDSLIENVNKAFYEKEERRKIISNMFD
EKAFFSIKASTKEEVIISLSNKLKERDFIEESSIKSIIDRENISSTEIGNLVAIPHTIVKGDKKSIIGVGILENPIIWDKQEVQLVFMVFFNTKEKHNFSIF
KYLYNFIKDEGGVRGIIKICDFNKLMALIGN

>CORE_REP|Org5_Gene1668#

MFTGIVEEVGILRKITANGKSGKVTILSNKILDGTNLGDSIAVNGVCLTVSNLGKNEFTADVMMETIRSTNLGLLNANDKVNLERAMSLSSRFG
GHIVTGHVDGKGTICKFEKDENAVLVSIRPDKKLLSSMILKGSVAIDGVSLTISYLDDEIFKVSIIPHTKINTILLTKNVGDFVNLESDVIGKYVNNF
MANNYKELNSNSSNHKSNIDKDFLFKMVFKNNKGVNYMFNTIEEAIEDIKNGKMVIVVDDESRENEGDLLMAAEMATPESINFMATYGRGL
ICLPATEKKFKSLNIPLMVRENTDTFQTAFTVTIDGADTLTGISAYERAETVKLFCDENSTSKDFKTPGHIFPLIAKTGGVLVRDGHTEASVDLARL
AGFKEIGLICEIMKDDGTMARVDDLMIFKEKHNLKIITIKDLIEYRKINETTIEKVSSAFLPTKYGNFEIIGYRDTYSNEEHIALTYGNINIENTLVRLH
SECLTGDVFHSLKCDCGLQLESSMKKIVENGSGVLIYMKQEGRGIGLLNKIKAYKLQEEGYDTVEANLMLGFEEDMRDFYMAAQILKNLNIKSI
NLLSNNPDKINQLEKYGIKIENRIPINEEINDFNKLYLKTKKDKMGHLLDII

>CORE_REP|Org18_Gene2740#

MVENVFKRLQEFNGYDGYKESFEMNYLCIYESIPLREQVELANNLVDEILNMYKSESNEIYLLEDSNSKSLICYFEIFMKKINTLVKEMIIDEKWLY
KLTKELIYKSKKVEYVKLGLVLSEKYLNVENLREVVDTFSKSGEYVFYLSNTIKKLEFYNTYLFNLSKKATGSIKVFAIVNMENLDSKINSYLIEDGYK
DTKYERLLMNYIISIVDLNEYLEKRDLDKEKINNLARLICNYLLSVEFKYIGNKLELVNRFLPTVVNYGTNFESLYSIFLIAINVLKDENIECNKIEFEKEI
NGILLSEKWKNIYFEALRDASGKTEDIIKMSEIYDVNLSFDDLLPYLNRDIRDFEVYWYISKKGTTSSRLKLLNFFEETFKIDDLIGKMKDIEKDKLT
QEYYDDMLFFIVLKGSKSLYPEGKNISLKGIFGNINEVRKESINILKRYREKLSLEELKIVKEAYEKEKNVILKDELRRVLYESNNLKKEFVNIEKIKVD
EHGKDIYLTSIAVAGSRFRNREYLEKELEKSKIYYLTREKDNLYDEKAIKIVGETGYVIGYVPRKENYILSNLLDGGKLLYCRVTEYNLYEDCIYANVY
LSYKDVIETVENSLKMVLDKSRIKLIN

>CORE_REP|Org36_Gene1073#

MYKYLDKVNSPKDIKNMSIEEMDLLAKDIRKFLVKSVSKTGGHLASNLGVVELTLALHKVFDSPKDKIVWDVGHQSYVHKIVTGRKDCFVSLRQ
FNGLSGFPKENESPHDIFDTGHSSTSISIATGIACARDIKKENYSVISVIGDGSITGGMALEALNQLGYIDTNMIVILNDNEMSIDKNVGGMSKYL
SSIIRNSTVEKMTDEVDKILNVTQTGEILSKTAHRFKDKLMYSFSPQDCSFFDSLGIRYYGPIDGHNTKELIDILRKAKHKKGPVLLHVITKKGKGY
RFAEEQPDKYHGVSKFDIKTGVTSAKVKSMSISVGEKLVDMANSNENIVAITAAMPSGTGLNLFESAYPKRYYDVGIAEQHATGFAAGLAKNG
MKPYFAVYSSFLQRAYDQVIHDVCITKKPVTFLIDRAGLVGNDGETHHGMFDLSYLNSIPNIVVMAPKDTREMELMMDLSLKLDCPLAIRYPR
GSSYYLDKGEYGEIVLGKYEVLDDGQDTVILCIGSMVKHALEAKEILSREGINPTIVNARFLKPIDEGMLKALLKNHKNVVTIEDNIVTGGFGSRIN
KFIIDNEYNVNILNIAIPEEFVKHGNIDELYDFVGLSPKSIADKIRKLVIE

>CORE_REP|Org62_Gene1531#

MKRFLRRIILVLFILLIFISFISIKLIHNVGDYGKLINYVGIVRGASQRLTKLEMNHKPNDELIEYIDEILQELITGHGNYGLVLTDCNKYNEDLLLLEKK
WEDLNSEIKKVRMKEPNNQLLSISEEFFSLANDTVFEIENFSKEKSNYLMTLIIIISIIGILACIILILQYSKKMIKLEKLNVDLKNIAYKDELTGVNTIEK
FKLDANQNICMHKDKKFAVFYIDFENFKYINDIFGYDYGDMILKRYANLMMNDIGKYEIFAREIADRFVALRCYIDKEDLVVRQRIVDSELINTT
NEIKNKHSITVVSGICCIEDVNEKLSIDGLINRANFAQKTVKNKPGTNYAFYNDSIRKKMIEENTIKSRIHEAIEKREFIVYLQPKVNLHNQKINCAE
ALVRWLTPDKGIISPAIFIPVLEKNFFIALVDKYVFEEVCKWIRKRLDENKPFVQISVNVSRIQFYNTKFVETYSNIQNKYRIPKNTIEIEFTESVAFE
NQNHLLEIIHDLHENGFTCSLDDFGKGYSSLSVLKDLPFDALKLDSMFFKASLDKDKEKIVIKNIVHMLKELNITTVAEGIEYEEQVEFLRDIGCDL
VQGFVFYKPMPILEFEEILDKEFVYNS

>CORE_REP|Org94_Gene998#

MNKVDLKKILKKVEKPARYLGNEINSIHKDTSNSELIRYAHCFPDLYEVGMSHLGSHILYDVINKDEDVFCERVYSPAVDMENIMREKSIPLFALE
SREPITNFDFVTFTLQYELSYTNILNILDLANIPILKEERTLEDPFIMVGGPCAYNSEPLADFVDVVILGEGEEVNLEVVNEYKEWKKNKTTREDFLY
KISSIEGVYIPSFYDVKYNEDGTVQSVTPNREGITKNPTKRIIKDVETVDYPEKLIVPYIDTVHDRIVLELFRGCTRGCRFCQAGMIYRPIREKSVKRL

KEILDKLVKNTGYDEISLSSLSTSDYSKLSELTDYLVDEYASNNIGISLPSLRLDNFSMEIADKIQQVRKSGLTFAPEAGTQRLRDVINKGVTEEDLE
NATERAFEMGWNSVKLYFMIGLPTETYEDLDGIAKLAYKVIDIYRKVNGGKLKRSFSVTVSTSTFVPKPFTPFQWHGQDTTEEVINKQRHLVNK
LRNNNIKYNYHDSKTSLMEAVVARGDRRIGKVIYDAFRLGAKFDGWAEHFNLDIWKEAMEKNNLSIDFYAHRNRNYEEVFPWDHIDVGISKK
FLIREDENAKKEKITSDCRHNCNGCGINIHDIGRGLC

>CORE_REP|Org10_Gene2464#

MEEIDDTILDSMFKLTLNERLLTNNDFIENKIDVVKNLIDCYKTEQNSLMLLKSNFLLALLYGIQGFSEKMKEYILISCKYIDKCLPKDYKFLARFYS
QIAILSLKNEDVNKANLYMDKFNLICDENNFLIEEIIFKSQLIYIKASKCIESSVIIKEIETLYIKIKEINDFNCKKIYFFIIGKIYFLFLDDALIAKVNFLKAR
KYADLLKDMQVSSLCNIKIGECECSFENYECSMEYFNEVISNKKYRNVNIIQKYRASNNITKILIKTRNYPVAINNLAKSEVYLEKIKNHSLKEVEKF
DLFISLAMYYAKSNEKSFEQSICYLDRAKNILNMIKNIEEYIIYDLEIIYHQAKIYYIFGYYDNALNTNKKLLEKSKNAKNYNYVKLAYKSIYLCFEKIQ
NYEMSMKYFKMYYELKMMYIKARNRNYIDSLNYRHEYIEKEINNMRKVKLDLDKKKYVDHLTSAYNRTFLNDFLEKQEVSEYCTAFMIDVDYF
KEYNDTYGHYNGDIALKNITIIIKKYLKKDMLMIRYGGEEFLILSVCKDYKKSKIFGRKLCRIVKKFLNNNLTVSIGIDTCKNSSIDIKEIIENADKALYK
AKESGRNRCLHYHDFKNF

>CORE_REP|Org35_Gene1187#

MKKKAALATLAMLPLGVVNAHADGDIGIVTINYLNVRNEPTAESSIAFVAKKDDKVLIKDSSNGWYKIKAESGQEGWASSKYIAKSNSDSLRTS
TNKEKQVISNSLNMRNGAGTSYRVITVLKKGQKVEVISESNGWSKIKYDGRLGYVSSSYLGDVSNSTNKSKTKQVNTTSLNVRSGPNTSYGLLG
KLPKGSKVEVISESNGWSKIKYNGKDAYISSMYLSDVSQSNSDNSSQSNDKKNTDKVVNTASLNVRSGPGSTYSKLGKVYKGSKVTVLSESSG
WAKINFNNKEAFVVGNYLSTSADTSNNNSNSNSDNSSNSNGNNSSSSGQVNGMSGISGAKIDYKSLSYTLESHISKQVEKAASGGNVIAPSNR
KSTPSPEFSTFSAQRTSSFVNASSSDIEYYLNPKNFTNTTKGMMQFLKINSYRDGISESSLNSYLNGLSSSVFKNQGAAFINAAKKYNIDVVYLVS
HAMWETAYGKSTLAQGQTLTSYKGQPLSKPVKVYNFFGIGAIDKSANVSGAEAAYSNGWTSVEATIDGSAKWISQNYVNSSKYNQNTIYKM
KWNYDYTWHQYATDVNWANGISGIMENLIGLYGGGSSLVFEVPQYK

>CORE_REP|Org88_Gene3147#

MLSKLKEFQQEMIKYTETVASVLDVDIEIVDDRLIRISGTGLYKSKINESVVTEGFIYDNVIQTGQELVVLDICDNQLCIECSHYMKCLNKVIIAVPI
KYNNRTIGVIGAISTDKTKKVEISAKIDNYLKFVNHICDLISMKIEEHEVSKNSSRKMDMMIEIIENVEKGVIILDINSKISYINNIALKKLDIDKNIIEN
IVNIVSVESSSNGHELLEIDIDNKIYNINAKIIPVYPYINQYDKIIIFDKTYINHKGHVKVNSGWGNSDIESIIGNSEAMLKVKERTKKLAKSNSTVLIT
GESGTGKELIARAIHAEGSRWNKPFIAINCAAIPENLLESELFGYIKGAFSGASSGGKVGKFELANEGVIFLDEIGDLSMPLQAKLLRVLQERKFAR
IGSNKLIDLDIRVIAATNKNLLKLVNEGKFRDDLYYRLNVIPINLPPLRERKDDIEAIMMKFASKYSLELGIQLNKIEENVMNMLINYNWPGNIREL
ENAVEYMMNLVGDDGIIYKDMLPLDILNYYNINGNICKNKDINIIFEDDIVGGIVENQERILSIKELELTYINKLLNKYGRDTKTKKKIAKDLGIGLA
TLYRKLEEEQS

>CORE_REP|Org88_Gene1297#

MNDIKDIIEEIKARCDIASIISEYMSIKQSGANYKGLCPFHGEKTPSFYINTSKQIYKCFGCGEGGDIINFVMKMENLDFMDAVKILANKCGIEINT
NMNEETRIKIEKSKKFQDIHTEAARFYLSNLLGSKNLGYEYLRIRGLDDKIIKKFGLGFSLDSWNSLMNTLISKGYKKQDLLECGLIAKNRDGTNCY
DKFRNRVMFPIFDYRGNIIGFGGRVLDDSLPKYLNSPDTLIFNKKQNLYGLNFARKNLESKTIVLVEGYMDLISLYQYGIKNVVATLGTALTEQQ
GLLIKRYADTAIISYDSDEAGIKATLRAIDILTKLGINVKVLDLKDAKDPDEFVRKYGLSDYKKAMDVSTHYIKYKIDHLKKEFNIQKDEERVKFAKE
ASKIIKQLTSPVEIDFYTKYLSNQIDINVESIKREVYGKNYNKPYNNKNQKKIEEKVIEKVEVRQDGKQLVEETLIKIMLEDKKIREIALLKVEESDFLL
KESKEILNYMIKNQELDKITIDKLKSLNISEEYLKELNSISLNSINLENTKEIEGIITNIRKNSLEEQINSLLREQQELENNNDMKEVDGRVMEIALKIV
EINKILKSL

>CORE_REP|Org49_Gene1154#

MSQYININSQLDALKLKEFEKIFYENINKDVKVVPKVTPFKGINTDLLYVKDGKILFIKFMDTTEDIFFILEEELLEVMNEEYELLKLKMGQKNRNIS
YNYVYIMPYVEVEETYEFEEFVNNNIIDKNKLQDIMNKGSLDEYLNDENDEINLNLFLLDVCSEYYIINDKLHLNEKFKKISFYNDDYKYTATMME
EVQIKDVISIKYGNTLIEGGSGIGKTAIMLSRAIKLAKVYPHHKLIIFTHTKQLRNELRERIELLYKDNNNLEVHTFSSFIFKLAKKFNLIVDYNMLKN
DYEKAFNNLVKQAQNIIKNKNMFKAIFIDEAESFLEYEIDFIREFLYKTKFIFNVCSCNSLNISNRLNIFKKLYNGIEFDDKIILSKNYRQAKEIVDFTN
KFSNNSNSYINELRPNTEFSTFFYTKALRGGNKSVDIIKVSDLDDQISSVIWEIEYLISKKGLDYSEVAIVYPYNKKKLKSGKTIYFQYMLKKALEEAK
IPYICAEDNLTNISKKVGTTIANIYAIKNLEYKAVIVCELEMLYNQTINDIEQDYQVNDFVGDLNKVYLAMSRATDYLSIVTTFNEEASDIIRLITESK
DI

>CORE_REP|Org44_Gene1958#

MALDGLVIHSIVDELSSKLTGGKIDKIHQPEDDEVIFNIRNNKENFRLVLSASASNPRVYLTSNYQKENPLKAPMFCMLLRKYIQGGNIVEISQIG
FERIIKISVESLDELKEKTIKNIMIEIMGRHSNIIITHGEENKIIDSIKRVPFSISRVRQVLPGHDYSLPPEQNKLNPLDAISKDLFIKNLEESEESIFKSIY
SKFLGISPIIAKEICYRAGINQNTIIKDISDEQFDSLHKVFCNLFNDINSNKYSPCIVIDKKVDRVVDFSCINLTLFSDLSYINKDSMSRILEDFYRTKDI
KDRINQRSSDLKKSISVKLDRLYNKLKKQEEELSESENADIYKIKGELITSYIYMVEKGMESIEVANFYDENCNNVTIELNKNLTPSENAQKYFKKY
NKMKHAKVEISHQISLNKEEIDYLENIILSIENCENLAELQDIKEELAKVGYIKTQKKNSKKDTIPSTKPHEFMSSDGFKILVGKNNKQNDYLTLRLA
DNDDLWMHTKNIPGSHVIIKCAGKEVPDNTVFEGAMLAAFFSKSKLSSQVPVDYTKRKNVKKPSGSKPGMVIYETNSTIYVTPEEETVAKLKVK
SE

>CORE_REP|Org18_Gene2718#

MSMTNGSYKMKNLVEISAMVTESTDFFNIKDDIIEKMLEVVHPTKACVNLFYKNDSKYAYLVCSQTLEYVPQIFPINSLKGAKIDFDTYPEYIHE
AVNEKKIIYVENVFEDSRAEGERDLAKAEGYIGRIVFPFIINNVVVGFMTCFLKEDDYITEQDIDFISSVASLLSLSIEITNKNNNVQILIDKLRGSISA
INEATKKLYLNKSIDGFLENLSKQACNITNSKEALIIINSHHNKDAIVSCYNVEQKKKTNLYPMIDMFLKKESLGGYLNNLKPCSKKGINLESYIYYK
LQDKNDTIGCIVCANSKNYTSDDLNILSILSKQVSVGMQLYEHNEKEVKHKVLENELNILNKQQQLIMDKGKMDCNDEKELYFYHKPARVVGG
DFYYATKVDDEHIVYIVADVMGHGMVSNYVVAMIKGAFKVLCNQYNTPREIMTNLNRMLYDEFDKMGVFTTCLIGIIDTKENMITVSNAGH
YSPVVVKKDGTIENNLNCKKGIPIGIMEDATYENNTLSMEDYAMVCMYTDGILEIKNSSKEEYGINRLENFLKENFRLNQQLIVENLKLDLKNFS
SKDNYDDDILIVMLKDR

>CORE_REP|Org5_Gene2467#

MEISYVLKDCTFKHNKYSVIEAETWKEKDLDIVVAKGEKFAFQIMLKATEEFNCTIDKSSTISWKGLENRVRLALNVPNSLENNFSINILGYVQDD
TKAFVNDAILRDKDVLVEQYLPQTFWIEGQVPEDFEENNLNIGIDIFKSFGYEDEEKVCTIDVPVKVRNVVLKPLDKSKFFLDLWQHPSCLARM
YKVELWSDIHFEIVDNYLKELASLGEKVATVIVSDYPWAGQSCYKVYKNPSNLYEYNMVSVSKGLDGKIKCNFESMDRYISIADKYKMSKEIDLF
GLLGNWCAGEFGNPVEGYKDPIRVRYFDENDKVFKFINNTNDLKEYIGLVLNHLIECGLWDRVRIIADEPNNPEVVKECIEFINSTVGTHQVKY
KSATHDQNFLDRAKDEIDDMSINLKLTIQNYKDIENLKKKINDKGGILTWFVCCFPEKPNSFLSSPFVENRIIGWYTYYFGLDGFLRWDYNLWTE
DPWKDSSYKFPIWKAGDMFFVYPGKDLKPVRSVRMENLRFGIQDFELFTMLEKEKGREYIEVELMQELLNKKENAEIKGFGDIELGYSLDNWG
YDKVKKYVLELLDRV

>CORE_REP|Org24_Gene932#

MKCGKYKKYDKMQIVNRKWPDNEIFKAPIWCSVDLRDGNQSLPTPMSVNEKVRMFKMLIDTGFKEIEVGFPSASNTEYTFLRKLIDENMIPD
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VIDVWKPTPQKKVIINLPSTVEMATPNVYADQIEWFCKNISCRDSIILSLHTHNDRGTCTAASELGLLAGADRLEGTLFGNGERTGNMDIVNVG
LNLYTQGIDPELDFSNIDKIIGIYEDCTKLMVHDRHPYAGNLVHCAFSGSHQDAIRKGMIAMKNRDNDYWEVPYLPIDPHDIGREYKEIIRINSQ
SGKGGAVYIMETDYGFMIPKNMHSDFGNVVKMESDRIGEELSSEAIFNLFKKEYIEVESPYKVKKYKIKSMDELNYENDDSNDTNMIEMTARIS
YMGNEQRIVGIGNGPVDSFNNALKQCGMKDYKFRYYWEHALEEGSHSRGVAYVGIEHNNEVYFGVSISENINTAAINALMNAINKSYIEEEIK
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>CORE_REP|Org45_Gene290#

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QMILEVNQRCTFEIIEDREKLLVKHMHISNPYGEMQLDEYFPTKIGTQSYDYLQRLLKEKTEVIEMITNNINGGLKGSNDDSTYSFFYVNEGLPKI
LGYTYNEFMEMSGGSAVGAVYPPDLPKALEDCEQCFAKGPTYSSEYRIRKKDGTLMWVLDSGMKSLNSDGIVKINSIITDITQLKNIESELKLER
ERYRIALQNITDIMFEYDMENDNFIKYQRVEIDKKIELENFETKNYSKLLESGKIIHLDDIGKLLEVLRGNLHETIEIREINSLTKNEWRWIRVQCSVI
YDSDHNPIKTIGVLKDITEDKSKLESLINQAQRDPLTQLYNQRVSQNLIQEYLCSSDSKNNDALLIIDIDDFKTVNDTFGHLEGNEVLVAVSKILLH
NTYDKDIVARIGGDEFTIFIKSLTKDLIIKITNDILNDASKIKVKDNHKITLSIGIAFTDDSTKLYKDLFSKADKALYLSKADGKNCYSVYE

>CORE_REP|Org32_Gene2922#

MDDISQDNFLLSKEYENSLDVDTKKASGIYYTPKIIVDYIVKKTLKNHDIIKNPYPRILDISCGCGNFLLEVYDILYDLFEENIYELKKKYDENYWTVD
NIHRHILNYCIYGADIDEKAISILKDSLTNKKVVNDLDESDIKINLFCCDSLKKKWRYKFDYIVGNPPYIGHKKLEKKYKKFLLEKYSEVYKDKADLYF
CFYKKIIDILKQGGIGSVITPRYFLESLSGKDLREYIKSNVNVQEIVDFLGANIFKNIGVSSCILTFDKKKTKETYIDVFKIKNEDICINKFETLEELLKSS
KFEHFNINQRLLSDEWILVNKDDETFYNKIQEKCKYSLEDIAISFQGIITGCDKAFILSKDDVKLNLVDDKFLKCWIKSKNINKYIVDKSEYRLIYSND
IDNENTNKRILDEIIGLYKTKLENRRECKSGIRKWYELQWGREKLFFERKKIMYPYKSNENRFAIDYDNNFSSADVYSFFIKEEYLDKFSYEYLVGIL
NSSVYDKYFKITAKKMSKNIYDYYPNKVMKIRIFRDNNYEEIENLSKQIISILLNKSIDKGKVEKLQIKMDNLIMDSLGI

>CORE_REP|Org2_Gene2491#

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QEIDGKPIKIVYQPEAYLHQDLQRHLYIHGIVNVGMTDFTLEINDEGRPYWVVSLYEHKIGYGGANATGIATVDAETGKINVYDVKNTPKWVD
RIQPQSFVTDQIKDWGVYVNGFLNSVISEKGVLVPTEGTSLVYGNDNRSYWYTGITSSGGDESTIGFMLVDSRTKEARLYKQPGATETAAMKS

AEGNVQEKNYEATFPVMYNILGQPTYVSSLKDKAGLVKRVAFVSVEDYNVLGIGEDKNEALRNYKDALESKGNDLKLDNDLKDEVLEGTVTRIS
PDVRGGNTNYYVTLDSNKDIIFRATSKVSSELPLTQVGDKVKISYSKEESGVIEMSEFDNLNIANFEDKKQKKKQELMKIQIPKILKIKVMYNLNK
KIDNSI

>CORE_REP|Org2_Gene2090#

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VAGLAIISTWIGLEVGLIHDAFESISIDVDAFGIFLNTIPFRFYNILILAFIVISALLLKEFGPMRKAEIKSRSRKISIDLDEGVEELDDLAPKNGVKLSV
WNAIIPIGTLIIVALASFYYSGYTSIMGGDDKALIQLFTNSPYSFEAIKEAFSASDASRALFQSALVASLVAIIMAVVKKIFTISEAIDVWIDGMKSLV
ITGVILILAWSLSSVIKELGTAKFLIHLLSGSLPPFLLPSLIFGLGAIISFATGTAYGTMGILMPLAIPLAYSLNPDMSYVIVSTSAVLTGAIFGDHCSPI
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>CORE_REP|Org72_Gene1252#

MKRIKVLTVVLAITLMVAGCSNTKTKQSSSDSSLQSQSSIDAKYINLTMVTPKTINPITNTDKSVGYIMNLVYDSLFTIDENYNVIPQLVKEYNIA
QDGMSIDIKLKDAKWHDGKNVTSNDVNYTIGLIQKSADSPYNEFTKNIASVNIKSDKDFTIKFKARYAFSIDSLIFPIVSQNHLDSKDVNDKNNN
MIGNGKYKIESYTEREGMVLSVNKDYYEEVPKTMKNIKVGMVPNEDARTSMVMALDSDITNVTLNDLSKFQEKEFNITKYQGRDYECVLFNY
NNPFFKDVNFRKAIAHSIDKDRIISEGYMDDATPVNFPLNSKSKYYNSEMKDLEFNKDKAIECLAKVEYANVNSVNQNDNKVKNQKESAKKNS
KKLTPEEEAKAKKAEEDRIKKEAEEKKNREKEEVKKSLSEMNLKIIVNRDNSERIKTANIINENLKTIGINSTVNQLSDKDMENALNSKNYDLALV
GWKLSIIPDASSIIAGSGYTDDKLNGYMSALTSSTSEIETKKAYKDVQTYIKDNATFISLAVRNNYIVSNSRLKGKITPNDFDVYEGISNLDIKSNES
N

>CORE_REP|Org94_Gene2766#

MAYKGIGASPGVALGKALVVEHSELVIEKKSIDNVEAEIAKLEDAVAVSKEELVKVKEKASEELGAEEAEIFEAHLLVLEDPELIGSAIDKIKTESVN
AEYALNEIKEMFVSMFESMDNEYMKERAADIKDVTNRILRHILGIKVVDLSALSEEVVLIAHDLTPSDTATMNKKMVLGFLTDIGGRTSHTAIM
SRTLEIAAIVGLNDITSKVKDGDFVVFNGDTGEVIVNPDEETINKYTELKAKYEDERKALQLLKGKPSVTLDGKHVELAGNIGTPNDIEGLIKNDA
EGVGLYRTEFLYMDRDSFPTEEIQYEAYKAVLEGMDRKPIVIRTLDIGGDKELSYLSMEPEMNPFLGYRAIRLCLDRKDIFKTQLRALYRASVHGR
LRIMFPMISSLEELLQAKEVVKEVLAELDSEGVAYAKDVEIGMMIEVPSAAVISDVLAKHVDFFSIGTNDLIQYTCAVDRMNQKISYLYNQFNPA
VLRLIKTVIDNAHKEGKWAGMCGESAGDQKMIPILLGMGLDEFSMSPISILPARKLITSVKESDMKKLADDVLNMGTAEEIKSYIEKTFNI

>CORE_REP|Org71_Gene1913#

MGNLKRQCDVSSGREKADIVLKNGTIINVFTEELITGDVAVVGDTIVGIGDYKGNVEIDCSNKYISPGFIDAHMHIESTMVMPIELSKKLLKSGTT
TIVADPHELVNVKGASAIDFLLESTKDIPLNVYIMIPSSVPATSFETNGVGKFSAKDMESYVNNPRILGLGEVMCFNDVINSENEILDKLELFKNK
VVDGHAPNINGKSLQTYVCAGIENDHECITFDEVYEKLRAGLKILIREGSAAKNLKSIVSGMLKHNLPIEEFMFCTDDKHLDDIEKQGHIRWNIK
CAIDLGMEPVRAIKVATYNSARAYGLRKIGAIGAGYKADIVVLNDLDKMEVDSVYKDGNLVNEEMFSNYNYEIKDKELLNTVKFKYINKEKIQLK
VSEKNYVMEIVPYQILTNKVYESLPCADGYFVPNKEYSKLCVVERHRMTGNVSIAPLKGFGIKNGAIATTVAHDSHNIIVTGDNDDDILVAINYL
KEIQGGYVIVSNGKVLAHLSLQVAGLISTFTAEEVQEITDNMLEIARKMGVPEYVDPFITLSFMALPVVPQIRLTDLGLFDVEEFKFI

>CORE_REP|Org78_Gene1295#

MKFSEFKYERPNYNSMKKEFLSCVEDINNSRNYKEQQKNIHKINLLRNKIETLSNIASIRYSTDTFNKFYKEEKNYWDEYMPLYEELNSYFYNAIV
NSKFKYDLIKEFGEQFFTIVEYSLKSFSKEIISELQEENKLCSEYTRLLASAEIMFDGKIRNLSGMGKFMYSKNRKTRELANKAYYNFFEENETKFDD
IFDKLVKLRDKMSKKLGFEDFVELGYVRMMRSDYREYMIKNVRKQVLKYVVPMANELYEKQAKRIGLEYLSYIDEGVEFLTGNASLKGDSRYIIK
NGKRMYSELSKETNEFFDFMLENELMDLETKKGKGAGGYCTYIPDYKSPFIFSNFNQTADDIDVLTHEAGHAFQLYMSRWIDMPEINFPTLDS
CEIHSMSMEFITWPWMDLFFKEDTDKYKFTHLSSSIKFIPYGVIVDEFQHYIYKNPNVDKSKRKEIWRFLEKKYLPHRKYGDNSFLERGCWWFK
QGHIFKNPFYYIDYVLAQICALQFWKKMIQDRDAGWKDYINICKVGGTKSFLDIVSMGNLYSPFDDGCIESIIGDVKSWFDEINDSKL

>CORE_REP|Org18_Gene1567#

MGGTIFMVQIVIVLAIFMILVIPMGKYLYHIATNQKTFGDRLFDKVDNFIYKVCSIDKKKEMNWKQYALALLFTNAVMVFIGYIILRTQSMHIFN
PSGIKSMEQGLSFNTIISFMTNTNLQHYSGESGLSYFSQMTVIIYMMFTSAATGYAAAMAFVRGLVGKKKTLGNFYVDLIRITTRVLLPGALIIGL
ILVTQGVPQTFAGTETVTTIEGKLQDIARGPVAALESIKHLGTNGGGFFGSNSSHPFENPTIISNIVEILSMMILPGACVVAFGHMIKNKKQGWV
VFGAMSIIFLIGLVVCFKAESAGNPILSQLGLNQSMGSMEGKEVRFGIAQSSLFTTVTTSFTTGTVNNMHDTLTPLGGLVPLLNMMLNVVFGG
KGVGLMNMLMYAIIAVFLCGLMVGRTPEFLTKKIEGKEMKLIALLIILHPLLILMFSGLSVAIPAGLEGISNPGFHGLSQVLYEFASSAANNGSGF
EGLGDNTMFWNITTGIVMFFGRYVSIIVLLAISSLLASKKAVNESIGTLRTDNFTFTIVLVLVVLIVGALTFFPALALGPISEHLVLWH

>CORE_REP|Org21_Gene1500#

MEKSYCIIYQGDIESALQENGINRYMVLNSQLAVIYVPLDFDETILNNIIQVAWWEESEPMSSLIEITNNVNNGETITTAAETDYIYENPYNDITG
RGILLAVIDSGIDYLHPDFINDDGTSKVLYLWDQEANTNPPPEGFIFGSEFTRSELNIAINRNDGSLSQDNIGTGTLVSGILVGNGRINSQYRGITT
ESDLIVVKLKSYTDTYYAGRINYSVSDFLAAITYVTNIARTENKPLIINLTIGVKSSAVATTSILDTFNILSSAGVVVVSGAGNQGNTDIHYSGRFSSV

GEVQDVIIQDGDDYALDITLNTNGPDKVGAQIISPSGEVSHDIRYSPDFYIYRGKFNLENTTYAMRFIYPYITSGKENLEIRLRDIKPGVWILRLTSELIINGEYDIYLPNKNLIAPDTRFLDPDSVATITMYAASDDVITVGTFNNKTDSMWIGSSKGPIRGRGIKPDIVASGVDIISTYKNGTYNTGTGTGVSSSIVTGVLALLMEYLEKQDNVPRLSLFTQVLKTYLILGATKLEIYTYPNVSQGYGILNLKNTIQQIANTL

>CORE_REP|Org58_Gene1169#

MSKKKTPFLKKVGKRSWCIFTIILIIYSVLIYRLVDIQVLKGDKYKQSVESQSVEKVELNSGRGIIYDRNNKKLTDTSKSQVLIVEKEKLNNNYKILELIKKATKMNDLDIYKAVQEQLTRPIIQIQTKNIDINKSMKKELEKNGIMVEEKTMRYAKDGLLSHTIGYIKEDDKSGQSGIEKSMDSVLRNSNEKYISAFKAGDAGNEKSLNILKGSVKTVDNKDKDRHLKTTIDYNIQKKLEQILNKEENPTAAIISEASTGEILAMCSRPNFDQNDISKSLKGKNGEFENRVIKATYPPGSVFKMVVLFSALENGVIDENYTYNCTGKTKVGNTNEILRCNKRDGHGFQNLRQAFSNSCNPAFLDIAMKLGKEKILKSAEKLHLFEKVDIGLDEEKIREAPKNISIRNLAIGQENIEFTPLQINQMTQIIANNGTFKPLYLYKSLVDNNMNTIKTYKSSKKEELISPYVCTQVKEYMKSVSRIGTAKDLKDIEGGCGVKTGTAQSSLNKKAIDHGWITGFYPEERPKYVITVLVEGTQKGNKSATPIFKEICESIK

>CORE_REP|Org42_Gene2135#

MMFKIFNKSLLKLVAILSIVLIISNFSLSSYASEITSRTDNVLIVYDSKKETDYNRDILNIMRTLLGRFSSDIKLLKLSNYDGEINKNYYSHIFILGINENSYDNDNKTKNLISSLNLYKGTICWLGYGIENLLEHKKYNLDYIGKTNNIVSVNYRGKSYNLEEHYIFNIVESKDTSNKVIGSINDTLNKYPYIINDKNLFYVSKLDLDGVLFYIFCDSLNDIFNIKRFDKGRIFVRIEDVHAFRDPKDLVNIADYLSSKDIPFTIALIPAYVNPKNHKITTLSESPEIVKAIKYMQDKGGTVILHGYTHQYKKEEVSGEGYEFWDGKKDEPLKENMKIFVKDRVLSGLRVCIENGIYPLAFEAPHYAMESDGYKELKKYFSTYMGQHQNNNKKFSTNTYPYIIRDTEEFNILIPENLGYIDPEDKFTFQHIKENLDKLSIVRGFSGGFFFHSYLNIEYLKNTIEYLEKQNIEFMNLRDFNNWVKVDEIQIRNNGDEIIVNYDRDLEENIKSDIRFKSISNISKILIFIVSISVLIFMIIFIYFKRIDKKKFLK

>CORE_REP|Org55_Gene1923#

MEYFSESNNEVQKFDWGEVMWIHEPSKTQFNRLSAGIVRFFPGNYQEKHFHLSEEQLLYVIQGEGIQIIDGKKVNIKETSIVYCPPYSEHEIINTGKIDLVILITYVPHKFSSLRQIPIVFSENNIQELVNVNIIENLANQISNILKLRISVYDLKYKEIFETKKENKFCDICKNIKQCTKKLVKSINNDNFEKVYHCEYGVSSLEIPIVLEENIVGYIECGNFIVYKSIDIDKNLSELSSSSGIDIKYINKIYNEFPLNPKSRLYVLKENLLMMSEFIQEIAKRNFFENQLSIKDEEILKSRKENIRLEEALKKANSRLLEEEYIINPIDMFNNSSKEYPFELELYIEKEIKNMNLEGVYNLIDTNKLRYNDVRDTIQEMIFVLSRTVLRDLEDLKLISYLRNKYNKKISLVNSDEDLWNVLFEFSKECIDKNRAFWRKDKGNLIENINEYIKKYYKENINLNSISDVFFISPNYLSSIFNERNKVSITEYINLLRIEESKKYLLDRSMSISDICKKVGFNNSSYFSQIFKKFNSITPNEYRKNMLDNKY

>CORE_REP|Org72_Gene2695#

MIQYIDGKRLREMFISGANNLQNNKELVDKLNVFPVPDGDTGTNMSLTISYALKELAKVENDNISDIGKALSKGSLMGARGNSGVILSQIIRGIAKSIEGKSKLSTEDLAKAFKNGSDTAYKAVIKPIEGTILTVVRESGEFAIKTAKKEKDVVKFLSMLVKESNSSLERTPDLLKNLKEAGVVDSGGKGLVLIYEGMLASIKGNNIEIKNADLDTNISTSMDFAKSTTSTDNIKYCYCTEFILESSKVEDTKIRDIMMAYGDSLAVVGDDGVIKVHVHTNDPGNVLQEALKYGQLLTIKIENMKLQHENTLLDVEEKKENDSEPLEEEKEFGFIATSMGEGLANIFKDFGVDHIIEGGQTMNPSTEDFMNAIKDINAKNIFIFPNNSNIIMAANQAKELSDKNIIVIPTKNTPQGFAALVTFNGELSEDENKEAMMNALNSVKSGQVTFAVRDTVMNEIDVKEGNIIGIAEGNLLSAGDYVDEVTSNLIEKLVDEDTAIITLFFGEDVTESQANELRTSLEEKFEDVDVELYYGGQPLYYYLISVE

>CORE_REP|Org28_Gene2532#

MKNHTYKEIKNIYGKISPFEFKDKLIDIAKYTAKENNRELLDAGRGNPNWTCSTAREAFFTFGHFAITETRSNWDLGHLAGMPQKKGIKERFFKFINENIDMPGAYLARDIINFGINELGFDGDEFVHELADGIIGDNYPLPDRMLPHMEKIVHDYLVQEMKYDISGKYGDVEIFAVEGATAAMCYIFDSLMANELLKKGDTIALMTPIFTPYLEIPNLPRYDFKVVNINANEVDEKGAHTWQYTKKELEKLRDKSIKALFVVNPNNPASIAMDETSCNNLIDVIENYNKDLMIISDDVYGTFVEDFSSLMSKLPYNTVGVYSYSKYFGVTGWRLGTFALHKKNVFDKKINDLTGELKKSVDKRYSDMSLNPSSLSFMERVVADSRLVALNHTAGLSTPQQVQMAFFSAFALIDKVDAYKKLNMSICHRRQKLLFEALELPINENKNNAAYYTQFDIEEWAKLNYGEDLFKFISKTASPVDVLYKLANDYSVVLLSGNGFYGPEWSIRISLANLYDEAYTKIGKAIREILNGYIVEWQKIKK

>CORE_REP|Org96_Gene890#

MKEQLIFNITNLVTVVFEAFVIHMFLSDFLGQKEGYIKVVRYAKLGFIICLGFCNLITLNPKITMPLIFILIFSTSFLYKGNLKTRLFTTVLLSIFFILSEIVVTSIFVLFVKEGFEIMLENNSIRVLATILSKIVFLLTCKIICLFKKDVHLDMPIKYWLPLFLIPIFSLFLSVSIFDVSKFFSLESLKFLSLISSVGILYINFIVFYLFKFIIDKTKLSMKYELLEKEIIHKEELRLSNECYKIIVEQTDSVVFEWNIKENKSFVSQAWTEKFGYNNACKNIFKEIKDKDLVHSEDKAIFEGFLESIKKKNMHNQAVYRLKKSNGEYIWCRTSITSIYNDENELLRVVGVIVDVDSDIKKYEELRTRAESDSLTNIYNKGTFEKLVEETIVMNTGDKKDALFIIDLDDFKEINDNFGHPFGDFVLKTFADKIQTSFGSKDLVGRIGGDEFVVYMQDYVTEVNLHKKAKELNRVLSDNYTDLSFSFDASVSIGIARYPQDGTSFFELFKNADRALYSIKASGKNSYCLFEEELYVQ

>CORE_REP|Org39_Gene2934#

MKEKIYYNGNIITMEDSICGDAILIKDKIIKKIGTKEEVFALKNKDTEIIDLQGKTLMPSFIDSHSHLIAFATTLKLVPLEDATSFKDIVKKIQDFKESNNIKKGDWIIGFSYDNNFLEENKHPDKSVLDSASSENPILISHASGHMGVANTLGLEQLGVTNETQDPEGGHIGRAEGSKEPNGYLEENAFFNVASKIKQPSSNEIFNSIEKAQNIYLRYGITTAQEGLMEENQFNILKAMANQNKLKMDVVGYVNLKKSKSVADNNREFIKKYVNRFKIGGYKIFLDGSPQGKTAWLSRPYENSDDGYCGYPIYKDEEVEKFIDISLKEKMQLLTHCNGDAAADQLIDAFEKVLNLKEQSSENNIRPVMIHAQTVRADQIDDMKVINMIPSYFVAHTYYWGDIHIKNLGEDRAFKISPLKTTIEKGLIYTLHQDTPVIAPNMLETVWCAVNRITKKGIQIGENEKISPLDALKGVTINAAYQYFEEDKKGSIKEGKLANLIILDENPLTIDPMKIKDIKVLQTIREGEVLYSLK

>CORE_REP|Org43_Gene1179#

MMYDLILKNGFIIDGTGNPGFYGDIAIKDNLIAKIDYKINGNTNKEIDCCGKVITPGFIDPHVHEEIVAILDGKFEKFLKQGVTTTINGNCGHSITPYSSENVYEYMYKNGLLLEEEKKYLIDKNKYWNNFTEYCDLISKSGISINMGFLLGHGTIRWSVMGGSKDRHPTEEEKNEITNIINDGMKSGAFGISTGLAYIPSKYADIDELVDIAKQIKEYDGIYTSHIRDYIGRYNAVKEAIEVGQKSGARVQVSHLSPVEIEAFDEILKARYNGVDIMVDTVPRSSGHCMKKKRVIQFIMAISSSLFELGIDGVMDALKNEEGRALILKEAFILGDRGSIILLNTKDIDMEKKSIREIAIQKDIDEDKLLLDLLLDGDEELIFCLGGMYRSDFPDKLHDNKIIDNPFVMVGSDCLFSVGGDMSWFELQRRGAFSIFFNMYRKSGVRLEEIVRRVTSLPARQFKIKNRGILKEGLIADIAVIEIENYSYPRSEDIDFSKPQSLAKGVEYVIVNGKIALEDGNITENKCGEVLRR

>CORE_REP|Org22_Gene2983#

MKMNKKILSLGLAVSLILVNFKSVNASSVVEKIYGKDRYETAAKIADKQTYETVILVNTEKSLADGLSASGLSGATKAPILFTQQNKIPADTNRCLKNIKKAYIIGTEDTISKSVEKELDSKNIEVKRIGGEDRLKTSYLIAKEIATIKKVDKVLLTNAYSGEADAMSVSSVATRDGAPIILTDGKSVPFDVKNIQSYCIGSEEIMSNPLVKNTNSVRIEGTDRFETNKNVIDYFFNSADGFYVSDGYQLVDAIAAAPLTKNSPMVLVNDGSDKTVLEGAKNITSVGEINEKVIQQCINASKSNGQPPTITVGSTEVYKGEKFDTSKLNIVAKDNTGKVLPIEVDGFIDTNRVGTYILTLKATDEWGKSTGKRVEIKVLDDKSHDYNSPEFKKMVSTEMYNLINSYRKEKGKEPLVVSSRLEGMANAWSKYMMDKKVFAHYIDGKNAPQVFSEFGMRSEENIAYIYIDSKNVQTTQDAKDLAKAIFEVWKKSPEYNANMLSDEFYSTGFGLYILSDGQVHATQEFLNGNEGSL

>CORE_REP|Org19_Gene1156#

MLSIINSSNLVGIDSFLVKVEVDVSNGIPSFNIVGLPGKEIKEARERVKSAILNSGYKFPSTRIVVNLSPADIKKEGAFLDLSISIGLLRELIKKDENYIRESMFIGELSLDGKIRKVRGILPIIMGAKTQNIKRIFIPIENIKESLLVDEIDIIPIKSLKECVDFLNEEIKVDKVSIMSFLDDKSRKENGELEKDNSYIDCKYTKINNEESKYDEDFKDVKGNYFVKRSAEIAAAGNHNMFMIGPPGSGKTMIAKRVRTILPDISIEEMIEVSKVYSILGMINESKGIIDKRPFRAPHHTTTKQSLIGGGMDARPGEIALAHRGILFLDEIAEFDRKILETLRQPIEDGYVNISRVKYSAKYPCRVLLVAAMNPCPCGYYMSETECRCRSNEIDRYINKISGPLLDRFDIFVEVNSIKYSDFNSLKQEESSQKIKRRVENARKIQINRFKKDNIKNNSEIKAYNLFKYCKLEKEASKTAEMIFNKYNLSSRSYTKLLKMARTIADLEERDLINSQCIIEAFSFRKAYYSYFK

>CORE_REP|Org31_Gene2046#

MEKMFCFQCEQTAGGKGCTINGVCGKKGGTANLQDELTGVLIGLSRATIGNKNRPTSETDKIMIEGLFTTITNVSFDDEAIKRQIEKTEVEKSKLVPRCSDCSTTCNRNDNYDMKDLWNDNEDIRSLKSLILFGLRGMAAYAYHAMVLGYTDKDVNEFFYEGLIAVGGDLSIDELLGLVMKTGEINLKCMELLDRANTETYGTPEPTQVSMKIEKGPFIVVTGHDLYDLHKLLEQTKDKGINIYTHGELLPAHAYPKLKEYKHLKGNFGTAWQNQQKEFDNIPAPILFTTNCLMPVKDSYRDRVFTTEVVAYPGMVHIDEDKDFSSVIEKALELGGYREDVHMTGINGGDTLTTGFARGTVSSVQDKVVDAVKSGAIRHFLLVGGCDGAKPGRNYYTEFVKQAPKDTVILTLACGKYRFNDLDLGDIGGLPRLMDMGQCNDAYSAIKVAVSLANAFECGVNDLPLSMVLSWYEQKAVCILLTLLHLGIKNIYIGPSLPAFLSKNVLDILVDKFALTPISTPEEDMKKILG

>CORE_REP|Org81_Gene1177#

MKAPKTILTILTIALTLSSISIIPSYALTEEKLIGNGRYETAVKISQKAYSSSSNVVLVNDNSLADALSATPFAKAKGAPILLTESDKLDDRTEKEIKRLGAKDIYLIGGTAVLNKDIENKLKGNGLNVERINGKDRYETSLILANKLKDIKDIKEVAVVNGEKGLSDAVSVGAPAAQNKMPIILSSPKDGVEAFDKFIRDEKVIKAYVIGGTTSVSRAVEKSLPNAERLSGKDRNETNAKVIEKFYTDTNLSNLYVTKDGSKNENQLIDSLAVGVLAAKNESPVVLVGNKLNTKQRDILSTKKLNTITQVGGNGNEEAFDEIKSLQEKTVFEAKTVEELTDMINIASPNDIINFKPKENTVNEAFRMVTNKPITVNIKGDCSKTITVDMPNGEVNNYATLVNVIVRNIGEGGFNNHDTITILSVRDKNGRVIENTRNSDIDTLMILASANDTKLINDGYIGKLIDNSSNSDITNNGTIDKKVNQVEDLEAKVDSIEKAIDSISQKVNKIQDILDKLGFLKKFLS

>CORE_REP|Org66_Gene1571#

MGDSKVFEKIFSSQSDRGNYTPSKGYLSYFISYIGLEDEVLYNLEIFKTKQNIDSKKDIALFTDVIANPSDFDIINYFKSGLQKYRTSMEDVDINILGFEEIDYKIKQAMDRVLKEEEKEFTNDRVKQNFIVKIMAWIKIYIGALDINKNEAPKVIFYGDIKKHEVYLLLILYLAGFDVLYLNPNSKSNIDILKSERYNIEFEEANIIEEKISFEERVILGEKIDKSSVKKAFTVGAEASKRISEELLNDAGFIKPWQLQDRKIKNLLLSSTVDEISIYWNQPLKLRPGFKFNDAIVEAPNFLSKINGIYNDKNEYIKFLDLLRDSESSTFIEFNGDVDRFSKAFTREAFSLSFLLDSKGAIDKNSVLNNKDYSISTLALNQQIMILEKVEELLEGSMFLNGLSGEDKIKGLFTVLHMDKKFVHMMNNFDYSLINPKLIIYMYKSIVFDKEIVFLMLLLSKIGFDIIILCPGGENNIENVINNQLIDVHRLDKMVYDLKLNSLENDIPLLKKIFGKRRRF

>CORE_REP|Org64_Gene2747#

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AIVIAIIGLLFTEQFVTIFAAGFRNDPAKFQAAILFTKIMISGVLFLSGSKIFSSFLQVNDSFVIPGLIGIPYNIIIIAAIALSAGKNVWILPAGALLAMAS
QLLFQLPFAFKKSYKYKPYINLKDESIKELVNLVLPMLVGVAVGQLNIFVDRLLATTLGDGKLSALNYANRLNEFVMALFVTSIITVIYPKLAKMSG
KDNKEGFISTIVKSSNCIILVVLPISIGAIILAEPLVRILFQRGKFDALSTDLTSIALRLYSLGLLACGVRDVLYRAFYSLSDTKTPMINGSIALIINIVLNLI
LIRPLGHAGIAISTSTSNIITVILLFISLKKKNGYFGGDKIIKTGLKSLVASGVMAVATLLIYNNLYAFMGSGTIKEIISVGAGVLGGASVYTVLIVLFKV
EEMDLAFEFLRKGKQKLLRRR

>CORE_REP|Org64_Gene2241#

MKSKKLLSLGLAMSMFVACYPISANALDKIDKIQGADKYETAGLIADKQSYATAILINADSTMADGLSASGLAGATNAPILLTKKNNIPNATLKR
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GIESYAIGGTSLMSDKLVNDTNSTRLGGADRYDTNKKIVNKLYNGIKEFYIASGTDLVYALVGSTIAKNTPIVLVDDNSNKTVLKGATKITAIGNL
NNNAIEQSLNITKNIASPTTGGKYTVKEATERIAYILDEKVFVDYESAIKAKTDPDECFRYYIKNFTYQGKDYYAIGADDDDFRFLVNMNNLNDIL
QWYSNNTIKRFDAEGYLKERKAIDMAFEACSSKYDISENDLILDREEHNISTDFYVVVLYESSGIDSYWVFIDTDTWTVHDIQRLNQNEELVSYH
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>CORE_REP|Org94_Gene2771#

MNKNSMTKIYSLNKIIFIIIGILGIVLLTRHIEVDIKVLILILLTLFSINVFISYLKIKLYEDKINLGLINNSDKFINITKDENFLKHVQNYIISNEKENCVMA
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IKKAIDNADMARLKSKGLKHIEYVEFDNAMEEEIQSIMKIERDLFLAIKNKEFVIHYQPKVDSSTGNIIGSEALIRWLHPSLGMVGPNKFIPIAEKN
GLINNIGRWLIQEVFITINKWISEGINVLPVSINLSRVELYKNDLVDFFKLMFNTYNIPKELIELEITETTALRDVKFISERLYEIKSLGMNISLDDFGV
GNSNFINLKGIPLDIIKIDRSLILDIVTNTKTKFMVKAIVNLSHDLNVTVICEGVEDMHQVKVLSELGCNFIQGYVFFKPLDEMNYKKLLTDGSYIN
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>CORE_REP|Org20_Gene1142#

MDNFKKILLNELPNFKEYSSKFLNGEINKMQYKGFSGGYGVYAQRDKKSFMIRLRVSAGVLSQYQLNKIYEIAIKHNLDKIHLTTRQAIQLHDLSI
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DEPYFRVFLGGGLGKQPKVALELDELIKPKDALYCVEGMIKFFMDYGNYENKNRARVRYMVESLGEELFLEKFKEYYKLEKENGSLELNIEEIDYS
KPGVKIDIQDSRLIPQKQDGLYTVYIHPVGGILLTKDLSTLLKELDNVENPMIRLGMTEGLYILNLNGNEAKRILEISKTISCNSQLEQSISCIGVPIC
QMGIQNSQKMLHEIIDYFRLQNNEEILNKAPKLYISGCLNSCGVHQVGSIGLCGKKKNVDGISTDTFELFVGGSFEIGKTRLGKSLGDFKASDIPE
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>CORE_REP|Org7_Gene1684#

MYRVGIDVGGTNTDACILDGELKVIHSVKVATTKDVETGVYNALKKVIDESKIDHSLIKYAMLGTTHCTNAIVERKRLNNVAMIRIGKPATTAIL
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NGAILNSALSQVGKAVSLGFEKALKDLGIDAQIYFSQNDGTLMNLEYTMKYPIFTIGCGITNSIRGASFLSKVKNAIVLDVGGTTSDLGVLYNGFP
RESSIPVTIGGVHTNFRMPDVLTIGLAGGTCVKGEKDNIKIGPESVGYRITEDAIIFGGDTLTLSDVVTKLDMAFEDRKSNVENLDKEYCNEVYKK
VILKLEDAVDQMKTSQDDVELVLTGGGSIIVPEKLKGISNVIRPPHYTAANAIGAALGQISGDVEKVYSLDKMSREDAIEDAKKEAVNKALKAGA
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>CORE_REP|Org90_Gene1316#

MSKVAKATFYLMIVTIISKILGMGRELVLSSIYGTGLYTESYLTAMNIPNIIFAAIGTAIVTTFIPMYQDISSKQGEKQALKFLNNVLNIIVGICIVVAI
LGVIFSKQLVSIFAIGFEGERFLLTVKFTKILITGIIFIGITSVMSAFLQIKENFIVVGFGSIPYNIVIIISIMLSTVFGPYILPIGAVVAMVVQLLFYMFFV
KKTNYKYLYYLNFKDDSLIKLLALLSPVFIGVAVNQVNSLVDTTLASTLVKGSIPALTYSDRLNGFVTGTFTASIVSVMYPMLSKLSAENNQKKFTS
SVKSSINMIIISMIPISVASIFFATPVVRIIFERGAFDARATQMTATALIFYAVGMTAFGLRDILGKVFYSLQDTKTPMVNGIISVGVNIVLDLVLIKP
MAHGGLALATSSSSIACILLLFLNLKRKVGYFGQDKIIKATLKSVVASLIMGVLSYFTYKFIFGILGVGTFNEFVSLAISVIVGGGIYTLLMTIFKVEEV
DMILNIAKRKLHLKK

>CORE_REP|Org10_Gene2423#

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PYQTNSILRNNINKGVVDYIDMHLSHSTQFLNYGTIPKVDVAIVEALAITEEGNIIPTSGIGNSPSFIKSADKVIVEINLAKPMEMEGMADIYITEN
PPNRKPIEINHPKDRIGTTYIPCGLDKIAGVVITNMQDKTRPLGVVDEASKKISNNIIAFLREEVKSGRLSKNLLPLQSGVGSVANAVLYGLCESEF
ENLTCYTEVVQDSMLDLIRMGKVTMASTTSVSPSPEGLIKFEKDIDFFKDKIILRPQEISNNPEIARRIGVIAMNTAIEVDIYGNVNSTHIMGSKM
MNGIGGSGDFARNGAITIFSTESIAKNGDISSIVPMVSHVDHTEHDVMVIVTEQGYADLRGLAPRERAIKIIENCAHPDYKEQLRDYLNRACKS
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>CORE_REP|Org76_Gene2172#

MNDNVVKKKNFFDRTLNRIETVGNKLPDPVTIFLGLCVLLLILSSLVGSMGISVVHPGTGETITAVNLLTVEQLQILLGNIVSNFQGFAPLGLVLV
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ASFTVPAAQMIDSGFQANATMNLFFMIASTFVLILLATWVTEKIVAPRFGKYEGNAELDVDGSLSDVEKKGLKKAGISILIYVAIIVALSVIGKKPF
LADPETGDLLSNNAPLMKGMVPIIALAFFIPGVVYGKTIGKIKKDKDVVSIMASAMSDMGGYIILAFAASQFLQLFTNSNLGLILAVKGGEFLKS
AGINGPLLLIGFIILSCFINLFIGSASAKWAILAPIFVPMFMMVGYNPALTQMAYRIGDCITNPLSPLFPYFPIILAFTRKYDKDAGMGTVIANMIP
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>CORE_REP|Org74_Gene2348#

MIFVKNKKYRKIAIIISIPILLVAQYYLFKFGILRPMVKGVEIEIVDGEYVKDIDKYVVKLNETVTLSTGEYIKVPSYAKNPNIWFNVLDNSGTLKIDG
NKMTALKVGYSSVGIMKNSRVLKKATIKVVDPEVESLDMEINGDLKHVGDSATIESTIEVDYDKFKKSYKPVYKSSNENILKIKGNKVSAVGVGK
ATIYAKCGNKEIERTFRIQARVAEINMDDIKIEVDQNEKLKPDIITSPPGLEPPKIYYELVDSKLPVERAISLSSNGNVVGLREGKDRVRITCGDKSK
VITVTVVKETITNDYIQNLVGSHKIVNNKVIIKLEWDYMKDVFDYDIYLKDKLSGESFKKIKSITINESDLGKSNKVYATIEVDMKGNQNIDFDIYVI
GKKDSDTTKPSNVINITNGNGNSNNDNNIKDMRVENISANVDRDNNVIRVNWSSISHKDCTYSIYVKNNTNGDGEFTLYQSDIQGNEHTISIP
EGDLNLDIYVVANYNGNSSQNSDVINVR

>CORE_REP|Org38_Gene380#

MTYPVLKGAGYVLIHTPDMIVQNGSTCTVERATNPDSEFLKEVSNHIRSYEDVVNYMPNQVYIGNRRPEELRDLPMPWCEQKIEGTRNGKFG
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FENLVVKASGVLSAIQMLRHSKIDPAEIDYVIECSEEACGDINQRGGGNFAKSIAEIAGLQNATGSDTRGFCAAPTHALIQAAALVKAGIHKNV
MVVAGGASAKLGMNAKDHVKKGLPVLEDVVGGFAVLVSENDGVNPVIRTDLTGKHTVGTGSSPQAVMTALITSGLDRANLKITDVDVYSVE
MQNPDITKPAGAGDVPEANYKMIGALAVKRGDLEKKELKDFVSNKGLPGWAPTQGHIPSGAPYIGFLIDDLTTGNRNRAMIVGKGSLFLGR
MTNLFDGVSFIAERNTGVTEETSGISKDEIKKIIAESMKKLALDMLEE

>CORE_REP|Org39_Gene1313#

MIINRSKDSSSNEISFVSKDMGFLLTQSEVSYNFKDKLVEDIAKQVFAENRLSVGTIAKTNVKYTKMFIGVNGYDTIMSAYTEASKKTKKKYMIE
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GYGDVSCITGRGVKVKDSYTKLVGLFYIDTDKHTWQNGEYQIELELNFQNLMDEKSAGQDEPKEESNLGGEDYVGGTEFSAIFTAYYPGPGIE
GGDTDCREKKLNPSKKTCAAPMVGAYEKSYYTKEFLSKHPLFKYGDEVSIVTGVSGRDGVYKVNDNGSAIIIEKDGTYHIDVLVKNAEEMKRFG
KRKGKIIIGGYSGNASNKAKIVISEAKKHLGKPYKWGGNGPSSFDCSGLMVYCFKKVNVSLPRTSNQQSKKGKKVEQKNLQAGDLVFFHNPVS
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>CORE_REP|Org6_Gene2184#

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ENTPVVDLEKGKICRVKTREDNIIEAENVIISSHSPWYDGLNFYFAKEYAERAYLMVAVLENKLADGMFISIDDPSITFRQYNNGSENLLIFGGGD
HKVGQGGTEKEIFDDLEHYGKEVFKVKDFKGKWSAQDNMSFDNVPYIGYINKREDNIYVATGFSKWGITNGTAAGIIIKDLIINNNSDYKDTFN
PSRLGSYFSKDFIKENANVAINYVSGKLKIGSGDMPKNNGEGKIVNIDGKRYGVYKDDNGDFYIVDTTCTHLGCELNFNSEEKTWDCPCHGSR
FDYKGNILEGPALKPLKLYGHGDNDVNPKLL

>CORE_REP|Org18_Gene1870#

MLKRVRCSYLKKNRLIAKNISIAFIVLFFFSVFTFFYVGNINRVLEYETNDIITVTIAGWIILSFLFLGIIIYILYSKANSQKTIEKVAYTDFVTGYSNWRK
FELDVTNLLKKTSQNNKYAMVIFDIDKFKAINDIYGHKKGNLILKDIADTLNELTDINETFARVSADNFNILLTYNKKEDIINIIKKIMANNELVNLS
FGIYEIKDKDLSVSVYSDRASLAKSSIKNNSDVNFAFFNDKLREKLLFEDKIEKEMEYALESGQFVMYLQPKYNIKLDKFCGSEALVRWQYTEKEV
IYPGDFIPIFEKNGFIRKIDMYILEQACKEIRSLFDKGISPLPISVNFSRVDFFKKDFIENIVNICDRYKIPYSLIEIEITESSMFGDTDTLFNVSRNLQDI
GFIVAMDDFGSGYSSVNMLKNIPLNVIKLDRGFFVDDKDVDKSQIVIKSIVSLIKQLGIRVVAEGIETRSQIEMLKKANCDIVQGYYFSKPLPIKEF
EKLVYKI

>CORE_REP|Org20_Gene724#

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QKSSNQFVCEYGITIYNIPILYKSNSIGVIRGGYVLLSDLNLDTEHNNLYDIPEGAARSIKRLLKQISKNIINFCSFNDIRKDLQEKEKTIARTYHYGEQ
LEMNLKVAQDMVTNLRINHHFLFNTLNSMASIALDDGSYDLYSAIIDLSRMFRYTMRSDLRFVELESEILYIKNYLNLQKLRYGDALKVKYLIPEK
LYNLSVPFNFIQPIVENAFTHGFRDIDTEKRIEIIARLDSQYAIIEIHNNGTILDGNNIDKIKAGIRSNNGHGLSLIYTKFTSAYGNNFDMDIKSSDNE
GTYIMIKIPIENYKEYV

>CORE_REP|Org34_Gene2184#

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RGAKAHQTGSINSHEHLIMPTISMTEADKDYAVSFAVPSDAEGVFMIYGRQSCDTRKLEEGADVDLGNKEFGGQEALVVFDNVFVPNDRIFL
CGEWDFSGMLVERFAGYHRQSYGGCKVGVGDVIIGAAALAADYNGANKASHIKDKLIEMTHLNESLYCCGIACSSEGHKTEAGNYQIDLLLA
NVCKQNVTRFPYEIVRLAEDIAGGLMVTMPSEKDFKSDLKVGTSGMTIGEVCNKYFKASSVASTEERMRILRFLENICLGSSAVGYRTESMHGA
GSPQAQRIMISRQGNINQKKELAKTIAGIKKEEALNL

>CORE_REP|Org62_Gene1723#

MYKEPKYRTILESTKEELNDLRNISLNDKYKPIFHIHPQHGLLNDPNGLAYYNGKYHVFYQWYPYDVTHGMKHWAYVSSDDFVNWNREDVA
LIPIESYESHGAYSGNSIEVDGKLHMYYTGNIKYSAEDRYAYQNLAIMDKDGKITKYENNPIVSEIPKGYTGHVRDPKVFKRKDKYFMLLGAQTS
NKKGAIIVYESKNSIDWNFKGELNVKNIDEDFGYMWECPDYINIDGKDILIFSPQGLEPKGFNYQNIYNVVYAIGNMDLDNLTFEIDIMKEMEK
GFDFYAPQTFIKDSQTILFAWAGMGEVLYPTDKNKWAHCLTVPRKLNIKNNKLLQMPVDELVKLRYDEISGQNTIKKNINIIENDENVYELNINI
KNIDSNKFGLELFSSQDEGVKLEFNKVENTVTLDRSNFKKVFSVEYGTNRKEYINIDENTNIKVLADRSILEIFINNGEAVFTSRIFAKENSNQIKIYS
DKIVCYKYTKFKLKQGIEL

>CORE_REP|Org22_Gene2553#

MREIKAKFYRSGDIVRDIGIVYFYELLMDLKNELEKNDYKLKFTCELNRNYLSLESAEYIDPKYISDYILENQLFKVFKNGKKETLEKIFSNIDNLTYV
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RERKDSKYNFLFRGAEKSGFKRSGQVESNICFECEFFNLMCLLYINLKRPMVFAYTNDLRELAFLNHKIMLKRKMYSDKSFYKKLLHEKISSIRLYR
FDIDTNKGIILKFDSIIEYKELLKKIELIDIIDNYNFSREPGNTRNLGKKMIDNGNLSNLKELLLDNISVLRQLTGTSREMDFVSSSYNIGLYIKLCWIV
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QEIMK

>CORE_REP|Org3_Gene2541#

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DCVGYIVEGALGHEEGGKQRLVSTPWSQEAMTFEKAAEIGTKKVIKDHSTIGIVVLTDGSVTGIDRKSYVEPEERVIQELKNLKKPFAVVLNTLSP
KSEETSMLRSELEEKYEVPVLPMNVVEMEEEDIEEVMEAVLYDFPLTEIRINLPKWVEGLERNHWIKSSIITTLKQSIIDIGKIRDIEGIIQGFSELEF
LEDTGVDNVELGEGVINIDLQTKQDLFYNVLEEKSGFKIEGDYQLLSLITRLSKVKNEYDKIESALIDAKIKGYGVVAPSLEELSLEEPEIMKQGKQY
GIKLKANAPSLHIIKADISTEVSPIVGNQNQGEEMIKYLMEVFEEQPADLWESNMFGKSLHDLVKEQLQSKLYTMPEEIRVKMQKTLQKIVNE
GSSNIITILL

>CORE_REP|Org20_Gene1651#

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PTETSARLKNVSKVYIIGGTYSISTSVENSLKSKKMKVVRIKGNDRIKTSYNVAKEINSIKKVNTVMLTNAYKGEADAISIASVAARDKAPIILTNGQ
SIPFSTSGLKSYVIGGTASMSTTLVNNTKSTRLGGSTRFETNKAIINKFYKDAREFYIAGAYELTNALVGSSLSKHGPMVLVNDGSNKSILKNAKKI
TSIGYIDSNIVQQCLNITNGIGDINTGVVKNVKPTTKTIKDGMYKVGKDISAGEYLITSNSGSYASYYEVTSDSTGNADSILSNDIFSGTRYITLKNG
QYIKIEDSTMTLAKYAKAQKAKNGKFGNGMYKIGLEIPAGEYIIMSNSSDAYYEVRNDSLGNAEGIVTNDTFSGRRYITVEEDQYLILNDCYLIEN
E

>CORE_REP|Org29_Gene1330#

MSNVNKKLVIAIGAVALVAIIFIGIMCMQFKGEKIAKNTYVNGVDIGKLTKSQAKQELAKKYKLENVEFNYNDKSWKVKSKDLNLSTDLDKTVE
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NYKNELVVKATPAKVKKEQLTNIDTNLGTYSTIFKTSQINRSINIKLATDNISNVLLMPGETFSFNKHTGKRSKENGYKSAPVIMEGEMEEDYGG
GVCQVSSTLYNSVLYAGLEIVNVKNHTIPSSYVPKGRDATVADSGIDFLFKNNLKHPVYIKNYVSGNQIVCNIYGSAEDKQNITISTKLDGVSQTT
MKRVNDPTMPKGKEKVDKSGRNAYSVSTYRTFNDANGKKIKTEKIANSYYPKKEGIILVGTMEPKPEEKPNTDENKNNQNTNNQNPNNQQK
PETPPTDNKPNETQPQPQA

>CORE_REP|Org69_Gene2322#

MTTFLIGLAILLIGGALYGAYCEKVFGPDDRKTPALAQSDGVDYVPMKKWKNSLIELLNIAGTGPILGPIQGILFGPIAFILIPIGCVFGGALHDYM
SGMISIREKGAQMPSLISRFLGNKVFQVYNIFLCLLMLLVGAVFIYTPGDLVVTQILNMKSTINNPVVWIVYGIIFLYYLCATLFPIDKIIGKIYPIFG
AILLLSAAGVGVGIFTQGYDLANLSLANWKGIHPDGIPLIPTFFVTVACGIVSGFHSTQATLIARSVSNEKEGKTTFYNMMILEGLIAMIWAAAA
MGIYNKGIPKELIGSPDVIGLVARDLLGSIGGIIAIIGVIVLPITSGDTALRSLRLMLADYFHYDQKEKKHRVILSICIFIPVIAILIFAKLSASGFNILWR
YFSWSNQTIAIFAFAMITVYLIVKEKNYIISLIPGMFYSFVIFSYIFNAQIGFNLNMNISYVLAAIFTVLYAILTVHSGRKLKSRADTKLAD

>CORE_REP|Org62_Gene2690#

MKLNDIIQGLDIINVKGELNIDINNVQYDSRKVTKGTLFICIKGFVSDGHKYIKDAIEKGASAFLVEEDVEIKGCTFIKVKDTRKDMAKVADNFYN
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KLGIFTNLTPDHLDFHKDLEDYRKAKEKLFFKTTMANIINIDDEGGKKIYENIKGINVPCYTYGVDTNADFMARDIKSDSDGVSYRLITPSYEEVIFI
PVPGMFTVYNTLAVIAACYVLGIPKPIYKEGLRLSNGVSGRFETVPNDKGISVIVDYAHTPDALENVLKTTQQFAEGKIISVFGCGGDRDTEKRPL
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M

>CORE_REP|Org50_Gene1780#

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KMTMGIGLGILTAIVIFGGVHRVAKVSEIIVPVFAGLYILVALAIVVMNITEIPSVIALIVESAFDFKGMAIGTFMGVVMTGVKRGLFSNEAGMG
SAPNAAATAHVTHPVKQGLIQSLGVFTDTIIICSCTAFMVLLYSGYSSSGATGIELAQEALTHHIGPVGNIFIAVCIFLFAFSSIVGNYYYGESNME
FMSGSKTKLNVFRVFVVGMVLFGSLTQVDVVWNLADLFMALMAIINLIAIALLGKYAFIALKDYTSQKKSGIKDPVFIADEIEGLENVSEWHREL
SEENLG

>CORE_REP|Org14_Gene494#

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KTYAVGGSISMSTSLVNKTNAKRLGGSDRYDTNKKVIKEFYPDASEFYLSDGYDLVNALTGSTIAKENPIVLVSESSDKSILAGADKITRLGSISDS
VYNKCVSVAQNNGDSSTKGDSPMKNETSILGQPTASLEACLKWAKSKKANDLFIELIPILYDTAVQEGVNPVLAVAQSAKETGFCNFGGVLDA
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EIEATK

>CORE_REP|Org43_Gene1303#

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MFYTTGPAYVICVVLYTVIGFKYSNNTIDYVQINQIKDVLNSNFHIGLVAMIPIIFLLLLLLLQKPPIISILSSAIMGLIIAVFQEGEKIGDVLNYMLSG
FTIDTGFVYADKLLNRGGIMSMAETVLLVFVVFVIAGILQKTGFLEVLLQPLINKIGKSRTKLVGSTFIVSYFANAFSSSMMFTSVFVGTLMSPIYK
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>CORE_REP|Org46_Gene2479#

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NSNRANGPFITINCATISPQLLESELFGYTSGAFTGASTKGKVGLVELANGGTLFLDEIGDIPQNLQAKFLQLIQDRTFTPVGSLKNKNVDIRIISAT
NADLVSKVKEKKFREDLYYRLNVIEIKLPPLRERRDNLVEIIKYYFNRYSSDFNLNKTISKEAMETIANYRFPGNIRELQNIIQKILLTCTDNHITIHNL
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>CORE_REP|Org2_Gene1389#

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AGDQMQKKLSEGISGEALNILIGNMPLEDEEKEPITANILKILNEKYNIVEEDLLSAEIEVVPAGKARDLGLDRSMVLGYGHDDRVCSYAAVKAIL
ETEQPEFTSVALCVDKEEIGSKGNTGMHSKFFENTVAELIALEGDYCDIKVRRALANSKVLSADVSAGYDPNFGEAYEKRNSAYMGNGVVLTK
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FFNINL

>CORE_REP|Org8_Gene2127#

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LGGEGMGYLGTYLFFAAGCLLVFWFSSTEIIKSGAEEEVLQKEEKPKIKASEMAKALFTNVPLMMAFCLEFLICIRSIGLGPLAPYYFKYVIEDERG
LAVFLSIMPLVSVAFMFFAPVFIKICREQKLASIISFSICALCHLLVAWTPWGKTTLGVTMLLAIGGGFSNVVSIINLNFFAGSCDYGHWKSGKDL
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>CORE_REP|Org63_Gene2748#

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TSGISSFKDFIESKNINKSYIIGSTNAVSDKIKQSLPNSERIGGADRNETNGKVIEKFYTSNKLNNVFVAKDGMKKQNQLIDALAVGVLASKENSP
VLIVGEQLSATQKSVFSNKNATSITQVGSGGNENAFKELKDLQANSNNKRVMYVTNTDKVNIRNDATIEASVIGYLSNGDEVEVLDVLKTGW
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>CORE_REP|Org23_Gene2342#

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FLNNAINHGILGPIGIAEAKEAGKSIMFLLESNPGPGLGVLLAYWMFSRGSVKQSAPGAVIIHFFGGIHEIYFPYILMNPVLILATMAGGAAGILT
FSILGAGLVAAPSPGSIFALMALAPKGGLLPVLAGVAVATVVSFLVAAPFVKRASANQSEEDSTSLEEAKAKMSDMKSASKNSEKNIEEKQLEV
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>CORE_REP|Org41_Gene1867#

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NVNDDIESIITNSYDKYSELKSILRGIDKTYVDKLCLEENRDVFDLYRIESKIEKLLNKKVWLKSGGYLIIEKTEALTVIDVNTGKFIGTGKLDETVYRT
NLEAAKEIVRQLRIRDIAGIIIIDFIDMHKKKHQNEVLNILEEEFNKDKRKAEVLGMTKLGLVEVARRREKESIDKYYLMSCPCCDGEQTIKSVHYIL
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>CORE_REP|Org35_Gene2612#

MVSFLGSIVVLIVGYFIYGTFVEKVFGINDKNQTPAIACRDGVDYVPMKWKRIFLIQFLNIAGLGPIFGAIQGALFGPSAFLWIVFGTIFAGGVHD
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MAVGVAGGLIIKGYNIPNINLQNMNPNGTPLFPYLFITIACGAISGFHATQSPLMARCVEKESEARPVFYGSMVAEGIIALVWAAAAMSYFHG
IPQLNVIFNDGGAATVVNTVSVGLMGPIGGALAILGVVACPITSGDTAFRSARLTIADAMNYNQDAVKNRFLIALPLFAVGVALTFIDFNIIWRY
FSWANQTLAMIMLWTGSAYLVKANKNHYITTLPALFMTVVTFSYIMQAKEGFRLPVNISNGIGIVVAIILGLLFFKKAKDIKEQNAHKLAS

>CORE_REP|Org70_Gene2467#

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KVLISNNMAIVADYIYTMNSQGEIAASLAWLGSIAYTLQIFFDFSAYSDMAIGLGLMFGFKFEENFNYPYISKSISEFWRRWHISLGMWFKSYIY
FPLGGSRVANKDIMIRNMFIVWLFTGIWHGAEWTFVIWGILNFVFLIIERFIMFEKIENHNFIKHIYALLVVNFGWVLFRAPNLKEAYNYFKAM
FGGNGVIWSDYTYMFLKEYWIFFIFAFIFSVPIAKKINKFVVEQAKYSMIFNVFYPISAILLFFISVTYLVTGSYNPFIYFNF

>CORE_REP|Org12_Gene2600#

MIVLSKRELFAMLPSVDEVLSDNRIVEIINEYPRSLVLESVREVIDLKRQFILRLKEDASNSVTIEFGEIIESAIERVKLNYSLSLKKVINATGTVIHTNL
GRSLLSEDIKDELWCAASRYSNLEYDLDNGERGSRYSHLTSTIKRLTGAEDVLVVNNNAAAVLLVLSTMAKGGEAIVSRGELVEVGGSFRIPSIM
ALSGAELVEVGSTNKTHLKDYKEAITEDTNVLMKVHTSNYRIMGFTESVSIEELVNLGKKYKLPVIEDLGSGVFIDLSKYGLSYEPTVLDSIRQGAD
VVTFSGDKMLGGPQAGIIVGKKEYIEKMKKNQLTRALRVDKLTICALEATLRMYLDETKAIENIPTLKMLTYKIEELEVKANKLFEKITALNLNANI
NIEDGFSQVGGGSMPLETISTKVISITPEHMNVSSLEKKLRLSEAHIIARVYDNKYVLDVRTIFDDEFDVIVEELRKAFN

>CORE_REP|Org11_Gene1489#

MEVSIILVKDIKQDIESMPRKILDISLIEDNKSDLTFFNIEEEDGDETLKALKQSYVTTNYKEETLLNLQGALNSKSDTTSKELKLESYKRYNNALDLA
YKNYITSAINMVNKALEINPKDIDILNLRGLLKLLKCDFAKSFESFYTALCYENNHISRKYVNLISSEDFKTFLGRYNHSIRFINEELNYESIHILENIIEE
EPELIEPYVILSLLYDKLGNVKKREGYLDKLKELDKDNPVFEKNEEEKEEEKEDTSKNEEIKKVKRKKSILPYIIVGCVLIGMGIYLIQSKKRIENLNNQ
ISSKEEKLSETDKKLGETSKKLEKTNKELNEVKNKEPEREITVADEEDLYYQALNLKKNKEYEKAIDNFKSIVSSGKTKKYISESIYQLAITNKLLGNK
DEAIKYYKKYINTYTKNDQYYDDSYYELGMLYYDNGDLKNAQQTFYSLRSEVPDSMYNNSKIKEILSEK

>CORE_REP|Org81_Gene1711#

MLEFMKSIIDTFGSAIIVPIIIFIIAKIFKVTTKKSFLSAVYAGVALQGFTLILNSFTPIITPVINRMVESTGVNLPVFDVGWQATSLVAFSTSAGMIYL
GLGILLQTILFLIKWTDVFQPSDLWNNYSYMVWGAMVIGVTGNFPLGIACMVLLNLYSLLISELVAKRWSSYYRYPNCTIIAMHNVEASVFAVF
ADPIYNKLGLNKIKLNPKELEKKLGFLGEPITLGLFLGMFIGILGNMTRINTMEAWGEIMKVGISTSAVMAIFPKVASMFAQAFAPITEAARKIM
QKAGNREWYIAVNDAVGYGEPATLISGLILIPIMLVIAMVLPGNKVLPVVDLLAIPYMVQGLVAIHNGNIPKVLVSGIIWFGLGLYVCTSTAPLF
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>CORE_REP|Org18_Gene3090#

MGRLKMSSLKKKKFTMPQTLTIIFLLIVLMAILTWIVPSGNFERVDIDGRSVVVAGTYEKAPSNPQGITDVFTAPINGFIDAAEVVGFVLIVGGAF
GIVNKTGAIEAVIAHTVNKMKKFQFLIIPISMILFGLGGTTFGMSEETLPFYMIFIPLMTSMGYDSLTAVATVFIGATAGFGAATTNPFSVGIAQA
LSQIVPGSGIEFRVVMFIIYMAISIGFVMMYANKVKKDPKKSLVHDISLNQELMVNSDTNIKEFTKREAMVIAIFTIGMAIMIYGVLRLEWYITEI
AMIFTAIGIISGIASGLKQDEIVNSFISGAGDLITAGLCIAFARGIVIIAENGFIIDTILNSAANLLNGLPKTIFINLTFLIEGLIAFLIPSASGLASLTIPVLA
PLGDLVDVSRQMIVTAYQFGIGVTNLITPTSGVLMGALAVANIPWSKWVRFVIPLMVVLTILVMAFLTIGLYLGF
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>CORE_REP|Org91_Gene2348#

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KDKKEILKVVDPEGKLDVNTTTSLTQEQIDKYIAYAEAGVGIGHAVAYPFGVLIVILGVNFLPKLFRMDLKEERRKYEKEMKEARDSVSGKTIPEV
PFNIITFFLTCLAGYLVGGIHVFMGPLGYFTLGATGGSLIVSLVLGYIGKIGVVNFRMEEKVLNILKQIGLVFFLAIVGLRYGGKVVDSIMTSGMHL
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>CORE_REP|Org94_Gene1661#

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YTPKKYTPFQMVNNYKYIETKYVNFVLEKYLNKKHLNIIVGIPSRDISRIILTYSQNNIKKTLNKVIIITLVIDSVVALGVGYLFSRKLTKPISSVLWSIE
TMANGNYSLYLKDRGIYEEVFKNINMLADTLRVNEVERKENEELREEWLANITHDIKTPLASIQGYAEIINDKDYEFEEDEIQEYTEIIYNKSKYIK
DLVDDLNLSTRLKNDTIVLDKKKINLVSLVRNIIIDILNDNRYKNRNIEFESNEDLIEVYVDSILFRRAITNLIFNSIVHNSEGTLISVEIVKKDNIEIIIKD
NGIGISKSDLKHIFKKYYRGTNTGEMHKGSGLGMAISKEIIEIHKGKIYVSSEIGIGTKIIIEIKQN

>CORE_REP|Org38_Gene3647#

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ERLNKAKTVYIIGSESTISKNVENQLLSKKKVVQRIFGENRFDTSIKIAEKIKEIKPIDKVIIANGFTGEADAISASPVAARDGVPIILTDGNSVGFDTT
GLKSYALGSSEIISDELVKSTNSIRLGGTDRFETNKIVIQEFYKNSKEFYLSKGLQLTDALAASTIAKNAPVVLVENGSNKSILSGADKLTVLGGINQ
NVIKQCINQASPNQQGLYYNPNDRAFKERIKGKVYALTKQYRKENGVRALSVASRLEGLANDWSNLMANKKTLSHTINGKNSYSTFLKYLDW
SEIKPGYIAVQGENIIKYKIPDKPVYTNRDADDIGNFIFNEWKTNPEEGTNMLHKGYEIMGFGIAITGDKNLYATHEFYGRYKE

>CORE_REP|Org61_Gene2639#

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TMLVARVLQAMGSGSLMPLLQVIILYLCPEEKRGAAMSLVGITVGFAPAIGPTLSGWLVDSFGWHSLFLFLSPIAILDVILSFILLKNVGETQNLK
LDIPSIVLSSLGFGGLLIGFTNQGNYGWTNIATYLPILIGIMSLILFTLRQLKSKEPFLELRVFKNKPFLISTILIMIVYASMMSATLMIPLYVQSVRGF
SALSSGSLMLPGAILMVVLNPIAGRHLDKYGPHALSILGTGFLFLGTLSFAFLGRDTSLIHVSLMYCIRMIGISMVLMPLTTWGIKTLDRELISHAT
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>CORE_REP|Org14_Gene1#

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NIKMYFFVTIVSTITGIITGQLVDYFKLEEKLGLKNRRKSDKYDTSKNNSKENKEKHNHDEIILDTLAKSHGNTNRLAFIITHGKGYKIYIGIILIGFIF
MSLAHSGLNLPIIEKLHSLEEVIAVIGILFSIIYMWCFITISIDTTGDMRIREKANKAPIRETLAAGLIYLTPWKAGRVLVDPMCGSGTILIEAAMIGI
NMAPGLNREFISEKWRTLDKKIWWDVRKDAFNKIDNESKFKIYGYDIDEESIDIARENAEIAGVDEYIEFNVGDATQFKSEDEFGFIITNPPYGE
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>CORE_REP|Org5_Gene2034#

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KLILNTVNTPKKMILLSYILGILLIFFIPQPFPRVILVSAFYKEFLKEQQITEDSKSILLFSIFTASTFTSMFFVNGDTLLNYVVLELGNCNINWGQWAF
YMSVPTIITCFITYFLFIFVFKKELHSIKFISNENLEGNKLHFSYSNLKKEFNLLNKEQKHVFLCLGIMFFMFLTQFIHNINTLIIMSICVLLLLLRKIVGF
STLKEINWKVLIFFIAAFSIGGVLKYSGVVDIMGNYLIKFIPNSSEIISILFLITLTIILNICLGSAVTTSSVVIPLLGSLHILKENSVTLCLFVYIIVSIQYILPF
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>CORE_REP|Org45_Gene278#

MNFRDLFEKAVDFIDEKRKSIVAISLSTLGVIVLMIVFFLSSNEFSVGKEANELLKIIEKRQYSIAVDYYTSIEKKFSDSKMERFNKSVSKKINKLLLNS
GDKYLDGDISQESFIGLINTVKELKKISIDVDDLLAQADRVREMYKEENTTYDIAINYINTVSLLNGMGSNLDVYKQNIETIKESRDVYDSAVKDQ
KVYKYYEAIEKYNKVLKEDEKYYSMAQNGKEQCIEEMYDYYISRAEEANTSGDYERALQYIEYLKEDYSDDEKVQSLEKKYKKNLSLYTLTSDDIIN
VIAKKSGKDKANLSINSLPQMIKNNKYYYAEVYEYDKLINEVLVSAKTKDLYSYKDGKKDYKVDYGDGYFRILEDGSYQFGITKDKAKFVLTNALD
EKENKYKKIEILDIEKADRYSKSKKSLEELFGKYKNIYYYAVVNKGLFRGKEVYAINIYNEKIYAVSENGLNEY

>CORE_REP|Org2_Gene1975#

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MTLSVITGIIIMILGILFANKILTLFGASENTLIYAKSYINIILLGTVVNLLSFSLNHSIRADGSPKISAGIMIVGCLTNIVLDWILIFGFNLGIQGAAIAT

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QPIIGFNYGAEKYDRVKKAYLGSLVVATIILCMGMVVVMLFPEAIIGIFNKDPELMNISVNGLRIYLLMLPIVGLSVTGTNFIQSIGKAKMAMLLS
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>CORE_REP|Org37_Gene2294#

MEKAVENFEDLSKEYINGYIERARKAQREFECYTQEQVDKIVKIVGKVVYYNAEYLAKLAVEETGMGVYEDKVAKNKSKAKVIYNNLKDKKSVG
IIDIDRETGITKVAKPVGVVAAITPCTNPIVTPMSNAMFALKGRNAIIITPHHKAIGCSTKTVEMINEELEKIGAPENLIQILDQQSRENTRNLISSA
DVVIATGGMGMVKAAYSSGKPALGVGAGNVQCIIDRDVDIKEAVPKIIAGRIFDNGIICSGEQSVIVAEEMFDKIMDEFKNNKGFIVRDKVQK
EAFRNAMFVNKSMNKDAVGQSVHTIAKIAGVEIPEDTKIIVIEADGPGEEDIIAKEKMCPVISAYKYKSFEEGVAIAKANLNVEGKGHSVSIHSN
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>CORE_REP|Org28_Gene1960#

MERLARREQPHIKFGMFKIRIPFIHYRFEKPEAIQGIISSMTSLGTIGLSTQILGLPYEVAWSMAIINSILYCLHVFMGDPVVPGWITASITLTTAYL
LKFSMGIERIQALTALQIDLGIIFILMGITGVAGKLVSKIPNSIKGGILMGVGISTIISEFNPKGRFDSYPISITVGILVACFVMFSERFDTLKVKNKFLF
HLGEYGVVSAILVSLIVGIFSKEIEIPRFSFDNLVYIVDFKNLINTVSPFGIGFPSVMLFIQGIPMAFMIYIIAFGDFITGENLVLSESENRKDEYIDFNS
NRSNVISGIRNIFMAIISPYIPMCGPLAATLTGSVAQRYKVGKEAMQSVFSGMGTLVWVSAIFICFYPIAQIATPLIPLALSVTLLVQGYLCTKLS
MELCDTGIEKGLIGLMGGVIAAKGGTWGLAVGFILYFVLIDSKKRKEKDINSIEDCVYEILDKKKSI

>CORE_REP|Org18_Gene2460#

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IIARDANIVEDLMSENIISVYVDEDREEAVRLVSKYNLIAIPVVDRQEKLKGIITVDDIIDVMEEEATEDMYKFAGSSEHEREVAEKENPTLREQIIS
ALRGRLPWLIITLVGGLLASLILSNLDYIMNPVYAPLVFFIPVVIGMGGNIGTQSSSVTVITLSNKDLNFSNVVREGIVGIITGLLCSIITGIVIYFVMR
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>CORE_REP|Org85_Gene2194#

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FLMSSNNKITFIEMGTMNPDFTLEEMNTLFKHIVKEIDFKTIFQYGQRDGAKWQKEAIAKLIYKAGLETTADSLLPASGGQNAIVAILAGLFQH
GDRIGVDPLTYPGIKTAAKMLGVQLIPIKQEHNEISEEGLLYACKNENIKGLYIIPDYQNPTTHIMSQNGRKMIANIASKYNLIVIEDAIHSLLNET
HLNPVASYLPNQTIYITSLSKIIAPSLRLAYISTPKQYRESLSDALYNINLSQSYFLTEIAYRMITSGEADKLINARRKSARRRNKIINQYLSGYNLLGN
EECIFRWLILPEGIMAEKFEIQALKEGVQVYASERFAVGKEKPISAIRIAVCATESIEELKAGLSILKRLLEEKK

>CORE_REP|Org10_Gene1101#

MLNFMTELLVVLSIFIQFSIMNGILIYKKDSKKNEKIVFYIVLFLIYIIIQISRLFNGGNYFSNINYLFYILAFIAWGGYYNYFYKMGYIKYSIFFYLFSVY
YKCLDAVIYRILFFAITGNVISSKESLLVPYLESIKIQIYSNLIIILIYLIFSFFRKSIKLISQDKRNYVYLLFALLVNTMNMLVNYVLKKLERFGSLHSEGYY
FDNFVNPKLVGASSIFLILLFKEIIKENRLKSQAELIKNKLDMQYAHYLSIQESHMRVKKLYHDINNHIYCIDNLRNNSKEINEYVNNLKDEIKTFKYI
YNTGNMILDIIINEKSEVCLKKGIKFTCSINFSKVNFVKPIDVSSIFSNILDNAIEACDKIVDENINKYIRIKGTITRSFFVLKCENSKLNQLTFNKNILLT
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>CORE_REP|Org94_Gene2824#

MITGYGLLIAFVISIGILLVSIIKFKVNPFLALLITSIITGFMVRMPINEISTTISTGFGNTLGSIGIVIGLGIIFGNILSESRATESIAKGLLAKTGEKNSAL
AVTTAGFLISIPVFMDAAFVIMMPIIKYVSRVTKKSLMVFVCALGVGTIVGHALVIPTPGPLAVAANVNANVGSFILYSIIVAFPAALIGGWIYGK
RFEKYPAYAIDENDREKNLEQGKDSIKIEDDDSSKVPGFGISMFSLLFPILLILISNVFSMFLEKGSTMSGVLAFIGDKNIAILLGILVAIGFLKKYINK
PMGDVVIEAADSAGLILLITGSGGAFGSVINASGIGNFLVDTMSGLSISVVVLGFLLSALLRISQGSATVALVTTSSILGPTILATGMSPVLVGLAIC
AGGVGFSLPNDSGFWVLSRFSGLSVKDTLNSWTIGGTIAGVVAFIMVLLLSVINGIIPLPGL

>CORE_REP|Org13_Gene2861#

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SIKINNIHNIKIYPNSIGNRDKVSVMKVAYKSAKEFSNDISQVSVSYLDKDQKILIANTEGIYVEDRRIRTRLGISSIASKGNENQTGFEGPGGCKGF
EIFEEIDPEYYAKESARVAHTMLHAKNCPAGNMMVAIDNGFGGVIFHEACGHSLEATSVAKGNSVFADKLGQQIASTKITAIDDGTIPNYWGS
MNIDDEGNPTQKNILIENGILKSYMIDKLNGRRMGMNPTGSSRRQNYKFAPTSRMTNTYIAAGEDRPEDIIKSIPDGLYAKKMGGGSVNPVT
GEFNFAVSEGYLIKNGEIQEPVRGASLIGKGSDILMNIDMVGNNVKQAQGMCGSSSGSIPTNVGQPMIRVKEITVGGR

>CORE_REP|Org7_Gene2173#

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DRIATDSLSFSGIKSIAKMIGIQLVPIPQENNEISIEYLESYCKNENIKGIYLIPDYHNPTTHTMSDLSRKKIAKIAKQYNIIIIEDAINSIFRDGIQTPIFS
LASDNTIYIFSTSKFLCAGLRVAFVVAPKRYIENLENALYNMNLMVSPFTAEIVHRLLYSPIIDKIIEEKRDAIIERNEVADKVLSDYNLIGDKNCSFR
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>CORE_REP|Org77_Gene1193#

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CLNVAHDCNLKCKYCFAAQGDFGGEKELMSFEVGKAAIDYLIANSGSRKNLEIDFFGGEPLMNFEVVKQLVYYGRSVEKDYNKNIRFTITTNGV
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VGDESNPYALREEDLPKIFEEYEKFAVEYADRQLQGDGFKFFHFMIDLNQGPCVIKRITGCGAGNEYLSITPNGDIYPCHQFVGNEEFKMANIF
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>CORE_REP|Org39_Gene2136#

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KFKRKKLTMEEIKEEVKILEKMGHKRLALEAGEDPKNCDINYILDCLDAIYSTYNENGNIRRVNVNIAATSVDEYKLLKEKGIGTYILFQETYHKPTF
IKMHGQSIKNDYYYHLTAFDRAMEAGVDDVGAGVLFGLSDPKFEVLGLMMHNEHLEEKFGVGFHTISFPRLKKAEGMSLEDFPHLVSDDMF
KKIVAITRLAVPFTGIIMSTRETAEMRNELLKYGVSQISAGSLTGVGGYKAYEDGDNTEQFEVGDHRSPVEVLKELITDGYIPSYCTACYRKGRTG
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>CORE_REP|Org52_Gene769#

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ESILNTFKSLVNEITLQNLDKNKSATCIVTVNSSEYINEDLIFKNDEIQNQIYNTILNSLSRHGFYGVQVKKNDMKIEIHTTKEMLNNMTNNYTDF
FISEDLKEIKYSLNIGWGIGNTNIHAEQNARQANGKSASLNGNCTFIVNDTNDTIGPLYSNKNSNNIEDSSIANKVASFIPLSNTNVSKIMCMIN
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>CORE_REP|Org73_Gene2599#

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FILIFIRVIQAIGTSTLYPSGVALIQNNIKERQSSALAVLTIFASTTAGLGPTLGGLLLDLGGWHAIFLVNIPVVLVSICLGYFLFPKEVKEKKSIKETLK
NVLSRLDIIGILLFSIAMIFILLFLLSMKESFNLEQLVFGIILMCLFIWHELRTKLPFIDIKLFVSNPKLSKVYLQFIILNFFNYILFFGLPSYFQDALHYSA
KSTGLFMLFMSGIGIFISPLTGKWIDKSGTRFPLVTSSIFMFISAVLLSVVFIHIPVIGKGIILSLAGISYGVGNVALQSSMFEESPRDSIGTASGLFQT
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>CORE_REP|Org80_Gene2690#

MVLTGAHYIYILFMVIILITMIMKKDTIVPCILGVFFMGLFFEKNIFGAITAVFNSFIISLNELGPIILIIAIMVALSKALEANNAIQYMVRPFSRVIKN
SNTAFFVTGFVMLVLSWFFWPTPAVALVGAVFLPVAMRAGLPAIGVAVALNLFGHGLALSTDFVIQGAPSITAGAAGVAVSYVINDGMILFW
VMGIVTISVAFYTLKRDINKGMFREELKGFESEEVEEFNGKSKIATILVALGFLADIIAMYMFDLKGGDASALLGGTAVFLIIIINVINFGKDSLENV
CENIIDGFVFGIKIFGAIIPIAAFFYMGEVAPLTGVFGKVLAPGSQGLLSDIGIALSQTIPLNKFAVSGIETVVGAITGLDGSGFSGISLVGSLASVFG
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>CORE_REP|Org82_Gene2492#

MECLTIKELVLATNGKLIYGDYNDCVSDIVIDSREASAQNAFVAIVGENLDGHTFMKPAYDSGCKTFIKNESNGIKLESSDINLIEVKDTSLALGDI
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HVEKLGSQEGILKAKMEITSNFDETNTLIVNGDDKFLSTLKEKEHVYKLKTFGFNKNNDIYCESYTMEEDSLTFICVINGKKEEIFIPTIGEHNIYNA
MSAILVGLCLNISLDYIKKGLKNFKGTKMRLDIIKNEKLTIINDSYNASPDSMDAALKILGRYKGRRVAILGDILEMGEISEYGHRLVGKSSMNNT
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>CORE_REP|Org18_Gene2516#

MIIMELFKAESKKYEKEFLKLLEQWVSIPSFYDRKTVSKDMPFGKGVYDALNWFENLGRENNFKVKNIDNHAVQIEYGNGKEYVDIFGHCDVV
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KGGAIIKLISNIDDKSLYISGGIEFNTIPDKVYIKNVEKLGKDNICFDINNISINYDNGNYIVYGKGGHSSKPEKSINPILATIKLLSENIDEKWTKDLYK
LINQDNINGNLFGLNIEGKCGILSMVPTIINIVDGKLEVVLSVRYPEILTIEDIIKKFNLYMEQNNINKFELIGENLKQANYIDRNSKLVRSLHDIYIKY
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>CORE_REP|Org93_Gene1653#

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AVFVALVVFGGLKSISNVATKIVPFMAVIYVVICGIILISFWNKIPETFMLIIKSAFTPTAATGGFLGATMSLAIRNGIARGVFSNESGLGSAPIAAA
AAKTEWPAEQGLISMTGTFIDTIIICTLTGFSLVISGVWCSDLNGAVMTQAAFNGAIPTFGPILLTVSLTLFAFTTILGWSYYGERCFEFLFGVKG
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>CORE_REP|Org49_Gene1535#

MGLKEFDFIEESIDMLRTMSPTLETISDEIEEYFENILDEKNQEYINVTSRIKSESSLREKIIRNRYLKKYGEASNLIHNVSDLIGLRIECRFIEDENKIY
RLLRRYFNKTDDKINYYNKENKNIKLKLSERQPNKQKNGFEIYKIDGVFAYLDREVKFELQIKSLVNVFWSEIEHKIIYKNNTYLLADKFIKDMMD
SIKNNLTMIDNQLLSIYKNFHSGKSFNMKVSKKEIEKLFAKLVYDAFSEKMNKSIGFVVDFKKPCETILSYSFNKQDISDEVLGNFMLDEFARLNEI
VNKDIDFNEQIEFEREPTFDDKFCKDLGNHFRSRLNTEFPWNLFFRILFEIEPYNNTKDFENFVEFIKENVLLEENREQLLCQFEEDSKLIIEDIYDCI
FNSISEIDSVEILYNYNLEKINFTSSEIITFICREHECYGEYLEEKEKLMNTFKEKIIQIFE

>CORE_REP|Org19_Gene876#

MENSNTNLGSESVGKLLFKLATPAIIAQIVNVLYNIVDRIFIGRMENGEVAMAGVGVAFPIIIIITACSYLIGMGGGPLAAIKMGEQNNDEAEKI
MSNSFSVLVILAILLTIGFKIGKEPLLWMFGASESTIRYSMDYLNIYLIGTVFVQISMGMNTFINTQGFATTGMMTVAIGALINIILDPIFIFGFNM
GVKGAALATIIAQGVSAIWVLMFLFGKKSILKIKKKYMIPKASIILPVLGLGISPFIMQSTESLVLIALNSKLQMYGGDLAVGSMAIMSSIMQILML
PNMGVTQGAQPIISYNYGSGQLDRVKKTFKLCLLSCFTYSTILWLLLMIFPAFFVSIFNKNPQLLSMTSWSIKIYFAGAFMFGIQIACQQTFLALG
KATISLVLALLRKIVLLIPLIFILPTFFNEKLFAVILAEPVADITAATITAISFFIFYKCFLSKPKAIKE

>CORE_REP|Org40_Gene2163#

MGEKKINNMNYSHNNYSKKTGEPTRKIKNSHITLKSKEEKICSSCNKENNTKDNYCKFCGNELYEIASLRPLETKLDLKSKIKELSYHANKRGVFLT
TFTTIFILFIIALIFKAIITIQFNDISYLINPAHIILALNLGQISVSMSTMMGSGFINANIGLLILLIIPILVLLISNLIFMRKRCRDSKTVLANSLGVGIFYGL
VLAILSIFTNVKTSSHSMLEYGYALEYSYEFFSVLLNGFVLGFICTYITTYKKSYEKENMYLSLFSNSIRTFILGYVLVLVILLVLTISDSSYLNELDMSSY
SNGLNLFTILPQIASYMWAFANGISVTIINSTVSMFTLSSSSLFGDTKLMFYAMGALSMLILLLNGYKLRFKYNTDSIRPIIVFSIYYAFLMGILALFS
TFILDSNINFFNTTNYGTTLIMQFKVLQAIVISFVYSFVISLIGYKLNSAD

>CORE_REP|Org6_Gene2128#

MLLLIVTCAIYIWIGFYFSKKVKTASDFLIAGRNLPLPILAATIAATSFGGGCLVGGVQWGAERGLWVGMYSTIGAALACFINAFFAGKLRSLSCD
ITPADYIETRYGHSVFLRAYQSLVTPISILAIMGSQLISFGSVSTAFGIPYDIAVIIGVIVIIIYTYTSGMWGVAVSAFIQLAICIVFLPIVAYISLKLVGD
NPLLMLQSMVKEPFFPGNKSISDFMYTVLPLVLGSIFSYESFLRYQCADNAKNAVKSSVIAGFILLFLAFPIGIIGAIGGSLFPNISSVQVLPQMIST
TLPPLISVLFLAAILAAIMSTADSLMTSMSAIISRDIYNKLLHPNIEFNDLKNTLKYSQIASALTAIIGAIIALKFDSLLELLFWPAPLCTGVIFAPFVIGL
CWKGATKKGAIYAVIVSVILALLNMIGILTVFDRILVPIIGGSITIFIVSKFSKKD

>CORE_REP|Org27_Gene2060#

MKTRNTSKYDVDGIPPLKESIPLALQHLLAMIVGNMVPAILIANVVGLNQGQATMLIQGSMLAAGLATFLQLYPIPLFKGFKLGSRLPVMMG
MSYVFLGACLSVAAKDGLAALFGAQIAAGVIVFFVGFGVKKIRHIFTPIVSGTIIACMGLGLFATAIKNLAGGEGTQTFGSPINFTVGVIVAFVIIM
INKYGKGLVKNSSILIGILVGYAISLVLGLVDFSAVQGAAIVSLPTPAAFGLEFRPELIVMFTIIYIIGIADMMGACTIATVGAMDREVTDEELASVV
LGNSITSIISSLFAALPTGVFSQNTVIVSMNKVTSRFVIALGALVLLLAGISPALGAIMTTIPSCVVGGATLVVFSSIAMSGFSIMSMDGFTEENNLI
AGVSIATSMGLTTAPQVLDQFPETIGTVLGGSSIVSGAIIAILLQTLFKLKSRKSAENVTSNLEENIG

>CORE_REP|Org77_Gene268#

MSNIITNLIESIFTNPITILFLLAITVYSVFKIIENNRVYSFVSSKLDEINRDYKTSEFYKKIRDDYYTYSKENPYADVNITSFIEEVVSDLKHNNLPLLEKI
RSIKNSSSISILLGVLGTFVGLSTMLLCVDTKDIINSLPSTISSMQTAFTTSIFGVVFSLIIGYFTKIKDCEHVLIQIMLKSENLLTSEITHFKSERIDLKVE
EVKNTIKQISKSIEAIEKFDKISKDLNDFNDEFISGIEALKSLLEGSQSSIKTFDQSVRKLDKQFNILNIKFVKLFDKYDNQDNINKEILFDIKESSKNIY
NATESQFKIRDYIKNINAGFALYERSAQDLLTKLMTHESKISQNQKILLDEKFTLDDSIKNLSNIIENFSNDLQVKLDMMFENSLDIQDKLDVMFN
NSFMNDEVPLDSEELFNDDVNNVFNPFSEEIYEIEDKEIKVIGEDELNE

>CORE_REP|Org18_Gene1417#

MCNMIREINTKLNSFEIFTIFRNEHDSFILDSAMDKEKLGRYSFISSQPFKVLKYKDTDENPLEVLKEELHKYRVVNDTNLPFVGGAVGYLSYDLG
NYIENLPRTAVDDIEMPDMYFGFYNHVIVIDHLVQKTYIATPNIDIELEEKIIDDIEQRILKEEKKGIDSICYEEKEVTSIRLKSNFTKEEFKNAVQSV
REYIRQGDIYQANLTQRFSGETELTSFELYRDLRRFSPAPFGAFLNFEDAHILSNSPERFIRCVNKRIETRPIKGTRPRGKDKEEDLRLQQELRNSE
KDRAELLMIVDLERNDIGRISKTGSVKVPELFVIEPYANVNHLVSTVVGELKDDKDATDVIKATFPGGSITGAPKIRAMEIIDELEPTQRNVYTGSI
GYIGFNGDMDFNIAIRTIIKNDKKVYFQVGGGMTWDSDPDEEYQETLDKAKSIMKALRGYYEE

>CORE_REP|Org95_Gene1227#

MDTKISINENMSLGKRFFKYLAPSVVAMWVFSLYTMVDGIFVSKGVGELALAAVNISMPFINFIFAVSLLFSTGASTIIAIYLGKKDIKSANEVFSF
NLVSIIILSIIILAITFFNLDRLALFLGATESTIGMVKDYLGIIIFFNGFFIVSYSLEVIIKTDGFPILATVGVIISALTNIILDYLFVIEFGWGVKGAGIATGL

SQVFSTIFFLIHFLRKNSTLNFSKFRIDFKTLRKIVFIGFPDSTTELSCGIVVLLFNLSLTKYIGENALIYYSVINYINTLVLMTMMGITQGMQPLTSFY
YGAGNIDNVKKLLKMGIKATIIASVAVFAICMAFSGPIVSLFIHPEETMLFNEGVRVFKIFSISFLLVGINVIISGFFVSVEKPSISTVISLGRGLVIVVL
SLISMILIFGGQGIWMTTIVSEFICLILSLVFLKKNFSTLDSNLNKVA

>CORE_REP|Org63_Gene2662#

MDLKGKKVLLVGLAKTGISTIKHLDKLGASIIVNDIKDENKLRNILDELESINDIKYILGHHPEDVDDIDMVVVSPGVPLDLPFILKLKNSGKYIIGEV
ELAFKLSNNPIFIGITGTNGKTTTTSLVGEIFSRAKRDTYVVGNIGNPVIDTIETSSEESVLVTELSSFQLESIDEFRPKVSAILNITEDHLNRHHTME
KYIEAKANIFMNQTVEDFCILNYDDEIVKSLADKCNAKVIYFSRTKKVNGGVYLENNDIIIDIDDKIKFLNKDDVSLPGGHNLENCMAAIAIAYVC
KIDLEVIRDVLMTFKGVEHRQEFVRNLDNVIYVNDSKGTNPDSTIKAIQSYDRPIILIAGGMDKGSNFDELLETAKSYVKSLVLLGETASNIENCA
KNKGFNDIHIVKDMEEAVKTSYEISKSGDIVLLSPACASWDMYESFEVRGKDFKDNVNNLK

>CORE_REP|Org46_Gene1302#

MNVGNILETIKMIDEEQLDIRTITMGISLLDCIDPDGDKAREKIYNKIMSSAKDLVKVGKDIEREFGIPIVNKRVSVTPISIIAGATDESDYVKFAQT
LDKAAEDLGIDFIGGFSALVQKGYTKGDKILIKSIPKALASTNKVCASVNVGSTRCGINMDAVREMGEIIKETAELTKDAKGFGCAKLVVFCNAV
EDNPFMAGAFHGVGEADRIINVGVSGPGVVKRALEKVKGEPFDVVSETVKKTAFKITRVGQLVAKEASSRLNVPFGIIDLSLAPTPAIGDSVANI
LEEMGLEVVGTHGTTAALALLNDAVKKGGVMACSHVGGLSGAFIPVSEDAGMIDAVIKGALSIDKLEAMTAICSVGLDMIAVPGNTTAGTLG
AMIADEAAIGMINNKTTAVRIIPAPGCDVGDMVEFGGLLGRAPVMPINTNSSELFTQRGGRIPAPIHSFKN

>CORE_REP|Org74_Gene2607#

MIITIVGGGSTFTPGIVKSIALREKELELEEIRLFDIDKKRQDKVAVVVNWILKEDVKTDVKLTVTNCEKEAYTDATFIFAQMRVGKYEMREQDEK
IPLKYGCVGQETCGCGGMAYGLRTIQPMIKVIDDVEKYAKKDYWILNYSNPAAIVSEACRKLRPNARIINICDMPIAIIDMIAGSLNINDVHNIRY
DYFGLNHFGWFTSIDYKHRDLMEEIKEYIKENKILLPKSYIENLNKSRSTGNRHAVSSWIHVWESVYTMLESFPKYLPNTYLTYYLLSKETVEHSNI
NRTRANEVMESREKDLFEGVRHYLETGEISEKAFYAGSHGDWISDLAVSIKNDTRSRFLVITENRGAIPNMPYDAMVEIPAYIGKDGPEVIARG
PIPLFQQGLMMQQLNSEKLIVEAYIENSYEKALQAFTLNKTIPSMNVAKEILDEMIEVNKEYWPELR

>CORE_REP|Org6_Gene2794#

MELKNFKDILFKKALSEGFEECEIYYYTGENLSINIYEGEVEKYNLDKSFGLSFRGKVNGKIGYSYTEILDDKAVDMLIKNVKDGVNTIENEDVQFI
YEGDKHYNDVKTYSKELENLEADKLIDLALEMERETKAYSDKVVNLSKCTISYSVSSNGISNTKGLNLSNKTNMLIGFVVPIIEDNGQKYDGIGYN
RANSIEEIKPCEISKLGVDNALSKVGGKSIPSGKYKTILLNEAMVSLLSTFSGIFNADSAQKGLSLLKNREGDMIASPIVTIVDDPLLENGMASTPF
DDEGVATFKKEVVLNGKLITLLHNLKTANKAGVKTTGNGIKSSYSSPISIYPTNFYIDKGDKSLDEIIKDIDEGLMVTSFAGLHSGANSVTGDFSLA
AKGFYIKEGKKVFPVEQITVAGNYFDLLKDIEVIGEDLEFPMSSIGSPSVVIKELSVAGKDE

>CORE_REP|Org19_Gene2030#

MKDLTTGHEGKSIFFFAMPMLIGSLFQQLYNTADSIIVGRFIGKEAMAAVSGANPIMFLLVAALMGVSLGFSILVSQFYGSGDLKKVKATIDTTY
ILLFIGSILISILGIVFGGPMLKLMNTPESVFAQSKLYLTIIFSGILFSAGYNSVSAILRGLGDSVTPLYFLIIATILNIVLDLTFIVVLRMGVEGVALATIM
AQAVSFIISIIYLNKKHEVLKFKIKGIVYDNKIFKDGLRLGLPSGIQQMLFSIGNMTLQFLVNSYGTSAMAAFGAGLRIENFISLPIMNLGSAVSTFV
AQNIGAGENERVKKGIRESIKMTLVLAVTVIALILLFRENLIALFNTDKDVIKIGSSYLFIIGPFFLFIGTSFVLSSAMKGAGDSMFALISSIVSLWLGR
LPASYMLSKFFGTDGIWMGIPFGWTLGLIVTVIYYKKGYWKTKAIVNHRINE

>CORE_REP|Org24_Gene2491#

MISFIRGYYVIVVEGVGLEQFLNHLIRNGISVYNVTRIKNTKMEFHIDRQDIKDFKNVYRGSKFDIKVKQKTGVPFIIKRVYKHKGMWICALVSLF
LLMSTSQFVTDVYIQSPEGIKKEALRNELYKVGVRPGVYKKSIDRKEVRDHMMSKFNDVAYLSINVKGTNIFVTVTKKAESLKSTDQSNYCNVIA
LKNGIIEKVIPRSGKSVIKSGDIVQKGDVLLNGANTKSIPEVWASTFYESTKKASYVDTVNKKTGEKKNIYTLSFYDKEFTMRKNIKYKDYVVENKE
KKLSIGNYTFPIKIKTSTFYETKKVEVKRNKEELKKELSEKALKELEYIIPASARIIDVKHNFKVNKNMLEYLITVQTSENIAKIYPLSKSEAERFIKEESK
PDEGEEEVPSNPEKRPLNDIRNEFDEDNKDNKDQNNSDENNSNQNSNNSQNNNSNNN

>CORE_REP|Org18_Gene2666#

MKILEVNVKKVNNIISKVYKDSIAEEMGIEVGDLLISVNEQPIHDIIEYRFLLSDEYLDVEIQKKDGEVYIYEIEKDYDEDLGVEFTNPIIDQAKSCRN
KCMFCFIDQLPEGMRETLYFKDDDSRLSFLQGNFVTLTNMSEEDINNIIKYRISPINISVHTTNPELRQKMISNKFAGKLYGIMKRLADAHIEMN
CQIVLCPGINDGKELDRTIKELAQLYPYVNSVAIVPVGITKHRENLVELNIFNDKSASKTIEQIHQIQQKYLEKLGTRFAFLSDEFYILSNSELPGYEE
YEGFLQFEDGVGMIRKLKTEIEEYLNILPENILKREKKVSIATGHSAYEFIQSMADAMMDKFKNLQVNVYEIKNKFFGETITVSGLLTAKDLKEQL
EDKELGEALYITRSMLKADEEIFLDNIELNQLEELMRIKIIPCLNEGKDFVDKILK

>CORE_REP|Org26_Gene2648#

MSIIAPIGIIIGIIAIIYFSVKEIHITIAAPIATLIVVILNKMDVVTSMLGADKNNYMGALGNYIMSYFAIFLLGSILAKFMEESGATVSIADFILNKFGS
NHPYRVLVAIFIVSFILTYGGISLFVVMFAVIPLARTLFKKLDISWNLIQIPLWLGIATITMTIIPGTPAIQNVIPIQYLNTSLTAATIPSIVGSIGCATF

GLVYMKYALNKSIRKGETYATYTSELEEESLDRELPGFFASIFPLLALVIIAITGSTFGSEFMKKNVIYIALIVAILLSAFLFHKFLSSKIQTLSIGASGSIG
PIFATSSAVAFGAVIMAAPGFDVFSKLIMSIPGSPLISLTVLTSTMSAITGSSSGALGIVMPNFADYYLSTGLNPELIHRVATIASNILTIVPQSGVFL
TFLSLSKLTHKTGFKETFIVVAVGSLIAEIIVITLGLLMY

>CORE_REP|Org18_Gene1066#

MIFLKVPYLVLSTVILFISNFIVRIFGFLYKIFLSRALGETGLGIYHMIFNFLMICLAVTTTGIPTALSCLVAKRKALNDRHNTNALFISTLYISFFVALIIS
IVASFNSSFLSLKFLKDAKLNLFILAVCPAIVIITLSNVLRGYYYGIKNVKIPAIGQIIEQIGKILFVFLLVMYINNKSMNCYIALLGISIGELSNIIFMLICL
WRDSSFDNRYIISIKDFYNSSMETLKMSIPITCNRMSNILLQSISSMMIPSRLALSGMTYQQSLSMYGIVSGMVMPFIFLPFTVGSALIVNLIPTIS
QEMALRKRKSVIKKIKYSILLTLFVGILSSIFFYFFGKDLCILVFKNTLAGEYLKAMFLVPLFMSLNQTLSGILHSIRKELASSINTITGMLIQLIALYVFL
PIPGLNIYAYIYTMTIVSIFTCLLHTIVLFKSLKSIR

>CORE_REP|Org22_Gene1525#

MENLFTRKFTTFEFLKFVSPAIISMIFISLYTIIDGIFVSTLVGSDALASINIVLPIINLVCGFGIMMATGGGAIVSIRMGENRQDEANSTFSFIVLFSLI
VGILFTVISYFFIKEISILLGATDKLLPYCITYGKVMILCTPFYILKFIFEYFARTDGNSKFSLFLSVIGGVTNIILDYVFIKYFGMGLLGAAVATAIGIILTC
VLGIIYFLSNKSTLKLRKPKTDFRLIRDTMINGSSEMVTELSTGITTFLFNVVALKLAGENGLAALTIVLYAHFLMTSVYLGFAAGVSPLISYNFGAE
NSDKLKETFKHSLKFIFVSSLLVFIIALVFAPFIVRVFVSPDNTVFKLALQGLKIFAFAFLFVGINIFASGFFTAFHNGKISAIISFSRAFVFIIIGIIILPPM
LNMTGLWLTVPFAEVITIFISILFIKKYKGRYKY

>CORE_REP|Org83_Gene1650#

MKILIVDDELEYGVVMKKILQKKGYLVDVTLSGEEAINIIKKDKNYDLVLSDVMMKNMDGVQLLDRIKAINKDIEVILVTGYGSIENAVDAMKK
GALSYFIKSNPIENLLEEVEKVKTSKTSVSLQKNNLEFTLESKNRDFNDVIKIAKKAACKDVNILILGESGVGKDILARYIHSISPRKNEIFVPVNCCSF
SENLLESELFGHEKGSFTGAVDSRKGRFELSNKGTLFLDEIGDIPLNVQVKLLRTLEDKSIERIGSNKSIKVDFRLICAMNKEPKVEISNGNIREDFF
YRISTITITIPPLRKRREDLATLIEFFLNKYQIEHDKKIHSIDKEVKDFLLNYNYPGNIRELKNIINRLVVLSEEGNLSKDNLNLISNNVYIDDKISIKPLR
EIRKEFECEYIEKVLSLCGNNISNTAKKLEISRRQLTNKIAEYNIK

>CORE_REP|Org59_Gene2420#

MSKIVAIGCGVGIITANLIPVYADNNTSSIKKVDNSILSDSNKRTSEKEILTAREAVSAALKNSEKLKMKSEEIKMLKEKLEVQDEFDSFTGSDNSF
PYDQIGLLKNQSEQAKGFMEDQIANDITNKFNDLVSRENELDKIKNNLEIKTKEIKDMKLKKDLGLVTSLETESAELELQTLQNTQKAKLQELKN
NQDYFKLLTNIDLNNYQLDKEYRFESFRVGGSVDSYMEGKVNEYLKYDQLILERTEESFNDKDENKADLPDRPELKKPTVPPKPIKPSLDKFSTQ
EEYIKALDEYNKKLDEYESAINALNQYNAEKTNYATGLTTYANYLQQKFNTENGLVTLEDSKKALKKGLIDSYAQLLALEDTIQITKKQLDLSEKQL
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>CORE_REP|Org76_Gene847#

MGSLKIYPSKLSGDVKIPPSKSMAHRAVICSSLSNGKSRISNIDFSDDIIATIRAMTSLGAIIEKKEDILEISGIFSKEGILNRENQLNQPKLTIDCNES
GSTLRFLVPISLAFDGVKRFIGRGNLGKRPLDTYYEIFDRQNIKYSYKENQLDLIISGKLKPDEFRVKGNISSQFITGLLFILPTLESDSKIIITTELESKG
YLDLTLSTIKDFGVEIINNNYKEFIIKGNQTYKARDYKVEGDYSQGAFYLSADAIGEDISILDLKEDSLQGDSEVVEILSRMGMEILREGNKIKGITN
GLNSTLIDASQCPDIIPVLSVVASLSIGRTTIINAGRLRIKECDRLHAINVELSKLGANIEEKEDSLIIEGVSKLNGGVEVWSHKDHRIAMTLAIASCR
CDKPIILKDFECVSKSYPHFFKDFKMLGGRIDEWNMGK

>CORE_REP|Org1_Gene2002#

MIAIKSKYLISSADEIYTNSAAVVENDIIKDILPNEEVEIKYKNIEEIIDKSDAIIMPGFVNGHMHQYGVLSRGIPANVHFTDFEGFLNDYWWPFIE
NRIGLKEVKATTKASAIELIESGVVAFCDTLEAPNTEEGTLIEQGKILEEIGMKAILSLESCERISFENGLRCLDENSNLIKWSRENSKLINGIMCTHT
SFTCSDRFIKKAKEDAKKLNAPMQFHLCESIYEPNYAEKHFGKKAVDYYNDLDILDETVLASQCVKVNDEEIDILKEKGVKVVHMPLSNCEVGG
GFSPVPKMIKKGIKVALGTDGYINDFFEVMRGAFLMHKSVEEDASVMPANLVFRMATEHGAYVLGLQNSGKIAVGNKADIIVMEDEFKTPVT
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>CORE_REP|Org57_Gene2857#

MEKFMSFMDKYIVPVAAKIGAQRHLVAVRDAFIVMIPITMVGALGTLINNLPLEAYKNLMASIFGENWTTFGGDLWWGAIGTMAVFLVIGV
AYFLAKSYESDGLQSGLIALSIFFIMAPQIGKIVPEGGTTVVEGWGMIQQTYLGTAALFSSILIGLLSTEIFVRLSKVKKLTIKMPDGVPPAVSRSFA
KLIPGMLTIMIFTVIGIFIKMLSNGSFLTDILNTYLGAPLSNVADSLGSTMLIAFIIHILWTVGLHGANIALPFTETILMKLGGENAALAQAGATEGY
HVLAGAFFDAFVYLGGSGMVLGLIVALLIAGRRRKEMIVLGGPPAIFNIGEPLIFGLPIVLNPIFMIPFVLAPVICSAVSYLAIDFGLVAPVILPKIPW
VTPPILGGAMATGDWTGGALALFNLILSILIYIPFVIASEKMEANKLKINN

>CORE_REP|Org45_Gene2817#

MGKLKAVHYINQFFAGIGGEEKADTKPHVAETLPPISLQLDKLLGEDIEIVGTVVCGDSYFNENIDSASEEVLSMVKGFEPQLFIAGPAFNAGRY
GVAAGTITKVVKDALNIPALTGMYVENPGADMFKKDVYVVETSDSAAGMRKALPKIAKLAVKLANGEEIGTPKDEGYIARGIRVNYFHEDRGS

KRAVDMLVKKIKGEPFETEYPMPNFDRVDPSKAVKDLSKCKIALVTSGGIVPKGNPDRIESSSASKYGTYSIAGVMDLTEETYETAHGGYDPVY
ANLDADRVLPVDVLRDLEKEGVIGKLHETFYTTVGNGTSVANSKKYASEIGAALVADGVDAVILTSTUGTCTRCGATMVKEIEKTGLPVVHMC
TVVPISLTVGANRIVPTIAIPHPLGNPALDPTEEKALRRGLVEKALNALTTEVDGQTVFEK

>CORE_REP|Org91_Gene2905#

MKKGLKIVTIGGGSSYTPELVEGFINRYEELPVKELWLVDIEAGKEKLEIVGNLAKRMVKKAGVDMKINLTLDRREALRDADFVTTQLRVGLLDA
RIKDETIPLSHGVMGQETNGAGGLFKALRTIPVIFDIIKDVEELCPNAWMVNFTNPTGIITEAVFKYTNFRRYIGLCNVPIHLKNDVAKLFNVESD
RISMDFAGLNHMVYGLNVSLDGEDVTKEAIDKFVKADISMQNIKAIDFNAEFVKSLGAIPCPYHRYYYKTKEMLEDELREFKEGKARGQVVKEL
EEQLFELYKDEKLDVKPPQLEKRGGAYYSDAACNLISSIYNDKKDIQVVNTLNNGSIRDFKDEQAVEVSSVITKNGPKPISIGYLPDSVHGLVSQIK
SFEVLVAKAAVYGDYESALLALCINPLIPSDDLAKTILDEMLEAHKDYLPRFNR

>CORE_REP|Org50_Gene2615#

MLKNMNLKDGLSVKDDYIMRRVIGYSILSVLIVTLVFILFEYSRLHKLYEYQIKNTQNIAGILIEKYPNDEIDIVKSIYNSDYSKVSIGEKAFKKFGYGL
ENKMSNDKNFSLYLKSFFKESFFIFLMMFIVVIDIIYYFIRYINKRLSKIYFIVDKMAQENYLKDTTESEETSYLVEYNEYFKEGTFSKINNCLYELNRS
LKIKFIKLEKEKESVKSLVTDISHQLKTPLASLKLYNTLLIEEELEEDEANEFLLTNKASINKLENLINSLVNISRLEISMINIKKEDNDIKNTILNAVKSV
TPKAKSKSITLNLNEFNSRIIPHDKKWTEESIFNVLDNAVKYTQINGEINISVEETANYFKIIIEDNGIGIEKNEFNNIFKRFYRGSADEIESVEGSGV
GLYLSRRILEEQGGNIIVSSKVGIGSKFSLFLTTM

>CORE_REP|Org31_Gene2489#

MKKENKMEGIKVGMLKKLCSLAMVAIMTTTLITGCSSGNGKDSKKDGEKEKLVLWMPPVENNMKEVWDPILDKFEEKNNCEVDLQIIPWD
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WEDFKRICKKATQDTDGDGKIDQWGLAQGWGAKTFGNLNWNWYPYLWQAGGDIFNDDLKSVKFNDKSGLEAANFLKELQAYVPEDSLSK
DSNEMIESVFGPGKAAFTIMLSSAATSVFDESFPDLNWGFVTGLEDKKAATFGAVDHLSLMSSAKNKELAYKLIQHMLSVESMTEFHKAIPRA
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>CORE_REP|Org56_Gene1740#

MKEIADAITSEYLSYGINEDISIYEGRFCIYLDKKYRCNGKIYYKMTPPISISFKADIGCVEEIDNEDDNLVLDYDNAILEVHGYKIISITINTLSEFSVE
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DRISTALSFMCGRYVGFCLAKGYRSGNEVYRIWNENQISPFRYVPTWSDTLSNYHNMEKYISLMCKKLEDFYYGSAIKSVVDWYIESLGSATM
ENNIISVQIALETLSYVILVEQSKILTDEAFDCNLASKNIRLLLDTCKIPYGKHELNIFDNIIKNKFDDGVDLVIYLRNSIVHPSRKTHRAVLEVEDIWN
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>CORE_REP|Org77_Gene774#

MSWRELYQSKLCSATEAVKQIKNGDTVVFAHCVGEPPALVEAMIENAEQYKDVEIKHMVSLGSGGYTAKGMEAHFRVNPMFVSGNVRKAI
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EPAKIGEVEEAIGKNCASLIEDGSTLQLGIGGIPDAVMLFLTDKKDLGIHSEMISDGTLALYEKGVINGKYKNFDKEKMTVTFLMGTKKLYDFVN
NNPAVEVKPVDYVNHPAIIMKQHKMVSINSAIQVDLMGQVVAEAMGLRQFSGVGGQVDFIRGVSMGEDGKAIIAMPSITTKKDGTVISKIV
SIVDEGAPITTSRNDVDYIVTEYGIAELKGKSLRERARNLINIAHPSVRESLAIEFEKRFKEKY

>CORE_REP|Org32_Gene2624#

MGVIIIQIRRPLLIILMFVVAISFIITNNTKNDEELNDKIITIQGVVKGKIEKKRYNQYKVGVFLINDYTKNKNLKIGQKVNITGKFKSLDKMKYDDF
DYGRYIKSTGYKGIVYINNYKIIDKNKLYSLIGEIKFYISKTYRYLYKKNSDFINSILLAEVENLTEEQKEIFTRTGTSHVISISGLHTGILCVIISFLLRGIN
KLYKLLILSIFITLYCIMVGASPSIIRSIAFVMIFYLSIFIDRKKDGISALSLIGIILIMNNPYVIYNVSFQLSFLATLSILIFYNKINSIIKLSMVSLTISSNILTL
PIIYYTFKGIPLLSIIGNLIIVPFVGVIMYLSIASLIVFKVSVVIAKIISFFNSTFIESIFFLLEKISNLSFAYINIENPKFYIVVIYYIGVFFYIFYIEGKEIKEQEN
ELQGYYKECKREKL

>CORE_REP|Org58_Gene1641#

MNYTTQMDAARKGIITKEMEIVSQKEQVDVNELRELIANGQVVIPANKNHKSLSAEGVGKNLRTKINVNLGISRDCKDIEKELEKVRVAIDMK
AEAIMDLSNYGKTREFREKVVEMSPAMIGSVPMYDAVGYLEKELKDITEEEFLNVIRQHAIDGVDFITIHAGLTRSVCQKIKNHERLTHIVSRGG
SLLFAWMELNNKENPIYTNFDKILDICEEYDVTLSLGDACRPGCIKDSTDGVQIQELVVLGELTKRAWERNVQVMIEGPGHMAIDEIEANVVLE
KRLCHGAPFYVLGPLVTDIAPGYDHITSAIGGALACAKGVDFLCYVTPAEHLRLPNLDDMKEGIIAAKIAAHAGDIAKNVKGAREWDNKMSKA
RADLDWCEMFRLAIDPEKAKRYRDESTPTHEDSCTMCGKMCSMRTVKKILNNEELNLI

>CORE_REP|Org18_Gene1107#

MLGGVIVVKKAIAALGIGAVAVSVSSINASALEKGTVTASALNIRSGPSSDCDKVAKLYKGKTVEILEKSNGWYKVRVSSSVVGWGSAKYISTSG
SSEGTSSQNNSTSSGTTISGNGKVNVSSRLNVRSGAGTNYSLVGKANNGDVVKLLEQSNGWYKIKLSNGVTGWASSQYISKTSEDVGTNNSS

NSNSTNNSDKKPSSEESIEGKNGKVTSAVSLNVRSGPGTSYSIIGKLNGGDVVELKAKSNGWYKVKLSSGTIGWVSASYISETNEDTKEKPNSSS
NQNSQSNSNSKPSFTGNSDKSTAKGSTIVDFAYTLIGIPYQWGASGPDKFDCSGFTQYVFKHSVGVSIPRVSREQANFGSAISMGNYAPGDLV
YFDTDGDGTTNHVGIYVGNSKFIHCSGTQTNPNKVKVDNLTSSYWSKVLLGARRFV

>CORE_REP|Org34_Gene2261#

MLDLNRKLAKLEEEGKKIRVALIGAGHMGNGMVSQMANMKGIEASIVVDINLELAHKAFTDAGIDEEIIDNVTNENDAEIKLQEGKVLTCNDF
LVACKTKSIDVVIDATGGIAIGAEIALNSILNKKHIVMLNAETDCVVGPILKKLADDAGVIFTGSAGDEPGAVMELFDFADAMGFEVRVIGKGKN
NKLDLDCNPDTVREEAEIKGASPHMIASFKEGTKTMVEMALMCNATGFVPDVRGGHGIEATVNEVPKKYALKSEGGVLDNYGVVDFVNGIA
PGVFVVVAHKLKAVNDELKYLSMGDGPNYILYRPYHLCSLETPLSAAMAVLEHKATIVPKAGLVAEVMTIAKKDLKKGEYMDGYGAYTCYGTI
EKYDVAKAMKAVPIGLISKKTKVVKDIKKGEVITYDMVEIEKDTTLYHLRQLQEKIFG

>CORE_REP|Org48_Gene1183#

MGKTKDIIVFGFALFAMFFGAGNLIFPPYLGIITGPEWLIAFLGFTFADAGLALLAVMATAKFDGNVVEMFKRCGMKLGILIGCADILCIGPFLAI
PRTGATTYEMGIMPLFGTSIPVLLFCILFFAISYVLTIKPSKVVDIVGQFLTPALLIALAFIIIKGIISPLGDIVDKPMIPNVFAEGIGQGYQTMDAFAA
IALASVLIVSLNDKGYSTISDKLKMIGKAGVLACGGLALVYGGLCFLGATVSTMYGTDAVQSQVIVNITEGLLGNVGKVILAVVVSLACLTTSIGLT
SATGQYFSRLTKGKLSYEKIVLAVSVFSAVVASFGVGTIIKIASPILSIVYPPSIVLIILAFFNEKIKNDNVYKGAVYMSLLVSILTVISSYGVAVPVVNS
LPLHSLGFNWVVPVIIAGIIGNFIPSKSQSNTLGTN

>CORE_REP|Org50_Gene2566#

MKRNLSLLLICLLIFTSFLGRSNISFADNEPAIVAKHAVLMDYETGKILYNKDGNSKLYPASTTKVWTACLVLKEVKDLNQVIEIKDLPQIDGSSMY
LKEGESFTVKQLLDALLVHSANDAAFVLARYVGGGNVQKFIDLMNSEAKKIGATNTHFNNPHGLPDPNHYTTAHDMALIAREAMNNDTFRQ
IVKTKSLKFEATKAYPYERYFVNTNKFLTSHDKITYKGQPINIKYDIVDGIKTGYTDAAGKCLLSSAVKDGRRVIVAVFNSTNADLYLDSRILIDYGF
DNFKCATIVDKEKYTDTKKVLFTKQHELIYEPKNSYKIFLEKNESKGNYDTKTELNKIDLPIKKGAKVGTLNVYNNGKLENSIDLIAKNNLDSSLPFL
TENNVLMTFVKIIAGILILLVLFIITSNIKKKKKIKKARGKRNMKK

>CORE_REP|Org21_Gene996#

MEEEKINYALEQIPENQKRGWVAMFSVLVAIGVDLSSVILGAELAQSMPMKQAILSVIVGSFFSAILYTTCSLVGSSTSLSTSMITKYVFGEAGAK
IFSLVIGVSLLGWFGVQVGFFAQNAQIIIKDIFNLDVSMQILSLIGGLLMMSTAIYGYKAMEKLSVYSVPFLLVLMMLTIFLAFRANGISVDDNM
KSTMTFAGGVSLSMSIIIVGAIVSPDISRWAKSRRDCALSSFLGIQFGNAFMIIVSIVLVKCMGTSDIMRIFITLGIAIPGIIVLTLAQWTTNTSNVY
SASLSIALVLKKAPEKVLTIVLGIIATLLAVFGIYEGFIGFLNLLGIVIAPVGGVYTAEYYIVKQELKGFDKGVLYKPIVKRSIVSWIIGILITYLSTYGFITL
TTIAPLDGFIAGFVVQSIIGKVLCSTKNKQEIDKAV

>CORE_REP|Org73_Gene1864#

MKLELGNIFIKNVEFGEKTEVKDGVLYISSEEIEKIALEDERIVSVNVELARPGESIRIAPVKDVIEPRVKIGDESKIFPGIINKVKTVGSGRTHVLLGA
CVVTCGNIVGFQEGVIDMSGPTAKYTPFSKTNNICIVIKAKDGIDTHDYEEAARIAGLKIGAYVGEAGREVEPDEVIVYETKPLLKQVKEYPDLPT
VAYVHMLQSQGLLHDTYYYGVDAKQIVPTFMYPTEIMDGAIISGNCVAPCDKVTTFHHLNNPVIHDLYKRHGKDLNFIGVILTNENVFLVDKE
RSSDMVAKLIEFLGVDGVLVTEEGYGNPDTDLMMNCRKCSEVGANVVLITDEFPGKDGKSQSIADATKEADAVVSCGQGNLVVHFPAMEKII
GTLDYVEMMIGGYKGCLNEDGSMDAELQIIIASTIANGYNHLTARYY

>CORE_REP|Org49_Gene2497#

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NAFTNFTMTAYLFSATENFYESLEHLIDYVQTPYFTDENVEKEKGIIAQEIKMYNDDPDWNVYFNCLKAMYVNYPARIDIAGTVDSIYKITKEEL
YKCYNTFYNPGNMALFVVGDLDVEKVIDVTKKSNNYKVDKLSKSIERFYPEEPKSVKEKEVIEKFPISMPMFNIGFKDSNVGLKGKELLRKEIVTD
ILVGMLFKKGSKLYEDLYMQGLINDNFGAGFSSQVDYAFSIIAGDSKEPKKVKKIILDYIEKSKKEGLSKEEFDRTKKKKIGSFIKCFDSINFIGNSFIS
YVFKDINLLDYLDVIKDITFEEVEERLKEHFKEEYCVISIVEPK

>CORE_REP|Org30_Gene1291#

MEKVKVAVIGAGNRGTYAYAPYIYENSDVCEIVAVAEPKKGRRELFTQKYNLDSKNVFETLEDFFKHDKMADAVIIATNDDRHYDVAKLALEK
GYHVLLEKPMSNSLDGLVHIDDLCDKYKDKIFMICHVLRYSPFYNKLKEIVESKKLGELVSIQYNENIGYWHFAHSFTRGNWRNSNETSPLILAKS
CHDMDILLYLVGSRCKKISAFGSLKHLNNQNASGEMAQNCLQCLVEKKCPYSAKRIYLEKDRSINRAVHINPTEENLLNILKTSPYGRCVYRCDN
NVVDNMVNILQFENGVTVTFNLCAFTKENGRTIKLMFSHGEVGGDLNKNEIRIKEFGKNEEIVMNPSNQQNMVEEYDRNLIAEFIKLVSNKEL
EKGRVAAKEAIQSHVMAFAAEYSRVSDEVVYIEEFFDSAKQMTKEIEETIF

>CORE_REP|Org18_Gene2736#

MSKQMRDIFIVGFALFSMFFGAGNLMFPPFLGMESGKDWLIPLIGFVVADAGIAMLVIIATARCKGSMDDVLRRAGKGLARVMSVAALACL
ALLVIPRTCATTYEMGIMPIFGDHGPVAKAVFSIIFFGLTLAFTIRSSKVIDIIGKYLTPALLLVLFVLIVKGIISPAGPMSPEHMIDKNLFGEGISQGY

QTMDALGAASMATIMLMSIIAKGYTSDKDQIGMTIKAGFVACVFLAVVYGGLTYLGATVSTLYDTSIPQASLLVEITSILLYGQVGKVILGVIVAL
ACLTTSTGLTASISTYFEGISKASYKQLVIGICVASMLISNLGVDSIIAISVPILQTIYPVLLAIVVMELAGKHIKNDNAFKGAAYVTLVISLLSAINGM
TGAVPFIQSLPLAGLGFNWVIPAILGGIVGNFIKSNKQVA

>CORE_REP|Org15_Gene1095#

MNILGLIVEYNPFHNGHIYHLSKSIEKTNATHTVAIMSGNFLQRGEPALFDKYTRAKIAVENGVDLVIELPTLFACQSAEIFSHGAITILNSLNCINS
ICFGSEEGNTEILYNIAEILANEPTEFKLLLKKYLDDGLLFPTARANALFDYIHQDKKNNFIQNYSKEQLSKILNSSNNILGIEYIKNLIHLNSSIKPFTIS
RVQSEYNSEEIKNNICSATAIRTSLKENINFFHLKNVIPEKTYNILNEKIDNGFLPMFDDLFFDTLKTIILRDMDTLKDYFEVNEGIENRIYRDIFTSEF
LHELQLSIKSKRYTLTKIKRTLNNILLGIKKSDMQLIKNIDTIPYIRILAFNDKGREVLKEIKNKSEIKIINKFSNISFSLDDTIFKTLISYDIKSTNIYNSVYY
KNNKDLVKGPMDFYTHPIYVK

>CORE_REP|Org38_Gene801#

MLNETKELLKDYYGIDDDTFKLSQEIMEEIKDKFEEIKEIREYNQYKVLKAMQESKLSDMHFNWTTGYGYNDIGREKIEEIYSKVFNTEDALVRPI
IVNGTHALTLCIQGIVRPGDEILSVTGRPYDTLEGVIGIREEKGSLKEYGVTYDDVDFLEDGNLDLEGIKNKINDRTKLVMIQRSKGYSWRKSLSIS
DIKEAIEVIKSVKPEAIVMVDNCYGEFLDTKEPTDVGADVMAGSLIKNPGGGLALTGGYIAGRKDLIELISYRMTSPGIGKECGLTFGTTRNVLQ
GFFLAPYIVSQAVMGAIFCSRAFEKLGYDVLPKYDDLRSDIIQCIRLNNADEVISFCEGIQEAAPVDSYVKPVPWDMPGYESEVIMAAGAFIQGS
SIELSADAPIRPPYNVYFQGGLTFDHSKMGTLKAIEFIKKLKK

>CORE_REP|Org5_Gene1045#

MKKNKIIAFFAPAIIVGVLVLGIILYPNEAIKSAREGFSIWSNVLVPSLLPFIIGANLIVDLKIVDIIGFIINPITRFVFNVSGKSALAFAISTVSGYPVGV
SLASEFRSNGQISKHEAQRLVSFCSTSGPLFIIGSVGTGMFQNSNLGYLMILCHYLGTILVGLFFRNYGNENLPKTKLDLKTNIKNVINIRNSSGN
GFFVLFGNAVFNGVNTLLTVGGFVIVFSVVFKILSLFNVISLIASVIYLPLSFLGVSKELCQAFVSGLFEITIGCNKVSSITSSPEILRASLASFLIGFSGL
SILAQCCTFLSKTDIDLKLYILSKFAHGVLAAIFIFILYPIANSAVLVSSFADTYNVIYNNLIWFYYLSYYDTILQIVVIIYLISAVFIAKKHMKTLSTNGKL
MRYKNTFFIKKFSRKKIKLIKLN

>CORE_REP|Org85_Gene2013#

MRRIFDKWEKLSIKYKLFSITTSLLIALALIIYLILYFLLPSYYHEYKIESLQESLKSLVDSSIHFDTYTLEERLYYMAKDQNLAILLKDNQGKIVYGKNEV
VILRYSKYMINSLEDEYRTSIPIYTKDAKDGPYTLELVMPLQPIDEANEVIRKLMPYIISIAILIAIIGAYIYSIVITKPLINIIESEREQEYRRKDFVATISH
ELKTPITIISGQIEGMIYSVGKYKDRDTYLKKSYECTQELKDLVNEMIEVSKSEILEKDLKLVSINISELLNRLVKRQVFLIEEKHMKTILKIEENLEVKA
DQERITKAINNIINNAIKYSPEESEIIIRLYDKNKRISKKNSNQRVVLEIENTGVTIEKRYLEEIFNPFYRIEKSRSRKTGGSGLGLYIVSQIFKSHGFDY
SIKNKENSVIFTVEFKN

>CORE_REP|Org92_Gene1902#

MSNRIKNIHYGTQRQQLKNLTKKEYQALREMCFLAKNLYNVGTYNVRQHYFNQGEHLNYEANYHVCKENENYKLLNSNIAQQILKEVDSSFR
SFFGLIKLAKEGKYDFRGIKSPKYLDKEGFFSIIIGQIRIKEDGILNVPMSPAFKKLYGKVSIKVPQNILEKKIKEIRIIPKHKARFFEIQYCYEIPKSEEVS
NQKNALAIDLGLENLCTCVTNLGDSFIIDGKRLKSVNQWANKQNDKIEALKLKKNITAITRKQFKVWNKRNNQVKDYVNKTCFYIIDYCVKNNI
GNLIVGYNAKLEKSDNMERKIYRNFIRIPFGEIKGKLEYLCKIKNINFIRQEESYTSKSDFFADDFLPDINVDNVKKYDFKGERITRGQYKSSVGIIIN
ADVNASFNILKKSQVVNLSNLQNNPQILKQPQRVRIS

>CORE_REP|Org9_Gene1519#

MITISHITAKNMYKSLEERINKFPQGAPPSDTLYKILNVLYTEQEAKLVAQLPIKPFRVKTAAKIWSVSESEAYRVLDKLASKALILDIEDNKGKKYI
MPPPMAGFFEFAMMRTRHDIDQKLLAELYYQYMNVEEDFIKDLFYSTETKLGRVYVQEEVLTNDNEVSILDYERATHIIDESTHIGISMCYCRH
RMQHVGKACDAPMDICMTFDNVANSLINNKFARRVDKIECKELLHQAYEHNLVQCGENVRKGVTFICNCCGCCCEAMVAAKRFGNLHPVQ
TTSFIPNINHENCVKCGKCITACPIDAISKVKEDGKEYIKIDEDRCLGCGVCVRNCHKNSIMLLKRDEKIITPANSVHRAVLMAIEKGQLQNLIFDN
NALASHRAMGAILSAILKLEPAKKILASKQLKSVYLDKLLSMNDK

>CORE_REP|Org97_Gene2113#

MNEQTRISLERAAELKSKIDDYIQARKTINRGLEKEEEINKRKQKILSILNGTEEDWNNYKWQLSNRITDVDTLSKIITLTKKEKEYIKEVGTQFRW
AISPYYLSLIDPEDICDPIKLLSIPTHIELEDEQEDLDPMGEEYTNPAGCITRRYPDRLIINVTNECAMYCRHCQRRRNIGQQDSHKSKAIIQESIDYI
RENEEIRDVLVTGGDALTLKDDYLEWILSQLKEIPHVDYVRLGTRTLVTMPQRITDEFCNMLKKYHPIYINTHFNHPMEITKESKEACEKLANAG
VPLGNQAVLLNGINNDKFVMRCLNQELLKIRVKPYYIFQSKHVKGTKHFNTSVDDGLEIMEYLRGYTSGMAIPTYIVNAPKGGGKTPLLPQYLV
SKGTDYVMLRTWEGKVIKMEDEPAVDIKKLIKEQAQD

>CORE_REP|Org54_Gene2018#

MEASIHTIASNNLLIIFAIVSITGIICSKLSEIIKVPDVVLYLLVGILIGPSFLKFIDIRGFQIENQLILTFGSAFILYLGGKEISLKVLRNVKISVFLLATLGV
VISAFIMQQVIGFTFGISAMTALLAGTIIASTDPATLVPIFNQVKIKDRVKQTVISESAFNDATGAILTSAVLAVILSNKFSLGENIYELGTMVIVGV

LVGLITGILLLKLVNDKPYGIFKDFAPIISVISVVVAYELSTKLGGSGYMSCFIVGIITGNKKNFKIWLSQKSYDADFYVAETLGTICRMAIFIILGSQV
NLAQLSKYFMPSVITVLVLMFIARPLCVLVCTLVDREAKWSKSEILFMMWVRETGVIPAALCGIISAMKVPGYEVISSVVFMTILITLVIQGSTTK
LVAKKLGLLEEEVINISEKVSTF

>CORE_REP|Org77_Gene520#

MSKNIYVKETYEWIRVGNGENELTEIEYEKLLKYLENNNDVLKSNIIDIKYKKLRFINYVGIICFENIILEILPKLSLSDNLVKDREILLQMLSICNKIPII
MNEKIRLSLKNYNLLNFFIMYFIESMQIQMKKGIYFEYINKIENLNVIRGKILLSTYAKEKCISPMKIRCEYDEYSENNFLNQVLKKACISILCRINDN
SIQGKIKKILNYFQNVDLIYIDRKKLLDYKFCKNNDRFRDCYLLARLLLLNLSMDNSQDNEEAFSILFEINTLYEEYIGILIKSIWDNSFRETYIQDKSK
FLLKNEQTGKKNFNLRPDIVLYDLKSEYEIIIDTKWKAIEVDSNVFYRSSDIYQMYAYITTYENAKRCILLYPCIQKDKNYSSWKLSESFKGKFIEAKT
VRLDDIKNTKNDLKKIIFNYKF

>CORE_REP|Org22_Gene1698#

MKAKNIGKYTICFIIVCFLMITITLILSYFNKDKLSVKTLKGNVKDIGRVSVVYTPNISKFSYEEVIISKNGVRNNTNPKSRIRNDYLNIDKKYSDFVN
DKGKELIYKDDLNIGEAYTSVKSDLVQGMNALNDCIKISNKNLKSGVEENFDINLNKSDFKENSWKTLFNKIYKGNLYMVISETNISGSKVNNICI
LKIDIKNKSYKLLNRFNLGLQNGEQQNINEIKFSIGSKLYLEIVNNKSKNGYIEGHDSYSNLIIYDIEDNTFNISNKFMDNLNKEKNANPKEIGLLSK
TKLDYMVKNNKLNLIVTDMSNSITNLVYDINSNEIKLEDYEILDLKVDYNEASSGVRKVKLLDDKIYSISGIKNSISGELKGFKGIVDVVGTKPVKF
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>CORE_REP|Org47_Gene974#

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EIYPGVILGQTNIPIESCLAYVPGGQYPLFSTALMLIIPAKVAGVKRIVACSPTMKNTEKINPKTLVAMDIAGADEIYATGGVQAIAAFTYGTEKIK
PVDIIVGPGNKFVTEAKRQCYGQVGIDFVAGPSEVLIIADETSKPVYIAADLLAQCEHDLNARGILLTNSLEIAEEVEKNIETMLKDLPTKDIAYSS
WKNNGEIILVDDMEEAIKISNFYAPEHLEIAVNKCDDIFDRLTNYGSLFIGNLSAEVFGDYVSGTNHTLPTLKASRYTGGVWVGTFIKTCTKQIFN
EEAIESLAPVAEKLAKEEGLYAHAKAAEVRFKK

>CORE_REP|Org12_Gene2767#

MVNTKKIINLGNNINLTLIKTEKFKSNLISLYVQRLLDEKETTKNALIPSIIASGSAKYPSARAISNKLDDLYGSSMGADAVKRGERQVLSFKVINISE
KYLDESIFEEVVEFFNEVINNTLVVDGGFKEEYLNIEKENLREKIQSIINDKKEYAQDKCIEAMCKGERYSVSEFGYEDEIDSITSRELYEHYKNILKT
SPIDIVVEGNFDEDKVVDIISKNLKFEREEIINIPRADFIKNVDEVKVIDEQMEITQGKLVMGYRANVDYADIDKYYALVVGSNVLGGGPHSKLFV
NVREKESLCYYIFSSIEKYKSIMFISSGIETKDYDKAVELIKKQVESVKAGDISDEELENSKLALVNSMKSITDNIGGMSDFVFSQSMAKTNSEVQD
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>CORE_REP|Org61_Gene2620#

MAIKKKVINSSGASTTGGNNVGKSTPSSPTQSKGNGKWKEISKHIMTGISYMIPVLVMGGLIGALSQLIPYAILGLDPSVGIVDAMNSGEFTGF
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SHNWLAFKTTFLIPLIASLACMVLMIFIITPFGGLINESMKNFLTAAGAAGEYVYATALAAATAFDLGGPINKAAGFVALGLTTENVLPITARTIAI
VVPPIGLGLTTLLDKRIVGRRVYDRQFYQAGKTSIFLSFMGISEGAIPFALERPGFVIPLNIVGSVIGAITGIILGAIQWFPESAIWAWPLVDNLFGY
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>CORE_REP|Org19_Gene2292#

MSQSMVGKHAMWPKENDVIFSISGRAQAAEKAFGMDNVINATIGALMDDSGKLITMKTVYEEYKALDNCEIGAYAALEGQPDYLEAVKKVF
FRDYLPEGHIRVLASPGGSGAIKLAVWNYTNEGDEVLTSDWFWSPYVSIAEEANRKVVNYQLFDENRRFNFESFKEKFVNIAEKQGRVFTIINT
PAHNPTGYSVADDEWDKILDLSKEVAKDKDKKIIFFVDSAYIDFAGDDDVCRKFFKKFSNLPENVLVLVGFSMSKGFTAYGMRMGAIICISSSE
DVAEEFHYSCVHSCRANWSNCNRSAMAVLSNIVNDPKKFKEYEDEKEIYKNMLTRRADVFVEEAERVGLEILPYIAGFFVSIPCDNPKEVCEELT
KHNLFAVPLKMGLRFAVCAVSEDKCKKAPSIIKEALESLEVKINN

>CORE_REP|Org26_Gene2105#

MGRRTTRVSRLGKEKKRSVLIVLAALVLIMGGFTYFFNSKFLYNGKIAKNVYIEGVNVSDMTKAEALKAITDKYTPEDLNLAYDGKKYTISPKDID
LKYDTEDVVKDAYESTKKGSYFQNLKKYIDIRVNKANMKIKAEYDEAKLSSKVSSIADSINVKMKNASISVGSGGLSYTDSAVGREFDLAANKESI
YNMIKNKEHKTLELKVNLQKPDITTEQVKTVNSVIGQYSTTYSQAVEGRSYNVGLSARKTSDVLLMPGEEFSYNKLTGPSNKANGYKDAPVIVY
GKLEQSAGGGVCQTSSTVYNAALLSGMEITQVTNHSSASTYVPKGRDATVSDGGLNLKFKNPYKHPVYIKNYAGGGSVSSVIYGNSGDKPNISI
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>CORE_REP|Org29_Gene1788#

MSKVIVVGGGASGMMAALSASKNNNEVILVERNGELGRKLRATGGGRCNFTNNREIEDFFDKVVSNKKFLYSSFYTFTNKDLISYFESRNLEYK
IEKENDHKVYTKNDKSIEVIEVLNKDLLNHNVKIMYNKKVIDIITEEIALKDDSNKDKSKYLIKGIILDNGDKILGDKVIISTGGVSYSKTGSDGSMY

KILKKHGHTLNKLYPALVPLTIEEKWIKDLQGISMKNVEISCKIKKRKISKSGDMLFAHFGITGPCVLIMSSYINKIIEKEKVELNIDFLPNLSTDEISSI
IRAFPNKNVLNNLKQILPQNFLREIFSLLSLVDKKASDLSKADEIRIIEYIKNMKLTCNGTTGINTGMVTSGGISVKEINSSTMESKLVKNLFFTGEV
IDIDAETGGYNLQIAFSTGYLAGISV

>CORE_REP|Org74_Gene2365#

MDLSGIFKYYCKECENTWNNSSVELFENIETYSKDSQKKREKELDKLLNTISVHLERYPSDAVLRKMWVKKGEVFLQKTLEKENIFKLEKMDVED
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KSKDYHESKVSKMIDYIESVYPREKFTEVYESLLLIFKSQVNSLKQHGKENHLCKEDLLSISIEKGGSSVLVDGYLISGLMTKEEIEFCIGYGFLLQISD
DLQDIKEDLKYNHKTIITEMSKEGTLDKVVNKLINFTIELIDSFKINNKNKSVITMIKNDCLMLILFSVVYNAEFFSVGYIKEVEKFIPYTIDYSLEIEEK
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>CORE_REP|Org64_Gene1750#

MITLTFDIVQTLTLSIFFFLIGNLLKNKVNFLNNFCIPAPVIGGLLFCFLNLFFKYFNIADISISGNLMPNFITFFFTTIGLEISINLIKKGGSVLFRYWILC
GVLAFCQNILAITISKIIKLEPLLGLMCGNVSMEGGHGYSAAFGLTIENLGIEGAVGVGLSAATIGLIMGGILGCPVAKFLINKYKLKPSSNIDLSIPR
YNRNLKRFGSKFFRNKNRIKNNNFSQTITPSIFLEQVLLIFICINTGEIISRCFYITFNILLPSVVTCMFSAVIFRNLNDKINILELNFKLIDFLKELSLGIF
LTLSLMNIDLFELSTLLPPILLIVTFQVIFIILFSIFICFRVLGKDFDSAIIISGLIGHGIGATPNALANMSSLTQKYGASPKAFLVVPLVSGFLLDAISIPCI
LFFINILT

>CORE_REP|Org14_Gene3214#

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LKTPMTSLIMLNDLLYNDIPYEVKIDFLNKIKNQLNRMDWLIKSMLKLSKVEAKVINFKKDKVKFSELIHRAMQSMKIPMEIKNQKLTIEGSDNI
SYIGDIDWSVEALVNIIKNCVEHTPEFGNITITYKENPLFSELIIKDDGEGIHKKDIPHVFKRFYRGRSSSKEDSVGIGLAMSKSIIESQNGDIYVNSE
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>CORE_REP|Org12_Gene1026#

MATIKPFKAIRPNKYIVDKVAALPYDVMNSKEARRIAEGNPYSFLHIDKSEIDLDENIDLYDEKVYLKARENLDEFRKQEILVKDDKECIYIYKQIM
DGRAQVGIVACISVDESLNGTIKKHEYTRPEKEIDRTKHIKYCDANTGTILVTYKHQRVIDDIINDFMDNNEPLYDFITDDKIEHTVWKIDNDDII
DNLVDKFEKLDYLYIADGHHRTASAENVAKEMRAKNPNYTGKEEFNYFIAMIAPDENLMVLDYNRVIKDLNGLSEEEFINKIKENFELEEIEGKE
KYKPDKKGTFGMYLGDKWYKMKANKNLLEIEDPVDSLDISILQDYVIDAILGIDNPRVDKRIDFIGGIRGLEELEKRVNEDMKVAFAMYPTSIED
LIRVADANKIMPAKSTWFEPKVRCGLFLHEINE

>CORE_REP|Org62_Gene1505#

MKSYTKAKWSVWGIITFSFVLVLFLRMSTAVVSDNLENELGFNSIQISNIASFCLYAYAFMQIPAGILIDKYGARKISSLGIIMASLGSILFGLIQSIE
LAYISRVIVGAGTSVILLCILKVQGRWFNKSEFASATAKFSFVGNLGGVLATFPLVFLSELVGWRNSFLLIGIIGVVIGCFMYIIVRDTPKEYGFNVD
TELYEESEKVNIVDGIKSVIKNKSTWYNSMIMLSFVGLTSAFISLWGVRYIMDVYCVSKSFSAFIVSFFTYGFIFGSLIMDFVFAKIRSSKFNIIKYGA
IIDLFIWIVIVVVYQVKPPIIVLPISFFIMGCIVMSHLQVFNDAKYKNKEIYSGLATSVINTFEFIGSGIINLIIAISLQVNSYNVVDGYKKSFVVFIVLSII
TIVSSHIGVKNDDFKAL

>CORE_REP|Org17_Gene720#

MIMENNLNTAKRNNTELSQNDSLKVNLQIGVDFTLLSKSLKAFYKKEKDFYCIALAPCNVSSEEANRKISIYDMIKEINILIESITDKNELLSEELFTN
NLSEFYDESLDEIYIDLKQAYLYIKKNTNGLNIEDSIEYVFDVDISNDIKAKENPLINFNSLSLVVWSGETKHILQQMNILNLEDIHSYSMENNTNIT
IYENDNLQYKFDEESEDIKDSNIDIIEQMLILPDDLNYDKDEVENMKSRLAKINIKYLQALKEKDIKIKLINSNLTDEPEFSDLKYQLPPCWVRSGKT
WKDVPGIYRNNSIVAKIGYSNPSYTNVHSSKNLELHETAHAIDKNVLNKKSNSEEFMKVFAQERYKLYDPKQIAHAYISKFIEEFFAESFVHYYLD
EDSKNTLKENCPLTYDFLEKLELYY

>CORE_REP|Org46_Gene2737#

MELNKVELLAPAGDLERLKIAITYGADAVYIGGEIFGMRSAAKNFSKEDMAEGVAFAHERGKKVFVTVNIIPHNEDFLQLEDYLLELEEIGIDAVI
IADPGVLSVIKKVIPNMEIHLSTQANTTNYLSANFWYEHGIKRVVVARELSFDEISEIRAKTPLDMDIEAFMHGAMCISYSGRCLISNYMTGRDA
NKGSCAQSCRWQYHLVEEKRPGEYFPIYEDERGTFFFNSKDLCMIEYIPELIKSGITSLKIEGRMKTAYYVATVVRAYRMAIDEFYKDPENWKFN
PMWMEELKKGSHRHFTSGFYLNKPTTEDQNYQSASYVRNYDFIGIVRETEDEDGLIVVEQRNKMCVGDEIEVMGPYKETMFTKIEAMYNEE
GEAIESAPHPRQIVKLKLSVKVGKDYMLRKVIEEKVEE

>CORE_REP|Org1_Gene1708#

MQITTFGAIFGLLIAIILIIKKFQAVYSLMLGAFIGGLVGGANITQTVDFMANGAMNISPSILRALASGVLAGSLIKTGAVDKISEQIVKIFGEKRAL
FSIAISTMVLAGVGVNLDVSIITVAPIGLYIGRKLNYSKLSILLAMLGGGKAGNIISPNPNTIAVADNFSVNLSSVMMANIIPAIIGVVITVILASILIN

KGNKVQSYEILEQREDLPSLFKSLCGPIIAIFLLFLGNVSPIVIDPMIALPIGGIVTLIVTGNLNNSREYLAFGLSKMQGVCILLLGTGTIAGIIQMSEL
QQSTIGALQFLNMPQFLLAPVSGILMSLATASSTAGATIASSTFHDAIINGGLSPISGASIVNAGSSVFEQLPHGSLFHTSSGSINMDIGERFKLIP
YEALIGIVMTIISTSIQLVL

>CORE_REP|Org10_Gene510#

MEDEILKGKIKQLTILALIFIFITPVFAFADTPPVPNSSRAALLIDQETKRILFEKNIDEKMPLASLSKMMTFLLAIEAVDKNQVKETDMVKIDKSTA
SVGGSTCKLKDGDEISLGELMQGLMLVSGNDAAIAIAKHIGKTEKNFVNMMNKKAEEIGMIDTYYFNPNGLPIYTDPEHKEPPIENMSTAHDI
VTLGKYMYDHYENQVTRITTMQVYNDTKKDFTHYNTNPLLVSVPGVDGIKTGYTDNAGYCLAFSMMVPKDAKNERNHRLIGVVLGDGNKK
NRISSSATLLKYGKDNFHSKKIAHKGDIIETPCVDGIDDFKITVKVDKDLYGVVSDNENINPKVVFKNMNYPIHKGDIVGVAKYYNDSGKFVGSV
DVKSESNIGCIPLKDKIKIKVAKINKKLEIKNSVCFKA

>CORE_REP|Org77_Gene2939#

MDGDILMSKILKYKNEIFLFILVVITYLIITKIFFSKTTIFYDLNNTYDVLLDTDTGVLFNLNVFAISQDNSKHILFSAIISIFAYPIYLFCTSIANPGTTDF
NSAYGFGLICLQIITSAMSITLVFNHIKKIKMQRLTLILLTMIMIFSFPQLFMTLNVERFIYSQFSLIFFIVIANKMKGKNSYLVELAAIPLFGITISNIYL
YFFNMIFEFKLKIGKMLKHLLTFILMAYICVVSTKSYESFMNLGNVIQYDTKFISGEPILEKIAMIIERLLYSVFYFPGAGIKKGLFLQNGEVATIPVIL
TLLALCFCVLSVIENSEKRVPKLCMGIIIFNLTLHGIVGYNLVNSSIMAINFSFAVIILLAYFTKALRKNEKNIYNIFLSLLLVTIIISNINGFIEILNIGIKSY
PV

>CORE_REP|Org97_Gene1466#

MKNCLNFNCEIDIIDNPLNLELNDFLDVGIRNNSKRRFLFISKKLGKHLACKPSEMDNLGKLMATIYNEKNKEESNGTVIAFAETGTAVGHSFFD
YLCGDYEFIHTTREQFDELENLEFLEEHSHATDQNLYFGMLNNFKFGDEIILVDDEITTANTCMNIIRKIQSIYPKKKYTICSILNWVSDENLSKVT
RLERELDCKIDFVYLFKGNFKFYIDEDIISNYNDNYSITKLETISSDKVNLVVNHIYVDLEDYIGNKKYVKYTGRFGINRREQFRLKEIVKRESKKITM
ASKESLKNEKEKILFLGTEEFMYIPMLFAKEKENQYDIYYHSTTRSPIINIDKNNYPIKSKFMLKSFYNIDIQNYIYNIDKHNFSKCYLFVELNKSENS
YLEFIDIIKKTSIKELTIVCCS

>CORE_REP|Org4_Gene2664#

MQEREELVLNPVPKEERVGWLAPLFNMLGSNIAISELMVGGTLILGMTLSNMIITSIIGNLILVAIIMIQGYIGYKEGLNTYVLAKGAFGEIGGKY
LISLLLGITSFGWFGVQAGVAGLSVQKIFPSVNLTLVTVILGLFMVVFALYGFKAMAKFNYLVIPPLMILMVWGVFKAFSTYGVEAIYNYTPQTT
MSMVEGLNIVVGLVIVGAIISPDQLRYTRRVKDIWIISFLGLGIISLFQQVAAGVMSMGAPTWDITEVLANLGFGWVAFVILILASWSTNVSNA
YSGGLALKTIFPNVKRNVLTLVAGLIGTIIAATGIIFKFQSFLSFLGIAVPAIAGIMWCEYYFIQGRTYKHREGINWIAVISWLIGFAASYYSSKINFLI
PPINGIVVSMVIYYILMKCFGIKDK

>CORE_REP|Org52_Gene1914#

MINKNVFTSTKNHLIKMYIIVVGSFLIIFSIFIYSYFRGLTYSGIDSEINDELEYIVSQFKRTSFLNPIRLKDPKDMVYVYEDGRISYYTQNEYFDELLP
DRRLDKKNSFFKYTENGYTFRELNVDVGRYQIQIIRNIDSEMNSLRQLTSVLIIGILISVIITYFVAVYLTRKALIPIETAWKNQAKFIQDASHELRTPI
TIVSSKLESMLKSPESTVNDEVETIATAMKETRRLKKMITDLLSLTKEDSIVKVNLEEIDLEKLLEEISEDYIDIAEFQEKRFVFNSKLKNKVIITDKNK
LRQLILIFIDNAFKYTKLGDEISLELKEDIEDEVTLLISDTGIGIKKEEIPLIFDRFFRSENVRNKDLEGSGIGLSIARMISLNLSIDINVTSDVDIGTTFEL
SIPKKLK

>CORE_REP|Org45_Gene629#

MQDYKKNKRRMTNQPMPTMNEEEVYTEEINSEDMRGFKKSHHHNECNTDNKCDCHDDCKPCNPCKPNPCNPCKPNPCNPCKPNPCDDN
CGCHDHCKCDCEPCEMDSDECFENKCGPECCNPISPRNFSVSNAVPFAIEANRIFDTMQFQTFTDATGPNGEPLTFETEVVEVFGSVPSAGKA
SVTIEKICLSNDGIVIDTGMTTLEDFDLDPLGDIVGRNCETTFEFAVCGERNAECCRQGKGKSVAYKQRGLTVAVRNLVLELRGRCGCTEFVALA
FPAVRAGGGCKRRVDYVEFTFNTLSAPICLPADGRAVTLRQEYQTNLTVDCIGKSILKLECNECCEPFYELIIPNDIDLVLCLQNTVSTLISEQIVVL
ASPNPIQPRLVDTFSKVCDFSQCGPNHESGKPSCHR

>CORE_REP|Org29_Gene1424#

MSLLKNSLANLKGHKLRVFVALLWIIIGITSVILVSSIGNGFQKEIKKSVNNVNPNKTTISFESADNTGLTDDMSIFLKPFNAKDLEELSFVEGVERI
APSRDGFNLDSVYSSQASFDKKTTYVDVGPVKKDSKINLICGRDFSLDDEKRKVILLTLQSTSEIFENPEDALGHGININGTIFEIIGVLDDSQQNQ
AGGFFGGYQDMQFTTSLVPKKAFDTLMSQNSYSNEIYQLDLVSSKGYNVNEVANNVIAKLYEMHPGINGSYTTPDPTEQTAYLESINSNVNKY
VSIITVVAMFVGGIGVMNIMYVSVMERQREIGIRRAIGAKPRSILFQFLVEAVFITVCGGILGTIVGFAATNYVSKYIGFEAIPSLNSLFYAIVATILT
GVVFGLIPAFKASKLDPIKAIYK

>CORE_REP|Org79_Gene3042#

MSFLKKFKNKRFRNNSFKSNNFRSSSFGSSGFNSKNKGFKNNPFKNKRFKIYAGIAVIILLILGVLAYVDSKNTKLQANENFIETYTIPENEKIFING
MVVPKQTKDFNISGDYELSDVNVTNGQKVNQGDLLFTAKNPTIIAEIDSLKSQLSQYKKQKISLSDIAENRDAIASINAQITTLNSQIASLDKKAY

DRVTAPFDGTVYLNDQTGNPDQPVSFMTIQGLEFYMKGQASEQDLPKMKIDQMVNILVFSTDQKLTGRISFISDKPSTPNTEMGAQQNTLS
YYDINIAFDNQEGLVNGFHLQASLEVSNSSFKIPASCVLKDKKHSYVFKDLDGILKKQIVDVASQNDDFAVVRGGLEQGDIIIKHPTKEMKEGDP
VQGDGVTAGSNNNGDTTPNKKVEEVNMDVN

>CORE_REP|Org18_Gene2684#

MMKVLLSGGGTGGHVYPAIAIANKIRDEHPDAEIIFVGTEKGIESEIVPKYGFELKTVTVQGFKRKIDFDNVKRVFKLFKGLEQSRKIVKKFKPDIV
IGTGGYVSGPVLFNASMGKIPAIIHEQNSFPGVTNKILSKTVTKVLTSFEDSHKRFPEAAEDKLVFTGNPVRKEILLSRKNIARKNLSISDEKRMVL
CYGGSGGSRKINDAMRLVIKNMVNEDIAFIFATGKSYYDEFMGSISDINLKPYQKVVPYLEDMANALAASDLVIGSAGAISLAEITALGKPSIIIPK
AYTAENHQEYNAKSIEKQGAGIAILEKNLTPESLNTAVFKLLGDRELLVDMANASKTIGKPEAIDLIYDEIMKVYNSTQKSTSKKTKKEKVIKEVKE
IKKETTPSIEGQAKVIGIKKR

>CORE_REP|Org57_Gene2615#

MKKVVIIGGGPAGMIAASTACEKGYDVTLIEKNHKLGKKLAITGKGRCNITNACEIEELIENVPTNGKFLYSAFYTFTNDDVISMFNNLGVKTKTE
RGKRVFPESDKAFDIVNALERQLKSKKVNILLNSKVEKIISKNNKIEKVILNDKKEIKCDSVVVATGGLSYPLTGSTGDGYKFAISQGHTIIDTKPSLI
GIEVQESFTKDLEKLSLRNVEIRVFNSKQKKVYSDFGELEFTRFGLDGPIIKSASCRMKDTRKENYTILLDLKPALDEEKLDKRVQKDFQKYTNKKF
EKALDDLLPKKLIPIIINLSEINANTVVHQISREQRKNLVHLLKNLKFTVKRYRPIEEAIITSGGVKVNEINSSTMESKLVEGLFFAGEVIDIDAYTGGF
NLQIAFSTGYLAGFNC

>CORE_REP|Org66_Gene913#

MKQKVVERFLKYVSFDTTSNSQCENCPSSEGQRVLAKYIVEELKTMGVDDVSLDENSYIMATLKGNTDGVDTIGFISHLDTIEDVSGKDIKPRIIE
NYDGKDIVLNEALNVITYVKDSPELEEFKGDDLIVTDGTTLLGSDDKAGIAEIVTAIEYLINHPEIKHGDIKIGFTPDEEIGRGADLFDVEKFGAKYA
YTLDGGIVGELECENFNAANATITIHGRNVHPGSAKNKMVNAIHIAAEISEMFPADERPETTEGYEGFWHLNSIGGNVENVSMAYIIRDHCKE
KFENRKSIMIENIEKINKKYDNRVELDLKDSYYNMKEKIEPVMFIVDIAKEAMEELGIKPRLVPVRGGTDGARLSFNGLPCPNIFTGGLNFHGKN
ECIPVSSMEKATKLIVRIAEKYAERV

>CORE_REP|Org29_Gene2326#

MKRYLIVFLMCSSLFLVGCGKTKESEPEKPIAVSVQKAVGGEIENTNSFSGTTKVKDETAVTAQTVGTVQEVYVKLGQNVRKGDELLSISSPELE
NSVKQSKASLDLAKASYSSATGGSLEAQVNQAKTALDNAKIQYEESQRNYDNNKILYEQEVISLDQFKKIEFSLEQTKQQLDSAQRAYDTATSKS
IPQAKALAKKQLDQAQVSYNLAMSNLDKLTLTSPVDGTITAKNFDSKEMITQSQPAFIISNPNILEVDLNVAESDIGKFKKDGNVDVIIEDQRILG
KIDYVPSVVDPQTSLYPVKVLVNNANNKFKAGMSAQVNLSIEKENGAVTVPKKAIFEENGKKYVYIATKDNIAKKHLVQTGIVTEDKIEIKSGVS
DKDTVIIGGISLISDGTKIFPVEKEK

>CORE_REP|Org88_Gene1163#

MSILVQKFGGTSVESYEKMNEVCKIVKAYKKNDEELQLVLVVSAMGRKGAPYATDTLINLCSAVNDEPSKRELDLIMSCGEIISGTILANLLNAQ
GIDSVFFTGQQAGIITSDEYSNAKIKYINPKKIKRALDDGKVVVIAGFQGVTDDGEITTLGRGGSDTSAVAIGKALECETVEIYTDVDGIMTADPR
VEPNAKVLSFIDYEEVFQMADKGAKVIHPRAVQLAKSGNITLAIKNTMNPTFEGTKIGSLCRHLEDNIEYEQERDFKVAVANKDSVAQVKIKSA
EEVFTEVLNEIEKKFITIDMINFFISEKAFVVEDADIKSLKEILDKFELDYEVNRDCAKVTLICSRIADEMSGIMSKVVRGLSKAGVSLLQTSDSNMT
ISCLVSEEDMHTAVHAIHQQFYLK

>CORE_REP|Org70_Gene1218#

MSTKNITDKTKNKKDVGALIGAAFIMATSAIGPGFLTQTAQFTQDFGPNFSFVILITTILFIGAQVNVWRVIGVSGLRGQDIANKIIPGLGYLVAF
LVALGGLAFNIGNVGGAALGMNVMFNMNMTLGTVLSGLIAIFVFMSKNSNSLVDKITKFLALGMIIIVGYVAISNHPPVGEAVSRMVKPENP
KGLIFPIITLLGGSVGGYITFAGGHRLIDGGITGEENIKEITKSSLLGILVATMMRVLLFLAILAVVSKGLQLDPENPAASAFKFSAGAIGYKFFGLVL
WSAAITSVIGAAYTSVSFLKTLNPFIDKYEKYFIIAFIAISTLIMAFIGKPATLLILAGALNGLILPITLGIMLIASKRKDIVGDYKHPTWLLIFGLIVVLIS
AYTGITSLSSLGALFA

>CORE_REP|Org32_Gene174#

MQQALKLKYQTKELGKDFVIESCNSIKPWLINIRRELHKIPELALEENLTKQKVISYLKEIGIDYMEFTKHNGIMAYILKESADKTICIRADMDALPI
EEENNIPYKSIHSGKMHACGHDAHTTMLLGACKVLHSIKDKLNVNVKFLFQPAEEGFGGAKFLVEDGCLENPKADYIFGLHVMPHIETGLIETK
YDTLNASVDTIKISIKGKRAHGAYPENGIDAIVTASQIVTSLQTIISRNLEPNNAVVLTIGKIYGGDAHNVICEDVKLEGTLRTLNSKTRNFMIDKIA
KIVGDTASAFGCVGTLHVSDENYPAVINEKELVDTVISNTKELLGEEKFILRPNPSLGGEDFSFYTEHCKGAFFHLGCKNEEKGLISPLHTSSFNIDE
DCLPIGVMMHVMNTLYFN

>CORE_REP|Org7_Gene1542#

MENKVKIGVLGYGVVGSGLIDIIDNNKEKRSIEIVGILVNNLEKHKDKKYSNIITNNIDDIFNKDIDILVEVMGGLEPSLSYIKKALNNKIHVVTANK
DLLAECGDELAKLASENKVSIKFEASVAGGIPVLKPIIESLEGNNIDSINAILNGTTNFILSKMYDENLSYDMALRQAQELGFAEANPESDVLGYD

AARKLSILSTLAYDNRVYWKDVYLEGITDIDEKDIEYAKKLNCKIKLIGQSKYENDKVSAFVRPVLVEKDNILARIDNEFNAVIVNGDSVGEVSFVG
KGAGSLATGSAVYSDVIDIIDNRVSSIDSFTKDKIQVNKIVREKCGALLRFKKCNKDEILNIVENCLVKFDILNDDDELAIMVYADSEYEINNSLCLI
KDKGYCEKMNKMLKIS

>CORE_REP|Org38_Gene748#

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LVGLEEAKHNNRSYPFNIKLIAFAEEEGTRFETSLMGSKVFAGTFKEELLKSVDENGITLEEAVTKFGFNTKNLTNLHPRKDVDAYLEFHIEQGPV
LENESLPAGIVSSITGFKSFKISVNGKSGHAGTLPMNMRLDAGCCACECVLAIEKVAKTTADLVATVGKMNFYPSSSNVVPERAEFTLDVRSCS
QEILDNSVEKIFNEISHICENRKLNYTSELAFENVPVPCSNKITKIIEKSFIDLNLNPFYIYSGAGHDAQEMDNITDIGMVFIRCAGGVSHNPNESV
SVDDLDTAVKIFLKILDNLDLK

>CORE_REP|Org7_Gene2623#

MNNKKYYPTAIALYFSYFLLGIGISILGQYKPEFSSMWGAKTLSDGTLDVSIVLAVIAALGLGRLISYPFAGPISDKYGRKVSGLIGNFLHAIFFVGIV
FSPNFYIAYVFAIIGGAANSFLDTCVTPSCMEIFASLGTIANMFTKFTIALAQFLLPFIIGFVAANSISFKVIFIVTAILIVVDAILIAVLPFPPANNVID
NKGKTVKSEKMKFTPTSIALVCIGFTCTSTFVLWLNCNQELGKLYGMADPTKIQSFYSMGVICAVLITSLLIKKYIKPIRILVIYPIIALLMLLIVYFVQ
TPTICMLGGFVIGYSAAGGVLQLTTSTANEMFPTNKGKITSIVMIASSIANYVILNIAGIITKSGGVNGPKYVVLFNVAITFVGILLALFVNMRYEK
EKVYDYDV

>CORE_REP|Org44_Gene2527#

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TTLGFITTDANIDGVLLKEALKIAVDKSFNRVSVDGDTSTNDMVMILANGKAKNDRINKKDEHYQVFLSALTYVCIELAKLVAKDGEGCTKLIEC
YINGALSEEHAVKLAKTVISSSLVKTAVFGADANWGRILCALGYAGEEIDMEKVDIIFESMKGYIEVCKNGNGLDFNEEKAKKILEDDEISILVDL
NMGNARGNAWGCDLSYDYVRINGSYRN

>CORE_REP|Org26_Gene2843#

MNQEYVKGNPIFTNINKVPRQFPYLTDDIDTDVIIVGGGVTGCICAYYLAKNNIKSVILEKGRIAHGSTSVTTSLLQYELDDNLIDLTEVMTLKDAL
KAYNLCTSALEELDTFIELYGNKCDYAKRDTLLYTANKLEVKAIKEEYNLRKENGFDVEYIDESTNPFSFDLKSGLIAKNGGRELDPYKYSHHLIDVS
LKNGLQVYENTEVKKVDLSNDKVTAEVSYGYKVHGKKLIVATGYNTSLFTKRNFATKSNTFNIATKPLKNIASWKNNILIRDNCDPYNYLRTTKD
NRLIIGGEDVSFDDIENETLANEKYDILEQRLKSMFKDIKDIEVEYKYCGCFASTLDNLGFIGPDNKNNNLWYCLGYGANGILFAILGGIMLSELYL
GKQNKNMKLFKVDRFDK

>CORE_REP|Org79_Gene3598#

MLKEIKWKVNNLPKGDKENCIKFLNEEEITKVRNFHKSFPQYKETPLANLEGLAKKLGVAGVYVKDESYRFGLNAFKVLGGSYSMGKYLAQRLD
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HGVMVQDTAWDGYEEIPAWIMQGYGTMAQEAIEQLKEYGVDRPTHVFVQAGVGSLAGAVQGYVASIYDECPITVVVEADEADCYYKSAEA
GDGKPRFVGGDMPTIMAGLACGEPNTIGFEVLKNHATAFVSAPDWVSAKGMRTLGNPLNGDEKVISGESGAVTTGLLVAAMEREDLADLR
KDLKLDENSRILLISTEGDTDPDKYRSIVWDGEYPSI

>CORE_REP|Org40_Gene1535#

MQIKIGKVIQRLRKERNLTQEQLAKFIGVSTPAVSKWESGNSYPDIELLPLLADFFNVSIDKLLNYKIDLSEEKVMKIYKELESGFARIEIDLSTEEPK
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HKSIGDTSVNLAMIYLKQNRLEEAEILLQNKLFSNIFNISMDCKGIINVYKNQYKELKKKLENRNFNKNAIEREMEYIKNKLLWYANLSLEIKKML
SEDKGAFFSMYVDYMELSLIFLFFNMKEEAKKALYSLKEILEKYPIHESLDVSQMRFFDKVESKNLYTFNIYTNLLIVLNDDSYNELREEPIFKDVIE
KILDMEKMLKNKE

>CORE_REP|Org74_Gene2696#

MKKTIMSLQHLLAMFGATVLVPILTGFNPSVAIFCAGVGTLIFHFCTEGKVPAFLGSSFAFIPVILAAKEAYGGDLAYAQGGIIVAGLIYIIMSIIVK
VVGVNKIKLYFPAQVTGAMIVVIGLNLLPTAFSMASANFVIAFITLAIAILTNKFGRGFIKQLGILIAVFSGYIICLILRLVDITTITEASLFAIPNFTVPK
FSLGAIVIISPVVLAVFMEHIGDMTTNGAVVGKNFIENPGLNRTLLGDGFATIVAGCLGGPANTTYGENTAVLAITKNYDPSILRRTAIFAILLACV
GKFGGFLQSIPGSVMGGISIMLFSMITYVGLKTIRDSSCVESKINILIIAVILLIGLGTTYLSNKGISVGIPITSTVKITGLSLAAIVGIVLNRILNNQDFK
VEEE

>CORE_REP|Org29_Gene940#

MRFIHTSDWHLGKSLEGHSRIEEQAKFCEEFIKIVESNEIDMVIIAGDVYDTSNPPAQAEKLFYQTVSRLANNGQRCVLIISGNHDNPERLSAITP
LAHEQGILIYGYPLSATIEAKYKGFEITYATQGCTKLNINGENIVIATLPYPSEKRLNEVFSSEDEFEKQKNYSEKVGDIFRSLEENFRSDTINIAVSHI

FVIGGESTESERPIQLGGSFLVERKDLPEKAQYTALGHLHKQQKASERLNAYYSGSPLQYSKDERAYTKGAYIVDIKAGEKPIIEDVYFNNYKPIEV
FKCNGIEEALDICEQNQDREIWSYFEINTDEIISQNEIKKMKELLKDIIEIKPIITSCYEQESVDIKEKSMAELFREFYSFSKGVEPKGELMDLFLDIISE
EGESADETN

>CORE_REP|Org18_Gene1169#

MLMKKRFLPMIIGFLFTFFFVNIFAIMIFANEVPSSEDKEYGETKNSIDKYIDGQLDKLDINEIQDYINKEIVINDVNLKSFVKDLISGEKNILDLFNK
DGLKILMFDEFKASLKVVAVILVLALLSSILKSLENSFSSGAVSQIATYIIFITMVSLTLIGFKDVLQICYDAIDHTVGLMQVIMPILITFLLLIGFPITST
TLNPIFIGGVTFINVFFKNFLFVSITVAFGILIINNLSKNIRLKRFFSFVKQINYVSIGAMFTVYLGLVSIQGLYVTSFDKFSVKTAKFAIGNFIPVVGGF
VSDSVDILLSSSQLIKNIFGGIGLILLVGICLLPVIKILSVIVVYKLAAIIVEPVGEDGISNFLNEVANLMIIMLASVIAITVMFFVTVAILTSISVVSQG

>CORE_REP|Org48_Gene2468#

MNRFFKVRLITAIMFLIILFAFSIFNICYSGKDMIQEIKNSVAEKSSLKDTISSIDNKVNDKVIYKNTFIETYGYLQKLMGKNEFSKFSVVKDTSGKM
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TDHHWKVETSFWAFGELVEQLNKKYNMNLDENHYYRDKENYNSIVYPKSFLGSMGRKTGILYGGIDDFTLIYPKFKTNYTYYTDSKSQKFELKG
RFEESLILSYPFNADLNLMDGQSDKYFTYLLGNRPLVKIKNIENPEGLKVLFVKDSLIVPTAAFFSSVCSNIDMIDPRYYDGDILEYAKSHDYDFVFI
SVYPQNLTKEFFPFCE

>CORE_REP|Org74_Gene2205#

MSLNSTPQSVRVHIGLFGKRNAGKSSIINAITNQSAAIVSDIAGTTTDPVFRPMEILPIGPCVLIDTAGLDDVGELGELRIGKSLDVLEKTDIALLVV
DCQIGISQEDLSLIEKFNDKNIPHILILNKIDTIKNQSEILNLTKNKVKCPVVSVSSTDKIGIENLKNEIIKVLPKDSTEFKLVSDLIEPNDLIVLVVPIDK
AAPKGRLILPQQQVIRDILDSGAISIVTKEDSLKETLSNLGKKPKLVITDSQVFPQVDKDTPKDIPLTSFSILFARQKGDLKELINGAYALENLKDGD
KILMAEGCTHHRQTDDIGTVKIPNMIRKKTGKNITFEFSSGVSFTEDINKYALVVHCGACMMNRAGMLSRIEKAKSFNVPIVNYGILIAYVKGIL
ERSLELFNY

>CORE_REP|Org35_Gene1079#

MKLRALDISEANSYIKRILINDPILSNLKVKGEISNFKVHSSGNVYLSLKDETSKLNCVIFKSNFNRNLKLDNGVKIIANGYISVYERDGAYQLYINEI
EIEGIGNLHIEFNRLKEKLNKEGLFDPKYKIPIPKMPNSIGVITSPTGAVIRDIINVIKRRYPKVNIKLYPVMVQGDKSAEEICEAIRFFNHMKNVDT
LIVGRGGGSIEELWSFNDEMVAREVFNSQIPIISAVGHETDFTICDFVSDMRAPTPSAAAEIATPSLDDINYKLGNIKSRMSKSLTNQIELDQYRL
ETVFNKINNYLDSYTIKDKVIQLDKIYDKIIFGIENNLKLEDEKLVKIGALLHNLSPLATMDRGYSITQKNGKVINSIKGLKIKDSIDIVLKDGNLECMI
DKIENKEG

>CORE_REP|Org38_Gene120#

MKTSILIALIEKTSLIVVLFLLITKLKIFKQIFQKEEYSFNDLVCIALVFTFLAIFGTYSGINYMGSIVNTRIISIVSGGILFGPMVGITAGVFSGIHRYFM
DIGGITSVPCLLSSILAGVLSGFLYKRIPKQHRVMYGILVGMISESFTILLIYLISYPHSLAIQIIGGIYLPLIVGQIGIGFVISIVEGIEKDKKDIEARNKAE
IKALQRQINPHFLFNSLNTIASFIRFSPDKARELIINLSTYLRYNLEYSDNLIDINKEIEQVKSFVEIEKARFGELLTVSYDIEDVNIKIPSLIIQPLVENAII
HGILESGRAGVVKISIKKLPYSLENTVRISIEDNGIGISEEIINNVYQDNMPENKIGLYNVHLRLKLMYGRGLNIRRIDNGTLIVFYVKE

>CORE_REP|Org26_Gene1549#

MKSFVSPDNIWVLWAVVTGWAAFSIYLEQKYNWASKVSGAIIALVGAMLLSNLNIIPVESVVYDQVWGYVVPLAIALLLYQCNIKKIWKESGR
LLIIFLVGSVGTVLGAMIGFLALKNVVPDLNIVAAMMTGSYIGGNVNFAAMSGAFDAPGELVSATVVADNLLMALYFFVLIAIPSIGFFRKHFK
HPHVDEMESIGITEGETVAANYWGRKEISLKDIAIAIGSAFIIVAVSVELSTWFKAIIPLSNPFLAMLNTLFGNQYLIITTLTMLFATFMPNFFGDIK
GAQELGTFLIYIFFVVVGVPASITLIIQKSPLLLLYCGIMVLINMLVTFIVAKIFKFSLEEAILASNANIGGPTTAAAMAISKGWSKLVGPILIVGTFGY
IVGNYFGLLVGNILI

>CORE_REP|Org82_Gene1799#

MDRLVGTVSRGVRAPIIRQGDDLVKIVVDSVLNASKSENFEVRDKDVIAVTEAVVARAQGNYAHVDNIAKDVKDKFGDDTVGVIFPILSRNRF
AICLKGIAKGCRKVVLMLSYPSDEVGNHLISIDELDDKGINPWSDVLTEEKYRELFGYNKHTFTGVDYVDYYKNLIKDCGAEVEIVFANNPKTILN
YTTSILTCDIHTRQRTKRILRQNGAKKVYSLDDIMTASVDGSGYNDQYGLLGSNKATEETVKLFPINCDEVVNKIQGNIKEITGKDVEVMVYGD
GAFKDPVGKIWELADPVVSPAYTKGLEGTPNEVKLKYLADNDFADLSGDELKEAISKYIVEKDNKSDDLTGNMVSQGTTPRRLTDLIGSLADLT
SGSGDKGTPIIYIQGYFDNYTK

>CORE_REP|Org78_Gene1879#

MELWKRNLFVCWIGMFFSSIGMSQIAPILPLYIKQLGVTDVSLIQQYSGIIFGCTFVVAAFFSPI*GKAADKYGRKSMLLRASIGMGIVIFTMAFV
QNVYQLLGLRILQGVFTGYATACTTLIATQTDKNHSGWALGTLATASTTGSLIGPTVGGYIESILGLKSTFIITGGLLFVSFIISILFVVDNFKPKEIKE
SISIPKEQLNILPNKFLIASIFVTTFITQLALYSIEPIVTIYISQLTNFASNVALIAGLTFSASGLANLLAAQKLGKMSDKIGPQKVLLISLLWAGIIFIPQA

FVKTAWQLMLLRFLLGLSVAGLNPSVNSLLKKIAPEEYVGKIFGYNASAQYIGCSSGAFLGGQISAHLGIRTVFFSTSLLLFRNALWMYKFTGLFIKDKTK

>CORE_REP|Org69_Gene1011#

MKILVLNCGSSSLKYQLIDMNNEEVLCIGLVERIGIEGSILKHEKAGRDDKYVVEQPMKDHKDAIALVLEAVAHPEFGAVKEMKEIDAVGHRVVHAGEKFATSVVITPEVEDALKECIDLAPLHNPANIMGIDACKAILPDVPMVAVFDTAFHQTMPKSSYLYGLPHELYTKYGVRRYGFHGTSHNYVSQRAAEILGKDIKDLKIVTCHLGNGASIAAVDGGKCVDTSMGFTPLEGLIMGTRCGDIDPAILPFLMRKEGLDADGLDKLMNKESGVYGMTGISSDFRDIEDAAKNGDERAQATLEAYVKKVQKYIGAYAAEMNGLDVVVFTAGVGENGKAIRADIASNMEFLGMKLDKEANDVRGKETVISTADSKVKMLLIPTNEELMIARDTLRLVK

>CORE_REP|Org82_Gene2089#

MFIEFFYLLRSRGLNISLNEWMTLIEALDKGLCYSNFSNFYYLCRMILIKSESDFDKFDAVFLEYFKGIEHQEEIPEEIMNWLKKPDIDLEEFERLEQNPNINLDKLRAKLEERIKEQDSPHNGGNYWIGTGGTSELGHSGKGQTGIRIGGNSTYGRAVLEVAGERKYRDFRDDEVLNMRQFQVALKRLRQFSTRIDAPKTELDLDKTIEETCNNAGYLKLFFEKPRKNTVKLLLLMDSGGSMRGYSTLCNTLFQSVSKSNHFKDVKIYYFHNCIYDRLFTTPECWLSKSINTEWILKNIDKNYKVIIVGDASMSPSELLHIGGNYRGPYNYTPGIEWLKRFKRKYSKIVWMNPELRDGWDSINYWYQTQRMIQSEFNMFPLTVKGLEKALKNLMLSR

>CORE_REP|Org36_Gene1022#

MSKVFEVKKDIYFTGVVDEGLKVFDIIMETEFGTTYNSYLIKDEKTVLFDTVKANFKDEFLSNLSEVTDIAKIDYVVIHHTEPDHAGSLKYLLDINPNIEVYCTKAAKLYLDGQINRPFNCHVIKDGEILNIGKRNLRFITAPFLHWVDTMFTYIEEDKTLLTCDAFGCHFASVDAEVVNSEDYLKSAKHYYDCIVKPFAKHVLSAVDKVVGLNIEFDTILTSHGPMLTKDPMAAVKRYVEWSTEAVNTTNQNQVSIFYLSAYSNTLEMAKKIKEGLDKEGAKAELYDLEDMTLTEMHDTLVVSKVILLGSPTINKTMVKPMWDLFSVIDPMANQGKIAGVFGSFGWSGEGITMAETLLKSMSFKMPVESLKKKFFPSEETLKECMAFGAEFAKLVK

>CORE_REP|Org52_Gene1563#

MSIIVQKYGGSSVADTEKIKSIAENIIERRKENPQMVIVVSAMGKSTDEYITLAKELSNEPSKRELDALMSTGEMISASLLSIALNALGCKAISYNAYQLNIKTSGLHGKSQIDDINVNRIKNSLDEGNVVIVTGFQGINEDGDVTTLGRGGSDTSAVALAVKLNGKCEIYTDVDGIYFTDPRKYSKASKLDEIEYEEMLELASLGAQVMHSRSIELAQKYGVEIYVGRTCGTEKGTYIRGGKDMKLEDKVITGLATSDDDSSITIKDFKAENISSLFEDIATIGISVDMISQTAPILDKISVSFTVPKEELGECKKIVSKYTDEEHVVIDNNITKFSLVGLGMKNTSGVAAKVFKIFNENGIMIKLITTSEIRITCAINSDDKQVAIEKIAEVFNI

>CORE_REP|Org43_Gene1184#

MRKLIYFITPFIIGVVFLFGLDKFLDSKTDELLREKNLLPIMDDTLSDIKDKGVTANNHFLREKDIMILGSSELSNSTKQHPKYYFNTNRSKNKVFAIGRAYTQTLQDAAILGSMNPNIDNKKVVLLISMQWFMEKDGVTSHHYQSRFSPIQFYRFLDNPKISKQNKIEYAKKSSKLLWGSDEYKAEALYAKLYEPKTLLEKAEKVLLEPYFQGRKYCIALKEKGILYKRLIKLDKKRATKRKSPINWSHERKKAIEDAKKRVGKNPLNIDNYYYKQHFKDGIDQYKGRDKDVNLLTSKEFESYKLMLNVCTDLGIKPVVVLIPSMDKFYNLTGISEKERNQYYDKAQNIAESKGFEVLNLKDKGSDKYYLRDVMHLGTKGWVDVCERLFKIFKEQ

>CORE_REP|Org76_Gene334#

MNFNQKRIAASIMATAIIMPTMGNLAYANESEVESVSIESRTITGNAVNFRKGPGTNHESMGKLYKGDKVEYVGKEGSWVKVKYNGNTGYVHGNYVAINSLGSSNESSDTSVKSTKVVTAKGLNFRTGPSTSSSKISTLGYGTEVGYISESNGWSKISSNGRVGYVSSKYLGTSVNDSTNENVENSSNDLVKGTKVVTAKSLNVRTGPGTSHSKIATLSYGTEVGSISESGGWTKVSYGNQTGYVSSQYLAEKGSVDTSIPSYSTNSPSQGADSVISFAKTLLGKPYVWGAEGPNSFDCSGFTQYVMKKSAGVSIPRVSRDQSKYGTYVNRGDLRSGDLVFFDTQGSNNGSVSHVGIYIGNGDMIHASSGSSKKVTISNINSSYYSSRYVNARRVL

>CORE_REP|Org56_Gene2763#

MHELILISEKYKEDILDFFTDIHMHPELSFKEFRTTKAIKDLLVSLDIEILDLGMETGVVGLLKGKYDGPTVALRGDIDALPIYEEVDIEYKSRYDGIMHACGHDIHTSCLVGCAYVLSHIRDSLHGNVKFIFQPAEEVNKGAKMLVERGVMENPKVDAIFGLHNHPDIPCGKIGVKLGGLMAAVDTIKIEVNGFGGHGGIPNRTIDPIVASSAIIMGIQTIVSRNISPLESAVISIGTINGGTANNVISEKVDMTGTCRSFSNEVRKKISENLENIVCEIARGYQATAKLDYLFDLPAVINSKEMYTIACKSVCDLYSEDAIVDPIPSTGGEDFSIFMEKAPGFFYWLGVGNKEQDCIYQWHNPKFKADKNSILVGTNVLCQSVINYMDKLKNKI

>CORE_REP|Org18_Gene2810#

MRMVFMDKVKFLINMLLAFFIYPFNKHKFNGRDIWLIGGHSGDIYNDNSKFFYEYMLKEHNDVETYWVVNKDSKVFDKIPGKKLIRGSVENYLYYYNSKAIVFSHAPSADIAPYNFAVPVLNYFHKKTIKVFLNHGTISFKKRKPMNKKFKNIIDNLYKSYNIVTASSEFERNVMVNDWGMLDDSVYIIGNARYDNLPTNEVAQTRDILYTPTWRDWIKFSSGKFTDTDYFKNIMNFLNDDKLNKILDEKDINVKIYMHHLMHEFIDDIKENITGKRIVFLD

KGVTLANEIRKSAANITDYSSVAIDFLYMNRPILFYQFDLDEYMEKVDSYIDLKSEMFGSLAYNNDEAVNKLIDIIENNFEVMDNQKNERNKFFR
YNDNKNCKRIYDCVLSKIK

>CORE_REP|Org43_Gene1340#

MLRKITAFMLSICLIIGLTGCSLLVGKKDKEKVIDDFKVAVVTQPLSENKVQYNMVEEMAKEYEEENKIDKDKDGQTKVKQTIKHVVLPENFTSN
IDSAINKIVKLADDKEVQAIVVSTDQAGLLPALQKVKEKRPEIITISAPMGDDKNQLSQFVDVNLGVSAEERGKVLAERSKEMGAKAFIHYASTD
DLKDVNIAKRLEMIKETCKNIGLPFVQVNTPNINAEEDKNKVKQFLNEDIEKQVKKYGKDINVFGVNDYMDEVILTKALELKYIVAEQSNPSPIQ
TYPSVMGLKISKKDAQNYDKINDMISEKAKAFGMSNRLGGYPMPMDAFLPSLAIYLATEMVKQDLTQEDVCDPDYLEAFTELRFGIGSEFTPL
TEVLYNYQSVILSQLIY

>CORE_REP|Org45_Gene611#

MEAITAFCLVLISLTIGDVVSAKTKAFVPSVFVSAIIFIVGFWTFFPENIVDLAALGTPLAQLGMLLLITHMGTMMSIKELAGQWKTIVIALAGIVG
ICVGALALGTVVFGWDTAVIATPPLTGGLVASIMMADAATAKGLASLSVLAILMYVAQGFAGYPITALMLKKEGKRLLSDFRSGKVTVNTAEE
KVKDLPEQKSRFKIIPDLPEKYDTTYMIILRLGFVAWLAVQFTNLTNEVVSRYVMCLIFGVIASELGIVDRKPLNKSGSFGWLMTSLMAFIFAGLA
KATPAMLVEMAVPLVGIIIFGVIGMGIFSIIAGKLLGESKEMAFSVSLTSLYGFPPNYILTEEAVKALAETPEEKEFLMDKMLPKMLVGGFTTVTIA
SVVIAGIFVNLI

>CORE_REP|Org78_Gene1170#

MEIRYAKEEEIESIKDIWSYCFNDTESFMKYYFNDKYKSENTVVALDEGKIISSLQLNQYKLLLNSKVYNTSYVVGVSTLPEGRGAGYMNKVMKF
TLNELYKKGQLVSILMPIDYRLYRRFGYEHCYDQIEYTINTDDLKNFKSSGKMIKSNLSQIDDLIQIDRTFLNEVNGNVLKDEHYYENLFKEIQSED
GFLYIHEGNEKDGYIVYFLQEDKMFVRELFYKNIDALKSMLKFIYNHNTQCKIVTISTPTIDKIRFILDNPKDSDIKIKPFMMGRVINVKKFIEDIDIE
KDINSSFNLLIEDKFIDENNGLFKISIQNKKVSVEQLDKKGAEKPQEDFDIKLDINTLTQLSFSYIDVNEAIFLNDIKDVSEETLETLNCIFSKKNNYIN
EYI

>CORE_REP|Org51_Gene1430#

MKFKKQISSIVVSTMLVLGSMNLSYADGTNVVTLGANLSESQKQQMLNYFGVKKDQVLVLDVTNAEERQYLQGVATEGQLGKVTISCSYVEP
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VMNDIKTEIVKNGTKDTNQIANTINNVVNNYNITITPEQKEQIKGVMKKIADQNYDYNSMKNTLDNVSDNVNEQLKKLGESVKGSGILDTIGG
WFSGIGDWFSGLFSGGDKKDLGILNNTNDESLGSDAVINSTEGVQINPQNNTNSNNDSDTNSSKNDTSSNNENNDSSQTNENNTTNNSEN
QSNNNDSVGFFEKIKNWLSAYFRN

>CORE_REP|Org72_Gene648#

MEKLSDKRRVKAVSMETFVFIVLLAVGFGYVGSIMGAGMMFKVIMSTAHALLLDTVFLIMAMAVLAGALSALLSEFGVISLVNKIFKGLMRPI
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NYDPKNDTEKQINDKGAKLEEFREIRDGNVFQRTLDAILEGGKLGVEMGMAIIPGVLVVCTLVMLLTFGPSTDPATGQAVYTGAAYEGIKLLPA
IGDKISFIIEPLFGFTSPEAIAFPVTALGAVGAAISLVPEFIKSGAITPNDIAVFTAMGMCWSGYLSTHIGMMDALDARPLAGKAILSHTIGGLCAG
ICAHFIFVLVG

>CORE_REP|Org70_Gene1064#

MSRVIWIVIDSVGIGALPDAENFGDSKDVSTLGNIFREYPDINIPNMRKLGIGNIDGVDFFESIKTPIGCFGKCKEMSQGKDTTTGHWEMTGIIV
DKPFKTFEHGFSKEIIDEFEKKTGRKVVGNKPASGTVIIDEYGEHQIKTGDVIVYTSADSVFQIAANEEVIPLEELYNMCKIAREIMMGDNAVAR
VIARPFIGKKKGEFVRTSNRRDYSLDPFEPTVLDNIKESGLDVLAVGKIEDIFNGKGITDAIHTKSNMDGVDETLNYMKQDNKGLIYSNLVDFDS
KYGHRRDPEGYKKALEEFDSRLPEIMANMREDDILIINADHGNDPTYKGTDHTREYIPVMIYGNKIKKGFNLGVKDTFADIGATVADILNVKLP
KHGSSFKKDLF

>CORE_REP|Org18_Gene1426#

MSVENKSNKKELKKVTAKTLIEKGKKQGSLTLAEIMEAFSETELDKDQVENLYETLGNLGIEITETKNYKADIDFSVADDDLSIGHLDEDAEAISH
DDSSAIEIETVDLSLPKGISIDDPVRMYLKEIGKIPLLKPHEEVEFARRMHEGDEIAKQRLVEANLRLVVSIAKRYVGRGMLFLDLIQEGNLGLIKA
VEKFDYTKGYKFSTYATWWIRQAITRAIADQARTIRIPVHMVETINKLIRVSRQLLQELGRDPKPEEIAKEMEMTEDKVREIMKIAQDPVSLETPI
GEEEDSHLGDFIPDDDAPAPAEAAAYSLLKEQIEDVLGSLNDREQKVLKLRFGLEDGRARTLEEVGKEFDVTRERIRQIEAKALRKLRHPSRSKKL
RDYLD

>CORE_REP|Org31_Gene1241#

MGGVALKILKNKNKYIKGIMAFVFLSLATTAGVFLINDLSMKNMEEKVMESANVEGDDVKDQYKLLLENLFDYRNKAILEKNENILKGLYETDK
KFGLWAYENEVKKMKYLENWSSKQGVKFKDIKTRVKIKKIKEKEKDLYGIICSVSTEYKYSYENQKDKENAFRIGTYHYLNVKIIDNQYVITKEWY
TDPFADSLNLENIKSDDIRNYIGQQDGVELQLTDEQKKAIDYAHKYCGAAADEEHGMKFNPNYRDYNPEGGDCANFASQIMFESGRFKKNSI

WNYSERAGTKAWVNAQAFKNYALYSGRGSLIAKGSYEEVYKEAYNLRPGDFVGYEKKGRITHVSTVTGLDSRGYPLVTCHNTDRMLVPWDLGWSDKSIRFHIIKINY

>CORE_REP|Org71_Gene2296#

MKINWNTKYTTIAIYTFIIAASSIIFYLVSSQIDVFSNNLDAIFTTLQPFIIGFAIAYLLNFILKFYEDRIFIKSEKLKKLKQSSKRGLGLLLTYATAAVILYLFMYFVLPQVIESIVGLANDIPMYVNNATKLIDKLMTDLNLDEQYFNLAVDKWNEFVTYIIKFVTDLIPILGSMLKNVASSIWNIVLGLIVSVYLLIDKEKFYGLSKKITYAVFTEKQAARILELTHRSNYTFGRFLGGKILDSFIIGILTFVILTLVKMPYTLLISVIIGITNIIPFFGPLFGAIPSTLIVLFVSPIKAFWLLLIILIIQQIDGNIIGPKILGDSIGISAFWILFSLLVAGKLLGFIGMVIGVPMFAVIYSIIKDTVESKLDKKGLPTDTSDYM

>CORE_REP|Org27_Gene973#

MDIKEITKSYKDYVIKLRREFHENPEKSMEEVRTSKRVKEELDKIGIPYVSAGGTGVIATIKGANPGKTVALRGDMDALQVVECTDVEYKSKNEGLMHACGHDGHTSMLLGAAKVLNDIKDSINGTVKLFFQPGEEVGKGARAMIQDGAMEGVDSVFGIHLWTDVESGTISVEEGPRMASADFFKITVKGRGGHGSLPHQGVDAVLASSAIVMNLQSMVSREVSPLEPLVVSVGVLNSGTRFNVIASEAILEGTIRLFNPELRKQIPGILERIAKSTAEAYRADAELEYGYLTPAVINDKECSKIATDAAIKLFGEDCITLFEKVTGAEDLAEFMNIAPGALAFVGARNESKGACYPHHHGCFNIDEDALEIGTALYVQYAVDFLNK

>CORE_REP|Org33_Gene1231#

MKKLASTALAILIALTPLSFSFANNKENADANQLNISSKSAILMDVGSGQILYEKDAHKKLPPASVTKVMTMLLIVEALDSGKIKLDDEVQVSETASSMGGSQIFLEPGETQKVDTLLKGIAVASANDACVAMAEHLAGSVEGFVDRMNAKAKELNMNDTHFANTNGLPVANHYTSAHDIALMSRELLKHEMISKYLTTWMDKVVVGKKQVTVGLANTNKLIKHYQGATGVKTGFTQEAKYCLSASAKRGNTHLVAATLGAETSPERFNDASSLLTYGFANYESVKLCSKGDNIATLTLDKADENKVKLVAKEDLNALIKKGSSKEFEKKIEIVKNPKMPIKKGTVLGKIKICKDKKVIGEVELINTKDINKASYLQMLQRIIDNMI

>CORE_REP|Org31_Gene2820#

MKLMGYLRENGQFGIRNHVLIIPTSVCSSETATRIASLVPGAIAIPHQHGCCQIGSDIELTAKTLIGFGKNPNVAAVLVVGLGCDGIQAKELASEIATTGKKVDYVVIQECGGTLKTVSKGAEIVSKMAREVSKEVRVEFGMSEITLALECGGSDPTSGIASNPSIGVASNLLVDEGGSSILSETTEVIGAEHLLATRFEDEEMKDKFLKFVSDVEKRAIAMGEDLRSGQPTPGNKAGGLSTIEEKSLGCMYKAGNKPFKGALEYADIVPPDKKGLYFMDTPGQDIDSITGMVAGGAQIVIFSTGRGTPTGSPISPVIKITGNSDTYNKMPDNIDINAGRIITDGAKIADIGQEIFNEIIEVCNGKHTKAESLGHREFGIYRISSTF

>CORE_REP|Org77_Gene181#

MRTVKQVSDLTGISVRALHYYDEIGLLKPNKITDAGYRLYDDDSIKTLQQILFFKEIDIPLREVKEIMSSPYFDKLEALKNQRKLLILKRKRLDELIELINQTLRGEGNINFKEFDMSEYFDVLEEFKREHKSKIIKIYGSVEKYNEYIERVKFNEDKIAKMAIKQYGTIEKFAQAIKTNFSSDILNLGEKFDRYKNDCLKEQHPKLKELYRKLAEDLSKNPSSTELQEIAKEITDISKKDYEIFSMDTGDDNWYYMVQNYLVNPMWIEEVDKKYGSGAGKFIGQVLKTYLRDRKPKINTLYEKLVEDLSRDCSSKEIQSIVEEIDNEMKRSNDFYKIDNGERYFDYMSELYLQDSNYIKVTDKNYGNGASKFIGEAFKIYFDNNNC

>CORE_REP|Org30_Gene1287#

MNTLFSNPGSILAVMTSMIALGFYLQRYKAIKSLGPALTIIIMGIILSNLKVVPVSTELYGTISTYAIPVSMTIMLMSVDLKEMTKLSREPLIAIFVAVLTVSIMAFLFGLVFAEKISEGWKVAGMFVGTYTGGSANLTAIGTGLNVSRQTLAAANAADYVIGVPTLIFMFALPAILKNSKKFKKLWPYHVEESELEDCQNEEFMESKEWSIKDIAWMLAIGFVVTEVSTILAGYFNSSFSSAARILLVTTISIIIAQLKPVKKLKGNLDLGLFVALFFLCTIGFSVDIKEFLGSTFTITLYCFSIIFASFVFHLGITRLLKIKYQYVILSIVGAIADGPTSALVAASAKWNSLVSVAVVMGVIGGVLGNYAGISVAYAIKMSLGL

>CORE_REP|Org18_Gene2679#

MMLNFDVELEECAQIKVIGVGGGGNNAVNRMVEAQLKGVEFISVNTDKQALYTSKAEYKVQIGEKLTRGLGAGANPEVGKRAAEESKDEIVKLLQGADMVFVTAGMGGGTGTGAAPVVAGLAKEMGILTVGVVTKPFAFEGKIRMKNAEGGIAELKSKVDTLITIPNDRLLQIVQKNTSMLDAFAVADDVLKQGIQSISDLIAVEGLINLDFADVTTIMKDKGLAHMGIGSASGETRAIDAARQAIQSPLLETSIQGAKGVLLNVTGGPNLGLFEVNEASTLVMESCDPEANVIFGASIKEDLGDEIMITVIATGFEGLQNGALDLDTKPKSSIRSSLNTTVKQAVKEIEEEVIAEEKIEPPKKASIIEEDDDESMEIPTFLRRRR

>CORE_REP|Org96_Gene1765#

MIEISIKNKKNSKIKTLILLLIVSISIYLTGCTTLDNGNNQSNNNDSLSSSISSDKNVKIHFIDTGNSDAILIQDGKTFILIDGGDNDDEGLMVDYLNNQGVKDIKYLIATHSHADHLGGLDSVVKNFNIENVFVSNGSAETKSYRDFINALANKGLSPSVPLENNKFYLEDSYFEVLNTNGGDTTNEQSLVLVYTNGNDKVLFTGDAEEGTEKEILPKLEKVDLLKVAHHGSRSSSSQEFLDKVNPEYAVLLVGKGNSYGHPHQETMNKLKKMGVKVHRSDECSDIIFESTGDGVFTSCKDGSYNKGVREDGNSGKSNSNTSKNDSFKNKQNTSNSEEIVYFTPKGKSYHSTKNCSGLSRSKKILSGTIAESKKNDPCDICYGK

>CORE_REP|Org35_Gene2342#

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VLALGISHLNQAMKAQREVSNMTNELLLKNAETLKMGTIETAKESERGIVDIDTIKKTNQSLISTIDEVVKIQHDGRIKRQEAEVELSKIENELKSK
LLEFTVK

>CORE_REP|Org13_Gene2724#

MKTLNDDRNIMIRKYLYIFVLFIILLRKYMISFIDPNIDIGMIKSALFYSSIGILMLLFLFDKRKSITEMVLVGVCVLLYLLNREGAILLIVLLAVSAKQI
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TTYSRTGFFTILAGLIFVEIIRWIDIKKIKGLPMLLKTLPIILTLFSVIIGTIFDKSTLLNRLLASRPKFWHVYLAEKGNFLKPFGNSYSPAIKATNPLDSS
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>CORE_REP|Org94_Gene2126#

MKKISILGSTGSIGKQTLDVVRDNRDKFEIVAISANSNIELLLEQIVEFKPKYVTVFEENKALKLKEMLPKNIEIEVLAGMEGLKIISSLDEVDVLLTA
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KHPNWSMGRKISIDSSTLMNKGLEVIEARWLFGVEQENIDVVVHPQSIIHSMVQYTDSSIIAQLGCPDMRLPIQYALTYPDRMESSFERMNFS
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>CORE_REP|Org67_Gene2443#

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MNLADNLMAYIERKLFTLNTGHAITAYIGYLKGYKTIEESIKDKFICDIVKSAMVESGEGLIKKYNFDSEVHYKYIDKILNRFKNPYLNDDVLRVGR
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>CORE_REP|Org32_Gene1840#

MELRPRSAKLEEFDKVIELINYVFRISRNHKPTMMEEFPLLLSKNNIENMIIISEDDKVVSDVNYLIQDVSIQGNRLKVAAIGGVCTHPDYEKRGY
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TIAWGPIGYKKVFIKENNNIIGYLIIRTIKKEDSTVGEVAEIGLNSVNVENILKYVANKFGLESLNYKVHVKNLKDQLKCNGTKSLDYQQGTMKIIN
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>CORE_REP|Org32_Gene1859#

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TGLELHNVLYQAGFKFDRAELKHSLRKVIDDMKERYEKGECPVQKDKPRILITGSPIGGISEKIVKTLEDAGASVVAYELCGAIRSNDLLVDEEIED
VYDALTQKYINIGCSCMMNNDNRIELLDRIIDEYNVDAVIDVVLQACHTFNIESYRIREFVTKEKNKPFMSLETDYSKSDTEQLRTRFEAFVEML

>CORE_REP|Org12_Gene2962#

MIFSQYGDYFYLYILLLTSIPAVILGLMGKNIKYYGMLASLFMIFLIVGIDVQLKYLVIFIILEVIIVKGYEYVRRKTKNKYIYWGFLFASMLPIIINKISP
VTSFGIIGFIGISYLNFRTIQMVIEIYDGAIKEVKISKMLYFMLFFPTLSSGPIDRSRRFEQDLEKQISRKEYIEEYLLPGIKNIVMGVGYKFVIAFLINT
YWVSRIPKDMSFINILSYMYAYSLYLFFDFAGYSLFAIGTGYIFGIQVPINFDKPFISKDMKEFWTRWHISLSRWFGDYIFSRFVMSSMRKKRFKK
RTTAAHVAQMITMITMGFWHGLTWYYVAYGVYQGLALVLTDIYQRKSKFYKKHKKDKWFERVQIFITFHIVCFGLLIFSGYLA

>CORE_REP|Org33_Gene2469#

MNNYMLYVFENLIKTTIVCSLGICLLLFLKRYLFKKFSKRFNYYIWLIIVFRMLLFLFNYTIVYEVKEPKENALGNNITQIDISTDNNLMLYVAYLWL
FVTIVIAVYTFIKYTRFKNLVVDVSYDIEDNDINCIYKNLLKELNIKKKIELRGSDELISPAGMGLFKSYIFLPDYPYSKDELTWILKHELMHFKNKDIL
IKFLVLSVRIIYWFNPLVYVMSNKVNLDCELCCDESVLVECSLKDKKEYALALIKSIKFSKNYNSKILTTEFDKTNLEKRLESIVKKKGKSGILIAVLVF
MTSITSFVEVDAQVRIDEGNNGMNNNINEFLLNKTTDKIINIYYKDAPNEIRKFYEDKCELEGKIPRDYDIIEMDMKDYNQLIK

>CORE_REP|Org29_Gene2263#

MSKKVIADVFLEVANAIESGEFGKKVKIGVTTLGSEHGVENMVNGAQLAKSNLFDIVLIGPKVETDLEVVEVNDEKEMHAKMEELLDSGYIDA
CVTMHYNFPIGVSTVGRVITPAKGKEMILATTTGTSATNRIEAMVRNAIYGIATAKSMGNKCPKVGILNVDGARQVEKCLKELKDNGYDMEF
ADSIRADGGCVMRGNDLLVGAPDVMVTDTLSGNIFMKVFSSYTTGGDYEAQGFGYGPGVGEDYDRKVLIVSRASGSPVVANALKYAYDVVK
GDISNVARNEFAKVKKAKFDDIISSLTKKEVKAEKVEVKMPDKEIVTRQIAGVDIMDLEDAVSELWKNGIYAESGMGCTGPIVLVNEAKGDLAV
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>CORE_REP|Org45_Gene11#

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KTPPCVDKIIQNKIKRVVISTLDPNPLVCGNGVKKLRDNNIDVTVGTLEEEARDLNEVFFYYIKNKRPLCIVKSAVSLDGKIATKSLESKWISNESSR
YLTHKYRNKYQSIMVGINTVLNDNPLLTCRLNQEKVSHPTRIVIDTHLKLPLNSNLVKDKTSKTIVFTCCKESKKLSMLKENNVETIISPSKNNLVD
LEFVMYKLGELNIDSVLVEGGATLNDSLFRNRLVDKVKLFLSPKIIGGKDAPTFVSGEGINHLSDSTQLAINNVTLIDGDILIESDVLN

>CORE_REP|Org72_Gene2785#

MPKENLKKQIDIRMKTEFDGVVFYTTMLLVFVGIVMVFSASFIQSSFKHNDAYYFLKKNVIYAVLGFIVMIITSRIDYSFWKKNATAIGAIAVVLL
LLVLTPLGIEANGAKRWLGIGALTFQPAEIAKFATIILTAKLIEKNYDKIKSLTKGVVPLLVVPGIFFALIILQPNLSTAGTVILVTFVMIFVAGMDMK
IVFAMIGSGAALFAALVIAEPYRLSRVTSFLDPFQDPLGKGYQVIQGLYALGSGGLFGLGLGKSKQKYFYIPEPQNDFIFAIIGEELGLIGCIIVIMLF
VVLVYRCVRIALKTSNVFACMVVIGIGAQIGIQAALNIAVATSSMPATGVALPFISYGGTSLTIFMGAVGIVLNISKHVKIN

>CORE_REP|Org26_Gene1036#

MKKININYKSTIKLIKQLDWKLIVTVLAIFIFGLVILSSATHANSTGSYNQLIKQGLAFVLGIGMIIVILFFDYNLLGRYYKALYIISLILLAIVLLPGIGTV
KGGARSWINLGPLDLQTSEIVKLTFVLSYAKILESKKDKLNTLKEVMPVVVYSLPFIGLLIAQPDLGTGIVFCCMIFAMLFTAGLSSKLIKRGIIILLVS
MPLMYLMMADHQKVRIEAFLNPEDVTLKGNYQVMQSLIAIGSGGVTGKGLYNGSQNQEDFLPVQDSDFIFAVVGEELGVIGMAVLIILFMIF
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>CORE_REP|Org57_Gene2089#

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IHKIYSFMENYIKFPKENLPNRKVMSDINISDIESLAYKTREFWDLNSTPIVNMVSLLESKGIIISGMNVDRKGATIFTQKQRISKESKYLISLGNDK
KSASIRNYTLACELGYIISSELRIPSKQFSEDEYACAFLLPKESFLKDLTHPEDLDYYVELKKKWIVPISAMIFRAYNLEKINYKKYNYLMNEMDKKG
WLIEEPLDKMKGSSPTYLKRAVELLIENKIMSVNSIVSSLEEFGINLYPEDLELLMGLKKGLLSQEVNKKSKVIKFDGKK

>CORE_REP|Org42_Gene1152#

MNNDKKVIKVHNKSDKPDNIVIKENELIEKCLLLENKLPVFMKDYFIYLKGSVAVSTRLAYLEDINFFCSYLIETKELTNAECIKDITEDDFNTIKSRD
INLFLGDYCSRYYKNTEKNTLIFENNNRALARKKSSISTLFKFLYRNSQIDNNITDGFNPIKLPKPQPDAIKRLEIDEVAKMLESVETGEGLTEKEKV
YWRKTKLRDKAILALFVTYGLRLNELRELNISSFNFSRGEFKIYRKRGKEVLMPINHTCEHVIKDYLQNERTRDELLNDEEKDALFLSLQNKRITAK
AIRTLVKKYTSIPLDTTRENGYSPHKLRATAATSLIQTGFSIYDVQNLLDHDNVTTTQLYAAHKKNVKRDIVKNFEWIEDD

>CORE_REP|Org81_Gene2994#

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DTTTTLATSLTAFYNKTLVGHIEAGLRTYDKYSPFPEELNRQLTGIIADMHFAPTNLAKKNLISEGKPNNNIFVTGNTAIDALKMTIKENYNHPIID
EIGNDRMILLTSHRRENLGKPMKNIFRAIKRIVDDFEDVQIVYPIHLNPKIRTIADEIFGKFPKKIHIIEPLDVADFHNFLNKSYMIMTDSGGIQEEA
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>CORE_REP|Org94_Gene1709#

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KAGFPKFKSKKINRFSYKTNFTNGNIMYCGQHIKLPKLGMVKVRDKQVPKGRILNATISKEPSGRYYVSLCCTDVDIEAFENENTNNHIGLDLGI
KEFCISSCGEFIENPKYLKKSLNKLAKLQSELSRKTIGSLNRNKARLKVARLQEHIANQRKDFLQKLSTKLIKENDIICIEDLQVKNMIKNHKLSRSIS
DVSWSEFIRQLEYKANWHGRQIVKVGKFFASSQICNKCGYKNEEVKNLNIREWICPSCNETHDRDINASINILKEGLRLITIQNK

>CORE_REP|Org87_Gene1052#

MRVEAPIKVDRKTKKLAKRVESGEIAVINHIDIDEVAANSLVEAKIKLVINAAPSISGRYPNKGPGILTENNILIIDNVGEELFEELKEGETIEVVDGK
IYRKGKFLGAGEVLDKYEVSYQIKAAYENLAVELDRFIDNTIDYAKKEKGFILGEVEIPKVKTNYANKHVLIVVRGQDYKEDLSTMLSYIEEVKPVL
VGVDGGADALIEFGYTPDVIVGDMDSVSDEALKKASEIVVHAYTDGRAPGLKRVEELGLDAVVFPAPGTSEDIAMLIAYEYKAELIVAVGTHSN
MIDFLEKGRKGMASTFLVRLKIGSKLIDAKGVNLLYRSKLKIKYIWALIATALFPVLVVASLSPGVQQFIQLMQLKFRVLLQM

>CORE_REP|Org69_Gene1184#

MKDDKTILILTAQFGAGHISAAKAVKESIIEKYSNYNVVIQNFINASIPMMNKPMVKLYENNTKYTPGLYNYYYYFKKSFDSRHDFSHKLYTPKLS
EYIADINPDLIISTFPLAAACVNNFKIKNPDINIPTLTVITDVVDSMEWVFENTDLYFVPSPEIKNRFFQKGINPDSIKVTGVPVDKRFQIESKEICC
DKYRLLLLGGGRGLFDIDEDFMHWIDEFIEEHSDSIEITIVTGKNKKLYDNLTHKKPLKNIKVLGFVNDMYNLIRECDLMLTKPGGATIFEAIQSQ
TPVLVKMPKVGQEIENAKFIIDKGLGMIYSDDLDLKNIFYRLVSNEFDSIINFMKKNLEEFKTVIHPEKIADYISELIDKHYS

>CORE_REP|Org46_Gene1504#

METLKIRNIELSGTNYEIGYELGKLIANTPKILEGQINKSNVVTKEEEKEMLELFDKYCPGLNEELKGFADAVQVNCNQILYYTMTYLKPGCSQVA
LAPELTTNGHVLFARNFDFSHNMEDFVLCKTKVKGKYAHIGTTVMQFGRGEGMNECGLGVSQSSCGIPVGNSVGLRKPAVVGLQFWAVIRY
LLENCKDVDEALEYIEDMPIAYNINLLLADKSGNIALVETLDGKKGVNRINRLEKQREHFLHSTNHIHIDELHKLEPQSIKNSIHRYKLIKEYINNSK
KVGEKELMNLLSSKYPNGLSCNYYNDFFGTLKSIVMDLNTGKFNILWGGLESSSNNWESYYLKDDVKATTHLININIEKAPSDFFRFR

>CORE_REP|Org26_Gene3286#

MNIKSAFIRKRGGKFYVYVEYIEETTGKIKQKSYGSYEKKKDAEKHLIEIKSTINNNKFITPSKTTLVERCYKYIMSNEKKWSPYTTVNRKSWVKNYI
EPFFKDTILIDVNPSLLQIFIDKNFDGSAPSTAKVRYNFLSSVLKEAYRLKEISENPCDFVKLPAQNVTYEIEIYNREETLLLIEKLKDSLIEIPILLMLLL
GLRIGEVAGLRWSDVDLDNSIININQILIYANSKITFKEPKTAKSKRTLSVPKELIEKLKIEKVKQNKIKLQGTLENENNLVCLNTNLKPWIPTALSKT
FHNFIKRNNLRNIRVHDLRHTNASLLLLGGTNMKVVSERLGHTDIKITMNRYSHVLEEMDKEASDNLSKLLFK

>CORE_REP|Org86_Gene689#

MPFDKIILYIMAVGVLLGALDRIIGNKFGLGEQFEEGFNSMGPLALGMVGIVCLAPVISDVLGPIIIPIFNLCGADPSMFATILANDMGGYPLAM
ELAHNKEAGMLAGLVVSSMLGCTLVFSIPVGLGLIEYEDRPFFAKGLLIGLITIPFGGIIGGLIAGFNLSMVIINMIPVIILAVILAVGLKFNSTLMIN
GSLIFGKFISILITIGLGAAAFQEITGIVLIKGMTPIREGIQVIGSIAIVLLGTFPILHLLVKVLNKPLTIVGGKLGMDATSAAGLVFTLANSIPVYKMM
KDMSPKGKVVNTAWLVCATAALGDHLGFTAGVVPEMITPVVIGKLVGGVLAIALAILMTKDLTLEEEQSIKMKKDAV

>CORE_REP|Org29_Gene2365#

MKIIVIKIVIIVKIIIAITTNKIKLKILGGLIQLIIQKKFTIADGNFERELFGNFDENVKLIEKTLNIDVILREGNIILIGEEKNVDSALKLMNELHQTVSNG
KHLDKQSISYSLSLLLEGSEQKIKELEGTIVITQRGKAVQPKTLGQKEYIKLIENNDITFGVGPAGTGKTYLAVAMAVKAFKRDEVSRIILTRPAVEA
GESLGFLPGDLKDKVDPYLRPLYDALFEMLGADKFNKYLERGTIEVAPLAFMRGRTLDNSFIILDEAQNTTSEQMKMFLTRLGFGSKAVVTGDV
TQTDLPQNKKSGLIQATEILKGVPGIGSIMLTDRDVVRHELVQRIIRAYEKHDKREEFKKEERKKVKMQEKTFKRK

>CORE_REP|Org32_Gene2985#

MKISEVATPNFLLDLDQLEKNIDKIQQICTNNNKQLWPMLKTHKSTYIARLQKNAGASGFLVGTLDEGEALIKAGFEDIMLAYPYMGEVNINRI
VTMASKINLICATDNIECAKAYSEAFSKSKIECKLLIIVDCGLHRFGVEPEKVVELATEISKLENIKIVGISSHPGQVYGCSSPEGVPDVCVQEDSSM
EKAYKALTDNGFNIEIVASGSTPTVESEAASKTITAVRPGNYVYYDAIQIGLGCATEDMCALTVVCTVISKNSSGYYLIDCGSKCLGLDKGAHGNS
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>CORE_REP|Org16_Gene1985#

MNAFIRKRNKNYVVYLEFEDEKTGKRKQKNMGTFDKKREASKRLNEVKESLYNDGFLVPSEITVSEFLLDFLNKYSENISLATYNNYVSICKNYIN
PSIGKYKIQDLHPVHIQNYIDKLSYKLNPQSIKIHINILKLAIKRAYRLKLIKENVMDSIEAPRYKKFKNEIYDREQMIKLLDLAKNTEMELPINLAIGL
GLRISEVLGLTWDNIDFEENTITVNKITSRINGSVILKEPKTESSVRKISSPKELMSLLKEYKIKQNKNLLKSSIRNNNNLLFFNKKCEPIAEDVMSKK
FKRFLEKNELPHIRFHDLRHSHVTLLINSKVPIKVISERVGHSNISTTLSVYSHVLKEMDKEASDKISESLFNAN

>CORE_REP|Org18_Gene1237#

MDFMEKRDTYLWLKSIGGITTKTIEIIENEIVNIEDIFDFSEKEIYNLKNISLNIRKNIVKYRGHAYLENIKELLYKKAIKYICKYDKEYPENLKNIYNAP
KLLFYKGDIGLVNNNFNIAIVGSRKPTAYGINCAKTISCQLSQYGVNIVSGLAIGIDAYSHIGCMSGKSKTIAVLGSGVDNPLPKQNLHLSNKILEN
GGLLLSEYNINSTVAPYHFSNRNRIISGLSDGVVVVEAAIKSGALITVDFALEHGKNVFAIPGNINSQMSRGCHKIIKEGAKLIENIDDILNEYNIFN
IIDKKINQKYDNISLNAKSKQIIEAIKREGNLHIDSICDYTGIEIKYVNSIINELVLNELVVEMNNKTYSLNV

>CORE_REP|Org76_Gene168#

MSKKNKSLLSELKGHLMTGISYMLPLVIGSSLVVAIPKLTALAMGITSLDAYKNVSGFYHILYLMEQVGWTGIGLLNTVLAGFIAFSIGEKPAMG
AGFIGGLIASNTNAGFLGAVIAGFFAGYVCKFLKKKIKISGSASGMMPLIIMPLITVGLTGFLMSVVLAGPLGNINTSLNAWVAEMCQNGTNSV
VLALILGAMIGFDLGGPVNKAAWMAGNALLLEGIYLPAILVNCAIVIPPLGYGLATFIRKSKFSNALAETGKGNIVMGIIGITEGAIPFTLTNPLKL
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>CORE_REP|Org78_Gene1145#

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LNRLFIEKGDKVLGYSPQFSEYETDIKMHGATYDYVLLKKEDNFKFNEKEFIEKINPEYKVIYIDNPNNPTGQIIHLSSIENIVKEAAKYDIAVMVDE
AYGEYMPKENSAVKLLNNYDNVIALKTFSKGFGLAGLRAGYAVLPEQLVSPIKKISTPYEVSEISRSIAANLLDDVQFIEELKEKTKDIKNQLLIPWK
NLNIAETSDTVSIMTVEHKNKDIDLQQEFAKLKIRVISGSDFTGLDKNFIRFRMPEEKELPEVIKAFQIIDNIE

>CORE_REP|Org56_Gene1672#

MSFYDVIEKYRDFDFDGYLNNVTDNDVLRSLSKDKLEDFDILNLLSKTAVKHLEDMAQKAHKLSVQYFGKTVCLYTPMYIANYCVNQCVYCSY
NIKSGIKRKKLTMDEIREEGEAISKEGFKHLLVLTGESSFHSSVEYIGEAIEILREKFPSIGIEVYPMEVEEYKYIVDKGVEGLTVYQETYDEEIYKRVH

IKGPKSNYEFRLDAPERGAKAGMRTLSIGALLGLNDFRKETFFTILHGKYLKTKYPHIELSYSTPRMRPFKGCFEELVDISDTDLVQAMVCMRLFD
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>CORE_REP|Org97_Gene79#

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GTLVIMIAGAGAGATLSEYYGLNPYVGRIGMAIVSLITVSLGLTRLSKILGNIGPIIIIFTLLVGAISLFSNIDALSNAGNMVDSLNIKTATSNGYFSG
VLYTCYNVIIVITFLTGMGASAVNKKDAVWGGIVGGVALMAAAIMMNLALLSDIGNIYTKEIPALYLADKISPIIGILFSVVLLLGIYTTAVPLLWS
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>CORE_REP|Org81_Gene2774#

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SESKGLSKRLYSMPITRVQFLIYDFVGLWIYSFIFLLLYVLFFRILGITFKGNFAILLLLCALSSYFMTSISTFVTSFFSKKYGTVIVYALLFLQTIFGGIFS
MISDVFTKLTSLSPTYLIGELFSNYETFKTIDSIGNLIFTCLITSTILIALAIVKEKYKWREVQ

>CORE_REP|Org35_Gene2739#

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VQPTVVISTFPFCSQLVSRYKEKYNSNLPLITCITDISSHSEWISKNTDCYLVASKSTKEELVFKGIDESKIKVNGIPVKKEFKRIEHVNHSTKKNILIM
GGGLGLLPKSEQFYKELNSLEGVKTTVITGNNKKMYYKLYGRYENIEVVGYTNEVYKYMKDSDLIISKPGGITLFETIYSELPILAFNPFLQQEIDN
ASFILNNEIGRILGKNKKYYVDEIKDLIYDDATLKEMSSNMKELKKQFDNNTLENILFSLDEQGACRECM

>CORE_REP|Org63_Gene2841#

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FASEIISSIRNEVKDIPIDYKFAIRQENPHYGNAGVLLSEVEYFVKKFESLGINSFHVTLANHSKLEDTIPTNNHPYFKDEGCFLYLADEVKKHTNLP
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>CORE_REP|Org9_Gene2310#

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QIPTYIDKTEQFLFDLGKSLQSVDPNTLKEYGDKIMSVMPKFSNLLIGSLGGIFSTTFSVGKFIVQFLLGFIICFYILLEKEKFLLFTKKVVYISLGKKYG
DFIIELCQSLNLNIGKYFTGKILDSFIVGVLSGIGLYFLKSEYALLFGTLMGVMNMVPYFGPVIGMAPVVIINLFSNPTIALTSLIYLIIIQQVEVTFIEP
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>CORE_REP|Org92_Gene2621#

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SLLGYHPYIISVWGTDIYDFPNNGFIQKQIIKHNFRKADYIFSNSRDMAKEANKYTAKHVDVTFFGVDMDRFKPMEVEKEDAFVIGIIKSLEKKY
GIEYLIQAFKMLKDEYKDKKIILKIGGSGSQMDNLINLAKELGIENDVQFLGRISPENVSKTFNSFDVTVFPSLREGFGVAAIESEACEVPVIVTNV
GGHPESVWENETGLIVEPKQPEEIKNAIIKLMENDELRLNMGKKGRQFVRENYEVNLNFNDIEKIYDSIFDKYKK

>CORE_REP|Org22_Gene2456#

MKLSKKIQALILFGVMGTSILTGCSSKPKEKEEAKTGKDDYTITVGYYNCDHMTAGPVAESAGIYKDLGLNVKTVGNGKVPEAMAAGKMDAG
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FTSCDPWGSVAENDGAGKIIASTQYKEKANGKEYNCCSFSLNKNFIKEHPDLAKKLVLAHTKAIEYIYTNPAEAAKIFAKYYNVEEEVALRTIYKKT
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>CORE_REP|Org96_Gene2580#

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QLVDDYSNLFVIRGTSKFFSTPGIRLGYGLISNTNVKNEINKNLDLWNINIIASKMGEIMFSDLDFISNTISLMNTERDYLLKELKNIKSLDIYNTKG
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>CORE_REP|Org92_Gene1881#

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PMYTDYIDSFIEKNMSNIYFLKTLIPHIQHSLDNLLKEASNFVGKIPKNFLIYTLSISSMLFNMTMGFILSIYIIYDKEKIALGFKRFLYSSTARNKADN
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>CORE_REP|Org16_Gene2275#

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VFAGFITTIFPNSIIQKYLGNPGLLSLGSIAILACVMYVCAVGHIPFIAALVASGASPGIAITFLIAGAATNLPELISMFKLIGKRTVIIYSVTLTLSSIIIG
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>CORE_REP|Org96_Gene1992#

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CLKNLKEIGYQVGAGFMVESPFQNNEDLVRDLLYLKELNPHMVGIGPFIPHHDTIFKDYKHGDLEKTLLMLSITRLLLPKVLLPATTALASINPSG
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>CORE_REP|Org29_Gene930#

MRKYMNKFKLKRSILISLIILIFIFIVYFVSIELKDGSLVNNQYKGKIKSANLSVDYEINQVMKDIDKLGLNTVNVPIIINVESINSDIMSIDNNSKEKAI
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TYRTNWWYTKKDDSSSKLFYEQKLNNNFFDKLDFISIAAYFELSNKPVNTVDELISALHSSTVNNRGQNIKQEIYNLYKAHRKPIFFGELGFSNRE
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>CORE_REP|Org54_Gene2020#

MRKLSKREKDFIQYGFLLFLICITTYLVLTTLDIKLIPKIIRLVNKTYIFLGILTIIVYMIIESIVTHLIINAVQKTKVKFIGIKMATMGFYYNLVTPFASGS
QPMQIYALTKYDVSLSKSVAIVTNKTVVFQSTVTVFCGILILLNKSLLMEQVHSVKVLITFGMIMNVSMLLGGLLIVFSPKQVKMIAEVLINFLSK
FKTFKFLDSKRDRINHYIDDYNYSIKIFIKNVRILVLSILLTVLQLIAYFSIVYCVYKASNLRGVSYVHIMTLQVFLYMAISPIPTPGNVGANEVTFFT
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>CORE_REP|Org80_Gene1896#

MKIAIFLGAGASAAENLPIQNELFSEYFKKLNPTNYNTKMNRELYIFFKQMFNIDIVKDNIDNANFPTFEEVLGLLDLAEQRKEAFRNFGLENLN
NRSDSIRFLRQYLILLMAEAIHNTPRTDNKYHKLLVENLLKNDLLLDTTFISANYDIHIDNTVTGLRDKNDLPIMLDYGVEFTNFKEELNWRKPKE
PLIKLYKIHGSLNWLYCPICNSVTLTPHEGGVMKLIENSSETKCLECGELTEPIIVPPTYFKNMSNIFLSNVWNETEKTLRDTDLLIFCGYSFPEAD
MHIKYMLKRVQTNRKKPPLKIMVFNNHSQKQRITLKKEEGRYKRFLGEDVIFTDNSFQDFSVNPLKFIKNIY

>CORE_REP|Org5_Gene1807#

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KNLMRPGHADFTGNVRYSGFNDYRGGGHFSGRITAPLVFCGAICKQILSQKGIEIGAHIKKIKNIEDMSFDYVNISKQQLSNLQTLELPLLDLSKE
EAMKNTIIDAKNQRDSVGGIIECAVVGINVGLGNPFFDSVESTLSHLLFSVPAVKGVEFGLGFELADMYGSQSNDEMYYEGNQVKSKTNNNG
GIIGGITTGMPIIFKVAIKPTPSISRQQNTVNIKDKKDDILYIKGRHDPCIVQRAIPVIEAVTAIGIFDLMKGR

>CORE_REP|Org51_Gene1144#

MNFKENRLKIAVLIIVILIILAGIFVFIQIGPYDKNNKKDVIIDVPSGASVGKISDILYENKLIKNELLFKLLVKVSNKAPSIKSGTYLLNQSYSNNDIISLL
VSGKIYQDGIKVTIPEGATSKEIIAMLVSKNLGDKATFENLIKKPQEFYDKFPYLKEDGITSLEGFLYPETYYFNSKKQSEEDILSEMLKVFDSKYTDK
FKKKQKELNMTLQEVMEMASIIEKEAVLDKDRPIIASVFYNRLKVGMPLQSDATIQYIFEERKKIVTYDDLKIDSPYNSYKNKGLPPTPISNPGIES
IEAALYPDKTDYLYFVAKIDGGNNYSTNYQDHLKYVKEYKEARDKQSKDTKATNKENTKR

>CORE_REP|Org73_Gene1837#

MRFLTEESVDKIAVGAAVLGTGGGGDPYVGKLVAKQAIKKYGPVKVISLDELDDDALVVPVSGMGSPVITIEKLLSEVELTTPLEIMEKLLNRKV
DVIIPIEIGGINSLMPIAVAAKKGLPILDADSMGRAFPEAQMVTFYLEGYEASPAVMSDEKGNSAILYPVDGIWSERLARTLTVEMGGSSSISDY
NLSGAQVKKAAIGNTLTIAETIGGFLLESKSDSKGAVENILKELRGYKLFEGKVIDIKRELKGGFTRGHAFFAGINEYDGEYSILFQNENLIAKKGNT
PLCITPDLIAVLDLETGFPITTERIKYGSRVMVVAFPCNEKWRTEKGIETVGPGYFGYDVEYKTVEELQGK

>CORE_REP|Org80_Gene123#

MSKIFKILTINPGSTSTKIAVFDNEDLVFEKTLRHSSEEIGKYEKVSDQFEFRKQVIEEALKEGGVKTSELDAVVGRGGLLKPIKGGTYSVSAAMIE
DLKVGVLGEHASNLGGIIAKQIGEEVNVPSYIVDPVVVDELEDVARISGMPEISRASVVHALNQKAIARRYAREINKKYEDINLIVAHMGGGVSV
GAHKNGKIVDVANALDGEGPFSPERSGGLPVGALVKMCFSGKYTQDEIKKKIKGNGGLVAYLNTNDAREVEERIEAGDEKAKLVYEAMAYQIS
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>CORE_REP|Org78_Gene2069#
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MKYFDYICKDDLERIFLKEPEDFSAKTEKDVLKYALGAFLYVPATQYNMIYKSIIGDVKGVRPLAICLEDAVGVNGELEAIENLRLILKNISNESITN
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GMYGIRRDKNFSIYNNLICSSFILDIITYLQRPELDIPISGGVSEFFDMTNKDIRNKYIEEILLDKYHGLIGKTVIHPMQIQIVQALSTVSYEDFTDAL
DILDSTDSKYGVSKGVLGERMNETNPHFLWAKKTLILSKIYGVLNKGVDYEELLKF

>CORE_REP|Org58_Gene2738#

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YVWNSGMFVWKVSKILEDFKRYLPKVYEKLEDISKYLGTKEEMEKIKEIYPTIQSISIDYGIMERSNDVIVVPGDFGWNDVGSWDSLGAIYPTDD
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>CORE_REP|Org62_Gene1798#

MSYGRYLLCLKKIVAIASSIIVSTICLTGCDFNSNDKKDESSSSKNLDKVTIAEVTHSVFYAPQYAAITKGFFEDEGIKIDLINTQGADKTMAALISGE
ANVGLMGPEASIYVYNQNKNDYAVNFAQLTKRDGSFLVARKKMPNFSYNDLKGTEILGGRKGGVPLMTFEYVLKEKGLTIGENLKAGNVNVR
TDVQFGVMAGAFAGGEGDFTTAFEPTATAMEKEGSGYIVTSIGKDSGEIPFTAYSTTRSYMKNNKDLIQRFTNAVYKGQLWVQQASSKEVAK
AMQPFFEDISLEDLTTVVDRYKSIDAWSQNPVLKEEGLKKLMTVMKEAKELDKEAPYKDIVNTEFANNAIKNIK

>CORE_REP|Org50_Gene1192#

MKLGNNIIIGIDTSCYTTSIAAISLDKKVIFNEKIMLEVKDNSKGLRQSEAVFQHINNLGILSDRIKSFKDKFNVEGVCSSKKPRPVENSYMPVFNV
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GGSKDISFGQLIDRVGIKLGYKFPSGKYLDENALNCNLKIESGLKTSVRDGYMNLSGLENQVNKIINDNGDNTNQKEYISKLVLDSVVRNMFKSL
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>CORE_REP|Org39_Gene1155#

MISKRVGIVESIVSQTETLDDIRVNINGEIQRAYNYPKISGTINIGDEVVLNTTAVELSLGTGGYHFVITNLNNIESTLTEGGHIMKLRYTPLQIKVD
SVEEQESIYHDKFANFKGLEGLSVVVGTLHSMLTPFAASFKRNNPNKKLVYIMTDGASLPIYLSKNVDILKEKKLIDSTITIGNAFGGDYECINIYTA
LITAKEILKADAVFVSMGPGIAGTGTKYGFTGIEQGSILDAVKKLEGRAIAIPRISFADKRERHQGISHHSMTVFKEIVNVNVDIPITIYDDEKLNFI
KEQINLNGLDKKHNIIYIDNNKTKEDLDYFNLKVKSMGRNYEQDEAFFKAASTAAYYLMEV

>CORE_REP|Org57_Gene1882#

MKRVDERNTMFARANYKKDSTAYNDYYKKNPDKKEIDDSIRNRPNLCSEGTMTYNELNSPMASSAFDFLSDIKSLCEGKVSDTKVDVDAKSM
TKKIKGLAKQYGASVVGITKLKDYHIYTNRGRHEENYGEEINLTHKYAIVFGCEMDKEMINRAPMICEVIETSKCYVDASIVGMILSYYIRNLGYD
ARNHMDANYLVMPVFIARDAGLGDIGRNAILTNKDYGSRLRLGVVTTDIPLLEDEYVDFGLEDFCKVCKKCSFNCPSHSLSNDIKIGDDGKYN
WVIEHETCYIKWRYLGTDCGMCISACPFSQNLETIKNTTSFKGNNELIQKALDEYTSKFGKRIFIPGNPSWLK

>CORE_REP|Org8_Gene2639#

MISKTEKKNKCLGSVAFLVLLMGITGYFVFRGQSVESLIKSLKGASPMFILIGFAMMFIYVACEGINIYLGMKALNQKTTLLKCMGYAFIGFYFSSI
TPSASGGQPAQVYYMKKDDINISYSSLILLVIVVIHQVVILAYSGIMFIMEREFILNNVSGMNILLIYGVITNVALVIGVIAIIFSKKLVNNFIISITNLL
GKLRIIKDVESSRKVIISQIEEYVKGAQYIKQNPKLVVQILVITIVQITAMFLVPFFVYKAFHLSTYTVFEILAIQSLLNIAVSSLPLPGAVGASENSFM
TLFKIFFPGHLLVPAMLLSRGISFYAFVAISGLICIVVHVKSSEKVKAVKKVAYVR

>CORE_REP|Org25_Gene1192#

MIRLTIANIKRYLKNHTLLINMVMLPIILIFSLNFFINNSGNQSMYFSPVAIVSDSSGKYEHKLINSSKLKENSFRLNEQDKAMNLLKNNKVSAVFV
LDKNFSNSIDKLQRPVVKCFKIENGGGSLWAESQIESFITKSLKLKVDKNIDDKLTKTNIIDNKPAKNKGSFLVVFLICYFMYINAAHLASDLFTLKK
SNVLKRLISTDNKDIKIIFSIFLGLFFIQSIVYTFALLCFSIIEDFNLSLNVLMIVLANSFVSTGFVFWVARVFKNESSISLISTFYSLIGLAISISSLIPSMD
KLSFMTNLSKFTPFYWTIDAIKNNGSILINIIALILIGIIFVTAGSLKLRDFAKN

>CORE_REP|Org80_Gene2219#

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VCSIDFLNQDTIAISNVEFWVKEINSKSKSVDLDLEKKKILYKRYIKLSQDANSDIESIRYMEEAVNIGKSMITKEDKELGFWKGLSTRAYMIALESL
ARKLESINNLNESKKVLEYLIEINPSDEQGIRYKLLNVLIRLNDRTSINKLFELYKEEKSATWMYSKALYYFKNKSMFLANDSIKVARGKNKYVGLYL
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>CORE_REP|Org59_Gene2275#

MDIQKQKNFIIKFTYVVLITSIVYIVLKFLLPLLMPFVISFIIASILRPIIRLITNNTNLNRTLISIVILLIFYGLCIFLLVSFGVKIFASVSDVFFRLPEIYKSSI
QPTLNTLFSKIDASTPNVNLALILGWDNISQSMMSLVASISTNALNAIASIASKTPAFMLKLIITLIASFFFTFDYQKIVNFILKQFPEKSQFMIINIK

NSSINALLKLLKAYAILLSVTFIELLIGLTILKVENAFTISVIIALVDILPVLGTGSILTPWMIISLINGNINLSIGLLILYIIITVVRQILEPKVVGHQIGLYPLI
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>CORE_REP|Org56_Gene2044#

MIIKELIIRDLVAKVPIIQGGMGVGISRSSLAGAVAKLGGVGVISGVQIGYDEEDFETNTINANLRAIKKHISKAKEISNGGIIGINFMVAMKEYET
YVKEAVKAGVDLIISGAGLPNKLPSLVKGSNVKIAPIVSTAKAANVILKMWDRKEKTTADLIVVEGPKAGGHLGYSNEELDNIDSIDYDKEFVEIL
KVANTYGEKFGRNIPVVAAGGITSSSDVKKYIDMGASGVQVGTRFVATYECDAHENFKMAYINASEEDVHIVKSPVGLPGRAIRNKFIEEVKIN
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>CORE_REP|Org50_Gene1876#

MRKIIEIKHHSHDYECMWNGIEDLYINKTGECLPNDFFFLLSGFGSFCYIKTNKADLKRMVALGDGRTKQMYEFLAPIVGFEYKHHEFKKYEQA
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KYNIAREAIAIKRDMFLSPPKGFLGYKGFEKFIKELPQWNTELDKDDYDKILTNMVMFFGTVPTIPNAIKGIKEPDTVQFKGGFDKMSRMLNSI
GEEYKNNSFIQVAEIFDKTAIIIEKISNIIIDYLTQTCDDTEQLPLLFSEVLEHMKTGYLILDVQKIYC

>CORE_REP|Org96_Gene1979#

MNCKWISKIDERKKCHREADSSGYCIFHKENKSDEEIQLMMDTLHKEEISEFNGFVFENEFNAEEILTYNYKILDFSESIFKQKANFKKYIFKKNIIF
NYTEFRDKVLFNGCVFLENCDFNRTIFSKHYINDRIFEKVKFKGPDLVVNKVENFPRMDGIIFSMCTKFVLKNVEYGKSEYEHGKINYRIARNQA
TKIGEYEMIGFYYYKERIYSSKIMKRSNYPTFSDYLVEKFFDQIARYTTGYGEKPWNILLVIIAIISVFALLYLFVGIESSNSTLVALDINNIGDYSLSEIF
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>CORE_REP|Org48_Gene3539#

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FLDLKNFYIENILSNNSSVKSNTDKVVSTSENPSIRKMFNSINKIVGRYLDPSEKMSIMDIMNKYNMSPDMILCAYEYVKDKTGTSKPVKYIEGII
RNWYDSNLYTPKDVEESFLVRSERYILYKTIFNELGFSRQPSKSEKELMDTWFDKFNMDIDLIIKACSKSKNISNPSISYINGIIKNWNEKNIKNLN
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>CORE_REP|Org60_Gene1214#

MSVIKIEKALKLDKVIFVDVRTEGEYEEDHILNAINMPLFKNNEHNEVGTIYKMQGKHEAIQKGFDYVSYKLKDIYLQAAELALNYDNIVIYCARG
GMRSGSIVNLLSSLGVNVYQLEGGYKAYRNFVLEYLRHVMDTKNFVSVHGLTGTGKTDLLHLLDEKGIDVLDLEGIAKNSGSTFGFITFDKKPPS
QKNFETKLFESIFFSKENYIFVESESKRVGSVTVPNEIFEAMTREGHHILLECDIENRVDRLCRDYIYDKDEGNILILKECINKFRKRLGNKVVDDYID
LLESGEYKELVKRYLLEYYDPLYMHSVEKYKYDKIINFNDTQKALEDVIDLYESILEGENEC

>CORE_REP|Org52_Gene1117#

MNKKKITFIFVILILALILFSFFRSSSQNTKYSKTSYYLGTVNEVTVFNVKESKSDKILNECDSILRYIDNKMSTHIPGSDVSKINDNAGKKFVRVSDD
TFFVVKEAIQYSKLSDGYFDITIGPLSNLWAIGTDKAKVPSDSEIQKLLPLIDYKNIILDEKNKSIKLTKENMKIDLGAIAKGYAADKIVAYLKSEDVK
KGLVNLGGNIFTLEDGKNDKPFKIGIQDPTSKNGESIGNIETTNKSVVTSGIYERFIEKDGKIYHHMLNPFTGYPFENNLSSVTIISDKSINCDALST
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>CORE_REP|Org10_Gene1232#

MNKINKNFKNIWIILGAVSIFTMVIIFNKNCNVNKETQIEAFTIKNHDKKFVYPMGNIIGVKANTDGVLVLGYEEEDVDYIGGIQIGDNIVKIDNK
RIKNSQDVSEILNKIKKSKVEVTFERKNKYKTEVIETKKENGKYKLGLWVRDKISGIGTMTFYDPSMEKFKAIGHAIKDSDTNELLKIKQGYIYKPE
QLKIVKASNEKVGKIKGDFNDSNLMGNFSNNSELGISGNITENHNKEFNVANKEKQLIEVGRPQDVKIGDAVILFEDKNKNITSYDIKIESIVYDK
GNYRDMVIKVVDDKLLEYTGGIVQGMSGAPIIQNNKIIGAITHVFRDNPKKGYGIFIDEMIKL

>CORE_REP|Org94_Gene2793#

MIKKISTILSLVLLISISSTIGVFADANPKRELIEGSIPEISTELNKRAFKDSKEVILVNEESIVDSISATPLAYAKNAPIVVTKSKNLGRVTRNYLKELGP
EKVTIVGGLKAVSKDAERNIEKMGMKVERIRGKDRYDTSLKIAREMYRTVGFDEAFLLSSTTGLENAISVYSYAAKSGMPIIWAKDEGFEEQIDF
LKGKNLKKIYALGDSKEFIAEIDSNLKNIEGIKQINKSSTNVDLIKKFYDEKDIKKIYTARLDFGSRSDVNEYISLGVVSAKENMPILICSDNLSRAQD
KFLKDSNINDVVEVGYTVGDYSLFKSIFNLTFLSCIVLILLLLLITFRALRYESK

>CORE_REP|Org18_Gene2133#

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DGIRINPGNIGSIERVKMVVEKCKERNLKIRIGVNGGSLEKELLKKYGSATAEALVESAMGHIKILEDLDFHNIVISLKSSDIYKTVDAYELISKKVDY
PLHIGITESGSVHKGTIKSSIGVGALLLKGIGDTVRISLTGDPVEEVIVGKQILRSLGLLNDKIKVISCPTCGRCNIDLISVVNEVEEKIGSMEKNITVA
IMGCAVNGPGEAREADIGIAGGKGEGLLFKKGEIVRMIDGNKLVDELLEEIEKL

>CORE_REP|Org81_Gene783#

MYSSQTYDVVKNRTLSNIDLDIYKGEGSFLSDMVSPVNSELAKFYIELSYLHKKAFIEDNFDDFLDKRVNEFGVYRKLGTEATGEVIFEGKVGTTIQNGTIISYNELLFVVIKDIVISSEIEQNTSPVQALEIGIRYNIPASTEFKLQDEINGITKIYNDLAFRGGTEIETDKELKERFYKIQKNQATSGNKAHYEAWALEVEGVYNAKIYPRWDGPGTVKVLIFGENNQAVDSEVIERCREHIEEEMPIGPMLTVLTPSVLDISISASIKLETGYTLDFVKESFLESINSYLINVNKEIIYTKVSAILASIEGIHDFSNLLLNNKAENIVFEEDKVPSVTNLEFSEVVVQ

>CORE_REP|Org77_Gene3013#

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>CORE_REP|Org77_Gene3011#

MSILENNFLYKLKNNTIFFCIYTLLFIFIYKAFPYIAPFFLGGIIALMINPISQKLENKFHINKGISTLVLSFLAVAIVSTVTTIIVINSVKELMGFLNNISANPEDISNTIMYFLNKINDFMKSFQEIANFDIEQLVNKFSGEVMQITKNLLTSILGLATSIPYIIIFIITLFIATYFIAKDLDKIENSFYNMFTVDVRKKVKNVKKEAGLSLVGYIRAYTILMAITFFAIWGSFALFGLKYGLIVGFVGALMDLIPFLGIITIYLPVIVYYFLIKNYFIAISMTVIFFVLSLIREILEPKLVSVNVGLNPLATLAAIFIGIQVKGIIGVIFCLGLVCMHDILKKVDIF

>CORE_REP|Org39_Gene1501#

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>CORE_REP|Org87_Gene2187#

MKKMWKGNHAIAEAALRGGCEFYAGYPITPQTEVMEFLSHRMSELGRTFIQSENEMAAIYMVYGAYASGMRSMTSSSGPGISLKQEGISYLCANHYPCVIVNVQRWGPGLGSLDSAQTDYLRDTRGGGNGDYHLIVYAPNSIQETVDLMYNSFDVAEKYRVPVEILTEAALGQMMEPVEFPEFKKREEDLGWTYDGSNRDHAKVADNQKPTFCMEKRMRISENEQQWEDYQIEDAEYVFVAFGIPSRTTMNAVRRLREQGEKVGIIRPITVWPFPYKAFEKVSKDVKGFISVESTDTGQLVEDVALASKKVCKENVPVYGLFSGNHIPKTLQVMDTYSKIKSGEIKEVF

>CORE_REP|Org88_Gene1169#

MSVDQEKLKALNEALGKIEKDFGKGSVMKLGEATSMSIDVISTGAIGLDIAIGIGGLPRGRIVEVYGPESSGKTTVALSCVASAQKDGGIAAFIDAEHALDPVYAKALGVDVDNLIISQPDTGEQALEIAEALIRSGAIDIIVIDSVAALVPKAEIDGDMGDSHVGLQARLMSQALRKLTGSIKKSNCVAIFINQLREKVGIMFGNPETTTGGRALKFYSSVRLDVRKIDTIKQGDKVIGSRTRVKVVKNKVAPPFKQAEFDIMYGEGISKIGDLLDIAADVDIVKKSGSWYSYNDTKLGQGRENVKKFLEDNLDLTNEIDEKVRAFYNLNEEHEEAGNSVSKEIVEE

>CORE_REP|Org78_Gene2222#

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>CORE_REP|Org96_Gene2359#

MNYKDIIRNVKEKNFEKMYLFYGREYYLIENAIKAFKDSLNEGMLDFNLDIIDGKEIVLNQLISSIETLPFMDDRKIVIIKDFELLKGKKKNFTDSDEKYLIEHLDNIPDTTTIVFVVYGDVDKRKSLVKKIGNNGIVFDCDKLSDMDLFKWIKKSFALNDVIIDNSQIMYFIEQEGYRDKSSEKTLSDLENEINKISSFVGKGNNVTNDVIDKLSQKKVENDIFKLIDYIGEQNASNAMKILNDMIQEGESVLGIFSMIARQFKIIMQVRQLQLDGYSTKLIADKLKMHQFVVGKALKQTKNFSDDIIVEILNYILESDYKIKTGLIRDTLAVEMLVSRYCKREAI

>CORE_REP|Org25_Gene1481#

MEFTKKSKLKNMYVNMNVARMLSKINEYKGRQLLYKKQPKEILENLEKKSLVDCSESTYIGNQRDSSNFNLEKLISNEVTPRSREELSIVEYRDVVKTINSAYESIPISSQTILELHGYLYKFSSTRGGSYKSDNDFIEHNLKPSEFISIDSSVNKVEKAVEEICEAYNTLIEEDEIDILILISAFVLDFILIHPFKEGNIKMARVLILLLLNKNGYEVGRYISLGKIFDDSSYEYYSNLNYLKASIGSEKADMNAWIEYFLETILTAYEKLDDSLNISDKKRQTKTSRIEKIINSTLGYFTKEDIRDLCPDIPEPTINRVFNNLRKQDKIEVVARGRSAKWKKKY

>CORE_REP|Org88_Gene2627#

MSEILLGTGLLLLVLCCFTIFSYKAPYGMKAMGALANAACATFLVEAFNLSLLGDVLGMEFFRSVGAANGSLGGVAAAILVPLALGVSPVYAVLI
GLSCLDFSILSGFVAGYFVSFLIKFIEKKVPPGVDLVVVILLCAPLSRLIASNVDPLVNSTLLQIGQVLIEATNISPIIMGIILGGLITVVGTSPLSSMAL
TSIIGLTGLPMAIGALGAFGSAFMNSTLFAKLKLGSKKDIISVAIEPLTQSDIISANPIPIYSTNFFGGAFSGIIVALMGLVNMTPGTATPVAGFAIM
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>CORE_REP|Org78_Gene1253#

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KGIYTFGNLDLTCFNNTDMRSAKKNNHPRFVNNIRDLFVDIKEKYINCGMRCMNYISLKNLLEFVNLEFSGDAHDPLNDAYNLFILDEAITNNV
DIQNLLIIRDIIRPPFNDINSNLDNCFNKFKESLYKKEGNYNIVDFSVEIIKTVRMYLLTIIDVNIQNLEIMKDISKKMDTIDKLKDIEEGYFYLLEDVY
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>CORE_REP|Org1_Gene1963#

MNKIKVGIIGATGYVGAELIRLLMNHDKVEVTAIGSNSYVGKNIVDIYPSIGYKNNMICIENEKVIDMCDVVFTALPHGVSEKFVIKAIKSKKKVI
DLGADFRIKDEEVYSKWYGVSFIDKILHKKAVYGLSEIYKEDIKDADIIANPGCYPTSISLPLMPLLSSKLIKNNNIIIDSKSGLTGAGRELSISSHFTE
VNENITAYKIGKHRHTPEIEQNLSESCKEKVSVVFTPNLIPVNRGILSTIYCTKEDNISINDIHRKLTDYYEFKEFIEVLPLDKVASLKNVRFSNKCVIS
LHENGDTLIICSAIDNMIKGAAGQAIQNMNIIFGIEENTGLKNIAPSF

>CORE_REP|Org39_Gene1940#

MNFKKFSFNSIYLIIVVGIIFTVILFNISIYIITDDLKLVALLLIYTIVLCGFIALIIFLLHKKIVIFCSKICHTLDSMMNSEYNIEIELEEETILSRINHRLIRMY
EVIQESRNSIAIEKADLQELVSDISHQIKTPIANLKMINTTLLNQTFKTEIQNDFLMDMENQLDKLDFLMQSMVKTSRLETGIITLSKKKNSIYETI
ATALSGILFDAEKKNIEVTVDCDPNLYIIHDKKWTSEAIFNILDNAVKYTSSNGKIRVATECWVMYTKIDIIDNGKGISESHQAEIFKRFYREEDVH
DIEGIGIGLYLSRKIISLQGGYIKVTSEIGKGSTFSIFLPNK

>CORE_REP|Org47_Gene1973#

MEKKKIVLKNFTEDELKEFMKTIDEKPFRGSQIFSWIYKGAKTFEDMNNIPKSLRNKLEEISCIGHIDIELKLESKVDNTKKYLFLLDDGNIIETVM
MDYDSRVTVCVSNQVGCRMGCNFCASTMDGLIRNLEPWEILDQVIKIQEDTGKRVSNLVLMGSGEPLDNFENTKQFLKIINEKNGLNIGYRHI
TLSTCGIVPKMYELADLEIAINLALSLHSPYDEERRKIMPVANAYSIKEILDACRYYIKKTNRRVTFEYSLIKGVNDSEKEAKALAKLLKGMLCHVNL
IPINKVEEREYEKPDKAFIYKFRDSLEKNNIPATVRMSMGSDISGACGQLRRKYK

>CORE_REP|Org5_Gene2394#

MFKKCIKVVTLTFILACILPGKSLALNQDDFLKFLVNSSYPEAKVEGNDTENKKNNKNKETSKENKEESKEENTKSKDASKVDNKKESEKEYIKLY
VGKENVPDIESKNSDTTETNTTSSSDYKDDLRVTKENPRILIYHTHGCETYSNSPDGNYHSRDKKNSVMEVGSALTSALDSKGWGVVHTTKYH
DYPSYNNSYASSLKTIQSILPKYNSVDIAIDLHRDARDLTNPATKEKDHLKYTTMINGERVSKFFFVVGGKNTNRKQLRALAEDITAFAEKKYPGL
VSPIVEKDYARFNQFAVKNHMLVEIGNNATSVEESKATTKYLAEILDEYFKQKKLEL

>CORE_REP|Org95_Gene2649#

MKTSDFKFDLPQELIAQVPIEDRASSRLMVLDKETGNIEHKVFRDIIEYLNPGDCLVLNNTRVIPARLIGEKLETGGKIEFLLLKRTEEDTWQALVK
PGKRAKVGTKFSFGNGKLIGEVVDLSDEGSRIIKFHYDGIFEEILDELGNMPLPPYITARLDEKERYQTVYSKHNGSAAAPTAGLHFTEELLNKIKE
KGVDIAFVTLHVGLGTFRPVKVEDVLNHKMHSEYYMVSQEAADKINRAKENGKNVICVGTTSCRTIESACNEDGKMKETSGWTEIFIYPGYKF
KVLDKLITNFHLPESTLIMLVSAICGKDNVLNAYNEAVKERYRFFSFGDAMIIK

>CORE_REP|Org31_Gene2310#

MEDNKGLARDSSKYKIVSISVVVIILITFWYMLNMVLLTFIMTFIFYNLLVATRKRIKKFSSLNIPDSLIIIVLYALFAILLVLISYAVVPIIIVQLTELSRV
FSDFDVNQFAQSLGPKLYPIVSKLDFNKYISQAGLLIASTATKVGSFGVNILLAFLLSLLLLLEKNEIKNFGDKLSDSKISFIYNSLVFFGKSFVKNFGE
VMKVQVMIAFINSVVSMIFLGFMGFPQIWALGFMIFVLGLIPVAGVIVSLIPLTVIAFNTGGITKVFGVLLMICIVHAVETYILNPKLMSNRTKLP
VCFVFIILLVGEHYLGVWGLLIGVPIFMFLMDILGVKFTSR

>CORE_REP|Org71_Gene1826#

MFSDMTLLQYINSEDRGFFLPDMGTNGLFLINKKAYEVYDSVDLQLELAKTMDKYFESDFIYSFCDGITFCETLGLETLRPDYDFPSVLTHTITDR
DKLRKLDVPDPYTSGRMPLNIESLSVISKSIKKPLYESIQGPFTLAGQLAGATQLLRCIITDKKFVEELLEFTTELVRRYAVAANKAGAKYISIAEPTS
VTLSKDRFDEYIVKNLNKIYDELDCWKGMHICGDTRELLDNMLDCNIDAVSLDQILDYEEIAPMIPRDIVLIGNLDPIKLLGRSKPDKIRRETLKLL
KKMRGYDNFLCDFGCNCLNTTPVENLQAAIKAGRISYKELDRIDINEL

>CORE_REP|Org27_Gene1040#

MKIVIDGMGGDNAPKSNVEGAVNAIKEYQVDLIITGDKDLLEKEFSNYEFDRNKLEIVHTTEIIENEDKPVKAIRSKKDSSMVVALNLVKEGKAD
AIISAGNTGALLAGGLFVVGRIKGIDRPCLCSAIPNVKRGMTLIADCGANADCKPKNLVEFAAMSNIYSRKVLGLENPKVALANVGLEEGKGND

LVKRSYEEIKKLDLNFIGNVEAREVINAYTDIIICDGFTGNILLKSAEGVALSVMSLIKETFMASTKSKIGALLIKDDLRKLKSFIDYSEYGGAPLLGLN
GGVIKAHGSSDAKAIKNAINQGIKFSKGKVVEDINQFISKYNEENKNNEDE

>CORE_REP|Org94_Gene2555#

MFGGINIKRIGIIIMFFLSIAFIGFYLVIRDNSDTVKMQRGINIGNALESPKDFPWDVKMSNKFFDDIKDAGFDTVRIPVRFSDYTSDSDNFKIDEE
FFKKIDKYVDYALDKDLIVVLDLHHFEEIMKEPRVHKEKFLKIWQQIANRYQKYDKKLVFELLNEPKENLYSQLLNEYIEEAIKIIRKTNPKRTIIVGP
YNFYQIDYLNELNIPKDSNIVVSFHYYEPNDFAFQGNIYHKGFEHLSNITWEGTNEQMDYLKKRFDTVENWANKNKVKIFLGEFGITKEAPEAS
RRAWIKAVREEAEKRNFSWAYWELASGFGIYNQIEGTWDRDILSALIEKR

>CORE_REP|Org81_Gene1915#

MKLIKTIDAVGQVLCHDITQIIPGEFKGRKFKKGHIVKEEDIPVLLSLGKDNLYVWEKSEGMVHENEGALFLKELTAGENLDFSEIKEGKIDFIAAC
DGLLKIDVDALFDLNCVGEIMMATLHNNFIVNKGLKVAGTRVIPLIIDEKKLEDAKKVVGNRKIVNVVPFKPKKVGIVTTGNEVFYSRIVDKFGP
VIEEKVKGFGCEVIGQTICPDDKEIIKSAIKEFISQGAELICCTGGMSVDPDDVTPTAIKETGADLVTYGSPILPGAMFLLAYYGEVPIMGIPGCAM
YHKTTVFDIVLSRVLIDEKLDKYDIARYGHGGLCMNCDVCTYPACNFAKI

>CORE_REP|Org56_Gene2385#

MELNERKLNILKAIVKDYIETAEAIGSRTISKRHDLGVSAATIRNEMADLEELGYLIQPHTSAGRVPSEKGYKLYVNSLMSKSELDDNDKILIEQC
MNHNINHIKELIHETSKLLSQLTNYTTVAVTKSLINQSVIKHIQLVAMNDNNILLIVVTDKGDLKKANLTTNVYLDQSKLNLISDNLTRKLLGKSIT
DLDDNLIAFIKYEISEYSGLIDELLNALNSNMKEEDFSLSLNGATNIFSYPEFNDVLKAKSFLNMLEKKETIADIIKSKGIQKDNLNIIIGSDNDCELA
QDCSIVTATYNVDRDLVGRISFIGPTRMDYARIYSIINYMSLLINRK

>CORE_REP|Org61_Gene2585#

MNEKRVKGVTLTILTESPVPLSYDQGYGNYTPIKKEQYREKIHAKTSIATITYDLRRMLHQEYGWNLSNIIFGKKGNIYPSIKKNVGCVDENGLET
DVFGYLIPLKDKGSISKASPLRIIPFRSLNPYIGSTQLITNRGFLSSEFGRKYYDEKEENEVPRDENFPTSQALAIEETLSDYYVYTITLELDRIGVVEVE
VEDGKLLLPEERKFMSKELREKAVKDILDAITVFTRNIKHSSVLLKPLAVMGGAFDKVVPFFWNDVDYNADSGEINLEGVIETIESYSLKESNTILA
INDRLKISNKKELNKFNLSKYPVKEIKNLADRLEIGEDNMWYLKE

>CORE_REP|Org56_Gene961#

MKGNITIKDVAKQAGVSISTVSRVINDSKPVTDEVKQKVLEVIKETGYIPNPLARSLVTKKSQLIGVIVPEVSDSFVNEVLNGIEEVAKMYDYDILL
ANTYSDKEQELKSINLLRAKQVEGIVMISWIVEQEHINYIQNCGIPATYISKTARNYDIYTVSTSNEEATFDMTEHLIKKGHEKIAFIMTSKDDTVL
EMERLAGYEKALSNNNIELDKSLIKYGGTDYESGYNSMKELLDDGIIPHAAFVTGDEAAIGAINAICDAGYKVPEDISVAGFNDVKIARMYRPKL
TTVYQPLYDMGAVAIRMVIKLINKELIENKKIELPYRIVDRESVTERKK

>CORE_REP|Org82_Gene1721#

MIVVLKMGADKNEVKKLIEAIGREGVEVNPIDGTELTVLGLVGDTSKIDAKRIEANKIVEKVMHVVEPFKKANRKFHPEPSIINVNGMEIGSKKI
AMIAGPCSVETEDQIVSIAKDVKKSGAGFLRGGAFKPRTSPYAFQGLKYDGLDLLKKAKEKTGLPIVTEIMSTQDIDIFEENVDVIQVGARNMQ
NFDLLKELGKTNKTILLKRGLSATIEEWLMSAEYIMAGGNENVVLCERGIRTFETYTRNTLDLSAILAVKKLSHLPVIVDPSHAAGKSWMVDSLS
KAAIAVGADGLIIEVHNDPAHALCDGKQSIKPNEYDELISELKTIASAVGREI

>CORE_REP|Org82_Gene2254#

MEENKILKIEKGTSGWGGPLYIKKEGNRNKILSMTAGGIHEVTLKIKELLGCEIVDGFKTGVSDEEVAVVIIDCGGTARCGVYPKKKIPTINVNPV
GKTGPLAKFITEEYYVSDVNPNCISVVDGEDMPQKSQENKSENKSSIRKPDNYDEVKSKAQGEYAKKNIILSIGQGAGQVVSKFYDAGRDTIQ
MVMNNVIPFMAFVSMLMGIILASGLGDWIARVISPLAGNIGGLLIISVICTLPFLSPILGPGAVIAQVVGTLVGTQIGLGAIPAYLALPALFAING
QAGCDFVPVGLSLGEAEPETVEYGVPALFYSRLITGPIAVIIAYGVAVFALR

>CORE_REP|Org54_Gene1900#

MNFKKLGILGLVSVFTLATITGCSSNNNKDKNNDKDTSSKKVTMVLDWTPNTNHTGLFVALDKGYYKEEGLDVEIVQPPESGAETLVATGKAD
FGISYQEQVTYAKTSEDPLPIKAVATVIQHNTSGFASPKEKNITTAKDFEGKTYGGWGSPSEEAVFKAVMKKNGADFNKLKIVNTGQDDFFAA
MKTVDFAWIFEGWDAVKADLIGYDLNFIPVKDLDERLDYYTPLIISNETVLKDNPELAKKFLKATTKGYEYAIKNPEESAKILVKHAPEVDEKLAL
KSQEYLASKYKDDAPRWGEMKDSVWNNYTSFLKEYKLIDKDMKASDAYTNEFLPQ

>CORE_REP|Org54_Gene2802#

MTKLSKKNITYLLILVSIVVLVFGIVLSITIGAKDMNLSTVIDSLIKMEDGINMRIVKDVRLPRAIAAALVGGFLAVSGAIMQGITRNPIAEPSVIGIT
QGATFAISISLVLQKKLPQLIHGSFSVMMFAFIGASISGLFIYFISSKSRGRVNNVKLALAGVALGTLLISLASAISMYFNLSQQLSFWISGGLVGVK
WEGIKLLFVAGGIGFILAIIMAPRITILSLGEEVAIGLGQKTNFVRFICIVLVILMTGASVSVSGNIIFIGLIVPQIAKGIVGSDYKYIIPSSLVLGAVLLV
YTDILSRMINPPYETPVGSITALIGVPIFIYLVRKGEK

>CORE_REP|Org18_Gene1056#

MIYMIIHKFIIHVLDKNSDVPILNDFEGKVNQEVDGFFQKAIKRIAKDEDLRKGVFKDYNDNLIKNCCEQIIYDESTFLKNSKEIASYLFDVMKINA
ALESCDLAICLYTIKDEKSVAILKLDYKKLYTHSIEFVDDKFNIQMVSNEIGIPETLRQKQGALISLSGINDEFHLRLLDKDAEKEGSESKFVTEFLNA
KKIDDDKYKTKVFKNTAENWITNALSNDIKQAEDVRSILNYTLKEKHEVDINDFVDNSIKDDELKDSFKEHMEEKGLDESFSIDKKWVEKKLKKR
SIKTDNGFDIKGNLTDFEDPMKYTVKQNQDGTIDIIIKNVTFYEEK

>CORE_REP|Org22_Gene2332#

MKLKLDSSKFNEGLNYLKKDYKIFAPVLIPFKGTFSDTDVIRYKEVNAFEEMEFAKKANFSPKEVVLPINQVLFYFTEKEFKESDLDNKKILIFLRAC
DINGIKRLDEIYLNNGEEKDYFYKNIRDKVKFALVGCKESFRNCFCVSMDSNKTDNYSIGLNIEGDTLYLDIKDSEFEVFNGEATEFNVDYVTDNL
ISVDVPENIDSNEMIGNSIWDEYDTRCIGCGRCNFVCPTCSCFTMQDIFYKENENVGERRRVWASCQVDGYTDIAGGNSFRKKQGERMRFKT
MHKIHDFKKRFGYHMCVGCGRCDDACPQYISFSKCIEKINDLVTSKEEV

>CORE_REP|Org73_Gene2904#

MSTIIPKDYKSSLNVIDTQIAIKKLKDFFEMRLSNELNLIRVSSPLFVLPETGANDNLNGEKAVSFDIPFMNKNAEIVQSLAKWKRLALKKYGFEV
GSGLYTDMNAIRKNEELDNIHSLYVDQWDWELVIDKSSRNEKTLKDVVKRLYGVFKDTEIFVCSMYEGIKEILPEEITFITSQELEDMYPELSPKE
REDKIVKEKKAVFITQIGKTLISGEKHDGRSPDYDDWELNGDILFYNPVLDSALELSSMGIRVDEESLDRQLKLAGCEERKEFDYHKMLLNGELP
YTIGGGIGQSRICMYFLQKAHIGEVQVGVWPQDMIQNCSSAGIELL

>CORE_REP|Org58_Gene1995#

MEQSFINGKVNLLIENYKALNEVKGSWQIGLIQHSCALAFTLKNKRISPRLVEERIELIKKNTGLFSNFRGYNMFYMATLLSFESNPESSFKMILDI
YKELKSEKFWGDTYLPLTASIVYENREKMDYLTCISKMKIIYDYMRKKHPFLTSSDDYCNIALIAIHSKNLDEDLEYIEKCYEFLNENGFYKGNDLQ
ALSQILLFSDDRTMLKCKKTIELKKAFKENDCKMNYYGYPIIGAISLLDYREDEIIEEIKNVSNKLKEEKGFGNWSLGKSNRVMISSAIVASIYADLIR
NENNIGSITNNIFLNIVVAIQIACVMAATSAAIASSSSN

>CORE_REP|Org56_Gene890#

MKKYISIILLVVVTMVVLVGCSPGKDNPKNKELSVVKQVKVAVPDGLPAVAIAKLANENPEIKEGYETVYSIEKTPEAISTRVMKKDADIAIVPSN
MAAIAYNKTSSYNIVGTVGMGSLYLVSTENIKDYSDLVGKEVGCTGKGLTPDITIKSLLLQKDINYSNIKFNYVNSASELVPLLATGKVKTGIVPEP
ALSALMSKNPDIKIIKSLNDSWKEVSGSKDGYPQSTLIVKSEFLRDNKDFVDSFVGQLSNSIDWANKNPEELGAYSEKIKISTESKIIGKSLERANL
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>CORE_REP|Org78_Gene2307#

MIKRNKKILAVMTSLIMVLVGTVGCSTTNDKKDEPAKKEASLPKEINLTYVKSPLNVPSILEKKDDLFGKEFKKDNIKVNFHELTTGPEQTQALAA
GELDFLHALGGTSAIIAASNGVGLKITNIYSRSPKGYMLITNNDNIKSIKDLKGKKIVGPKGTILHQLLIAALAKEGYTIDDVEYVNMDIPSAASALE
SKSADVAMLAGPVALKTINSGAKMIVNGEGLVSGIIVTAVSDDFAEKYPELVKRFMKVHEETLKYMNENKDEVMDVVSKEVGLSLDETKEMY
SWYDFSSKITDKDIKELEDTQEFLMSNGMQQKKINIKDMLYNQN

>CORE_REP|Org62_Gene1406#

MIYGGSVLNTTKKLTEAALLSSLFIVVTIISVSTGFGYAIYLDFIVPIFFCIICLKCDLKYTILSGITSLLIISLVLGNLGTAIWATQSVLLGIMCGYLINKP
TMVMDDLVYGSVFGVIVMVFIDIYASTLIGYSFMKEFQGYSKWIYFNGYTNFIYYLMIALFPFGMVFCIYLLSLILGNKLHILDSNSLKKLLIFKNFR
TLNQFLCCSKKVFYICVSYLTIFEVVKLLNVKVDFVYLKTVFISIAYLCVYFIIRDSCMSLQNFIIAKFRKLLYARISFLIIILLLFFMFDVTVISLIIINAFLN
KKINIRLSQNNIVNKQINLLIEK

>CORE_REP|Org18_Gene1818#

MCFRFMKYKLFIDFEFNILDDNKNKPKEYNGAELISIGGVLVDNEFNTIDNYYSLVKPKYNKILSNKCKNLTKLNQLDINNAPNLLYVMDDFYKW
FCKFDDVTIYNWGDFDITGLLTSFRVYKYTGKCLELFNMMIDIQPFISQHITYNNRILSKQISLLNMKKIFSVEGDIKHNSLSDAVDLMNVCKCFF
FNSPKNIDILEELYNKLPALKTPLYYIPYFEDENFELKFDRTPEDIIIYLKQILTILNISKKEIYFKKRSVLVNNSKIINFKNLSSSFKLIKLNEFEEYPDFILK
LGDKKSFVESVIKINKSNRKSIKNLILKLSKKP

>CORE_REP|Org48_Gene1100#

MNTKAGILGVGSYLPEQSYDNFHFEKIMDTSDEWISTRTGIKERRFAKESEATSDLASKAALKAIECAKLNVEDIELIILATITPDMSLPSTACIVQ
DAIGAVNATAFDISAACSGFVYGVTIAKQFVETGCYKNVLVIGAETCSKFLNYDDRTTAVLFGDGAGAAVIGPVSEGGILSTHMGSDGKGKDCL
KVPAGGSRLKASKETVEANLHTIEMAGSDVFKFAVRKMAETSLRALEKANLNTTDIDYLVPHQANIRIIQASSKRLELDMKKVYVNIDKYGNMS
AASIPVALDEAYREGKIKKGDNVVLVGFGGGLTWGASVVKWTL

>CORE_REP|Org12_Gene2189#

MSKVKRLTDVWIYINDKQKFTIKELSEEFNLSAKTIQRYLKELNKMGLPIQAEQGRNGGYRVLNNSYIPPVIFTEKEVMIILFALKSLQIYNYKLMEIEINSIMRKVSYERKSSIKVGIENIKRYIGFVANDTNDGDFKSSNVTEFFRASSESLILNIKYKCGNQILEKNVCPIGIYLNKGAWFSPAYDCKSDKIILVHIDNIIDIKRTGESKKIHINLEEWLHEVYNNLYGNSSTTKKFGEIIYLNVLLTKEGVSKIKDSSWNLDMELNEDGSGIISTFIKVEDIDCYASILFFIGNNAKVIEPKFLNKLLYDKANELRYFYEENMV

>CORE_REP|Org50_Gene1894#

MKKITINDIANLAGVSKSTVSRYLNNKDISDSTKEKIKTIIDEYGYEPNAFAQSLRAKKTYFIGIITPCLDSFVKSKIMMAIDEELKELKYTSLIINTSRKIRSEIDSISKLASLKVDGIILIGTEITKEHKNVIEKLDIPIVVVGQKVDGINSIVNDDYGAGYKMGQYIANKGYKNIVYLGVDESDISVGLNRKNGVLNGLKDKGYDAKVFYTDFDQETSIQRSGEMLESENPDIIICATDNIAIATMKEINKRGKNIPRDISVAGFGGYDILSIISPKLTTIKFENKNAGKVAANTIVNLIQERKEPLLKEIKFELIEGESTINKN

>CORE_REP|Org23_Gene1323#

MGFKVELGGFQTLIQDRGRVGYGQYGVSGCGAMDEYAHRVGNILVGNSEDEASLEVLMLGPTITFDEYTQIAVTGGDLGAKINGKEIQNWRSYQINPGDVLSFRGVKSGARAYVSIAGGIDVPLAMGSKSTYTRAKIGGFEGRALKKGDYINTFIQEKDFTINKKLSSKYIPTYSSEIVLRIVKGPQFDAFSNGEVEKFLSNKYKVTNEIDRMGCRLDGESIKHLNGADIISDGISYGAIQVPGHGKPIIMLSDRQTSGGYTKIGNVISVDLYKLAQAKPNDVVKFELVDIYEAHRLLREQEDKIQDIYKSMKNIRVVKAKVLNDIAV

>CORE_REP|Org8_Gene1196#

MKIMMNNMDSIINYIYEGDYFIVTSHISPDGDNVGSTLSMYYTLKNLGKNVYYVLDDEAPLNLRFLVEGVKIYKSNEFNMKNYSLIALDCGDKMRICVSDEIKNNASKLICIDHHASNDSYGDLNYVDIDASSTCELVYNLLVRFQQTKDINIINEDIATCLYTGLVTDTGNFSYSNVHASSFEMAKNLLVLGAQKNTIIQNIYQSNSSDYYKLLGEALKGLEIFDSKVSSIVLTQDMMNRNNISFNDVDGITTYTRDIKGIEVGILFKEKKQNEIKVSFRSKNYVDVSEIAKLFGGGGHVRAAGCTIRDSIDNAKKMVLEAVLKSI

>CORE_REP|Org61_Gene1084#

MGDTSRFYESVKNKYPKLKDGTRVHLWPKENIIIGPIYDEEDGYKKSIGNVDSLSWKQIVILAECDGKNTTDDIINILSNRYRNIHNMKEKVMEFFMFYENVYLTFEDDIQTLSSVFEITGNKSYITPLYFTIEIDGDNNTNDYFSEITSLLNCMYEKGCRFIEVIGEDILKNKSMREIFQYMLDHFDLIVVTKDSFTIDRSLIKELDNYRHKVIWKVYSKNDDTRIKLKEDIKITSLIKRGHTVVRGDREKAIKIEDMRFKDTKERFSKYGAEWSHLYISSDGSVKSYSFQKDKRIYLGNIFNNSVEEIFLEMQNKIDKLEIVYQ

>CORE_REP|Org91_Gene1013#

MENKLIVSSSPHVRSNEDTSYIMKQVIIALLPAAVAGVYFFRLNALSAMFFCILGTVGTEFLYQKFTKQKSTIGDFSAVVTGLLLAFNVPASLPWWMCLVGGIFAILVVKMVFGGIGCNFVNPALAARAFLLASFPVAMTAWTQPGVNWIGKNLDAVTTATPLSFLKNGAAGLADLSSNGISLADMMIGNIGGCIGETSAILLLLGGVYLMYKGIINYVIPVFYIATVFILTFLLGGFNITFAIYQLFAGGLMLGGFFMLTDYTTSPMTKKGQIIYAVLAGLITTVIRMYGGYPEGVSYSILLVNCLAPLIDKFVRNRVFGEVAK

>CORE_REP|Org34_Gene1705#

MYILNLNTRETIEDFRDKFYVAENSYLILSAPKNLKLLKETLDIDEITFNDCLKFDEITKLDLFDNYDFLSLNTFELRDGEAVIEEVNMYLSDNFILVVVNEEHFLFEFVKNIILKNSQLEKNPVINLFKINYLILREVIKNGFESLEKVEELILQIEDEMMDNINKNHVSRISDVRGLTRIIVKNTRPLLYIGDRIVKENIRYLKYSNVKKYNLENFQGIDFGIDKLYSFALSTRELADKLLDIYSSRVGEKTNNLITKLTLLTAISAPLTIITGIYGMNFRYMPELNWIYGYPATLFFMLCIIFVGIIIFKIKNYCKLQMIFN

>CORE_REP|Org18_Gene1114#

MKMVILTAVLVLGIMGLIFGIVLDFASKKFAVEVDERVEAILGVLPGANCGGCGFPGCGGLANAIVEGNAPVNGCPVGGADVGAKVGEIMGISAEAGEKQVAKVICKGTCSSAKDKYEYEGISDCRAANVLNSGAKMCKFGCLGLGTCKDACKFDAISIVDGIAVIDEEKCVNCGKCKEVCPKGIIITKPESQEVVVECNSKEFGKAVKEKCTAGCIGCGMCVKACKFDAIIFEDKIAKIDPNKCVGCMQCVAKCPTKVISGDITKKKKVTIDQELCVGCTVCKKQCKFDAIEGELKEKHKVDADKCVGCHLCMEKCPKKAIKIL

>CORE_REP|Org45_Gene665#

MARKLIKNLGKSKSAKRVKLLFKKIFITVFIVASIVAIFNITKYFEELYKVRDLKSTKIEYYMDVADEAGDGKVQLSWKALLAIDMVIHDEDLSNIKKKDTLDIGEKFIVEDKNDKGEKVYKVKKFNKVLSELKFDSSQKSRARKYMKDLEYTYLGNKQLDSSDEKIKFIKKLEDSAIREYIDYGILPSITIGQAILESGWGNSKLTKQSNNLFGIKADKAWKGKSVEISTSEHYNEKIVASFRSYNSLQDSVKDHSLFLINNKRYRKHGLFEAKDYISQAQALENAGYSTAEDKKGNRIYAELLVDVIRSYNLQLIDNKVETK

>CORE_REP|Org34_Gene2734#

MHILKSVKKIPGGLMVCPLLLGALFNTVYPQALEIGGFTTSLFKTGAMSILALFCLCNGAQINIRQAGNPLTKGIVLTATKFIIGAVLGIIVSKFIGPKGIIGITPLAIVATMTNSNGGLFAALAGEYGDSTDVGAISILSLNDGPFFTMLAFGVTGLANVPIVALFAALIPILLGFILGNLDEDIREFLAPGTTLL

IPFFAFPLGAALNFNQIITAGLPGVILGLGVTIITGMGGYFVMKLIRAEHPAVGAATGTTAGNAAGTPEALAAIDPTLATIAAVSTVQVAAAIIVT
AICCPMLVSYLDKREKKKKAIFKTNKNIEVN

>CORE_REP|Org17_Gene3542#

MIRDLNTKKVMKNAYRITKTKYETSLRVRVPGGLIDPESLTIVSKIASEYGNGQVHITTRQGFEILGINMEDMEEINKIIQPVIEKMNINQSEKNA
GYPAAGTRNIAACIGNKVCPKAQYNTTKFAKRIEKAIFPNDLHFKVALTGCPNDCIKARMNDFGIIGMALPIYEKDRCVNCGACVKKCSKISVG
ALKTENNKVVRDGDKCIGCGECVLNCPTNAWTRDEKKYYRLAIMGRTGKKNPRLAEDFLLWVDENSIIKIILNTYKYVEKYIDKDAPGGKEHIG
YIIDRTGFMEFKKWALEGVELPEITKMYENIYWSGVKYL

>CORE_REP|Org26_Gene1077#

MNKLSDEIINSLSTTIREKVEKVSNNNLNIEEIRLRSQKPLILNANSKDYFYNQKTMTLDLNQQNSYVVTREDVEQTFQIICKYSIHSFMDDIKKGF
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ERNEIAGAYLGVPQMDVGIRTDIIETCPKDLGITMLLRSMSPNVIVTDEIGSEKEIKALYTALNGGIGLITTVHGDSIEDIQNRKELNRLLDKELFKK
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>CORE_REP|Org85_Gene1579#

MEKRKVIIDCDPGIDDSLAILLALNSPELEVIGITTCCGNVPANIGAENALKTLQMCSSLNIPVYIGEEAPLKRKLVTAQDTHGEDGIGENFYQKV
VGAKAKNGAVDFIINTLHNHEKVSIIALAPLTNIAKALIKDRKAFENLDEFVSMGGAFRIHGNCSPVAEFNYWVDPHGADYVYKNLSKKIHMV
GLDVTRKIVLTPNTIEFINRLDKKMAKYITEITRFYIDFHWEQEGIIGCVINDPLAVAYFIDRSICKGFESYVEVVEDGIAMGQSIVDSFNFYKKNPN
AIVLNEVDEKKFMYMFLKRLFKGYEDLIDSVEGVI

>CORE_REP|Org73_Gene1768#

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DEKYADLGGLKEPDLEGIKSANPDLIIINGRQEDFYEQLSKIAPTISTSKDDKKYLESVKNNIDKIAKIFGVEEKANQEFSKIEKKIEILNKKVTDKNL
NALTIMVNEGNLSVFGEESRFSILYNSFGFENKDKNIKESSHGQNITFEYIAKQNPEVMFVIDRGIATGSDVKESSTAKSVLNNDIIKSMDAYKN
DNIIYLDSPTWYVNDGGLTSLNKMIDDASKAVN

>CORE_REP|Org44_Gene1774#

MSKLKKFVILLAFLVVIFPISVYGYFYYKLSAIHDSSISSDLLDNNDHKNEDGIINILLMGTDARPNEDSSRSDAMMILTIDNKHNDIKLTSLARDSY
VDIPGHGKQKLTHAYAYGQADLLIQTIEENFNIDIQNYACVNFESFMYIIDAIGGVEVTIEKGEIRELNKFIPETYKWNKSDDKGSIQYIRNAGKQ
TLNGYQALSFARIRHNDTAFARDGRQRQIIQAIIKKTETLPVTKYPGLLDAVLPYVKTNMKPNAILSLGAQVLKMGDLNIKQFEFPIDDEIHSTG
GIYGKAGWVLRFDPDTLDILHDFIFNDIEFKQ

>CORE_REP|Org83_Gene2755#

MKKGYVYIILTTLFFSSMEISLKTVTNDFNPLQITLSRFFVGGLVLLPFAVKRLRALNLSITKSDLKYFAFLGFMCVVVSMSLYQLAVLNTKASVVA
VLFSCNPVFVMLLAYLILKEKIYRHNVISLILEVLGIIVIINPLHTKLTLSGIFLTLSSAIIFSMYTVFGKRKTLKFGGIVVTCFSFIFGSLEMLILVLLTKIN
FIADILSKNKLNVFANIPIFSGYTLHNMPIMIYVFVFVTGVGYALYFMAMEATSTSLTSLVFFFKPVISPILALLILKEIIPINMIIGILLIVIGSIISIIPTIIT
QMHNKHVEALYKE

>CORE_REP|Org63_Gene2683#

MLKLILNRVKVLIPMLILISILSFGLLELAPGDPADAYINPLMSAQDIENIRVNMGLDKPVYIRYLNWLKNTLNGNLGISYINHMPVTEQIMEKM
GNTFILMGTSLIFSILVAIPLGIFLAVNKNSITSKVSSIFNYIGVSIPSFWIGMILISIFSVKLNIFPSGGMHTIGNDSIEDLVKHLVLPVITLGLYNTAIF
TNYVEAGVNEQLKKQYVVTARAKGLSEKVILFKHVLKNSLTSLVTILGMSIQKLVTGAFVTEVVFSWPGMGRLMIDSIFSRDYTVIMAITMLSAL
FLILGNLVADILYLLIDPKIKSSKGGF

>CORE_REP|Org47_Gene1557#

MGESKKSENLLLSIIYIIFFVYILMIIRIILFRDVPIYAISKGTFRTVNLIPFYTIYQFIVDSNIDFMKATINIIENIGIFIPMGIFLPIVCKNLNKKTIIITIILVS
LAFELTQYIFALGSSDIDDVILNSLGGIIGITIYINMNKLFPNDIKRFKVIIATSLILGVIGLGVISKNYHNLLTFKFRPDKKISKILIEENREIIKDINKDTV
DIVGTFESFKKGIITIKAGSNNKVKRPENLIDSDGNIRIYLNENTKLVSYIITKESKMDIVKYEEFDVKNLDLLRRYDTINVWIDKENQPKDKHGIM
ASKLLIGLYE

>CORE_REP|Org41_Gene1352#

MKLSLNQKIYFVSILLFISIALFVIYGIDINHLEYALSQRIPKIFAMILGGGCIAFTTVVFQTITNNQILTPSVLGLDSLYVMIQTIIVFIFGSSSSLIINEN
YNFIINVAIMIGASLLLYKMLFEKNKNNIFFLILVGMIFGTLFKSATTFIQVMIDPNEFLALQTSIMASLNNINTNVLLIAFIIIIAIIPFIYDEIKYLDVLS
LGKEQAINLGVDFDKVVKKMIILIAILVSISTALIGPMTFLGLLLANIAREIFKTYKHTYLILGSMLIGMITLITGQFFIQHVFKFDTTLSVVINFIGGIY
FIQLLLKGANR

>CORE_REP|Org18_Gene2192#

MDAMRITKTTFNDVFSNDANGSIIKVEKYVDKKCASVFEILTYTIIVTNTSRYKTGNIFFKDYISKYIEFINNTVKVNGIIKRGLDPQKGFYIGRIDAS
CKKIISFKSVVLPNSAHRIIKNSANIYYYYKCNLDKFPTRISIESNRVYTNVNKIVFKQLNISNTLKAPKNLRDILKVNVNSKIFDVKPMKNLINKGSN
LKLCNLIVFGCIEVEIDYSCKNRSNFKTVNKSNDIKKDKYYKNDIQNNNENINDCKKQISFGDNKVKKITKTFGFSCFICSPVGIIYEDMKNINIKIE
HTSINELNPEELFVNTSLLLYY

>CORE_REP|Org79_Gene413#

MINVRTDLALEASEMCEKSQEGSSIPGVKIETKELENCIVTKVEVIDEQGSEIMNKDIGKYITLESNLMKFDDDESREEMISYLKDELVDIFGQDE
NKKTLVIGLGNRNITSDALGPKSVSKTLVTRHLFKNYNKDYDDDFTEVSALSPGVMGVTGIETSEIVKSLVEKVKPDRVVAIDALASRKMERVNS
TIQISTAGISPGGGVGNTRKSLTKETLGVDVIAIGVPTVVDAATLTIDVLDMAIDNLIAQSEETESFYEMLKKLKEEEKYHLIKDSLDPYDKNLIVTP
KDIDDTIENLSIIISEGLNRSLHPGRLV

>CORE_REP|Org35_Gene1762#

MSNVTAEQKKEVKGRGFLPSRDGEHFAARIITVNGVINASQAKKIAEAAEKFGNGQLAFTTRLTVELPGVKFEDIEALSEFIASENLITGGTGSRV
RPVVACKGTVCVHGLADTQALATEIHEEFYKNWYDVKLPHKFKIGVGGCPNNCIKPDLNDLGIVGQRVPDYDSELCVGCKKCAVVEVCPVKA
AKLTDKGKLEIDSNLCNNCGKCIESCNFDSIEEKESGYKVYIGGKWGKSVRPGTQIDRLFSKEELMTLIEKAILLFREQGNTGERFGITIDRIGADKF
IEMLLSDEVLERKEEILEALLHLTGGAVC

>CORE_REP|Org40_Gene2370#

MNNWIEVTIKTTTEAVEPITNILYEQGAGGAVIEDPKDFLFQKKNELDWDYVEEEVFKKNEEDDVLIKTYVSEEKNVMEFVEIIKQKVLGLKDFG
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GSGILAIAAAKLGAKEVVAVDLDEVAVKVAKENVLENKVEKSVSVMHGNLTDVIKDKADVIVANIIADIIKILAKDVQNFMKEDAIFISSGIILDKV
EEVKESLIENGFEIVEVQKLGEWSAIVSKLKK

>CORE_REP|Org81_Gene2911#

MNRRKTIYRGFNNNRHKIDLRKYVITIACLCLIGYYSYTKIKDSKILEYVSAKIPFLNNSSDITYKDISDELNSIKKGKKSKSQTNSDDKQETNPEKAV
NNTKEPEEVKLATIEGWDMYTIQVAAIDNNDDLKKIQTSLVNNDIPFSVMEKDGVKKIQTYSSFDENDVRKQISSVRKVFPDAFLSHLDAPMLS
LEYTSNYAYIESISKELNKLITNFKEESSFWSNAENNVDMEKYNTILTNRKAISQNISKEAEKIDYSEMRLFKDNLMEYVKNVNEKIDTASKAANE
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>CORE_REP|Org26_Gene1310#

MGEKSKGYVFIAIAGLLWATLGLFGKFLMGNGLTSEQVAFTRLFFGFIVLGVYSSIRTPQILKINKKGIMYSVIIGIICQAMFNLCYFKAIDIAGVSI
AAVLLYTSPLFLAIFSKLCYKENITRSKLFSLILCFIGAIMAVTGGRLDFQGLNAFGLLLGVLSAIAYALMPTISKNALKEFSSSTILVYSFLFGAIFMIP
SSRPWEILNYAKDLDVLSCMLMLGIVPAALAYIFYAAGISKGVELSVAGVVASVELVGSVIIGCTILGESFSLGKLFGVMLMLISAVVALNLSYDEI
RIFYKSNKLKQIEKTESI

>CORE_REP|Org26_Gene1388#

MSRAERLIELMITINAKRSFTAGELAEEFSVSKRTILRDLQVLESIGFPLYSKVGAAGGYHVLKERILPPIAFSESEVKSIFFAYQSLEYYNDLPFEQET
ISVLKKFLNCIPNDIQYNIENIRRKFVFWTPDRHCSTPLLKELFNIVMNEFTIKIEYSSKQKNSVRTIVPIGLYAMNGLWYCPAYCIKSESIKEFRVD
RIVKILSIENLSSKKYKVLSSIHDYLKNMEVGTDYHIKINLTDEGVKRCETEFLLARGLKILSKGGYIDMYIPKSTLNWVAEYFLTFGKNATIIEPIELK
HLIKSKVLELYNHHCI

>CORE_REP|Org93_Gene1876#

MEPLFLKPIFMDRIWGGTALKDKFNYEIDSPTTGECWAISSHKNGDCLIENGKYKGKKLSELWNKNRELFGNTPGDKFPLLTKILDANDNLSVQ
VHPNDEYAKKNENGELGKTECWYVIDCSDDAEIIIGHNAKSHKEFVNMVNNNEWDKLLRKVNIKKGDFFYVPSGTIHAICKGTLILETQQNSD
TTYRVYDYDRTDNSGNKRELHVQKSIDVTNVPHINFDTDYKIVSTSDFKCTTFVSNEFFSVYKLDVFGKCNFTHNTPFSLYSVLDGNGKLIHNSV
EYNLKKGMHFILPNDFGDFSFEGNLEIICSHI

>CORE_REP|Org72_Gene2043#

MIENNSEKIKVLENDIKQLITISKANNIDLSDKINSLNEKLEKLKEDAFSHLSAYEKVTLSRDIKRPTTLEYIEHICSNFLELHGDRLFKDDPSIVGGIG
QIGKFNVTIVGHQKGRDTKENIKRNFGMPHPEGYRKALRLMKQAEKFNRPIITFIDTSGAFCGLEAEERGQGEAIARNLLEMSKLSVPVITFVIG
EGGSGGALGIGVGNDVCMLEHSVYSVISPEGLSSILFKDSSKAKEACDVMKLTSNDLYDLKIIDKIIKEPLGGAQKDVDAVSKEIKAYILERLNHYK
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>CORE_REP|Org5_Gene1420#

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VVQTFAGQLKMEAELSGYMGTMYLAVFSTTIGFLFQTICQKRVDGTRTAIILSTEAVFGTIFSIIILKELITAKLIIGSILIFVAIITAETKLSFLKSKKVK
LKDSEESSLESI

>CORE_REP|Org4_Gene2815#

MKKIKSLAIFISIITTLVLVTACSDKNTEDKDKSETRVVQSVKGEVKIPSNPKKIVDISGSSEELLLAGYKPVATANVDSYETDKLPSYIREELKGVKIV
GHSMMDTMDMEAILEVNPDLIIMSQRQEKIYDQLKEIAPVVMMKDYANDWRSKLTDVSKLFDKEEEAKSWLQKYDEKATKLGKEVIEKNGE
KTYLPVLASSGQFMVFSDGGIGTLINDDMKLARPKNMPKQDGITLPMVSMEGLTDIDADHIVVIATEADKKDLENSAIWSQIRAVKDGNVTIL
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>CORE_REP|Org33_Gene2808#

MFRKVLHYLTLLSISIFFIVGCSNSQNNQNENQNKETQLQEDKEKIDSGKDTSNVIVSDGTDKPSKATTNNDNNKLDVSSLDNTTLDWFYIPNN
KHKTPEVNTDIEFKFSDYDALYNGPTKDGQKTLYLTFDEGYENGYTTKILDTLKQNQVKAVFFVTAPYIKENKDLVKRMVSEGHIVGNHSKTHP
SMPTKTSNLKNFNDELYDVEKLYKDVTGKDMVKFFRPPMGKYSEKSLAMTKNLGYKTVFWSFAYRDWDTDKQPSHEEATQKIMDNLHDGS
ILLLHAVSKTSTEILNDFISNARKLGYEFELLEY

>CORE_REP|Org77_Gene552#

MIRYYKTIDSKLEKLSFFEDGCWINLVEPNHSEINEISNLLNIDVESIESALDEEERSRIDVEDNHTLILIDIPVDESDSNSSHYTTIPLGIILTEEAIVTV
CDAQTKILNDFIVGHIKDFFTFKKTRFLLQILHKNAAYYLHYLRKINKMTIIIEREIYKSMKNKELVQLLELEKSLVYFSTSLKSNELVLNKMVRTAGI
KKYPDDEDLLEDVIVENRQALDMAKIYGDILSRIMDAFSAIISNNQNNVMQILTVVTLIFSIPTIISGFFGMNVINMPFSDDPNGFWIILLISAIICI
VITFFMSRNKLL

>CORE_REP|Org70_Gene2380#

MYYIGVDIGGTGIQAGVVDNYGKIIFRSECKTVIEKGFEGILNDIKIMIYKLLEDNKLTMSDIKSIGFGVPGFINKEGLVTCVNLKWNKKAFNKELK
RRFPDVEIHGENDATVAALGEAKFGSMKGANVGVLYTLGTGVGGGIVINQKVFSGAHGLGSEIGHQIIGENYFNCNCGNNGCVETFCSATAII
KYSQKLIEEGEKSRILDLAEGNLENVNAKMVFDAYRENDLVAIKVINRFKEYLAKTFANTINSLDPEIISIGGGISKSSDIILDGIEDLVRKFVLYKTED
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>CORE_REP|Org77_Gene3357#

MNKFKYAFDNKRYHTWNYYLRNTFGEKVFKVSINAGFTCPNIDGSIGYGGCTYCSKEGSGDFAGNPKDNLISQFYNIKEMMLKKWPHAKYIG
YFQAYTNTYAPLEVLKEKYETILELEDVVGLSISTRPDCLPDDVVEYLSELNKRTNLWVELGLQTIHDSTSKIINRGHDYKTFVEGVEKLKSKNIKVV
VHIINGLPGEDYNMMMETAKAVGKMDVDGIKIHLLHVIKDTPMEKMLQNGMLTLMEQDEYINLVCDQLEILPETMIIHRLTGDGKRDELVG
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>CORE_REP|Org5_Gene2557#

MDRVFFVAVIIGITSRIIMLNLDQKQYPTQPNVLLSQLILAFVASSLGALLVPALINRSYTSITFLSLAAEQFRQVRANRRNTLQNLEEVQLVKRGA
AFIEEIARTYEVRNYMCIVTSFLTIGLYYVILAETKISEGMSLVISSICGLVLAFILKKLLTRKSIGDIADVMPAEISFVDESILKVGDLKGITNIGLKSDR
EVYINRGVGIQIIPKNKDYANAGILFDSGQRQAIVYNIYSRLGLYGDYGEPSFVPLPRRNKEDESIMIAYLPVDKNMEKVMEAVKSCPILSSSKGK
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>CORE_REP|Org51_Gene2634#

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NEELVPKGDAYVEEIASTYESRSYISLFSALVSSIVYIVFARKYDLSFFYCTILAIVSGAIVGLIFRRFLRRNSIADIADIVPAKISFEGPILMVNGVIITNI
GLESTREKYRNECLAIEVIPRDLGAFGIVNDIGQRQAIIHNLFIHMGIDRDVDEVDIVAISKTNLEKSTVVIPYMPILKDIDVMIDVVKSTPIIETSKG
KQSDFSRKTL

>CORE_REP|Org77_Gene54#

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PSLILAFAAVVVAMSLSNFANSSQFAIGVGSIIALISALIITKAKPATSVQDGSRLLQQMGPASMLPQLLVALGALFTQAGVGEVISTMISGVVPA
DSRLFGVIAYVLGMVIFTMIMGNAFAAFSVITAGIGIPFVLSQGGNPAIIGALALTAGYCGTLLTPMAANFNIVPAALLECKNDYIVIKYQAPVAL
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>CORE_REP|Org5_Gene2612#

MDIQLNILLFFQNLRNPILNFIFLVFTISTEAPLLILITTIIYWCINKKCGQKILFAIIGNFVVNLGIKEFVKAPRPIGIKGLESLRVSTAGGYSFPSAHTQ
TATTFWVSIMTIFKKRYLHLIGAVMVLGVGLSRLYLAVHWPIDVIVGWMLGIFFTVIFIKIFDYIDDNKNYILLVVLLIPFIIVAIFLNSPEYFEKFGII

VGFVFGYMVEDRFVKFNTDNNNKKINFSNKNKGSKNIIFSRICRFLVGIVTIGMLYIGIKLFISMLIVTLNISDSTMSIIFMNFIKNTVVVFYGIAGAPALFKLLKLN

>CORE_REP|Org22_Gene1177#

MNKICKILNIKYPVIQGGMAWVATASLASAVSNAGGLGIIAAGNAPKEAIKKEIVECKKLTDKPFGVNVMLMSPFVDDIIDLIIEEKVQVITTGAGNPAKYMDRLKEAGTKVIPVVPTIALAQRMEKLGATAVIAEGTEGGGHIGELTTMVLVPQVADAVNIPVIAAGGIVDGRGIAASFALGASAVQVGTRFICSEECSVHSNYKNLVLKAKDRDAIVTGRSTGHPVRTLKNKLSKEFLKMEQNGATPEELDKKGTGALRFATVDGDIEKGSFMAGQSAAMVKEITPCKEIIEAMVNQAREIMPAIEL

>CORE_REP|Org66_Gene1170#

MVIIKSIKEIANIKESVITIGNFDGVHKGHQVLIGKTVEHAKKENIQSIVFTFANHPVNYFRPNSTKNIISNDDKIKLLEDLGIDIVVIIPFDEYMTKIPAKDFVDEILVKKLKAKKIVIGHDFTFARAKEGNVNLLKSLEHEFGFEVEVIKPIKINDVRVSSTYIRSLVSQGDMANVKEYLGRNYKLEGCVIHSKHLGRTIGFPTANIDLKNNMLVPKRGIYASIVHIGDETYFGATNVGYNPTVNGKTLSIETNILEFDRDIYGENIIVEFLERIRDERKFNSIDDLKNQLYNDTNYVYENYVCKNK

>CORE_REP|Org67_Gene2232#

MNFSNIFIQVAVLFIIILVGYFVRKFNLLDDHCTSKLSTLTMTVFLPSMIISSMQINFDSKMIQKILLLLFTSLIMYIVSIIIAFLLKYILKCNDKKDLGIYQYIVVFSNVAFMGYPVIEAVLGHEAIFYTAIFNLPFNLFSFTLGIYLLSKGSTSRGFSIKSLISPATIAIVIGLFLFVTGLRLPQFINEPLEMLGSITTPISMIIIGSLLANSSALDCFVNKKLYIVTFIRLLVLPVIVYFILKGWINDKMILAIPVVISSMPAAANTAIMANQYDSNITLASQCVFFTTLFSVISIPFISILLLS

>CORE_REP|Org66_Gene2830#

MSKENKNVRIAVVQASPVIMDLEKTVEKALGLIKEAGRKGANIVVFPEAFIPAYPRGLSFGFVVGSRTMEGREDWKRYYDNSVPVPSATTDLLGKAAQEAGVYLSMGITERDGNDINCTLYCTNLFFSPEGKLIGKHRKLKPTGTERCIWGEGDGSTLTVVDTPYGKMGSLICWENYMPLARTALYAKGVKLYIAPTADSREEWQATMKHIALEGRCFVIGCNQYVEKNMYPTDLNYYKELDAEPEIMCPGGSCIVDPFGKYVAGPIFNKEEMLIADLDLEKIVLSRLDFDSEGHYSRPDVFELIVHE

>CORE_REP|Org22_Gene1536#

MGSGKVGTSLANYFLSKGYCVSGFYGKNQLSLLESINLTKTKIYSNLRDIIYENDILFITTSDDSIEIIDKKLSKFNLKHKYICHTSGSLKSSILFCSKKAGALIYSIHPIFAFSNKNTDIKKMKDICFSIEGDNEQDDLVIQNFIDGLGNQFFIRDKDTSSTYHLANVLVSNLVLSLLDIGVSYFIKLGLSEEESLKAISPLVKKNIENILDNGFTKALTGPVSRGDITPIRKHLSVLNKKDEDIYKILSLNLLKIIALRNDNSLKGTKNITIENAIENLISKSEKYKEIYKLLGGKNDEKYHTDF

>CORE_REP|Org60_Gene2286#

MYKSENFSKKSVLINSFLSKFLKIIGWGLVSLFTLSALVLSTISIIIGWAVILPIQVCAVFLLIGGVCIFKGKRLADQISRYKKYCTIINNRNIIPVELIAENTSKSLNFIIKDVQKMIDKNYFINTYIDKRNNQIVLTNEDFIPPRYEDVAYEVKEEEKTDESNEVDTIINKGMNYLTQIKEANKNIKSESMGDKIVQVEDVTSKIFDVVKHDPSKLTQIQKFMDYYLPTTLKLLNSYHTLEEQGIDRENITTTMESIENTMNTIVVAFENQLDYLFEDEAIDISTDITVLENMLVQEGLTSGKF

>CORE_REP|Org60_Gene2521#

MENLVREFEENSRRKKTKLNIKPYMYILPLGIILVAFYVIPIIMSIYFSFTKYNIISPATFIGLENYKKLFTDETLKVSIINTIKFTVVVVPCQTILSLILAVWITGKGNSKIASFAKGAIFIPVLSSMVLIGMVWRALLNGEGSIIYQVLGAFGIESSKLLGDSKTALPTLMFISMWKNIGYFMVIYISAIMNLPKHCYEVAKVDGATKLQEFIKITVPLLKPTTIMVVFLGSIWSLQVFDLVYTVTGGGPGISTMSIVMHAFNLNFKNFNSGYAMTVANVLFLLIAVVSILQNKLVKRDNSDF

>CORE_REP|Org17_Gene3504#

MIYTVTLNPSIDYIVKLNELKTGSTNRVNEEYVYPGGKGINVSRILKELGNDNISLGFISGFTGEYIIRTLEEKNLKTDFIKIKNGFSRINVKIKESEETEINGQGPNIDDEDIDILYKKLDKLNQDDILILAGSIPSTLDEKLYENIMARLEKKNIKVVVDATKNLLLNVLKYKPFLIKPNNDELEELFGVKLNSIEDMVKYARRLKEMGAINVLVSMGKDGALLITEEDEVLISDVPKGKVKNSVGAGDSMVAGFISGYLNTGKYDYALKLGAASGSATAFSYDLAKREYIDKLVNEISVKQF

>CORE_REP|Org65_Gene1379#

MIDNQKYVILSLELHLFFSRIMKEHALFLEAGFTNKNYNLAMEADHYKKQFEDLLSYTVSASNGIIRPDILYSEELVTTLTSVAEQKTEEFTGIEINKNITTRELNLQSGVNPQVGQDLVNYVAQLNSDAIRLLDGLINFKERVLDGVLSCTIFTSNYPLLLEHIIHEANLYRSYVVDLENKIDIESKNAKEIELFWDHIMMEHALFMRGLLDPSEGELINTSNDFAIKFNELIEKTNEMTDSNIKNITEETLNETVEFKDFKEAGASGIEQCKIKSIILPLLADHVLREANHYIRILESYKNM

>CORE_REP|Org72_Gene2503#

MDKDLTYQIKELKKEKNAIILAHFYQPPEIQELADAVGDSYYLSEIARDCKEEVVVFCGVRFMGESAKILSPEKTVLMPVSNAGCAMADMVDEE
GVIKLKQQYPNALVVCYINSTAKVKSHCDVSVTSSSAIKILENIDNKEIIFLPDKNLGGYIAEQFPDKNFIFWDGYCKYHNNIRAEEIIELKDKYKNA
EVLVHPECKKEIRDLGDYVGSTSGIIKYATNSKNKDFIIATEEGILHELKKNNPNKNFYIPGGKILCTDMKKTTLENLYSTLKNMENEVIVEDEIME
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>CORE_REP|Org49_Gene1157#

MYSTKILDDYEYETFNVFSTKLNPNTKHDYLSKVILFKEFLKGKELIYATKEDCKNFVDYIQTKYAKSTCEKIYSYLHSFYNFLKKEGYIDINPFRYVE
KPTVTRIKTKDDVLSIQEINKLIGILPKLNIRDRVIIVCLVTTGCLLNELVSLKWKDLMVDENDNSYVRLGKGRKERVVKLHPYFFKLLEDYRNYSGL
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NLDINKKY

>CORE_REP|Org85_Gene1827#

MFILAFIICTVVIFIVSTKINQKRYDELSLMLNQILEGKEVTYPDTKDTRASKISHQVKKIKDMIEIEVEQSKLEKEAIKGLISNMSHQLKTPLSNITIY
CELLENINISTLQKKEFLQKMKNETFKIDWLLQSLFKMTKLEDGVIEFEVEELLIKDTLIQSISTIFNKAEAKNIRVNLEPFSDIKLVHNKKWIIEAIVN
VLENAIKYSPSDSTITISVIKMELYTKITIKDEGIGIDSRELNDIFKRFYRSKNVANQNGTGIGLYLTRLILEKENGNIIVESKLGSGCCFSIFLQNCKSL
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>CORE_REP|Org60_Gene2752#

MYKYKFTVFTPTYNRAHLLENLYNDLKAQTYDFNDFEWLIVDDGSSDSTKELVEKFISENKLNIRYIYKENGGKHTAINLGVKNADGELFFIVDS
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LGYYKYIGQRKLVSK

>CORE_REP|Org79_Gene52#

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IEILYSHGVEKIEGEKTVSKIEVKNLKTEEKRTIDVSGIFIAIGLKPNNKMFENVLDLDEGGYIISDESCTTSVEGVYVAGDSRTKFLRQIITAASDGAI
AAVQAANYINVE

>CORE_REP|Org24_Gene2555#

MKGDNKVTEKQRLIITIAQKIFDQKGFQNTSISDVVKECKMSKATFYKHFETKESFICEIINYYDEKFLEIIHSINENNDIPSSEKLNRKIIAVWKNIF
SRTTINTYIRENFSEEQRKATSKLQTKSRANLLNEYKLSLFDNYGDKIEKIIFDLVFLLDALIHQFIYIIHVQKREINVYFIAKFTIQILDLVVENMDNL
NPLIEKSMFLHKQEDEVYFSLHNKSLFFKTIQDIEELIKTDTSLLENPKLLEAIKKLYVEGKNQQYDSLIMDAMIAYLEKEDTLRPKVLLLNSIKNQL
KKETL

>CORE_REP|Org46_Gene1445#

MFFKDIELNSKKELDPYFDLVDYEACEYCFSTLYMWQHVYKTGYYIGEDFAVLVGEYEGDSFSILPLAKKDKLPEVVDFVLEYFSKNNKKIYLRGIT
TEVVEFLKEKYPDRFEYIEERDLFDYIYDAESLRTLAGKKNQKKRNHINYFLKEYAGRYESKLLDKENFDECLVLMKEWESNKEENNEFDESMDD
ELIGIKKIFNHYDILKDKVKVFGVYVDGKLEAFSIGELLNPNMALIHIEKANPDIRGLYPFINQQFLVSEFKDVEFVNREEDLGIEGLRKAKLSYHPC
RFVEKYSVREA

>CORE_REP|Org33_Gene1037#

MDFKQLEVFVAVAKHQSFSKAARELFLTQPTVSAHIQNLERELETVLINRSNKVITLTKSGEILYEHAIYILNNCKRAIYDIKEYSGKIEGIIDIACSSI
PETYILPDFMKSFSMSYPDVKFSISHYDSQYAISEILNERISFGLVGSKINNPQIEYLDLLDDELVLITPSDFKIDNKNNCIDIGELAYLNFIMRKEGS
GTRNLILNTLSKNNFPVSKLNVIAHVESNEAIKEMVRLGLGVSFISYISAIDYLNAGKIKCYKIKDVDFTRKFFFIYSKKKTFSPLEDKFLNRLCEYFEII
I

>CORE_REP|Org63_Gene2774#

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VLVSIHLNAEKNGNTATGIETWYRNKATDGSKELAQAVQSTIVSYVKVRDRGIVENNFEVLRESNMPAILIECGFLTTPSEEQKIINEKYQDQLA
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>CORE_REP|Org55_Gene1707#

MYNKIKYIPINCEIACNKLKRSMPYKWDLNIYRGCEHGCKYCYAIYSHKYINSNNYFEEIYVKTNIVEKLERQLKSSKWKKEVINIGGVTDSYQPIE
ADYKIMPEILNLLIKYKTPAIISTKSDLILRDYDLIDKLSRITYINVASTITTVNEDTQRLIEPNGVDSMRRFKMLKEFRKTNASVGLHIMPIIPYITDD
FDNINSLFRHAKECNVHYVLPGTLYLRGITRGVFFDFVKKEFPELLDKLSILYSAGSLNREYKNQLYKMVNELRYKYSLSSSYSKIMKEKLKNSGDV
QISFFD

>CORE_REP|Org86_Gene2683#

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GIPPLILGIVFSDVVAQLVANNPDIEFDIVEKGAYDLNRMLILQELDYAVLLHPHKIDKSVVTEHVLQEDELTAFLNINHPLAKKDKIDWNDLNEQ
LLAIFNPTFMIHHKLMQKFTDENVKLKRYIMSGSWDFLLLSTTNSDFITILPSPVHDFFENSKIIEKPFNHPITWKVILCRPKKERYSHVDQHVFKF
IIDFFSKKNS

>CORE_REP|Org53_Gene987#

MSKKGRVVKVQHFSVNDGDGIRTTIFLEGCKLKCKWCSNPDSWSNIVKLGVMKDKCVSCNRCIDVCPQNISSLFDRAQINNKCDLCGECIKVC
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KEYTGVSNKIILDNICRLSKLNKSMVIRVPIIYGVNDSEENIRNTALFVKQNVPGGKMELLPYHKFGIDKYKALGLEDYIYEFDEICNNHMLKLKEI
VELTGVKIIEYK

>CORE_REP|Org89_Gene2365#

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NITKKMLRDSNLPTAPWVLVKSVDEIDYDEIDNIGYPVFIKPNSGGSSVATFFIHSKDEVGEAVRKGLEVDEFVMIEKYIPGGEYTSFILNGEVFP
TISIKSDSGFFDYEAKYSVEKGAKEEVVYLDEELQKRVNEISETCWKIFNCKAYVRVDMIISEGIPYVLELNTLPGMTQTSLIPRSAAARGIKYSELL
DKLIEYSLN

>CORE_REP|Org67_Gene1499#

MKLLSKVNNNIRLITQVAFTALTNGYVNGFLEGTIYGGESKKLCVPGLNCYSCPGALGACPIGSLQAVLSSREYKFSFYVVGFLMAFGAFFGRFV
CGWLCPFGLVQDLLHKVPFPVKIKKVYGDKYLKYLKYIVLIMFVIILPVAIVNVAGGGNPWFCKWICPSGTLLGGIPLILGNENLRESIGFLFSWKL
SILLLILLMSIITYRPFCKYICPLGAIYGFFNSISIYRFKIDKDKCTNCTACQTKCKLDIPIYKDVNSPDCIRCGECIKVCPQNAITTTFSKDKKENNICAK
KYRGI

>CORE_REP|Org18_Gene1118#

MVMALRFDKNKNEKKRINVKVIATGVVAITLIGIVGISIGKFSSGSPVNLGVASDAITSVGKGINDGFSFIKNGFKDVANFKDNSKKVKKLEEENE
KLKKNMIALNAKLDKTESLEELKKTLNFVQEEYKATSISASVVGKNDGNWYESFVIGAGKNSGVKKESIVMNGSGLVGIVYEVSNNYSKAISLLD
SKASVSFKLAKDANAKGTITQNTTLDNKDSYNSKGYLQGYMFDSSYNVIQGDIITTSGLGFFPDGIPIGEVEKVVDDKDKSLKYVVVKPYVDFKN
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>CORE_REP|Org78_Gene1683#

MKDKNTYFNRKGQENFIDIFLKDDIKKGANFKRHWHEHLQIYYFIDGIAYLECGLDNFKVVPGNIVIANSNELHYLESLSDNLKFYSIRIEPTFLFS
NQVDLLQTKYLAPLALNHIVFNNLIQNDSLILKCITTILDEYHNKEVGYELSIKANIYQLIVLLLRSHIDKIYSEDEFIKRKYSLEKFECIFDLIEEKYMD
KITLKELASRVNLSAHHFCRTFKQITGKTTIDFINGIRLDKAIYYLKETDLNMTEIAMRCGFDSINYFSRLFKKNYNISPTKYRNEHREVSNVILKED
MK

>CORE_REP|Org27_Gene2092#

MLEIIVPATSANIGPGFDCLGIALNIYNKFYVEEIESGLEIEGCEDAYKNENNLVYTSMKYFFDRVKPEKIPAGIKIKIQSEVPICRGLGSSASCIVAG
VIAANALSGANLDKNQLLNIASEIEGHPDNVAPAILGNMIVSVTDNENIHYDIIKIPEELKFCAMIPNFKLSTEKARGVLPKEIPYSDGVFNVSRVA
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AVLNII

>CORE_REP|Org62_Gene2216#

MKNKKFIVIILIISILIGVLVKEYSSREINKADINVSKYIKYADLASKNNVQVNWKYVASIVAVLNKNKLKNVKDSQIQEVSDLFVKNFSKNNKVNK
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IQSEM

>CORE_REP|Org9_Gene1590#

MSNKIVSKRQLTDSIYLMEIEAPRVAKSSQPGQFIIIKNDEKGERIPLTIADYDREKGTVTIVFQTVGASTKKLAMFEENDFVMDFVGPLGQASE
FIHEDIEELRNKKILFVAGGVGSAPVYPQVKWFKEHGLDVDVIIGARTKELIILEDDMKKVAKNVYVSTDDGTYGFNGRVTDLLKDLVDNQGKK

YDQAIVIGPMIMMKFMCQLTKELNIPTIVSLNTIMIDGTGMCGGCRVSVGNETKFACVDGPEFDGHLVDFDQAMRRQSMYKTQEGRAMLK
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>CORE_REP|Org47_Gene1206#

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LESAFLYGGYPSKALKNKFLLAKESEVDYIIPSNGKIVDTELEAISLPGHYFEMIGVKTPDNVLFVADSLTPENIITKYHFFFLLDIDSQFKTLEKLRM
LEADFFVPSHSVKTTDIKNLIDINKKKMEEIIDNIKKVCCEPVMIDKVIEKMCDLYNVKLDANQYVLVGSTIRSYITYLYENNMVEYIFDGGKMMI
KVLQ

>CORE_REP|Org73_Gene3005#

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SLGIVLVLSSILLSLLIHKNLCVIILLYLFNNIMYSLKLKNIILIDVFSIAIGFILRVCAGSIAINVSLSSWIILCTFFLSLYLGFGKRKKEIILLKEDASNHRKIL
KEYDEENLNQMMSISLSATIVCYSLYSANNIYNSNMIFTTVFVVYGVLRYNYIVNIGDEGNPTDVVLNDKSLKFCVLFWVIACIGILST

>CORE_REP|Org54_Gene1275#

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DANMLNKMSPFLVVIFCAIALKEKINVKQIGAIIIAFIGALFIIKPTFSVEVIPYLGGIAGAVFAAMAYTCLRVLGDREDYYTIVFFFSVFSLVTVGPIA
FAVYEPMTLMQLIYLLLGGVFASLGQFGITLAYKYAPAKEISIFDYSNIIFSAILSIFLFNVYPDMLSVVGYLIVFSAAFYMFLYNKKLDKLDKEKKK

>CORE_REP|Org45_Gene3308#

MALILPKGLPVINKLLDEGIDVIYKEDFKKKLTYEENIDTKIAILNLMPIKIDTELDLLRRIDKTGFNVSVEFIKISTRESKRSCNEYVKEFYKTFDEAKG
EYFDGFIITGAPVEQMEFEEVDYWNELEEIMDYSKSKTKSTLYICWAAQASLYKYYNVKKLPLSQKCFGVFKHKVDKNSKIVDGFENEFFAPHSR
HTTVNIEALKENKELSIVSHSKEAGPYIITNSRDVFVMGHSEYDKYTLDKEYKRDINRGDKISIPQNYYINDDPSEEPTVKWKKHSELLFRNWIKN
YLIQ

>CORE_REP|Org18_Gene1469#

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KAVEKYDYKKGYKFSTYATWWIKQSITRYIDDCENTIRIPIHLHQRINFVKKKKQELLNVLLREPTIDEIADACGLEVDKVLELLRRDKNVVSLDTP
LKEDEDSSLVEFIPSDADFKDVVIHEVEQHNLKEKIEELLTGLGEQEQQVLRMRFGIDDDDPKTLEQIGKVFGVTRERIRQIEAKAIRKLRHPSKLK
QLKHFY

>CORE_REP|Org6_Gene1877#

MNIKLELYKVFNAVVNNKSFSLAAKELFMSQPAVSQSIKQLEEQLDTLLFYRNNKGVKLTPEGKILSEHVTTALKLISSGEDRINKFKKLEYGSLKI
GVGDTAARFFLLKYLEIFHKKYPHIHVSTINRTSRELISLLKDGNIDIAIINMPIEDDTLNIVECIEIHDIFVCANDYIEYKGRKISLEELNTLPLIMLENK
ANSRLYVNEYFLSKGIKLNPDIELGSHELLLEFAYINLGVSCVIEEFSIDYLENEKLFKLDIKEPIPKRNIGYCHLKDISLSLATKEFLSMISNNI

>CORE_REP|Org18_Gene1671#

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SGNDMYEATTVILATGVEYTRPIKGEEEFLGRGVGYCATCDAPLYRNKKVAVIGYNEESKEEANFLSELTSKTYFIPMYKKDNLMRSSDNLDDSI
EVIHDRPVQIDGDKLVNKVSFKENHIEVDGVFVIKDSTAPSALVPGIEIDGIHIKVDNNMKTSIDGCFAAGDCVGKPYSYIKAAGQGQIAALNAV
YYLDKLKRA

>CORE_REP|Org68_Gene1591#

MDTTKIDDISKLDLNNLDINKMDMGGIMESLLEWATTSGVKLIIGILILSIGFKIIKKFVNHVMLLLSKRDIDLTLRKFLKSLLLSVLKVAVIIIVLEYW
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VDLTFSVGYEDDILHVRRVLKDIVNNHKLIINEPEPFIGVVEHGDNAIKFATRVWCKTEDYWTIYLDLLEEVKVKFDEEGITIPYPKMDLTVKELN
KI

>CORE_REP|Org20_Gene994#

MLEGKIIKGISGFYYVDTYNGIYECKARGIFRKQKITPLVGDRVKISIVDENEKKGILEEIDSRDTELIRPPIANVDKALIVFAIKNPKPNLSLLDRFIVL
AEKENLETVIILTKADLDDNDTLETVKNIYELSGYKVIPVSNITKLNIDKVKEELKENVVVFAGPSGVGKSSLLNEIDENFKLQTGVVSDKIKRGKHT
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>CORE_REP|Org31_Gene2477#

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KESKGIYDSVFDVDIGNRDLHQCADAIMLMRAEYLYQNKLYDEISFDFVDGFKAKYSKWAQGYRISVKDSGSSWYKATEYSTSYESFRKFMDIV
FAYSGTLSLEKELEPVKVEDMKIGDVFIVGGSPGHASIIMDMAENEKTGEKVFMIAQSYMPAQQTQLLINRKNPNLSPWYSLDFEGDLTIPQW
TFKRDQLKRF

>CORE_REP|Org72_Gene2726#

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KFDIIDDISVMNVAKFPDIVKIEEKEEDEDLLWSMLNQAVEDALIKLREMRSEEGKKLAEDIAMRCDLLKNHIEEIEKYSSSVVEDYREKLNLRISE
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>CORE_REP|Org66_Gene2694#

MNLYHLRYFVTLAHLEHYTKAAENLSITQPSLSHAISLLENELGVALFEKEGRNIVLTKYGKIFLKDVEKSLEILDSSVKSLKITGTGEGQIDLAFLRTL
GTDFIPDIVHKFLKSNPAKSIDFKFHTGVTTDIIQGLKERKYDIAFCSKLEKEKGIEFIPVAKQDLVLIVPYSHPLAAKDTIDLKETIPYPQIVFNQRSG
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>CORE_REP|Org18_Gene2252#

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TTDLGYDAISAVTPFYYKFDFEEIKHYYNTIINSVDNRLIIYSIPFLTGVDMSLDQFGELFENEKIIGVKFTAADFYLLERMRKTFPNKLIFAGFDEM
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YRKYF

>CORE_REP|Org57_Gene1891#

MITFDVNGAIIRFDDTKNNYNKIRKIFKLYALEISKNFERDCLNSFQNLKQISDRGLSLGEKYIEESFKKGIETIVSFGIITIDIDTFKSVYCEKYLDFKR
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NPYREDVYEFLVKEDGDFSKEIERLTEFLGYDIKEYKASLMDIYINELMESDENDVENAKEKIEKYARYIGCSDENLYVARVNAIYTFANA

>CORE_REP|Org40_Gene1092#

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SVVIAGGNDAKDSTKQFEKIEKFVVSKLKSENKYLVEVQNTGVKTSYVELYSKNKVATIDNIDEGIGSISLAILLQQGNIVGNFGRLDTATSLLPSIK

>CORE_REP|Org5_Gene2151#

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YGSPKSIEKKSDDELKELRKLGVKMIYLGLESGSNEVLEDIKKGFSSEQLIKVGRKVKKSGIKLSATVIAGLGGTKKTHQHAVDTGKMLGAISPDY
VGVLSLMVEPNTELYDLLKAGEFTILEDKAVLQEIKEMIKNIDANEKIVFRSNHASNYANLKGVLPDDKQRLIDEIDYYLSNQKLKEKNIEDYSF

>CORE_REP|Org67_Gene2731#

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>CORE_REP|Org77_Gene475#

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EMAHDYSDDFAILNKVLKSDIDNIRSTLEEIDERAFKEASNKLLRARKIYILGMRSSFVVAQYLGFYLDIILDNVHIIRMDMGDAFEQIVRINEEDV
IVAISFPRYSKKSYQIVNYAKEKGAHVISLTDSLFAPVASLADNTLLVKSNMASFVDSLVPALSISNALAISVGMKEKEDIKQHFDDLEQIWKRYSV
YE

>CORE_REP|Org10_Gene2425#

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LGTFLLSKILPRFNVIYPDIELKIFEVPTFVGAKMIEESTLDFCIGIIDSDIYDDIDSKTIYKTELYLVTNPKNELAKHPIISNYMLKNVPFVILSEGSYHY
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>CORE_REP|Org56_Gene2657#

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>CORE_REP|Org53_Gene1441#

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>CORE_REP|Org38_Gene1677#

MDYKTIILNRKSVREYKNTDIKEEYLSEIKKYSESCKKLVPEIDVDVRIMNRSEVFNNLDKVAGYKGNMIDSPSYIIILSDIKDNYIENSGYIGESIIFKVTELGIGSCWVTFEDGKKVKEKLGINSDKEVTGIIAIGYGENVSNAKVLNATKTGQNYSKSDMQVVTDKGSTRLGVEDVVYMNEWGNVASIEILEERALLDAFHYARLAPSTLNRQPWRFIVDGGTVVLAVRKDGHTNLYEEKIDIGIVMLYFATIISATMFDLKWNLGTPDKDYKVPEDYKIVGYCNI

>CORE_REP|Org61_Gene2808#

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>CORE_REP|Org14_Gene710#

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>CORE_REP|Org26_Gene2783#

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>CORE_REP|Org95_Gene1253#

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>CORE_REP|Org41_Gene1816#

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>CORE_REP|Org32_Gene1140#

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>CORE_REP|Org65_Gene2631#

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>CORE_REP|Org21_Gene594#

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>CORE_REP|Org5_Gene2634#

MLSSYVKRVSKIIKKKYIMFIDESGRADINHEDPFTLTGVIFEYKYAVSQGDYVCSLRKEMDAFKEYCFGTSNIGIHLTDISRKSRAFEKFDDSQIKL
FYDELPLFLSRLECTIISVTVDKARLKKYYAPSKEPYVVAFIHVLQNFYSFVNNETVESARIVIESRDDVSNLKVQKAFFDVFNNGTIYLDIDEELRD
KVKGFIIAKKEDADYREGLEIADILCNPLSRARRGLIEANPKCMQYGEKNKIFKSVRNKIYTPTSVNDIRNWGFKEVPIVEPVGPWLEKMR

>CORE_REP|Org18_Gene1829#

MMLLKKDRITFSEILILIVGCILMAISLNLFFNPHAIAAGGITGLGVVLNSLFGVELWIVNLLLNVPLFIFAYKILSKKDCFKTVLGIIFLTIALKLTANM
ATLDITNDMYLAIISGSILMGVGQGLIFRINGSTGGTDLMALLLNKYFPTFSIPVLMGIVDCVVVVLSGIVNRQVEIALYSTVALYILVKVSDLLIEG
FNYSKSFTIISDLSKDISKKIMEDLDRGATILKGEGAYTGENKNVLLVVVEKKEVVELKKLVKNVDPNAFIIITDIHEALGNGFKKIE

>CORE_REP|Org43_Gene2026#

MINIEKANTLIEALPYIEKHQGKTIVVKYGGSAMKKDGLKESVMEDLVLMSYVGINIVLVHGGGAEINKMLAKVDIESKFVNGLRYTDEETMEI
VKMVLAGKVNKDLVNKIHTKGGKAVGLCGIDNNMILCDPYKNYELGFVGEIKKVNVELIESCLKSGYISVIATIGVGDDGETYNINGDTAASAIA
KELNADKLILLTDVPGLLREPDEEKSLITEVILEDVDKLFKEGIITGGMIPKIQGCVDALNNGVNRVHILDGRVPHSIITELFTDSGIGTLIRKENE

>CORE_REP|Org82_Gene2233#

MSELSGKGCEIIVPFEERLPVRDIEKSIIKKYRKNLWSKFMKSIRDYKLVEEGDKIAVAISGGKDSILMAKMFQELKKHGQVNFDVEFIAMDPGY
HANIRQLLIDNCEYLNIPIHLFDSRIFEIADEIAKDYPCYMCARMRRGALYSKAEELGCNKLALGHHYDDVIETTMLNLLCAGNFKTMLPKLNST
NFEGIKIIRPLYYIREEHIIRFIQNSGIWPLNCACMVAAKKTGNKRYEIKDLIKSLESNFKNVEKSIFKAAENVNLDSVLGWQKDGEKHSFLENFE

>CORE_REP|Org18_Gene1941#

MKKQKSPILLEMLGLFFGCISMSIGINMFLKPHTIAPGGLSGLSLVLNKVTGLPVSAIMLIIGVPLVILAFRIMGTKNSLKTLFGTVVFSAIVQLTDP
LSKLRFTNDLLLSSIAGGILVGIGLGIMFKSDASTGGTDLIALILSKKFPGIKATKFMSCLDGMVVISSGIVNRSLETALYSGIALCVLIKIADMIMEG
FDHSKAFFIISDEPESLRQAITEELDRGLTILDGKGGYTRENKEVLLVVVSKKQELYLKRLVKRTDPTAFVIVTDVHEVLGEGFKNLEN

>CORE_REP|Org96_Gene2069#

MSKDVKVKRNKKYDTFSITMELERPLLYDEVENKDDKNNNRKFNIKNKIFKGIGILFVLILLGFFIWINKIYEPQKLAKEALVSNSKVEVTVNENISF
TPKGRKVSKGLILYPGAKVEIESYAPLARKIAESGYEVVIVKMPLNLAILGTNKAQKVMDSYNNIEHWVIGGHSLGGVAASNFARDNKLIEGVVF
LASYPMGDELKELGKKVISIWGSKDGVVNFKSLVESKQKLPDDTTYVEIEGGNHAQFGDYGKQKGDNDAIISQEKQLNITANSIIKFLKNIS

>CORE_REP|Org88_Gene1902#

MIKKFLSSKESKYVTISLDDNFKKNSVDDKFWTYCKGCDSHVFRKDIEENSFVCPKCSRHYGLRARKRINLLIDKGTFMEFNSDVEFQNPLNFPK
YKEKVDSYKEKTKESEAVVTGYGRINGIKTVICVMNPDFMMGSMGSIVGEKITYSIEYAAENNLPIIICSASGGARMQEGMVSLMQMAKTSQ
ALSKLEEKSLPYISVLTDPTTGGVTASFAMLGDIIISEPNTLIGFAGPRVIEQTINQKLPEGFQTSEFLLEKGFIDMIVDRRKMKEVLYQILAMHKK

>CORE_REP|Org50_Gene1316#

MKIKLVCDSLCDIPDEISEKDYIEIVPLTVIFNDREYIEGVDIKKEEFYKKVKEIKQIPKTSQATYMEFKEVFDKFVTEGYHIICMTGAANASGTFQS
AMIAKNDVNENEKEKIHIFDTRNLSLGSGQYVIKACELLEEGLGFEEIIDELENTRSSVRLLFAPYTLDFLKQSGRVPVATALIGNMLNIKPIFFFDN
GEAKLVNKVRGIKNIASKLVDIILEMNEGSLEGKIVTIGCGDNLHDCEILKDEVNKRIKARRVLFTRGGVSICSHTGPDILAISCSN

>CORE_REP|Org97_Gene860#

MNRINKKIDLLILALLVFIFLIVGIVILSIRTENKLNVFIMLAIIFFIIMLTYLSNSVVGLITSSIIIFMYTSYILYNNITHNMDVEFISYMWIIATPVSSIIM
GNLNKSINELQNTNKKLSEQYKELVTIDSETGLRNLKIFYNDVNMEISKSIRHNTDFSLMIVKLPYYGNLQTIFGENKTNKIVKYIGSNIIECTRNED
IIYSLQKDMIGILMPNTSLEGSKVVKDRIKKRIKELNLDLNNRGKYVNIDVKIAFLQYKSSFGDSINFKNIVEEELQYDV

>CORE_REP|Org92_Gene2560#

MNNQKNLNIPITISSYTLGTEVSFRDRVRIAKEAGFDGIGLRAENYIDAKNAGVTDEEMIAILNEYDMKVTEVEYITQWGREEDRTEAQREKEQ
NVYHMAHLFNVKHINCGLLEMIPEEQIITALGELCDRAGELIIGLEFMPYSGVPDLATAWRVVKGCNRENAMLILDTWHWARAKQTAEDLAP
VPADKIVSIQVCDVLETPYEKLRDESLHDRLAPGEGYGNTEEFVKIIKEHNISPRVIGAEVISDSLISKGLSTAAETVFNATKKVLDKAWSEVSPK

>CORE_REP|Org91_Gene2248#

MSILEQLESPTFKVTKSDKLLIAYIKENIDDVFYKPISQIAKESNIGEATITRFVKKMNFNGLQDFKVTLAQEISTINKKNIINKNIQNDEPALDTAKK
LLSSNVTTLENTVEIINSKDVHDCARLIINAKKVYFIGIGYSGIIAQDSNYKFMRIGLNCVSFDSSHTMIMMSSIMEEGDLIIAISHSGETEEIIKTVK
LARANNAKIISITENKNSELKDISDVHLSYVSGETVLETGSISSKLAQFFIIDLVYTQVVKELSNEAIERKIKTTNAIKLFKNE

>CORE_REP|Org59_Gene1409#

MLVKEIKLLRNIIKDWRKHGYSIGLVTTMGFLHEGHQSLIKKAVKENDKVVVSVFVNPTQFGPNEDFNSYPRDIDKDFKYCMDSGATVVFNPS
PEEMYLKGNCTTINVSGLTDFLCGAKRPVHFGGVCLVVSKFLNIVTPDKAYFGEKDAQQLAVIKRMVKDLNIDTEIIGCPIIRENDGLAKSSRNTY
LSEEERKSALILNKSLSLAKEKLVKGNLNPENIKELITAKINSEHLAKIDYVEIVDSETLQPVKQIEHSILVAIAVFIGKTRLIDNFTFKLNI

>CORE_REP|Org54_Gene1853#

MIYIIEILKISVINIFCFIGIFIVFGLIFSITENLNNKFIFSSFGKTGIIVTGAIGTFVHELSHLIMCLIFMHKINSVKFFRPIESKNDGILGYVSHSYKKDNL
YQSIGNFFIGIAPIIGGTIMIILIFKILLPDSYMKVTQNIDLKLYVSMINNLNINGFIHIILGDISNFIRIMLLTPSVYSLKYFIFMFLMYSISTHMSLSSA
DLKNSLNGLSFIVIVIFVISSITYLFGFDNLNISSLIVKYNIFISFFMAIGFIFSIVTLIISYILSLVSPFKNFS

>CORE_REP|Org34_Gene1266#

MFKEIFLRTFPGFLIIRDSNYRITFINDNLKNLIKSYMQDNPLGMTNVEIAKKLPDNIAKFFTDYHNIQLNWEKDYPYDKISNWILEFKKDTTSYW
NVLEYKVDVDEKSYIITMANDITKLYEENKKNLHYSITDPLTGAYNRKYLNDRFDMFIGDYIVLIDLDNFKMVNDYEGHNVGDKILCDFVSLLNK
ELINSTSIIRLGGDEFIVIFSSDVDKNYVYSQIEALRENFLKVFSKYKYLSFSYGVDTVKRNLKLTIVELDKKMYKNKEKKKKKFNKNNY

>CORE_REP|Org18_Gene1667#

MLNMNKIVKKSISLMIILTIFIFMLTACEKDEQPDSVDIQTEDKNEIKIDEGNAKVLNIGKSEIINIDEGDKVDTSTKVENNSTFNISNVELIYNEYD
ENKKIISSDSKALLDMTLMPGKVAYIECGHKTFVKGVEVYAYEYEAEGKIVYVNLKENTINIRNNNIKLENSSQYEVLSTSELKKVNESNEGITYQV
KVKNSSSKDLGNIILKTAEVNENGEYLTVNRVPSYKILKPSEETDIDILCSTKAKSVEIVGYTYDDIKEKANVDIDLKSHKVKIDK

>CORE_REP|Org42_Gene2157#

MINIGDFNKLTVKRKTEFGYFLDGQTNNTKDDILLHNRLIGKNEINIGDEVNAFIFKDSDDRTAATLIPPLAKVGDVARLKVVDNTDIGTFIDMG
LPKDILVPFKAKTYPLFRDEKYLFYIYLDKSKRIAATTDIDSYLLTDHTYNVGDIVTGVVYGFQTNNSAMICVDNKYAGVILHNEYFTELKTGDVLE
NLHVIKIYEDGKLGLSPRGNRKDELDTLENKILSYLEGSDGYMRFNDKSDPKDISILFNSSKKNFKRALGVLMKKGLIYQDEEGTYLK

>CORE_REP|Org4_Gene2335#

MLVKNLIIYAVSDSVGETAQQVAKACMSQFYVNETYEIKRFPYMINKGVLLETLENAKAENALIVYTLVDEELCSIVERYCEREGLSCIDLMTDIL
REISKRTGRKPKREAGIIRKLDESYFKRVEAIEFAVKYDDGKDPRGVLQADIILVGISRTSKTPLSMYLANKNIKVANVPLVPEIPIPKEVFEIDTKKII
GLTNSPEKLNEIRTQRLKALGLSSKANYANLERILQELDYSEEIMKRIGCPVINVSNKAIEETAGIILDIMKENGLKIYKEIEI

>CORE_REP|Org76_Gene125#

MDKIKLIVDSACDLPDDIIEKYNIEVVGLNVSFGEESYISGKEIDNETFYRKMSESKVLPKTSCPSPDKFLEAYHCQEESVLVINISSGLSGTYNSALL
AKDMFEKEGNNKKVEVIDSLSGSIGIGQLVLKAAILIKEGKEIEEIVSIINKYKDNPPFFGTLETLENAIKGGRINPIAGKIINTLNFKAIIQVADGVVT
PIDKARGEGNSLKKLITLVESKIKDKEEKVLFIGHANCPEKAQKVREVMEKDVKYKDVVICEIGSVMGTYTSKGAILITAI

>CORE_REP|Org81_Gene1297#

MIIQQIYNNNVVLVLDENIKKELILTGCGIGFQKKKGQEIDKSKIERTFVIQDESFLDKISKLASQVDEKFFEISTEIIAYAEENLNTKLYEYIYVALTD
HIAFAIKRYHENITIKNDLLHEIKRIHKKEYEIGKWAVDYINKEFDVKFPVDEAGFIAMHIVNSNYKGSSKESLLITKIVKDILNIIRYYYRVEFKEDDI
NYDRLLTHLKFFAKRLVKKEKINDTNNEIIDIIKVKYEKDYDCAYKIKTHVEKNYDYYVSQDELLYLTLHIKRVISVLNL

>CORE_REP|Org25_Gene1039#

MTTSSKKLETISPDSKITRKDFWKCFRRSLTLDSSWNYERMQNIAYAYMMAPIIRRLYKDDKEKKSKALKRHLEFMSVTPHISTLLVGISGAMEE
ENAKNKEFDANSINAVKSSLMGPVSGIGDSFFWGTLKLIAAGVGIALASQGNIMGPILFLLIINVPHFIIRYICLDKGFKYGTQFFKDVSGSSIVSK
VMEAASMLGLMVIGGMTASNVMLKLSVNVGSGEWAEPIQTYLDQIMPCMLPAMIFGIMYWLLGKKVKTTTILISVMIICIVLAAIGVV

>CORE_REP|Org11_Gene1255#

MGGFLVEKIKIVLADDNKDFCQVLKEYLSNEDDIDILGIAKDGIEALDLVKKTQPDLLILDVIMPHLDGLGVIEKLNTMDIPKMPKIIVLSAVGQD
KITQSAINLGADYYIVKPFDFVVFINRIRELVSNRVTQVEPKPRPVQETQMTRSDFVKNVGNIENVGNIETEITNIIHEIGVPAHIKGYLYLREAIK
MVIDNVELLGAVTKELYPSIAKKFNTTPSRVERAIRHAIEVAWSRGKVDTINQLFGYTVHNTKGKPTNSEFIAMIADKLRLEHSMVK

>CORE_REP|Org41_Gene407#

MNFKKLSNVKVSVMAVVLSVGILSGYSALNKQVTLVVRGEERTISTFSSNVGDLLESQNISYDANDIVTLDKNAKLSNGDKIEVIDVKEKTVVET
KDIPFEVTVVEDGSLLKGDSKVKEEGKSGKSELIYKETYHNGKKVEKEFVKKVVKAEPVNKVVSKGTKVEMQVASSRGESSRRMASSSSSSSSSSN
NGKNMRVVATAYTGHSITATGTKPKWGTIAVDPKVIPYGTKVYIPQFDMVFTAEDCGGAIKGNKIDIYMNDSKTVYNWGRKTIDIRILK

>CORE_REP|Org68_Gene892#

MRKIKSEQIVEQVKKLCIEASLYLGEDVLSCIKEKAKSEKSEVGKNILNILVENAEIAKEKNIPICQDTGMAVFFVEIGQEVLIEGDTLTDAINEGVR
QGYEEGYLRKSVVSPINRVNTKDNTPAVIHYDMVKGDKIKIEFAAKGFGSENMSKMKMLKPSDGLEGIKKFIIDTVSEAGPNPCPPMVIGVGIG
GTVDKCAQIAKKALFRELGEFNKDENIAKLESELLTAINKLGIGPQGLGGTTTALGLNIETFPTHIAGLPVVVNINCHASRHKKVVI

>CORE_REP|Org85_Gene1752#

MNIVIVGLGVIGGSFAKALKKAGYENVFGVDVDLETLKKAEKAKIIKKGCTTGKELFKKADLIILSIYPRLVVDFLNNNKNFFKKGTIITDTTGIKETL
INDVLQIIPDDIDFIFGHPMAGREKRGIDFASEQVFNGANYIITPTGRNNIRNLELVENLILKLGFKRVKKLTSQKHDEIIAFTSQLPHVMAVALIN
SDEEDRDTGKFIGDSYRDLTRIANMNEDLWSELFLGNRDNLLKVIENFESEVNLIKEAIFNNDKSKLIEYFKKSSIRREILEK

>CORE_REP|Org14_Gene3586#

MNIKIAKNAGFCFGVKRAMKMAWDEVEKSDSGIYALGPLIHNKQAVAKYEEKGLKTVNEIDTIPNHENMIIRSHGVPENIYKEAKNKKLKIVDT
TCPFVKKIHTVVSEYHNKGYEIIVIGDMKHPEVIGINGWCENSAIIIKTLEQMENMEFDNSKKYCLVAQTTINPELYISIVNKLSDKLEEIVFNDTIC
SATKTRQESAKELAKEVDCMIVIGGKHSSNTQKLVNVCEELVPTFAIETKDELDVNMLKKYKNLGITAGASTPNWIIEEVVTFLENL

>CORE_REP|Org76_Gene3622#

MLISLIMPTLNRYDDIYLLMDSLENQTYKNFELIVVDQNDNSKVKEIVDKYIDKLDIKYIKSSKKGLSYNRNVGIDNAVGQIIGFPDDDCVYENDT
LEKVINFFNKNEDYKIYSCKTMDSNKVDAFKKMYDGTCDITSSNVLDTITSITFFIDFEGKDYTRFDEKLGVGGEFGAGEEIDYVLNLLSLGFKGKY
FGNDIIYHPAKKHSKSKEKYQKDYNYGRGFGALCKKEIVYRKNYTFAKVMVSKLVRNIGGLILSSNRDYHSATIKGRINGFRQYKL

>CORE_REP|Org9_Gene1633#

MFGIDKKLIEYIIAKSNYSELSSKSAEVSFFLMLSIFPFLIFTISSIAYIPILHLNKYIALFRNMMPEGAFAVLSSIIVSAIDNRNLKFLAVSFVLTMWTF
SRAVKAIIKGMNRAYKVKETRSFFKILSISFLFTIMLLVLIFLSMIFLVYGEKIGYFIFNLVGLDEIFIKIWDILRYTVGIITIIVIFTLLYKYTPNKKLTIKES
APGAIFATFAWFLVSFLYSYYTNYYANYEVIYGSIAEIIVLMTWMYFSSWSIVIGYEVNSRLYFRKIRHEMLK

>CORE_REP|Org92_Gene1279#

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ENIIKRLSSIESVIQNTKIDEIEVVYIEKRKALELNADIKRDEDFDFLIQKLQKEYEDRFNILGNNNIGSAFSTEAINKGIFNEFKSVFCFLESNEKVYNI
VFDEGYYVTLNYTGSNSNNKMYMEKVFKFIEENNYKIIADPIEIYKIDIHETGIVEEFVTEIQVPITKYLYFNGLDGK

>CORE_REP|Org34_Gene878#

MKRKSFLAYPYVVWSAIFVIIPLILVVFFSFTKESGGGYAFTLENYKEVIDPIYIKVFGRSILLAGGATLICLVVGYPVAYIISKARVSRRGSLILLFILP
MWMNFLLRTYAWVAILGKNGLLNTFLGWFGIQPLAILYTNFAILLGMVYNFLPFMVLPIYTALSKMDNDLINAAHDLGANNMTVFRKIIFPLS
LPGVMSGITMVFMPAVTTFAISRLLGGGKIMLVGDLIEQQFTVVGDWNFGSAISIFMMIVILISMSIMSKFGDESDKEGGGLLF

>CORE_REP|Org68_Gene2500#

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PEQSTDSEAYQNLINSCTDKNLSIQHLYKNDVLNIDNNINIYVLSPSYIQEESNLNSIVFKLTFNDNSFLFMGDAEEENKKEILHSFKLNNINFIKIG
HHGSNSSSSLEFIKKISPDIAAISCGYKNQYGHPHREVINNLKQNHVSIYRTDRIGDIVFYSDGEIIFTKYNYEIDT

>CORE_REP|Org21_Gene484#

MRQEERTVCFDRELKIEAYRFKGIMQKFPNHFHEHYVIGFIEKGQRYLSCKNKEYTTSTGDLLLFNPFDSHTCEQIDDKVLDYRCINIKPEIMKKT
VFEITGKNYLPKFNQPVIFRSELVPLLQELHYIIMEEELDFKKEELFFFLIEQLIEEHTEPNLQSNLENTNIEIQAVCDYLENNYAEHIVLDELSTIAG
MNKYSLLRNFTKLKGITPYRYLENIRVNKAKKLLEKGVEPIDAAIQTGFVDQSHFTNFFKNFIGLTPKQYQNIFINDDSNNFK

>CORE_REP|Org72_Gene1673#

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NVKATFFMIDGNMKEYPQQVKNIIKNGNTAGFHSVSHDIHKLYVTSTSAKEEFDTNDQTFYKITGKHSKVIRIPYGSKPYTPQASYQALVDAGY
KIWDWDLDTEDWRSNSSQIVQNVKNHIKNRKGEDKDQLVVLMHEKKQSAEALDSVLKFLSDEGYEFAPVDQNQIPKNYWLRNLE

>CORE_REP|Org65_Gene3658#

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DAVKNAGRLVKEGGAHAVKLEGGANVIKQIESIVNAQIPVMGHLGLTPQSVNSFGGFKVQGITSEAAKQLIEDAKLIEKAGAFSIVLEGVPAKIS
EIITNSISIPTIGIGAGINCDGQILIYQDMLGIFEDFVPKFVKQYANVGDIMKDSIKNYILEVETGAFPQEKHSFSIKESELEKLYED

>CORE_REP|Org91_Gene909#

MSQVSKNYFTTGEFAKICGINKKTLFHYDDIGLFSPELKKENGYRYYSYHQLSIFGIISSLREVKMPLKEIKAYIDKRTPNLLIELLEKKTIDIKNEIEKL
NNIQALMESTISFTKNACNIDANTITLKEHEEEYLVKTPITYKEQFLGDEEENFLYECINFMDNYELSDYGTIGSIIKGEDIINKDFESYSYLFTKVNK
EYKKYPVSIKPKGLYVTAYHKGSYETIYKAYEKLLNFFNQNNLRIGDFVYEEYLLYDISVRDSNEYLTQISAEVKI

>CORE_REP|Org4_Gene937#

MNDKLKYFSYSQNSINTYKSCPLKFKYKYIDRINWKNDDVGSREYYETLKTGRDFHLICERYFSNIPLGIYFNEDDKNSKKFLKWMENIKKVVPIE
KGKTYLPEYEVRMTLNGDIIQAKYDLVVIGNNNIEIWDWKTESKKIDYKHVENRIQTIVYMFLAKEVIPKVLKMDINVKDINMRYYQPEFDDLPI
TILYDEEKHEANRNKIQNYISMIKNTNYEEHTYEDNLYNDIEKVYNKEERMCYRNKKHCKYCEFNKLCNGKEIDYSILEAEIYGT

>CORE_REP|Org59_Gene2609#

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KESFTVDTLDGIKDIKINLTNREINSIRVNMGKGSFIAKDVPVLTNKERFVQESIKVLDRELKVTSMLMGVPHTVVIVDELDVDDVCKYGKEIEN
NKIFPEKTNVNFVKVEDKYNIHVYTWERGCGYTLGCGTGMTASAIVCNLLNMVESSVNVTSQGGTVKIDVGDFSYMTGPAVKICEGILEV

>CORE_REP|Org87_Gene2703#

MKICITVGHSILKSGACTSADGVVNEYQYNKSLAPVLADTFRKEGHKVDVITCPERQFSSKNEEKSHKIPRVNSGGYDLLIELHLNASNGQGKGS
EVLYYSNKGLEYATRVCDKLGTVFKNRGAKLDKNLYILNSSKPTAVLIESFFCDNKEDYESAKKLGYEGMAKLIVEGILNKGVANNEVKQMYKHT
IVYSGDDKVSAEILGLYYKRAKENYLVSDIKDYEPHQTQNLYVIGGETCNKMKEMSNTTGEKFTEIYSDDVWSTMDKAIEFVKEKL

>CORE_REP|Org78_Gene1930#

MLNKLCMYLERPELYKQSEINFWDDEYISKQLLKAHLDTNFEGASRNFNFIEDSVNWIVTVANPANYPKLLDLGCGPGLYAEKFAQKGYKVTGI
DFSKRSINYAQNRNKETNLNINYLFQSYLNMNYNEEFDLATLIYCDYGALSTENRRLLMEKIYDSLKPGGKLILDVFTINKYNNFEEIKYWEINED
GGFWSNEKYMCLQDNCKYNDYNTLEQTLVITEKDENVFYVWNHYFSKESFLLEVENIGFKSVEFFSNVKGEAYSDDSMTMGLVLQK

>CORE_REP|Org52_Gene2358#

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GVIGILFEDDIDRLFFNSTVVAIALIVYGIIMIGLEKRNKKPKYKDFSQVTYKLALCIGLFQCLALIPGTSRSGSTIIGAVLLGTSRYVAAEFSFFLAIPT
MLGASALKLLKAGFGFTGFEWLILGVGSVVAFVVSIVVIKFFMDYIKKHDFKVFGYYRIVLGIVVLAYFFLL

>CORE_REP|Org75_Gene811#

MKDYILYTILLLTGLFGTYAVIPLFKNLLINGNVLRPNYKKDMIPVSMGIVFLPMIVINGIILAFFTTEFKDLAYIFMFMFGMISMFFAGILDDVIGN
RDVSGLKGHFKSLFKGSLTTGGFKALFGGFVGLIVSVAISKDIIDIIVNTLIIALSTNLMNLLDLRPGRAIKAYLFIMVIIFLTLTGFVQVLPLLIVPNVL
AYFNYDLKARAMMGDTGSNVLGISIGMLISFGYPFNIRLGWLIFVVIMHIFTEKYSLTKIIEKNKLLNFIDKLGR

>CORE_REP|Org3_Gene1320#

MKKDSLKKYIMIGAFALILFGIASINFKSLDKTKTQISSPTLDTHEYDWYFNPREDGKQPSPIKEADFFKKYGAYYVGNPNEKVIYLSFDAGYESG
NTPKLLDTLKKHNAKAQFFVVESYIKSNPELIKRMEKEGHLVCNHSKSHPSMAGITDFEKFKEEITSVEKAYKDVTGKEMPKYFRPPMGKFSEQ
SLKYTQDLGYKSIFWSFAYVDWYEKKQPTHEFAKNKIYSRTHPGAIVLLHPNSSTNTEILDEVLTHWEKEGYKLKTLDYLNNKK

>CORE_REP|Org84_Gene1512#

MNKLLYLINVDLRRSNKFYIAYISFFSLITLGLNLFEINKFKNSKFIINLAIGDFGGIFYGIGILSNLGFIQSILFFGMLGLFIYYIFMWKREFFSNNQSIY
TLMMLPQNKFKICISKSIALLTMIYGFLISQIATLFICKYIFNFIFRNVPIINMNFAKDLYYLNLKGIPIDFISFMAIYVFLLLIAISIVNCCILFIFSYINKFY
ILLITLLIIVGLYFSTIYISIITLFRKYYMAIGFQFNNLVAGLLSFLIIMFILNGISYLLIKKKISL

>CORE_REP|Org74_Gene2178#

MRYKKISSLPILVVALLITGTTTTFSLSTTNSEKTNVYLANTVSTVTKKVSDIQSSKGLVYNENIPLFINNSKIQYDDTPYHWPSNVISLTNSSEKAI
MDYEITCLAYDKNGKPLELYWDAQNVAADGEVGSVGFSPAGVDYGIVTGISPVSPKSYSHTYRKMQQSPPQDIISMFEKQQGKAWVENWL
KEWKQMEKEYAKQNAIAPGKNQNDAFLLFDKWKQSTGEHGVKYIISCVKQVTFNDGSVWKNSAYENWLKSFQGKEVSNSVLENYYK

>CORE_REP|Org56_Gene1236#

MQKKVAAINDLSGIGKCSLSVAIPILSALKVQCCPFPTAILSSQTGYPEFTFLDFTDEMVKYSNVWKNLKVNFDSIYSGFLGSKHQIEIVANFINDY
PNAFIVVDPVMGDNGVMYPIFTEEMRQEIKELVKHSDLTTPNLTEACFLTGNDYTKSDYNRDELIYIAKSVSDLGPSKVVITGILEDDNILNLAYD
RDNDHVFFTSVKYNNCSYSGTGDIFTSILCGMLVNKHDLGVAVNTATDFIYKTINYTSQFDTDRNDGVMFENFLSDLTNI

>CORE_REP|Org62_Gene1448#

MNIYEQAIRLIENNEDFAFATITSHSGSTPRETGAMMIVKNDSTIFGSVGGGSVEAECIKHAINVIKNRESMLYKFTLNKSDVAKLGMICGGTGE
IQIDFIDSKLKSNIEKFNKRLKENTSKAYIFGAGHISRDVAVILSLLEFRTVVIDDREEFANHERFPESEVIVLDSFEEIPDFPTDENSYIIILTRGHLYDS
SALEWALKRDAGYIGMIGSRTKIGLTYEKLMKKGFKKEELSRVHAPIGIKLNAQTPAEIAVCIAAELINCRANKEK

>CORE_REP|Org3_Gene2267#

MYKLIALDIDGTILNTQKRITPEVFESIQEAKRAGAKVVITTGRPLPGVKELLNQLNLTDEGDYVICFNGAIIQEVKSEKIIHDVEMTLDDFDFIYN
NVCKKYKTKIHINTMTNLITPNEAPGKYTLHEAKLNNIEVKYIQKDKIDESIKICKIMIVDEPERLEEIIQQLPKNLFNKYTIVRSAPFYLEFLGKTTNK
GTALKTLCTNLNIPIENAIAVGDEENDQHMIKYAGLGVAMGNARNSIKEIADYVTDTNNENGVAKVINKYILNKAI

>CORE_REP|Org85_Gene2106#

MNLIDNHIHTNFSSDGKDSMEDTIKKAISIGVRYLTFTDHLEHDEDRGFCINYNDYVPVFNKFKEKYKKDIELLLGVEVGYRKHLKNEIEEIINSNP
FDFVLCSTHTIDNIPVPSKAYFKGLSKEDAYYKYFNSILETNREFRDYNIYGHLDYISRYGIYSDNRVIYNDFKDIIDEVLKSIINNGSGIELNTSGYRY
GLNAIHPNEDILKRYKELGGFIVTVGSDSHRVEDICKDFDVAYDMLKYLDFKYVSLFKERETYFINIEKVKSNNIA

>CORE_REP|Org18_Gene2887#

MNEELSSLRFDGVGKCKGGIFDNVNISGTGKIEGSVKCSKFDSSGSAKVFGTTECNEFFTSGLSKVEGNILASKVEISGLLRCTGNINSVEIDTSGII
NVEGSIKSDIIHGEGYLKANENIDCENINLSGILECNGFLNCEEVNISLNGTSNFNEVGASSINIKKGHGDYCKKFRMLEKKHINFEKVSSNLISLGL
LSIRKYTESKLFANIIEADEISLENSEVKVVRGKNIKIGKGCYVESLEYSESIEIDEDSIVGEIKNISEKIKLKKDK

>CORE_REP|Org12_Gene2351#

MIKKEISNFRGSSDYVVSPELMASVNVAIALEKPLLIKGEPGTGKTMLAQAISNELKKDLVIWNIKSTTKAQEGLYVYDTVQRLYDSQFGGEGVD
DISKYIKYGKLGEAFSSNQQVILLIDEIDKADLEFPNDLLWELDKMEFYINETKETVRAKQRPIVIITSNAEKELPDAFLRRCIFHYIEFPDRDMMEE
IVKVHFDKVEEHLLEQVMTTFYWIRSLKDIQKKPSTSELIDWIQALTLSGMPIEKIEKEVPFAGILLKNNEDIESMQRHL

>CORE_REP|Org83_Gene1695#

MEVNFVKEKEKLDKLKKMLLELGSVVVAYSGGVDSNFLLKVAKDTLGENVVAVTIHAMMHSSREIEEAKQYTQNFGVKHIILNIENFDLKEFKE
NGIDRCYHCKKYIFSKIKEVAKEHNIKYIVDGTNIDDLGDYRPGLKALSELGVISPLKDSGLKKEEIRSLSKILGLKTFNKPSFACLASRIPYGVEITDE
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>CORE_REP|Org74_Gene2629#

MLSVTRYSIKNVRLKPWVKFIWYFETKSNILLNNKLLPTDSIDIILNLSDVMEYKIENQDYTASNMHFNGIRDKHGFIIQHGNIRVIGISFYPFGLY
PFLKIPISEFNRQIVDLEAVSQLFAKKLEESLNPTQSVEKIVLYLEEVLLSILEEDLISNKYVKLLNSFIYVNRYSNIKAFCDDTNINIKTLERICLKYTGY
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>CORE_REP|Org57_Gene2439#

MRVVKIFNNNALSTVTNDRKEAILLGLGIGFNKRPGDKVNEDKIEKIYYVQDHMQTKFLELLKNVSPEVMDASQQIISLIPGNEGKFNNKGILSL
VEHISFAIDRMKNNVFLPNLMLLDIKMMYSKEFELGVKALEIIYRVCHIHLPEDEAGYIALHFVNLQSNDNLAYDTLKFVKGSIDLIKECYGLELDE
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>CORE_REP|Org18_Gene1587#

MMKDLIRLFEFELKRNIKNYIFIIICCCSFVILNIVKNLNDYNYIIENAVKSEQLTKIGNTIETVNVTGFSSFRNIMGSTESWFMFGIIACICYAFFIWY
RDFNGRSKSIYTLIMLPKNRINIYISKLLNILFLVYSYTVVLTISLFIASKLLPRHMLGNVTNYGFVQETIYELKMLLPYSFEILFVEYIFLLIGFVSVVFTS
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>CORE_REP|Org57_Gene1082#

MKKRIDLLLVEQGYFESRERAKKAIMAGLVFVDNQRCDKAGTEVKEDCSIEVKGNPIPYVSRGGLKLEKAMKNFDLTIDGKVCMDIGASTGGF
TDCMLKNGAIKVFSIDVGYGQLAWKLRQDDRVVCMERTNIRNVTIEYTKQFADFASIDVSFISLKLVLPKAKELVRHDGEVVALIKPQFEAGRE
KVGKKGVVREKSTHIEVIKMISDFSVENGFEILGLDFSPIKGPEGNIEYLIHLRNGNEGYEFDGETYNNKIVEVVEASHNLDK

>CORE_REP|Org64_Gene2251#

MFKKLSVLALAMIISLSITACNSKKNKANDESNTKVTTADDSKEKETLFVYSGAGLKKPMDEIAQKFEKENNVKVEYSYAGSAQLIAQIETSHKG
DVFIVGSEPIYSKAFEKELVGEHKTVAHHTPAIVVPKGNPANIQKLEDLNKDGVKLILGDKESNAIGKTTQKILEKNNLKSINDNVVSTAATVNE
MIVQLTSSKADATIATKDSVFGNEDVEVIEIAQDKNIDQLISAGIVNYSDKKDLANKFINYIESDEAKQIFKKYGFEPVK

>CORE_REP|Org53_Gene2600#

MFTSILKKLKKDKSFAFACITLSIIIILIITSFILNIDSNAIDTTSKLQEPSLKHIFGTDELGRDYFSRALYGGRISLSVGILSMLISVVFGTAVGVISGYIGG
KLDQFLMRLVDMLMSIPSFLVLIVLNTYLTPKVSTIILIIGFLSWMEVSRIVRGETLKIKENEYCLAAKATGIKTRNILLRHIVLNLKETIVVAGSLNIA
NAILTESALSFLGLGIQLPLASWGNMLQDAQRHIFDKLYLAVFPGLLIFLTVMSLTIISKKFSSNT

>CORE_REP|Org33_Gene1887#

MNFFGLVGEKLSHSVSPQIHKRVFEILNIESAYKNFEISKEDISKLDGAIKLLGIQGVNVTVPYKERIMKYLDFISPEAKRIGAVNTILLRENMLYGY
NTDYFGLDSMFKMANIDVQGKVAVILGTGGASKAALTYFIDSGIEKLYVSTRKKDDKKLLNSKAILIDYEELKHIKGDIILNATPVGMYPNVGISP
VSKSIIQNFDILIDLIYNPGETEFLRIGNSMGKKTCDGLYMLVGQAIKSQEIWQDTKIDNSILDVIYNELKLEFL

>CORE_REP|Org63_Gene1738#

MNKIINNILNTCKQYTYILPHKLLRQYIAHYTISIPDTSIKENLTLIPDASGCMIFKFDKKGIESAFWGATTKTTIVKNDIENVLFRVFVEFRPGGVYY
LTGLSQRESTDLKISLEDFNTLFSLEANSIFERTSTIKELVEQLDMLFLSYLLKSNIVDMTIPILENARKQNSIMSVKNISQISCYSERHLNRIFNNSLG
MSVKSYLRLLRINLVLQEVQNNKIPFATLAQDIGYYDQSHFINDFKSICGVNPTTYIKNLSDFYNEKYKF

>CORE_REP|Org67_Gene2668#

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KLFLFMIMTLIIPSQVTMIPLYIIMKHLGWINSYLALIMPIPTAFGVFIMRQAILGVPKELLESAKIDGCSDFRILIQIVLPLIKPALITLAIFTFMGAW
NEFMWPLIATTKDAMRTLTVGLSTLKTFQITNYGQMMAGATITFLPPFIFYLILQSKFVEGVSLSGIKG

>CORE_REP|Org72_Gene3457#

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YKTNKGKVYAERVNKKLATIFKNRGAKSDVRGLYWLSHTKAPAILIEVCFVDSKVDTDYYIRHKDIVAKLIAEGILNKKIDNKENGEGKNMYKHTI
IYDGEVDKILANVLSWGYSPSKVLVCDIKDYVPGQTENLYVVGGGACEKISSITKENYTMIKGNDRFETLYKALDFIDR

>CORE_REP|Org10_Gene1435#

MNLILGDNMSKKSKRRKINKLKLTIVIIVLFLALLSIYEILFSNPNKKGNIKSQETMQNKNNTTDDSKNNQSSTKKQEDNNIKPTFSYSSIPDNIKN
KMIGKSMPTDEPISFDSLSYLKLTYYGFDEKTHQGEMIVNSELAPEVVDIFKELYEKKYPIEKIKLIDDYDAVDEKSMSDNNTSSFCYRTIAGTNVV
SNHGKGRAIDINPLQNPQVSGNDVTPKVSTVYADRSSTKFGMIKKGDDCYNAFVSRGWSWGGYWKNPDYQHFEK

>CORE_REP|Org56_Gene2374#

MKVLQCKLKQPTAHYRDPKVFQNEYISTLNLPSKTTIMGMITYLCDRRLNSDIDIGIIGTHHHRELEFSRGENIDFWNEYTNMRKGKDKEKFLL
QGNYYDYYKEHKAQNSILNYEVLKEVELTIFISCKDDEELEFIKKKLESPCKYANLGRKEDFVIPSEKGCFVKEVELKEVMPMNTRDAIKENIKLKN
TYVRVDLRDKENVETIINQGVLIALPYKYKDLEANRDDRVYEFCHYIYVDNDGIYPKNIKVNVCNVCIDTKEVFTWL

>CORE_REP|Org5_Gene2156#

MNPYIPVSAKILDIVKHTDKEWTFRVNCNTKGVLPGKFYEISIPKYGESPISVSGYGEDYIDFTIRNVGKVTSELFNYKEGDSFFIRGPYGNGFDVS
LYEGREIVVVAGGSALAPVRGIVEYFYNNKEKCEKFKLIVGFKSPKDILFADDLKRWSKKLDILVTVDGAEEGYSGNVGLVTKYIPELDMKDINNT
SIVVVGPPMMMKFTVEEFLKRDLDEKNIWVSYERKMCCGIGKCGHCKMDDTYICLDGPVFDYSYAKILLIRGRSL

>CORE_REP|Org69_Gene1655#

MKNILKKVGIFTIMLGLLGGVVGCSKPDNEKDKDASKESKKEVVVGFDNTFVPMGFLDEKGNTVGFDVDLAKETFKRLGMEVKFQPIDWSM
KETELNDSKTVDVLWNGYSITDERKKIVSYTEPYLQNKQIIVTLSDSKINSKADLKDKEVGTQQGSTALDAVEKDKDFMNSLKGGAPVLYDTYD
KALRDLEIGRTSAVVGDEVLIRYYMGQKGEDKYKVLKDDFGLEDYVVATSKENPELCEKINETLKEMKKDGTFDKIYDKWFK

>CORE_REP|Org61_Gene2284#

MENIDVFLLIGQSNARGLGNPKESVIPNENCFEYLSTDEIINMRCELETSEGDGTIAPAFSNEWNKLTGNKVCFIHNAKDGSRIKNWNHDNN
WFLNDTIEKFNAGCTTLSKHYNIENKYVIWIQGESDAKYGSDALYYKESLKKIAYRLKEECMIDKMFVSLTGYWLGEDEYFIRTRRIAAAQESAC
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>CORE_REP|Org18_Gene1421#

MSLIVFDYGKRTYIMGILNVTPDSFSDGGDFNNLDIAIQHAKDMVDQGADIIDLGGESTRPGHSYVDSDEELRRVIPVIKKLKQELDIPISIDTYK
ADVAEEALKLGVTMVNDVWGLRKDKNMASVIGKYDAEVCIMHNQDGTNYDKDIMESIKDFFKVSIEMAMSYGVKKEKIVLDPGVGFGKDF
EQNIEVLRRLNELKDLGYPILLGTSRKSVIGKVLPVEPKKRLEGTIATTVLGIRDGVDIVRVHDVYENLMAARMTDAIYRK

>CORE_REP|Org51_Gene2295#

MTFKNKKFTINKYEILSIILVLCLILTGFSSYVNYSHKKFKDYVVFYVQHQDDEVLWAGSAIVNAIKERGKNNVFVVLVSTGCGISVFDKYKKYENL
TNIQKSEYRNREFLASLNSLGVIRKNIILLPEINTNGNTDFNYMEKIALTFEEKFKNVTHIAHTYKLDDHLQHLKNGSVIQNLYNAGKIKDAKYFVK
PKFTDKITFNNKIVYKAHSTEDYEKVKNACQQYKIVDELEHREGIGYKSDHKSFDKLLSNKDVPAILHTPNL

>CORE_REP|Org41_Gene1023#

MRLNKRSEGYINYVKGVKREKRNVLFYQLLILIGFIVIWELLADLNVINTFLFSKPSDIYNLFIQYASSGQLFKHIGISVYETVLGLVIGTVLGILVAIA
LWWSEKLSKILDPFLVVLNALPKTALAPIIIVWVGAGIEGIVVTAVTISVVVTILSAYNYFMNIDEEKIKMLKSFGASKSQILFKLILPANTGNLINLT
KINIGMAWVGVIVGEFLVSRYGIGYLIVYGSQVFKLDLVMMGVFVLAICAWAMYAVVNIIEKIYNSR

>CORE_REP|Org13_Gene1645#

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YKIMAGKKLYVCPAILYSYKIKSVDEFKKGDTIAISNNPSSCSKNLRYLESIGLLTLPKGDGLVSPKDIIENPKGIQFKELDIAQIPSSLPDVTAAFIDTT
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>CORE_REP|Org13_Gene1564#

MEKREKRIIISSLLSVSILMGLVSIYSILNKEDIILTVKGQEQKVSSFKKTVEELLDEQGVKYNSEDKINPSLDTELKDDMKIKVVKVTKSKKEEIEKIP
FDTKHVNDSNLLKGKSKVYQEGQEGEKKLVYNLTYHDGKLVKKVLSKEVISKEPTTKIIKYGTKEKVLIASRGANIRGGKHMKVVATAYAGDTIT
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>CORE_REP|Org16_Gene2083#

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NIKGRVCLKNAIYFGVMSVLIIRFIHPFIKYFVSIIPYRILISMAIITTLWTILDLIVTIITLKKLDIKLNLLDDIITDLNDINVKLDKFDRGEIQALFKTINN
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>CORE_REP|Org67_Gene1378#

MKLYLSADIEGTCGIVNWDETKLECEFSQHYRTQMSKEITAACDGATQSGVHEILVKDAHDSGRNINPNILPENVKILRGWTKDPLVMMAGI
DESFDACIFTGYHSGATCNGNPLSHTMDIDYDYFKINDEIASEFTINAYIAAYYNVPVAFLSGDEMLCESAKKLNPNIVTVPVSKGIGNGSISIHP
NLALKKIEKGVKKALSGDLSRHLIKLPDKFKIEIKFREHYKAFKASFYPNMKKIDSQTVLFETEDYYEFLRMLLFI

>CORE_REP|Org78_Gene2970#

MNIVVCLKQVPDTNEVKINKETGTLIRDGVPSIINPDDRNALEEALKMKDELGAVIKVISMGPPQAKSALKEALAMGADEAYLISDRAFGGSDT
WATSTIIAAAIEKVGKYDVIFCGRQAIDGDTAQVGPEVAEFLGIPQVTYAKEVKVQDDKLLVTRYTETGDYLIEAKMPVLLTAIKELNNPRYPSVK
GILEAYNNGDAKITVLTLADLDVDTTQIGLKGSPTNVYKSFVPVKDKHNEIIEGINKKEKAEKLIEILFDLKLV

>CORE_REP|Org38_Gene699#

MITIKEYVVPKSLDEAYELLISRKNNIILGGCGFLKLGSKNIGSAIDLKDLALDYINETDDSILIGADTSLRTLELNKVIKNYCNGVISNAVSNIVGVQF
RSGARVGASVFAKYGFSDLIPSLLVVDAKVKLYKKGVMNLADFLENELEKDILIEVILPKKDAIGVFDSIRKCTGDFAVLNGAMLKEGSIYKIAIGA
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>CORE_REP|Org83_Gene983#

MFYDYHMHSSFSTDGKSTMEEMVKKSIELGLEEICFTDHVDYDVYADDSFSIVYEDYFKSLETLQNKYKDKISIKKGIEFGVQTQLIDTYKKEAHQ
YPLDFIICSIHAIDTMDLYLGNYFKDKTQHEVYENYYLYLYNIVKNYKDYSVLGHLDLIKRYAPYDTILDDRLFSDIIEETLRQAIYDGKGIEINTSCYR
YNLPDLTPSKYILQMYKDLGGEIITTGSDSHHISQVACEFDYIYSLLKNMGFKYVSKFNKLKPEFIKL

>CORE_REP|Org10_Gene1534#

MNELKPYIKFFNKNTKLYIIIFMIVGIVMNILPVFILKIFGEASKTNLSTIVNPILTYITILLFVYGVNIANKDFSGALSIRADRKSCIKAIVIDLIILSFVISI
LGIVLIFLSKLFIEIITGYSIELSVLLKRDMIWTSISALIDPSTSSMPLTYLNYFVQICINEICIGFIGVLLGAFTYRVRKVTSITILIGLPILMVIYIVNFATK
NMHKMLLYLEKIIYSFQNPFILFGTKVGIIVICIIFIILLLRKAPIKEYANDLL

>CORE_REP|Org32_Gene1738#

MIVFSDLDRSIIYSNKFLNADSKYANIEIYREKEISYISLDTINLIKQIQYYGMFIPTTTRTVEQFKRIEFNKYGIYFPWSITSNGGVILKDNEILKSWSE
KIDKLKSDYEPIESMIHKFKDYLNVDGITNFKVAEDTFFYIVVDLSRFNLDSIKEYTNILESKNWKFYVSGRKIYFIPKEISKENAIKYLTKELGIEYFYA
VGDSIMDYGMLNISNKSYVLKHGDINKNEIENSFISSSFNGMSGTEEILSNILDENCLLNI

>CORE_REP|Org83_Gene1388#

MKLKKLLSVALVSAIAISAVGCSNKEDKKILVGASSNPHAKILEVAKPLLKEKGYDLEVKIFDDYVLPNTALDEGSLDANFFQHIPFLEETVKEKGYKLTYTSKVHIEPMGFYSEKVKALDEIKDGAVIAVPNDATNGARALKLLAKNKLIEVKDGELITKKDITKNPKNIQIKEMNAEQLPTVLKDVDGAVINSNYALTANLNPTKDAIVIESSDSPYVNIIACRENNKDSDKIKALSEAMNSKEVKKFIQDEYKGSIVPAF

>CORE_REP|Org58_Gene1888#

METKQYLIDFYNTYDEDSRLALKHGMVEFLTTMHYIDKYIKSGDCVLEIGAATGRYSHTLARQGYDVDAVELVEHNIEVFYKNTQSNENISITQGNAMDLSVFPDNKYDITLLLGPLYHLYNKEDKQQALHEAIRVTKPGGVVFAAYVISDGCLIDEGFHRGNIDVSEYIEKGLIDPQTFAAKSEPKDLFELVRKENIDDLMSAFNVTRLHYVASDGLALYMREAVDSMDDDAFALYLKYHLATCEREDLVGVTSHAIDIFRK

>CORE_REP|Org24_Gene2359#

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>CORE_REP|Org32_Gene1395#

MYKVDLNSDLGESFGTYKIGLDEEVLKYISSANIACGFHAGDPSHMEKTVQLAKKNGVKIGAHPGFLDLIGFGRREMKITKQEAKDYTKYQLGALMAFASSNGCNIQHVKPHGALYNMAAKDKELAMGICEAIYEVDKDIILLGLYNSEMINSAKEIGLRFANEVFADRAYDNNGFLVPRNVEGAVIHDTKHAIDRVVRMVKEGTVETLTGEVIHIKADSICVHGDNPKAIEFVKEIRKRFELESIEVCPLENIEVCSSENIV

>CORE_REP|Org22_Gene2952#

MIKLIATDLDGTLLDEKSEINPEFYKVFKKLRERGIMFSAASGRQYQNLIKKFEDIKDDMMFISENGTLVVYKGKEILSNPLNKELVNEIIETTRSIKGKKIVMSGKKYAYIESKDEAFIQEVSTYYAKFKVVEDLTKVEGDILKIAVFDFKGAEHNNNIYFEKFSDRAQVCISGVEWLDLTAKGANKGSAIKKVQKMLDIKYEETMVFGDQLNDVEMMKSAYHSYAMENANEHLKQIARFRAKRNTENGVVDKIKEVIKIG

>CORE_REP|Org22_Gene2914#

MNQNEELEYKKNILKLALFVGELMIKNGAETSRVEDSVLRICRSRGFYHVNIFTTPTVIIISDEKFDGFSFMKTIQSRGINLNKISLLNSFSREFVSDKEYDIDNAIARLYEIQDVKPYPLWLFYSCTGIASACFACLLGGNYVLNFILTFIIAIFAAITYDKTMKISAISAFSCLVSSFLIALSGVLLVEIGILDDPKMLIVGAIMPLLPGVAFIKAIRDLISGNLISGISRAFDAAMIIIAIASGVGFVLDTWYRIGGPF

>CORE_REP|Org9_Gene2152#

MFTVMDIVQPDTVEEAYSILNKRKTNQVIGGSAFLRMGKKRIGTGIELSKLNLDYIKEYEDYVEIGSMTTFRTLETSSIIKNNFGRIIEDSVKNIIGVQFRNVVTVGATVFSKYGFSDLIVALLSLDTEVELYNIGRISLEEFLNRDYEKDLLIKIYIKKTNKNASYKSLRNAKSDYPILNVSVSKHMEQFKLCVGARPQKATIAKQASEFLSNNEINEINIDKAVEIASEELTFGSNMRASREYRKAMSKVLLKRAIMEVI

>CORE_REP|Org18_Gene1577#

MYNLIKDVKKLNPLVIHYTNNVTINYCANVTLAVGASPLMSFSYEEVEEMVSVANSVVINIGTMNSNMLDLFLLAGKAANKYNKPVVLDPVGVFASKARAELTSRLLNEVKFSVVKGNVSEIKFIGGFNVKGKGVDSFDEEEDSTEIIRKIAEKLECVVVATGKIDIITNGKGTYKINNGTDKLKGITGTGCMTASLIASFMAVTENILEAATMGVLTMSLSGELANLNNPPIGTFKENLMNAIYQMDIDTLSKNSNIEFLN

>CORE_REP|Org82_Gene1264#

MKENLFNNNSKIEINTNNKKITVKKDKLIIAGPCAIESYEQLLETAKFVKSQGANILRGGAYKPRTSPNSFQGLKKEGLKILKAVKDEVGMAVITELMDVRDIDELYSISDIIQIGSRNMQNFTLLSEVGKQNKPVMLKRGIASTITEWIGASEYIAIEGNSNIIMCERGIRTYNDYTRNTLDLAAVPIIQKETGLPVVVDPSHATGVRYLVKPMSLASFACGADGIMVEVHPDPENALSDGAQSLCFNEFEDLMKSINNY

>CORE_REP|Org19_Gene2533#

MDKLKLTNHIKDIDLKNKMFKVIDKANSCIKNYDVKSTEFLNPYEVKNAVAILNSTNEIKYSVDGGYEQAERSTVFIYPFYMEYEDIEDTLRFLQIEGNFKFKNISHKDYLGSILGLGIKREKIGDIIIHDSFCQVVVSSDICDFIIVNLEKVSRNNVIVKEISRENIVNSSSKYKEVSFTVSSDRLDCVISGIYNISRQDSAKYINGEKVHVNYEKITSTSKIVKNDDLISIRGKGRAKVTQIGDITKKGKIKVQARLIV

>CORE_REP|Org85_Gene1168#

MASEVLQKTRKINKTLQTSGGSSVSFDLLAGALGDVLSSNVYVVSAKGKVLGLHLNDAQDSSVIEDEYTKQKKFSDEYTQNVLKIDETLENLNGEKILEIFPEEHGRLQKYTTVVPILGSGQRLGTLVLSRYSNSFNDDDLVIAEYSATVVGLEILRAIGEELEEEMRKKAVVQMAIGTLSYSELEAVEHIFAELDGKEGLLVASKIADRVGITRSVIVNALRKFESAGVIESRSLGMKGTHIRILNDKLTDELKKLKNNQ

>CORE_REP|Org21_Gene207#

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AGEVYSQPTYGIGTMIQTEKINFNTSGIFAWIIIVLLISAILQIAQKFLARRAFLWKR

>CORE_REP|Org45_Gene2216#

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NFLRNTPPLALIPMLILWFGIGEESKIIIIVLASFFPIFTSTLKGIKNCDSKLIEVGRVFEFSKLQIIFKIIIPNAILDIAVGLKLALGYSFRAIIGAELVAASS
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>CORE_REP|Org76_Gene1352#

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>CORE_REP|Org70_Gene2161#

MHKETLDKLTNAAINKINLLNTSKVKYLVSSAFAGLYVGIGILLIFTIGGLLTDAGSPMTKIVMGLSFAIALSLVIMTGTELFTGNNMVMSAGML
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>CORE_REP|Org56_Gene2393#

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>CORE_REP|Org16_Gene1206#

MKDYREDNERFDKDNCSEESSCEERECIKQFGTNEMPPQPPKDIQCITIIGEIEGHFIGNPQKKATKYEHIIPMLYSIEESNDVKGVLVVLNTVGG
DIEAGLAIAELLNSTSKKVVTLVLGGSHSIGVPLATAGDYSFIAPTATMIIHPVRTTGLVIGINETFEYFKKMQDRIIQFIIRTSNIKKDVLEKLMHEK
DELVSDVGSVLIGKEAVDYGLIDEVGGLKEALKKLRELIKESEERKKIMIKICLNNKIYDIMM

>CORE_REP|Org50_Gene2499#

MIILNTQGIVLKAIRYKESDIILTLFTRKLGKVSAIAKGAKKNKSSLLSSSQLFSYSNFTLKKQGNMYKVTQSEIIKSFYNISYDIEAFSYATYITKLVEN
SILENQTNNRLFILLAQTLYLYTQDNTDNRFITAAFELKFLDYIGFKPIVNKCINCECKILQNSVFNIYEGGILCSKCSKLFDNNIKLDLTTISLMEYVL
RNDILTCSKAKVSKYITHELENILDKYLKVYVDNINFKSLHVLQSVKNNKGVDNDE

>CORE_REP|Org64_Gene2604#

MQVNKVEICGVNTSELPVLKNKQMKELLLQIKNGDEEARQQFVRGNLRLVLSVIKKFNNRGENIDDLFQIGCIGLIKAIDNFDLSQNVRFSTYA
VPMIIGEIRRYLRDNNPIRVSRSLKDIAYKALQVRERLIRTNSKEPTVSEIAKELELEVESVVMALDAIQDPISLFDPVYQDNGDAIFVMDQVQDK
KDTDENWLQEISLKEAIKKLNSREKLVLDLRFYKGRTQIEVADEIGISQAQVSRIEKNALKNMRKYV

>CORE_REP|Org28_Gene2625#

MRAIIVEDEFPARKELRYFIENKSGIEVVSEFTNGIEVLDFIQENKIDVIFLDINIPHLDGMLLAKTLNQFKSRPKIVFITAYESYAVDAFSLDVFDYIL
KPYSEERIISMLNKLEKSEMSDIELSNVNSNLYKYKKEAVNQEIEEITHKISLWKGDKLVVIDIDDIYYCEANERQTFIYTEKEKFILKEGISEVENLIN
DKTFFRTHRSYIVNLTKVKEIIPWFNNTYILKLKNSDYEVTVSRSKVKEFRLLMHI

>CORE_REP|Org28_Gene1975#

MKNLEIIDKVKDSIYPIATFLFILILWQSMVGVLEVPQYILPTPVDIINVFFKDYQNLSMHAVVTIGEAILGFIVAIIISLVIGILMDFVSIIKKCLYPIM
LVTQMIPTIIIAPLFMIWFGFGTMPKVLMVMLTCFFPILISFVDGIENIDKDYLNLFKTMDSNKVNTFIHLKFPMAMDKFFSGLKISATYAVMAA
TVAEWLGGTKGLGVYMLRSKSAYALDKVFASTILVVIFSLMFVGIVQAVKKVVIRHRLID

>CORE_REP|Org23_Gene1723#

MDKLVLGGHEFNSRLLVGTGKYGSNNILPEVIKESGSEIITMALRRVDLDNKQENILTYIPKEMTILPNTSGATNAEEAVRIARISRKMGCGDFIKI
EVISDTRYLLPDNEETIKATKILADEGFIVLPYMTPDLYAGRRLIEANAAAVMPLGAPIGSNRGLQMKEMIRIMIDELDIPIIVDAGIGKPSQAME
AMEMGADAVLVNTAIASAGDPVQMARAFKLAVEGGREAYIAKTGNVSEFANASSPLTGFLGNL

>CORE_REP|Org61_Gene1250#

MIIKLNSTYHSRVMKYLKKEPEYNLFIIGDIERYGYGNNFLNIWADVGEHGEIKAILLKYFEFMMFYSDGEYDVEGFYNLLRNTNYEEISGKICAVDALAKRLGLNNLKVVDFCKLQTKKFLIDNNCNAKVKRIRLGNLKKTVKLYDLIDEFHSTTLENLKNGLRTGRGYCIEINKQVVSMAKSTSENRTHAMIIGVGTHPKYRAKGLATKCLIKLCSELLRENKIPCLFYDNEEAGKIYKKLGFENIGKWGIYSK

>CORE_REP|Org79_Gene2855#

MTQLVRIFCSDLIKLKRTFIILMHFCIALIGMGLCLGYYKYSSADDISKIAAYLQVIAIAFPLLSSIMCSLCIEQEYYSGSYKHMLTSSNPKYLTLISKYIILICLGFGATLVSVLGFKFGVSSISNEVYFTLDFYMISIMILVGSNLFVYILHLFLSLRFGKGASIGVGIVETLLSAVLLTGLGARIWPYIPCVWGVRFISIWSSFSSSKTIEYIKVESIKGYQSIGLVCGFVTILAFIILCIWFSKWEGKKSEE

>CORE_REP|Org8_Gene2346#

MGEIINALDRALDIILLLYHEKREMGITEISKAMGVYKSTVHRTLVTLENKGFVIQNAENGKYWLGINLYAIGMVVGEKMSLTEIVKPYTKKLNQEFNEVVNVSILEERAQDSPRSIIIHKEYGSNQLLSVNPSVGSSSECYCSAVGKCLMAFNDSIDFEKYRKTPIHKYTEHTIDNWDDMMLFLAKIKEQGYAIDDEELEHGLTCIGAPILDKNNKAIAAISLSGPTIRMREGDFEYKIKRVIETAKSISELFR

>CORE_REP|Org36_Gene2165#

MKRKVQVKNITIGEGRPKICVPIIGKNKKDIIKEAKELKDACLDIIEWRVDFFENVENIKEVKEVLYELRSYIHDIPLLFTFRSVVEGGEKLISRDYYTTLNKEISNTGLVDLIDVELFMGDEVIDEVVNFAHKKEVKVIISNHDFNKTPKKEEIVSRLCRMQELGADLPKIAVMPQNEKDVLVLLEATNEMFKIYADRPIITMSMSGMGVISRLCGEIFGSALTFGAAKSVSAPGQISFKELNSVLNLLHKSIN

>CORE_REP|Org73_Gene1372#

MQDKSVREIKEIIETLEVEKYMEYIELLRVDERKSVQVLAIKLAKKLDNIRKEEERLETINIFENEGYDKGYLYIGGIDEAGRGPLAGPVVASVVVFKKDTKIEGVNDSKKLSEAKRDELFEVIKEEALDYGIGIVNNEEIDEFNILNATYMAMKKAINCLKKAPDYLLVDAATIPGIDITQNPIVKGDSKSISIAAASILAKVTRDSIMYQYDRVYPEYGFKSHKGYGTKEHYEAIEKYGITPIHRKSFLKNIL

>CORE_REP|Org75_Gene413#

MLGKLLKYELKASGRIFIPLYIAILIVAVFNGIFMNTNILQVQGIGILVLTSLFMALGVLTIVVTIQRFRKNLLGDEGYLMFTLPVSTSSLILSKCITALIYAVLSFIVAVFTFGVLMLFGTSGILLPEILDLFNTSFKWISENFLDILLLVVVMFISYSSFILLLYTSISMGQLPKFNKHRNIVAFASFIAINIVISIVGDAVGSILPNEDTNMVYHLYQSPSFMLAILGSLVVAIALFFATKFILDKKLNLE

>CORE_REP|Org41_Gene721#

MAYFNYNNKQCYYNEIGDGTPLLFLHGNTASSKMFNEIINFYKDEYKVILIDFVGHGKSQMVDKFAADLWFDEAMQVICFLEVMNYKKVNIIGSSGGALVALNVALERPDLVNKVIADSFEGEVPLESFVQNVKIEREASKQDDGAKAFYIYNQGENWERVVDNDTEAIFEHYKTIGKFFHKPLETMQPEVLLTGSREDDFVSLISNDFFENTFSSLLEKIKNGKMYLFDKGGHPAILSNGLDFSNVAKKFLEE

>CORE_REP|Org41_Gene806#

MFAEERIQAILNILKKEGRVTVKELSSKFNVTEDCIRKDLKNIEKISSIRRIYGGAVLARETLENQDTKDRKEINIPTKKIIAEKAFNLIEDRETIFLDISTINILLAKLLAESNKKVTLVTNMLDILNVVTSRPNNLNIISTGGLLNLSLDGFVGTPTIEFISKYKFDKTFMGSCGVDVFNSSLTTFEIEDGLTKKAIINSSKKVFIVMEDKKFKFDGNFKFAHLEDISSIITEKTPTPDIVDILSEFNVNVL

>CORE_REP|Org18_Gene1075#

MKMEFTQVILITLIAFFAYMHSFVGSTMHNRPIVVAPLVGLALGNLHTGIVIGSTLELVFMGAFPVGASNPPDFVSGSIIATAFVILTGQDVSAAVVLAVPIATLVLLIDNFLMTVVLTWGAHIADRYAEEGNIEGVERVQLLFGIGNKLILAIIVGIGFSLGVPVIEKILSFIPSYVTHGMDVAAGVIPAIGFAMLARMMLNKKTVAFLLLGFILVAYLNITVTGVALFGLAIALIYVNFVGEKEVIVDDNEF

>CORE_REP|Org35_Gene1455#

MNTGSKDIDTLNVNFRGIEIKAVLVYKNRKNISIKIDPFGKIIVMSPPKISKKIIKDIIIEKGDWILKKSEKYKGREEVYKQRMFITGEKFLYLGEEYHLVIKELLKDSVKKSNCRITINEYQIVVQTNDTSTDFIKKSLKSWYKMESERTVLERIDFLKLNCEIMKQLVPASVKVKEQNKRWGSCTAQKNIYINSKISMARLDVIDYVIIHEFSHLVHMNHSKKFYDLVKSIMPDYKDKENWLKINGYKIII

>CORE_REP|Org90_Gene1652#

MIGIYFSGTGNSRYCVEKFLQEYDITANSYSIEDNELLQHINNHENIIFSYPVQYSNVPKILKDFIINHSTLWNGKRVFIIATMALFSGDGSGVLARILKKYGAITVGGLHVKMPDSIGDEKVLKHSLEYNKKLVIKAEKKVTKAAKKLKHGSPPKEGLGFLSHIVGLFGQRLYFINKTNMYTDKLKINTEECIVCGKCVNLCPMKNLVIKNCMIVANGQCTMCYRCVNNCAKKAITLLGKKVVEQSNIKKYM

>CORE_REP|Org5_Gene2484#

MEYTVQKLSKLAGISTRTLRYYDEIGLLKPLKINSSGYRIYGQNEVNKLQQILFYRELGINLENIKNIINSPNFDSLSALKEHHNKLLAKRKQIDLLIE
NVTKTIALKEGKYTMTDIEKFEGFKEKMIDENEKNYGTEIREKYGKDIIDTSNKKLKNMSKQDYENWQNLNIEIISKLKKAFKTGDASSELAQEV
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>CORE_REP|Org18_Gene1530#

MLTRRIIPCLDVRNGRVVKGKKFKDIVDVDSPEVLGKFYSDCGADELVFYDITASNEERKTSLEFVTKVAENINIPFCVGGGVNKLEDFTDILRKG
ADKVSINSSAVKNPELIREASLKFGAQCVVLSIDAKKNEEGSWSVYVKGGREKTNLDAIEWAVKGVELGAGEIVVNSMDEDGMKNGYDIELLS
KITSLVNVPVIASGGAGKKEDFYEAVNKSNVDGILAASVFHFGEIKINDLKKYLKDMGVEVRL

>CORE_REP|Org52_Gene1151#

MDRFFVEKNNINLQDKTCTIEGEDVKHISKVLRCKLGEKLEICDKNNNEYICEIMNIDKSIVNLEILEKVDINRESELKVRLYQGLPKAPKMEMILQ
KLTEVGVEEIILVQTKRSVVKVDDKKEDKKFERWERIIYEAAKQSKRGKIPKLRGVLSFKEALEDMKKNNVNICPYENERTVSIKHALKKCDSNID
SVGIFIGPEGGFSEEEIEQIQKNNCNVVSLGPRILRTETASVVASTIALYELSDLGGEK

>CORE_REP|Org2_Gene2995#

MNIINKIFWQEDRIGMITNNLEADTHSHCMLQLFLGIEDSIEITVNEKLVKCNCIIVDKNISHSFSARKKVYYSAIIEPTSIYAEQLTSKMNDFGYW
ICDNDGLEKLRQQGTFLISNSSKEQYLRFMEMLNNYLNIPITLKHYDDRITELFNLLHTCNCDNHTISSFADKVSLSASRLSHLFKEQIGIPLKSYILF
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>CORE_REP|Org3_Gene1714#

MFSIGVDSGSVATKGVLFDGEKIIKKIIIPTGWSPKNTSKQVYELLSSEIDKKDIKKVVGTGYGRGVMDFADKKVTEITCHTRGIYFLNKNIRTILD
VGGQDSKVINLDRDGNVFNFIMNDKCAAGTGRFLEITSNLLGSDIESIDTLAKGYEPVNISSMCTVFAESEIVSLLAQNISTGEVAAGILKSIANKS
TSMLARGEVIDEVAFTGGLAKSKELVKMIEEILGKKIFIAEDTQIIGALGAAVIGFR

>CORE_REP|Org18_Gene1580#

MGMLNILWRSMKWRFKNPISFVVTILQPFLWLVLYSSIANQTMNNININNYTAFILPGIIVLVVFSSCSSGGIINFIMKNSGSFYRVLIAPISRYSI
VLGQLLEAILVSFIEVTILCIVSIFFSVRIESGIGGILLMIVLIFMTAFFLSSLAYSISLLLPNEIVYETIMTAIVLPIFFLSSALFPIESLSGGLKVAVMLNPF
THVINALRSLIFGETILIGDILPFILLFLILCCSSFSLAMWRLKKEMVS

>CORE_REP|Org36_Gene964#

MDEKRQKKEMDLEVNSFVPLYQQLYDNIKKQIASGIYKPGDKLPSEGDLCKEFNISRITVRNALNELVKEDILCKKRGKGTYVTIPERIEATCAGN
SFTNSCHRINAKPSTKIISVLIKKADKQVAEALSIELEEKVICIKRLRLIDEVPVIFEVDYFRIDYMFLLKEELEDKSLMEVISNNISTLPKRVENIFEVK
HSNKEYSDHLKCASNMPLLKVRQSVYTENNDVLYYNEQFIRSDKYKYAVSAEI

>CORE_REP|Org18_Gene2613#

MTDIKKYLTSVGILILILGILIGVVNFFIISLTQIFSLMINIIIISLILIILCSTAVTYRVIKGKYVNSNIMKINFNIVSGLFPIISFIASSFGMSKSDIRRIYIKLN
NEYIYSNKYNFNPEDIIILIPHCIQENSCKLKVTNDIDNCKECGRCNIGELIKLKEKTNVKIFVATGGTLARKIIMDTKPKAVVAVACERDLTSGIQDI
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>CORE_REP|Org86_Gene1966#

MFSVIFLCIGGFLAAFVDSIAGGGGLISMPVLMAIGVPVHLAIGTNKFAASAGCISSAYRYSKSGKINNDLLKKLVPFTIIGSVLGVRCVLSISEEILN
VLVVVMILIVAIYTFISKNLGQEDNFEAVNKKNLRLGMLMALIMGFYDGFFGPGTGTFLTFGFIKIYGYDFLHASANTKILNLTSNITSLLLFMING
QVDYKIAIVFALVMIMGAYVGAKVAIKKGSKMIKPIFLVMALFMVVKLVYQTLV

>CORE_REP|Org86_Gene2784#

MNEPLVSIITPVYNSEEFLSETIKSIQNQTYKNWQLLLVDDCSKDNSSEIIKSFRKEDARIKYIKLEKNSGAAVSRNVGIKNAEGRFIAFVDSDDLW
DSRKLEIQIEYMLKENVGFSFTSYRYMRQDGSKTNKVARAPKKIDYEGLLRNTIIGCSTVVIDKEIVGEFSMPLVRRGQDTATWLQLLKKEKYAY
GIQEDLVNYRLVGNSISSNKIKALKRTWNTYRNVENLSLPKSLYVFCFYVFNAIKKRV

>CORE_REP|Org29_Gene2697#

MKKNLVSIITPMYNSEKFIEATIKSVLNQTYQEWEMLIIDDCSTDNSPNIVKSYMQQDSRIKCIKTETNKGVSNARNLALSKATGQFIAFLDSDD
QWNSSKLEKQVNFMLENDYVISFTSYELMDENDKKLNKVIKVPPNVDYKRLLKGNILGCLTVVIDKSKLDFEIRMSGVRHEDYVLWLSILKKGHI
AHGINEVLALYRKSSNSLSGNKIKAAMWTWNIYRNIEKIPLYKAIYYFINYGINGIKKS

>CORE_REP|Org34_Gene1777#

MWEGTMNLANLIPFIISAAALSPINSNDKVLSENQLKDIFPDANLRAVVKRYINPDEMTISNIKALDGEFYATGESISNLKGISYLENVDNFIFWN
NNIKEIPKEALSLKDMDSINLANNYLIDDSVVNSLSHNGVDVNCDLNFIDTKDNQYKLDSKYHNVNIAKGESIDLRKIITKKIDSYYKYWEVTDNL
PKDLDFIVSVSDKSVLSCEDMIIKGNKTGQAVVKVILNDKNDLNTSQEVLITVNVK

>CORE_REP|Org16_Gene2574#

MDRVAFTLFGIDIMWYGILMACGMILGTLIAIKEAKRVGIKDDDVLNIAIIAIPVGLICARIYYVVFNWSYYAQNMSQIFNFRGGGLAIHGGLIG
GILAGYIYTKIKNINFLKMADTVILGMPLAQAIGRWGNFINGEAHGGATNLPWGIMVDGVKVHPTFLYESIWDFGIFIVLLLFRKNKKYEGQVI
VTYITLYSIGRFFIEGLRTDSLMLGPLRMAQVISLIGVIGGIIAHVYLSKKNKHNISEE

>CORE_REP|Org76_Gene1447#

MIMMVLNKSKLKKIIILILVVLLVLSGGVMVLKLFNNKPVFNLFNGVDLPYERGTKDKSGYVALTCNIDLGWETEYVESILETLKKENVKITFNVT
GKWAEKNKDELLKIKKQGHEIGNHGYKHLDYSTLSYEDNYEQIETSKKIIEEIIGEKTKFFQAPAGSFGPETVKAAKALGYTSIKWDADTIDWKYK
DQPEVIIDRMKKKDIKDSSIILMHPTNATTKCIDDIIAIVREKGLKPGKLSDVFK

>CORE_REP|Org49_Gene1271#

MKNNVGFDSSLSKFGIGLFETIKVKNGLPIDLNIHVERMLSSINCLDLDINYKKDFLINEIVTYIKKENVIDKALRITVFDEGYNISIRDIPYNQEMYE
KGFRLTISPIVRGNSLIHRHKTTNYFENIYTKNIANKTGYNDGIFLNSEGVILECSMSNIFFIKGERVYTPSDRLPILNGIIKKRIIEICDELHIELIENEIN
ISEISSFDFVFVTNSLMGAIKVTEIDKIKFNKENVVFDKIEELLE

>CORE_REP|Org20_Gene2537#

MKKKGILSVFKSKKPIIAMIHLKGDTPEDIFERAKKEITIFEENGVDGIMLENYYGNYYDLERILEYVSKANLSIPYGVNCLNVDTMGFELATKYNA
SYIQVDSVVGHVKPRDEATLEEFFKLQRSKCPAYLIGGVRFKYQPVLSENDVEEDLKIGMTRCDAIAVTENATGQETSMEKIELFRKNLGDFPLV
IAAGVTLENAKKQLKLGDMAIIGSYFKDNYKDFGDVSVEHVKTFMDEIKKIREEL

>CORE_REP|Org57_Gene1789#

MIIMLSPAKNMKNIEVFDRDLSLPCFIDNTKEIVENIKTFGIEDFKNKMKINEKLAVLNKNRFESIKFDRLGNPAILTYDGIQYKNIEAENFTRKDE
EFANSCIRIISGLYGVVKPYDSIYEYRLEMQTKLRVGEFKNLYEYWGNRIYKELIKEKTAIINLSSNEYSKSIEKFIKDSDTYITCTFKVNKNGILKVEST
QAKKARGMMTKYIVKNRIRDIEELKKFNLEGYKYKENLSNNSEYIFVKE

>CORE_REP|Org83_Gene2184#

MKNFRDLGGNKTEDGRTVKKGLFYRSAKLSNLSENDIKILKDLNIKYIFDYRSDQEARKHPSTIISNIKNIRIPAMRELEESGGSFGSIEDMIDGLFE
KDGAFNMLNNSYYNLPINNPSYKKLVELIRDYSNLPILNHCTAGKDRTGVGSAIILMILGVSRENIMKDYLKSNDFADKEIERFIDYKPKFKGIPKE
NLKYIFGVNEEYMKTAFRRIDEEYTSVEAYLYGEFNLNKEEIKKLRNQYLE

>CORE_REP|Org24_Gene2241#

MATEKLTPSVVSIPNKFCPGCGHGIVNRIIAEVIEEHGYEKNHVLTLGVGCVCNMNFSWNGDKMQTAHGRASSTAIGVKVALPDTLVMTYQ
GDGDAYVIGLSETLNTAYRNHNVTVFVINNNNFAMTGGQMSWTTMPGQVTTTSVNGRDIKTTGSPLKVPEMVANFFDVAYVARGSVHSP
KEIINLKKYIKNAIEAQLNGEGYSLVEILAPCPTNWGVSLEKSIKWMEEEIVPYYALGEFKQRDGE

>CORE_REP|Org45_Gene3418#

MKDFKDDIELIINDFFDCCNIPTKVFSKDLKEICSIGYDPTLETYFSSLNIFSNINSTDFISNKNLFYIMLSFCDDLHFLVMPIHKFDVSSGYFIVGPFK
SCINNDIEFSNIPFKPLSCLDYISNLLSEICLDKMKHRPALSFYVKKTIDYIHKNYSEDITVSDICNDLQLNKSYFCSLFKKESGYTFTNFLNKVRVEKS
KKYLLEKDLSILDVAVLVGFNSQNYYSMVFKKFNNLTPIEYKNIYN

>CORE_REP|Org5_Gene1174#

MRGKTHCAIGILTAIQTSLIFKIPISLVDILVSATFAVLPDLDKSNSMVSNFILKNNVSKYIYRIFIYAVNIIIFFISININDNFYLSAIITFVAIIIIEAKLTHT
FLRKVFLSLIFILLAICLYIIEVEIYFTIFCLMLSIFPWLKHRSFSHSIFATIIVYFLLKQIELITNINNLSFYGTIGYASHMFLGDLFTKQGIPIFYPLSEKKIS
LGFLTVGGPFSNFIEKSFIFVLIGLIIFSILKL

>CORE_REP|Org47_Gene1188#

MRNIKMIVAYDGSRYKGYQKLGDNNMTIQEKLENVLSKMTNETVEIIGSGRTDMGAHARGQVVNFRTNCMDSLDKIQKYLYEYLPEDIVVK
AVEEVDERFHSRYNVKSKTYMYRIDNNKYHNPFIRKYATHVSKKLDLDRMRKASEYLVGEHDFTSFASSKSKKKSNVREIYSINIKEDDNIIEIYVE
GNGFLYNMVRIIVGALIDVGLKRRAPQDIKYMLESRDRCQSSDTAPAKGLCLWKVRY

>CORE_REP|Org46_Gene1466#

MSRISVFMESCNGKFPNENSMLSVSFIKNILNAENKDFAKNIFNYGEERKNNKQIKDINTAIYIPNLIRSKNELLVDGDIIFNISFYNYSMFSKLYN
GILKVKELEYKGYRFKIKNIKIHKEHEIKENGVIFKTMSPIIVKNKEGKYLDVEDSNYIECLNYIANLTLESIRGSGLRKPLEFIPLNFKKRVLKEKIRGF
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>CORE_REP|Org24_Gene952#

MKIVNKSSNIPLHTQLSSIIREMIETGELKEGDAIMPERELCNIQNVSRMTVNKTIVGLVTEGLLYRVQGKGTFVAKQKKKYQFSNVKGFTDVM
KEKGVNIKTDILSFEMELPDDLVKRKLGISDNTTNIYKIVRLRYTDGEPFGLEIVYLSEEMCKGLTKGILDNSSLYRVLNEKYGYKIQKAEQVMEPVI
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>CORE_REP|Org42_Gene2081#

MKLKRSLVCVTILGIILVGCHKENTKEKNQVASKATQQKTMTKVQNDVNEIMNKDYKYIIKNMGIPYNTFYYIKPKVLKESNTMQDINTSSYMT
LVYPKYTGNDELDGSALYVDINGNKVVNVETNSFSSQGIAVVDAESSIVIEKSDHEKSAVSLENFRRIDLGEYVGVEESRITEIVGDANYDLTAYN
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>CORE_REP|Org18_Gene1810#

MVNIILNWRFYFMKEKILILEDEIGIRSFVSINLKREGYEIVEAGTGREAIEKMTTEKDITIALLDVMLPDISGIEVCKFIRENFDQVGIIMLTAKAQE
DDKIEGFISGADDYIIKPFSIKELLVRVSALLRRVAKDDSSVKSSEIVSPPFILDIDKRKLFKNGKEIELTPTEFSIVKYLISNAKQSLSRDQILDEVWGT
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>CORE_REP|Org64_Gene2254#

MNIFDILRDYLLVQVDKYNLNMDMISIVSKSLSSKEAIGNTKRKDFPIIVGKEIMLEADFKGAKGQAFTSTPSTFEGSLKDILSLDLYDNPHDRSLF
IASLNAVMKYLDKTDRTIHCKNNEPEVCAKKFPKFIKREFGNPKVAIIGYQPAIIDNIKDFFETRVLDLNPEFVDTIQYNVKIEDGIRDYEDVISWA
DLVICTGSTLCNNSIINFLSLNKPVYYYGTTIAGASNILGLKRLCFCSK

>CORE_REP|Org29_Gene1655#

MMFDRGKWNKLDYNELLEYMMSIKDIKYRDFNKKLIPGTENIIGIRVPNLRKLSKEISQGNWKEFLEVAEDTYYEEVRLQGMVIGNINSNFEET
LYYVKRFIPKIDNWSVCDGFCSGLKSMKKYKENMYDILKKYVYSKNPWEIRFALVMFLIYYVDDKHIKEIFEYCNNIQSEEYYVKMGMAWLLSIC
FIKCEEETFLYIKNNNLDDFTYNKMLQKIIESNRVDLEKKNIIRSMKRKTRRC

>CORE_REP|Org1_Gene2100#

MKTNYRLHMQQGSDYLKKFLEKHIDLLKKIPLFEGIKSDELEEMLECLGVVDKTYPKDSIIFSVGSEVTSIGIMLKGSAHIIKEDIEGNRNIVAELLP
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>CORE_REP|Org18_Gene1020#

MYAPIFALVLFSFNDSKSMARWNGFTWKWYGQLLQNESIMSALYYTIVIAILASVISTIVGTISAIGIHKMRGKSKKLILNVNYLPILNTEIVTAVA
LMSLFVFVKMEFGFTTMLLAHIMFCLPYVILSVLPKMKQLPDNIEDAAMDLGATPIYALRKVILPQIKPGIVSGFLIAFTMSIDDFIISFFNAGNG
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>CORE_REP|Org74_Gene1718#

MENRVLIIDDEVEILKLLETVLKKEGLNNIYTAKTKKEGLELFKSINPDLIVLDIMLPDGEGYDICKEIRKTSNSPIIFLSAKTEELDKLLGLAIGGDDYV
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>CORE_REP|Org38_Gene604#

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KENDIKNIVVTRMEVPCCGGIVNAVKTALQNSGKMIPWQIVTISVDGKIVDGEI

>CORE_REP|Org2_Gene3273#

MIPKKIHYVWFGGPKGNIENICINSWKEKLPEYEIVEWNEKNFDIEKEIKGNKFLEECYKRKLWAFISDYTRIKVLYEQGGVYMDTDMQILKDIT
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TENTFGIHWWGKSWAKKRNYFLESKHLTGVNKIWKCCKIFASNTLRS

>CORE_REP|Org94_Gene2086#

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DLELGREFKINNDSIFKFVDLMNIMVESISDSCMINIDITDLKEAIVGDKGIKYSFEEFEDTKSYSEIADILFDRMEYIGEEFISKKGIVFVEGSPEFSI
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>CORE_REP|Org6_Gene1990#

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>CORE_REP|Org45_Gene2586#

MNSYNILVVEDEKEIADAIEIYLLNQGYNVFKGYNGLEGLKVIENQEIHLAIIDIMMPKMDGITLTMKLRENHNFPVIMLSAKSEEVDKIMGLNI
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>CORE_REP|Org45_Gene2514#

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>CORE_REP|Org58_Gene1491#

MIIFPAIDIKDNKCVRLTQGEFDKVNVYYDNPLEVAYKWKNEGAEYIHIVDLNGARSEFGVNTKIIEDIANNIDIPIQVGGGVRDKEKVKSLINAG
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IASGGVTSIEDVKRLKAMNLYGAIIGKALYDKKIDFKEAQQLCLLGE

>CORE_REP|Org46_Gene2958#

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>CORE_REP|Org81_Gene1542#

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>CORE_REP|Org17_Gene1030#

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ASQDIKENITYVNERFYRNKEEIIIDDNVDLEDISIEAIKNILPYIFKVKTSQIENANDEKLDKIVRKKIISVEEKILYIRDIIKDKIEVTFTNIIKSYENDEII
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>CORE_REP|Org32_Gene1458#

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>CORE_REP|Org51_Gene2493#

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>CORE_REP|Org85_Gene1668#

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>CORE_REP|Org34_Gene1893#

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>CORE_REP|Org25_Gene2055#

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>CORE_REP|Org10_Gene1187#

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>CORE_REP|Org89_Gene2670#

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>CORE_REP|Org78_Gene849#

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HIENNRAHDGELSKEKARDIMLKYLEKYPDAKVKTVTPYKALGIHEDHRALGEAALELYREGKIKDLRFYVEPYDYNDFKKVNPNVRVWKVLSS
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>CORE_REP|Org96_Gene1332#

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>CORE_REP|Org31_Gene2712#

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>CORE_REP|Org54_Gene2394#

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>CORE_REP|Org77_Gene971#

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>CORE_REP|Org18_Gene1116#

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>CORE_REP|Org45_Gene2771#

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>CORE_REP|Org7_Gene907#

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>CORE_REP|Org55_Gene486#

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>CORE_REP|Org80_Gene2105#

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>CORE_REP|Org49_Gene2732#

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>CORE_REP|Org16_Gene2414#

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AVELLGGTTKEADLNGVNLSVRLEDEQHYIIPKIGEATSVTSNDDSNKPNQKNESRGEPKNKSNKNISNESKVNINVATIEELDSLPGVGEATAN
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>CORE_REP|Org18_Gene2394#

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>CORE_REP|Org85_Gene2195#

MERTQQLRESFIASIPIFLGYIPIGIVGGILLQKSGLSPFQIALMVTLVFGGSSQFIAASMISTGASVTSIVLTTFIVNLRHFLMSSNLNMYIKNKSPK
FILPFCHTITDETFAVNYEKFTAGNWSDRNAIYLNFFCLISSVLANFIGAFLGESISIDSSISGFILTSMFIALIVSQIKNKIYIVVFISSIIISVILYALFKSN
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>CORE_REP|Org15_Gene2509#

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>CORE_REP|Org19_Gene1745#

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>CORE_REP|Org90_Gene1656#

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>CORE_REP|Org15_Gene1080#

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>CORE_REP|Org88_Gene1291#

MIGCIYEVYNEEISKIIENQNTLAVYLVGSSKDVDFTLYDVEINDIDVFVFVKEGEKQERILFKKKGIEFDINYFSKDGIKKLLSNREYFFVKEMKDAKVLFDRENISHTIKDISRDIYLEGPSKMSLEEKSFIKQDIGAKISNLKNKEKFDVFEYHFLTNLYLKDIIIGYFNINDKWVPKDKKLLKVLKKENNELFELVSKVSENYDYQRLLDVYNYIFKEIETKEVIKLIF

>CORE_REP|Org57_Gene1952#

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>CORE_REP|Org18_Gene2759#

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>CORE_REP|Org18_Gene2640#

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>CORE_REP|Org18_Gene2877#

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>CORE_REP|Org39_Gene2018#

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>CORE_REP|Org35_Gene2882#

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>CORE_REP|Org95_Gene1194#

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>CORE_REP|Org34_Gene2492#

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>CORE_REP|Org93_Gene1048#

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>CORE_REP|Org50_Gene1030#

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>CORE_REP|Org46_Gene2434#

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>CORE_REP|Org54_Gene1326#

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>CORE_REP|Org69_Gene2191#

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>CORE_REP|Org3_Gene1649#

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>CORE_REP|Org12_Gene1240#

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>CORE_REP|Org65_Gene1877#

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>CORE_REP|Org68_Gene909#

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>CORE_REP|Org65_Gene2195#

MLEILKEEVLKANLELPKKKLITYTWGNVSGIDREKGLVVIKPSGVEYSNMTVEDMVVVDLEGNIVDGKLRPSSDTPTHLVLYKEFEELGGIVHTHSSWATIWAQIGKSIPSCGTTHADYFYGSIPCTRKMTREEICNEYEKETGNVIIEEFMGRNPIHCPGIIVNDHGPFTWGKDANEAVHNAVVLEEVAKMAYYTELMSPDNIMDKVLMNKHFSRKHGKNAYYGQK

>CORE_REP|Org29_Gene949#

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>CORE_REP|Org53_Gene1818#

MEKILVVEDDSILNKTLSYNLIEDGYIITSKFTAKSALKSIFECEFDLIILDINLPDKSGFELCNEIKGNYNIPIIFLTANDMECDMIKGYELGALDYITKPFNINIFKQKVKAFLNHLTIKTKQDYYRDGYLEINFSELSANINGNQIIFTPLEYRTLKLLTENPKSILTRKVLLEKLWDIDANFVDEHTLTSVISRIRSKIEKDNLKYIKTVYGMGYMWLGERNEF

>CORE_REP|Org51_Gene2784#

MSGYTNDECEIPKIKSYPGADKEIASEIDYSIVKGTVLFDLYQRIMDLVLSIIGLVIGLPLIAIFGILIKIEDKGPITYKQERLGKCGRRFYIYKLRSMRTDAEKFGAQWAEKDDPRITKVGKFIRKTRIDEIPQLFNILKGDMGLIGPRPERPNFTVQFNEEIPGFINRLAIKPGLTGWAQVNGGYEITPEEKLKEDIYYIKNRSILLDFKILFKTVKVVLTGDGAR

>CORE_REP|Org6_Gene2173#

MKTIGLIGGMSWESTITYYQVINTVIKERLGGLHSSKCILYSVDFQEIEECQSSGNWEKSAKILADAAIKLQEAGADFIVICTNTMHKVSDKIQESI
HIPLLHIADVTATVLREKEIKKVALLGTKYTMEQDFYKNVIINNGIEVLIPNEEDRIIVNDTIFNELCLGIISESSKKAFLSIIDKLGKQGAEGVILGCTE
IGLLIKQNDTSIPLFDTTVIHAIEAALSSI

>CORE_REP|Org61_Gene1114#

MSLREICSQELVEFKGNKRGIIVNIKREAPFEEIQEKIINKLEAYVGFFNGAKISKINSDCLTDMEILELKEGITSRFDVEFVEDQKIEENSNFPTKYV
NTLRSGENIEFEGDVVILNDMKPGSKVLSKSNTVVMGDINAGAKVVAGGNVFVMGKIEGFVHAGAEGNEFAYVVAGNLNPKILQIADNIAEA
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>CORE_REP|Org4_Gene2122#

MIEAFIFDLDGVITDTAYYHYMAWRKLAHKVGIDIDTKFNESLKGISRMESLDRILEFGNKKYSFSEEEKVRMAEEKNNYYVSLIDEITSNDILPGI
ESLLIDVKSNNIKIGLSSASKNAINVLNHLGISDKFDFIADAGKCKNNKPHPEIFLMSAKGLNVNPQNCIGIEDASAGIDAINSANMFSVGVGNY
ENLKKANLVVDSTNQLKFEYIQEKYNEYIVRRII

>CORE_REP|Org93_Gene2412#

MYRILLVEDDIDLSKEIALALEKWGFKVGLIDDFEVVLDEFIDRKPDVVLLDVNLPLYNGFYWCEKIRAISNVPLIFLSSRDSDMDLIMGINNGAD
DYITKPFSIEILVTKINGIIRRVYNYSDSNSILYCEDLMFDVGKGIIKHKYKDKSIELTKNEIKILTLLLKNKNRVVSRESLMMTLWDNDEFVTDNALT
VNMNRLRSKVKELGFDDFIKTKKGIGYIIQC

>CORE_REP|Org33_Gene2049#

MIWTFYSFICVILPCLIYQIVVIKRKNLKVEKNVMIHLVWVYIFLLYIYLALSKAGIGSIWDIGRYSGLFRIDEINLIPFDSVGILTYILNIIMFMPLGFLL
PLIWKNFRNIINVSLTGLGFSLAIELCQLFNLRATDIDDLMMNTLGAVLGYFIWVGVNNLFNLIKKKDIFPSIYKNIIQDEIAITIDDDISEKITSLYK
NEAIIYLILAVLGEFLLFNWSIIPY

>CORE_REP|Org77_Gene667#

MIVIEGSDKFKIAKEYIDVEYTLFSKVTFKYEKLKFKDNAELEKIKMFKYKNGYIPNKLNLSLGYGFSSYKKQIIRETVDTLRLTEIFSSENIEDIKFIKD
GTKKLEISIEKVVKFKRRKKRNYVCCYCPDMYRDIKLDKESIDKIYNRRKIKIEREVNIFEDEDVIINKKVLKFPKSWTKNMQKYWLSENKYPIHST
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>CORE_REP|Org56_Gene2638#

MKKLYRIVINIILVLVILYSGFNIYSKLTKYNHDTKTSSELQKKEYKKEDLSKINSDFKFWLSVENTNINYPVVQSKDNSYYLDKDFYKKDSISGTLF
MDYRNKSIDDKNIIIYGHNMKNKTMFNNLNKFKDADFFKNNNKIKITLNGKEFLYDVFSAYIVESDYDYLKTNFNNESDYQNYINDITSKSLYKS
PIKVNSNDKIVTLSTCTYEFDDARMVIHGRLI

>CORE_REP|Org26_Gene1470#

MFKHDKALLKEVKVERPNPQYAVLMQEQLGGANGELKAAMQYLSQSFRIKDPQIKDLFLDIAAEELSHMEMVAQTINLLNGHDVDYNAVNT
GEIETHVLTGLSPVLINSSGAPWTANYVTVTGDLVADLLSNIASEQRAKVVYEYLYRQIDDKYVKETIDFLLNREEAHNALFRDALNKVKDTGSN
RDFGVTEDSKLYFDLSTPGPNHDTKIDINPPSFEKPLKK

>CORE_REP|Org3_Gene2784#

MSKVKSIYNEEYLPFMIRYGRLTLSLGIIAALVPGIILSFGFGIMPPISALLASTMAIVSMSAPNYIIEPVSYSPILGIPGTYMSFLSGNISNMRLPCSI
AAQKAAEVESGTEEGSIISTIGIAVSILVNISILTIGVILGGSVLSKIPAEVVEKLNLILPALFGSVFGQVFLQDKKLGLVAIVISVLTIILSKQGIIPQSLV
VLICVFGTILIARAMYKDKLSD

>CORE_REP|Org42_Gene967#

MQLILDTGNVEEIKELCTCLPIDGVTTNPSIVSKEKKNFKQLINEIGEIIGEDMPIHAQVLSTKYEEILEEALYISSLRKNIYVKIPVTQDGLRAIKDLH
RKGVKITATAIFTAHQGFLAAKAGANYIAPYVNRLDNISGDGVAMVSELIKIIDTYKMDTKVLAASFKNAQQVIELMQHGVHSATVPYDICKS
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>CORE_REP|Org17_Gene187#

MTRRDLMRGRVILLISILSIFLVGCSFNKKDEINLVEQGKTYLEKHNYKKAMESLSSALEEDSTNENARAMYMQAMRMSNMTEFEELKNYEGA
IKELKLIEKIKNGSSVIKEEATKKKEELTKLEKEQNEAEEQRKKKAKDTAGEDRYRVESDARKSSYSGSSKNNKSSSKNNKKSDSDKSDNNNNSSQ
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>CORE_REP|Org28_Gene2247#

MLDKVKGRLIVSCQALENEPLHSPFIMGRMAKAAMEGGAVGIRAQGVEDIIEIKKVTGLPVIGIIKRNYEDSDIYITPTKKEVDELLTTGCEMIAL
DATNRVRPNNEDLKELIKYIKENGVLVMADISNYDEAIKAQEYGVDCVSTTLSGYTPYTKTLEGPDFVLMERLVKDLEIPVIAEGKVNTPQDLKK
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>CORE_REP|Org96_Gene1918#

MAKILGICGSPRKGATEYAVLEALKEAETIPGIETEYWSVRGKKISPCVHCDACIRKETMCIIKDDIQELEQKILEADGIIVGSPVYDMNITAQLTA
VFNRLRPMYLVHPGKLQNKVGAAITTGGTRYGGQELTKLPIINFFLMHEMLVSGGLGGCYIGGTIWSKDGKAKGAQEDETGMDTVKRLGKG
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>CORE_REP|Org51_Gene2816#

MATFKRLQEQAYDYLKELILSGKMIENEIYSETKLASEIGISRTPIRDALQRLSQDGFIDIIPSKGFRIHQITANEIVEIFQIRSAIEGFCTFLITSQYKEP
RAVETISKLKHLLDKQKDILLGDKNLNSFAEYDTLFHTTIVSYAQNTEFDKMFNNYMYRIKKLALDSLSHEGRLETTLKEHTDIFNNIANGCIEDIY
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>CORE_REP|Org27_Gene1678#

MKVLIVEDNKILLESVVEELSKHFETEKCEDGEEALYLINQNIYDLVILDLMLPNINGFDILKKMRINNIDTPVLILTAKETLDDKVEAFTIGANDYLT
KPFYMEELVARVYAILRTNGKIKERNGLEFKSLYLDTLEKRVYIEKEEIKLQNKQFNLLEYFVLNKGSILLKEQIYDRIWGIDSDATIEIVEVYVSNLR
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>CORE_REP|Org68_Gene1930#

MNLLIIEDDINLNEGLFYAFENDGFNVFKAYTKQEGLNIFNSKNIDFIILDCNLPDGDGFDVCQIIREKSDIPIIMLTARDSEIDEVKGLEIGLDDYIT
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>CORE_REP|Org74_Gene1256#

MFKIFLFSSEQFVSLFIFGLFLYYCPKLTKNILPYSYTVEKIICTLLVIIMALEQLLLISSGNYSTLNSLPIGINYICIYLCIAILIFKQYHLFNIFFSWSLVCS
VGELIFSKNLGYEFPSLIYFIFIFSKCLIIYADIYMVDVRKFRVNRYALRDNLAICFIYFSFIFLLNTFTNSRYYYGFLSHSTTAIFTFIFVTSIMYIPALLFN
RDTFILEKKKKSK

>CORE_REP|Org49_Gene1942#

MNSSILVIEDDSNIQELISEFLSAEGYQVDTANDGLEGIQKFKQGSYDLVILDIMMPNLDGYGVCKMIRKSSSVPIIFLTALNDEGDQLKGFDLEC
DDYITKPFSFNLLIKRVEAILRRSNKTINDKFIVFEKLKLDLNTYIAEIDGEPIELTLKEFNILKALIEKYPQVITREGLLDSIWGYDYYGDTRIVDAHIK
NIRKKISLPYIKTVKGIGYTLEKDI

>CORE_REP|Org89_Gene2194#

MNNKCNDIYTDEVDEFIRSIKFDDKGLVPVVVQEVVSKDVLMLAYMNKEAIKKTLKDKVACYFSRSRQELWVKGETSGNTQKVVKMSYDCD
VDTILLFVEQTGVACHTGNYSCFYRDLFDDTAKMELEVQTNILKELYDLINERKNNPVEGSYTNYLFEKGIDKILKKVGEESSEVIIASKNTDKSELI
YEISDLVYHTLVLMIEKGVEIDEIKKELLKRRK

>CORE_REP|Org10_Gene2783#

MSKLESTTEKVEVKWYGYVALILGALFFSGIFKDAPGPLKVLDFNNVLGSFGTLGTINDGVGTLAANFRGDGGTGPRDGWLYALTLIPSVMFAL
GVVRVIDHLDGMKAAQKLLSPLLKPLLGLPGFAGLTLIASLQSTDAAASMTKELKDDGYIDEKQKAVFCAFQFSGASAITNFFASGAALFPFIGD
VPIFIPLALILIMKFVGANLLRLYLNKFDKGEA

>CORE_REP|Org81_Gene2282#

MIKLIGILIVVIGFILKIDTLFTVLLAGVATGIVAGLDFNQIFTILGDSFVSNRGVSLFILTLPVIGVLERYGLKQRAVSLIEKLKRLTTGKVLTIYMIARQ
IAGALSIRMSGHPQFVRPLVNPMAQAAGLSNSDELKESDEEAIKALSAASENYGNFYGQNLFAGSSGVLLIASTLTQFGYNVTGLNIVKANIIM
AVIALVVATIQFTLYDKKLNKSHKK

>CORE_REP|Org32_Gene2916#

MKGNIVQYNFADIEEEVYSLDYAIAWNTDEENVNIIPFTNKFCKESIESFCLGKINNFVEILNEGFVENHHYVHLDKMISVPKKKVNLVYQQDTH
GYLLRDDNDNLIPAKITSEQSKSISSKMELFCAGEEKCLINILLKADPSYILDVDSIKDKNILNLGYESIDRYKEYNFDDDKILIFFINKKRYSVIMKKT
NNSDNDLVSRNNAIKELFTNKAGNLN

>CORE_REP|Org41_Gene10#

MRPSKKLLIAIISIFLISSVPVSAHAESTTIQQNKDILSQIVVFPTGNYDKNEANAMVNRLANIDGKYLNVLNQNNLKIKLLSGKLTDEKEYAYLKG
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FAYYYLNQDTNSKLKSACPQTYSCLQNLAK

>CORE_REP|Org63_Gene1809#

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YKELKKERVTIDELLEQLRVQGYFNLKDVQYAILETDGNLSVVPASTYNSTPPKAFNHLPIPLILDGRIINKNLDIAEKDTNWLMGILKSNHIETFK
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>CORE_REP|Org33_Gene1438#

MNSLIDFLTTLFPNALLQTLYMVIVPTIVATILGFILAIILVVTKPDGLKPNSTINSALGFIVNIFRSFPFMILIVAMIPITRLIVGTSIGETAAIVPITIGA
APFIARIIESSLNEVDKGLIEAAKSFGATKRQIVFKVMIKEAMPSIVSGITLSIISILGYTAMAGAVGAGGLGNIALIYGYQRFDTAVMVYTVIALIIL
VQIIQGVGNLAYKKLK

>CORE_REP|Org44_Gene1841#

MTKIIKVQKPKFTGELEIIENLEDILEDIFNDEKIFNKIIENEVISDLDSVRVSFESCIFRNVSFENCNLKKIDLLDVVFENCNLSNTFFDGGSIYRVEFK
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>CORE_REP|Org39_Gene2179#

MSKSEKGKETKASIISAARELFFEQGYHKTTTRQIAERANINLGLISYYFSSKSEIGAIIYEDIRNEMQSLIYNYHEEGTMMMFFLAMNADLCFLLK
NEAYRNFYLDIAYEEAILSYQRSVTEMVMKRYVNDKESIEHDELILSCIGILAMKPEIIRVYTSHKYDISSQAVIKHFTKQFLINLGHSTDLCEEILEEL
SKYYIDIVDNFTPIITRVRT

>CORE_REP|Org62_Gene1429#

MKKKLLYINVNSKPEDLSSSKTVARKFINKFIEKNKDFEVEEIDLYKEHIPRLEYQYFEKRNSIVSEENAKNLDDKDRKELTKIRNLCDQFVSASVYV
IAAPMWSLSFPAPLKEYIDCIIQDGKTISFEGNDKPQGILNDIDRSMVYIQSSGGHIPWVLKPVMNKGLNYVESIMKFIGIKKFDELLVDGTGTS
EEERQAAIEKASEKIDGIIDGMKF

>CORE_REP|Org38_Gene1235#

MYQFFLKGRDPISSLTHFIGACLSLLATIILVFQSVTLQETSLLMIVSVSVFGLSLIALYSASSYYHFLKGTPEQELFFRKVDHAMIYVLIAGSYTPICL
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MIGSLFHFLAVLLYVL

>CORE_REP|Org42_Gene1324#

MGNLVIAVDGPAGAGKSTIAKIVAKKLNINYIDTGAMYRAVTYKCLKSGVDVNNEKEVIQIAENSDIDFKDNSIYLDKEVINEEIRTIEVSNNVSN
VAKIKEVRQLMVQVQRKIGMKSSVILDGRDIGSYVFPNADYKFFLVATPEERGNRRYKELCDKGYNTTLKAVIEDIIRRDEIDSNREFAPLVKAN
DALEIDTTGKTIEEVVEEVISKINL

>CORE_REP|Org81_Gene2772#

MNKIKVLIVDDEKLIRKGLKIILSSYNDLEIVGDASNGYEALEFCKTNDVDIVLMDIRMKVCDGVLGTRLIKEYNNSITLLILTTFNDDEYIKDAMKF
GASGYLLKDSSDKVLHEGIRSSFFGNIVLDKSVAEKIMTSEKTIKQEYLYDMYNLTEKEISIIRLIANGLNNKEISQELFLSEGTIKNNITNILAKLELR
DRTQLAIFAFKNKIVIE

>CORE_REP|Org62_Gene1395#

MIRQTPLEKRYDKLGPHIVTALKKRYFDAYYCKTRNEALQQILDLIPQNHVVSWGGSETLKEIGVQTAVREKGFKVIDRDLAKTPEERTEIMRQA
LLCDTFLMSSNAISEDGQLFNIDGNGNRVAAMIFGPKNVIVVAGMNKIVKNIDDAIQRTRTIASPAVVQRFQDVNTPCYINGSCIDCTSPESVC
AYMVTTRISRPAKKIKVILVGENLGL

>CORE_REP|Org52_Gene1097#

MKKKICVAIIFALFIVFVEMFIDSSSEGSKIMTAELSKYRKGVNVLSINNIIVANKKYSLPKDYSPQESSEARDAFYKMNKDAQKSGLNLKAFSTYR
SYEYQDRLFKSYVKEHGEKEANRFSAKPGESEHQTGLAFDIGGDDQSCWANKKFNNTKEAKWLYENAYKYGFILRYPEGKENITGYMYESWH
YRYVGTEHSKNFAMNNLTLEEYLHIN

>CORE_REP|Org54_Gene2191#

MLDSLKGKVVEIAIKAEHYGLCKEKTGNFSIRDKDTGYILITPSGIGREELNVEHICVLDLNGNVIEVEKGIKPSSEVLMHIEIYKIRENINAISHTHSLYATAFSVAKKPIIPIVYESVNYGGYVDIAPYERPGTLKLAKSVSKLLIDTDACLLERHGLTTVGNDLDEALLKSRYVEEVAEIYYRSLVLNQFKELEVVDVDEFESWKYPEEIKF

>CORE_REP|Org18_Gene2054#

MQIILQGECTMTNMEKEILLLISRVRCVTESQFRKIYGDQKRYNKKNFKKTLRKMCSEYTLKKYPCDVDYYNYKDLSYVYYLNGSKLFKGDDLIKALVGSELVVRINTAGCDVKRFYRNVSVDDVKYDLFIEYTDQFGNIKQVLVDVDLNNEIDISKYENLSKKIDKSTIPFFKVPNVLVVTPDNLSELNDLERYDNEYSINFIDLGLNKLFNCI

>CORE_REP|Org92_Gene1987#

MEQNNKVGNFGDLLKILLDEKELSMGELSKKSGIDKSTISRIANNKQKPNINHLEKMAIHLNINLEELLKASGYEFRNSNNQIFNADSDFSNFDDILGFANLINDKNFNGNIEKELSKCKLYVQTDEGKKLLFDNFNKKIDSIEKQGQFTDRLRQMYADFCTDGLTIKKYLLIGSMLLYFVISTDVIPDFVFPIGFMDDLVALNIVTKLLKNDK

>CORE_REP|Org92_Gene1777#

MRRRRKKGADEKLLSYTKYVLRDDIDKLKGKWNLKFRNDNPIHVEFGTGKGKFITTLAKQNPDINYIAMELKEEVLLKAVEKADASNLNNILFLWGDVSNILDYFEAKELSRIYINFCDPWPKNRWSKRRLTHSGFLEMYNRVLEDDGEIHFKTDNEKLFEFSLNEIAANNWLLKNISLDLGNSEYENNVTTEYEDKFMSQGMRIFRCEAKKRN

>CORE_REP|Org91_Gene1640#

MKILLTGFDPFGGELINPAQEAVERVNNNINGAEIIKITIPTVMTKSVEAIDKAIQEHNPDIVISVGQAGGRFDITPERVAINIDDFRIKDNEGNQVIDTIIKEDGEPAYFSKLPVKAMVKHMNENKIPASVSNTAGTFVCNHVMYGILYMIDKKYPNIKGGFIHIPYTTSQVINKKNTPFMSLEEIVKGLELAIEACIIYKEDVKEIGGEIS

>CORE_REP|Org75_Gene799#

MAALKSFEKPLTPEEEIEYLTKFKIENDKSAKDTLIERNMRLVAYIAKKYNNSTEDQDDLISIGTIGLIKAIETYNIDKGTRLATYASRCIENEILMNIRSNKKNKTQVSLQDPIGTDKEGNEISLLDILGTEANYVLDEVELKVQVGKLYEQLNKILTPREREIVQLRYGLTPYGYKTQREIAQKLDISRSYVSRIEKKALKKLEKELVQES

>CORE_REP|Org33_Gene2035#

MKKAINKQFILSTLICFIPFIVSIYFYNRLPNEVAIHFDNYGNPDNYAPKVIAAFGVPLLMLCIHLYTWFRLENEPKKANFSNVIQNLSKWGVAILSVIIQIMMVLYSTGVSLESNFYTGLILGIIVILFGNYLPKCKRNYSVGIILPWTLNDEDNWNKTHHLAGWIWLIGGILLIINAFINIPFYNIFVIFVIVILPFVYSYLMYKISGKNN

>CORE_REP|Org21_Gene1670#

MIIIQLNERQLKIIDIVKENEPITSESIASSLNVTRATLRSDLAILTMTGILDARPKVGYFYSGVSEINLIGKSVKEKTVEDIMSMPVLAKKDESIYDVIVTMFLSDVGSIVIIDENEELCGVVSRKDLLKATIGGSDINKMPIGMIMTRTPNVVTLTKGASVLLASRKIIEHEVDSIPIVEYKGEDKNHMRVVGRISKTNITKLFLEIVDN

>CORE_REP|Org7_Gene1950#

MKGLILKDLLNLKGNVKFILLFIIMFGFMSSLGDGNVNNFIGVIIVLCTTMIVSTFSYDDLNKWDSYVLTMPINRNDIVLSKYLTMLIFSFIGVLVSLIVSVTIGYFKNTLILNETLLINALILSISVCFGSLILPLIYKFGTERARLLMILCFLVPTLALLVFKSILENISSPISIEIILNTLVYSLPFVAILLFVISYFISSKIYSKKEV

>CORE_REP|Org2_Gene1797#

MDNLLNELEALKSNLDNLPIEKIENYDLSKTALFIIDVNNGFARQGALYSPRVESLIKPIEMFTKKISNKLNRVIAFTDSHTPKSIELLSYPVHCLENDVESELVDELKSIENLQILPKNSTNGFFALENLDFDNIDNIIIVGDCTDICIYQFAITLKSYFNQHNIEKNIVVPMNLVDTYDIPNVHPAEILNLVFFNSMIQNGVNVLKEIR

>CORE_REP|Org39_Gene3238#

MEMWLRQSNDAFRFPIFPASFEISGNINTSTTNVLRLGEVIICGGTGLRTTEISSFFPSRQYHFCNYKDFPQPYDCVNKLKRWMEQGLILRYIITETDVNMEVIIESFKHGKQDGTNDVYFTLSLKEYKRIQIPSINSSDGKIEVVKNVPVTKGFETGKQKTHKVVKGDNLWSLSQKYYGNGDLYEKIVEANKELIKTADIIKEGWVLIIP

>CORE_REP|Org55_Gene2631#

MKKVKYTRLVILGILIYLVFNILVMIISKNVDTLVLKNEKVDAKIHVKGTIEKDANDQSNYLSTYISKEDSNNFEKNQNVIIEYHEQKLDAKVYKIYENNNKIMVKLKISNQIVANQDTSVEEFDIIYNQMECLKIPKTSIKTKDNKRGVYVIDEQSQSVKFVILEGITYENESSVFVDYYKNDINGVTSVNLYDKIILRPNSINTNIRIK

>CORE_REP|Org31_Gene1803#

MYLDLTEKQVLILEFIKSQIILKGYPPAVREICTAVGLRSTSTVHSHLNKLEKLGYIRKDPTKPRAIEVLERSKVNDVSGANQEIIELPLVGQITAGEPILAQQNIEEYIPFPASLVKGSNNFVLRVKGESMINAGILDEDYVVVDKKNTALNSQIVVALINGESATVKRFFKEGNLIRLQPENDFMEPIMLNDSEVEIVGIVTGVFRVIK

>CORE_REP|Org86_Gene1933#

MKVFDLTHVTHNDMPVYAEPNRPDIKKVAIIEENGYQETLISVFSHNGTHMDSPRHMYTKGETLDKLDIENFVGKAYVLELEKGNENIELEYLKKYEDEIKNSDFIIFKSGWSKFWDKKQYYVGYPTLTKEAANYIANTNIKGIGIDMLSVDRYDTSVFEVHHILFEKGKIIIENLTNLENVPEKFLFIAAPFKYNDADGAPVRAIAIVE

>CORE_REP|Org79_Gene3100#

MARRLFLERIGLIFLGSAILAFGVYNFYYLNNITEGGVLGILLLLKNLFNIQPAIANVVIDGLLLLVGYKFFGKKFLIYSIVASITFSVLYDLFEAIGPLVPQSQNMLLSTILAGVTVGTGVGIVVKAGCASGGDDALALVISKTTSLNIGQVYLATDVIVLLLSLFYLSAFDIFYSLIAVTISGKVIDFIYYHGKSLDMDISNDIVPEC

>CORE_REP|Org64_Gene1872#

MNNKYRRTVNREFEKSSFWPTFTDLLSTVLMVVILILFSSESISGSVEQDLAKNVNASVEETFKKSGIPVKVDKSNGQVTFGERTMFDVDSDVLKPEAKEMLKMFVPKYIETIYKDYGDYISKIVIEGHTDDVGSYIYNLDLSQRRAYSVAKFIVGDEIGDYKYKDKVTKHIIAIGRSKAELIKNSDNSVNRDASRRVELKYEININQNK

>CORE_REP|Org17_Gene716#

MIDKESLKKCLRLYLITDSEMLEGRDFYKCIEDAISSGITTVQLREKNTCGREFLRKAMKLREITKRYGVKFIINDRVDIALICDADGVHVGQSDIDVREVRKLIGNDKILGVSARTLEEAICAKNDGADYLGIGSIFSTSTKLDAKSASFETVKEIKEKVDMPFVLIGGINLDNIDKLKCLDSDGYAIISAILKAEDISKEVEKWTLKI

>CORE_REP|Org22_Gene1299#

MELNELFNFKYLIIAVIFIISVTMLILISHINILIIADINNKDICLKLNIKYMFNLININRQLYPAENSKNNDKKEGMKNNIDSSILLADDLLSIYRLLKKIKIHELYSNINFGTGNIGLTSSVYVLINTLYGNLFNMIDAEKMYLNVNPDFTKDYVLGNIRIHIRPRIKALFNIIIMINKIMNKNKGNKEGDSNESNRFDTESYGNNS

>CORE_REP|Org18_Gene2378#

MEIKISKDKSDRLTKKKTDGSMDILYKIILLVIIFLVWHFAAKDIGSSLLLPMPVDVIKGFFFCVTDAETVTNLFITLQRVLKGFMYALLFGLPIGFIMGFSKTFERVLSPVVDSVRQVPIMAWVPLTIVWFGIGDGPTIFLIAFSGVFPIILNTIQGVRAISKDYYNAARSMGASPIVIFTNVIVPASLPDILTGSRIAISTGWMSVI

>CORE_REP|Org92_Gene2421#

MVDSIIFDLDGTLWDSTEEVCKVWQDVLSEHKEIELSVTKDLFRSLMGLSFEEIANRLFPNLSEEERMNLLNECSLKECDYLSENGAKLFDDIEDTLKLLSKKYKLFIVSNCQAGYIESFLKAHKLEQYFIDFECPGNTGLHKGENNKLIIERNKLINPIYVGDTQGDANSAKFVGIPFIYAKYGFGNVDVYDYFIDSFKDLLEHDILK

>CORE_REP|Org60_Gene2099#

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>CORE_REP|Org58_Gene945#

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>CORE_REP|Org33_Gene1328#

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PMFLYENEK

>CORE_REP|Org44_Gene2913#

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>CORE_REP|Org92_Gene2660#

MFEKKKKELFPWKISALILVGVFVLSSGVYIGTRLKHNGVQTGEVVSTSANMNEKSKEAFGLNKNCEVWLQSEGENETNYKRTLTMAGIVPES
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>CORE_REP|Org36_Gene1621#

MSIKERRKNEKEEMKKKIMDASIEIINQHGYENLSIRKIATKIEYSPTTIYLYYKDKAEIISDMTNKLYNTVESNAIDIMNNCSSLPIDKQIIEIMTSFI
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GGLYNENSQQGY

>CORE_REP|Org44_Gene2653#

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>CORE_REP|Org72_Gene1714#

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>CORE_REP|Org67_Gene1541#

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>CORE_REP|Org59_Gene2098#

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GFMKIC

>CORE_REP|Org4_Gene1707#

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>CORE_REP|Org6_Gene2769#

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S

>CORE_REP|Org20_Gene1946#

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>CORE_REP|Org83_Gene1525#

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>CORE_REP|Org89_Gene2584#

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>CORE_REP|Org29_Gene1959#

MKKIILALTTFLLAISLTACSSAKPEDTIDSFFNSAKKFDFEGMNKVMENNDEKYKDILKELDTKDPNAQYVLDYLKQNASKITYTIKDSEVKGDK
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>CORE_REP|Org30_Gene2599#

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>CORE_REP|Org18_Gene2717#

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>CORE_REP|Org72_Gene1897#

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YYR

>CORE_REP|Org10_Gene1749#

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TKV

>CORE_REP|Org58_Gene1161#

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>CORE_REP|Org75_Gene481#

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GEMIK

>CORE_REP|Org11_Gene1877#

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>CORE_REP|Org35_Gene2821#

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KSLK
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>CORE_REP|Org18_Gene2457#

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>CORE_REP|Org76_Gene1032#

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>CORE_REP|Org38_Gene1668#

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>CORE_REP|Org90_Gene1711#

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>CORE_REP|Org26_Gene1892#

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>CORE_REP|Org76_Gene1472#

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>CORE_REP|Org66_Gene987#

MNLAKVFKNGLIDENPTFVQVIGMCPTLAVTTSAINGIGMGLSTAAVLICANLVISLIRKITPDKIRIPIFIVVIATFVTIVGMLLKAYVPALDKALGIYIPLIVVNCLILARAESFAFKTGAMPSIVDGVGQGLGFTVALTIIGAVRELLGNGSLFGMTLFGASFQPVLIFILPPGAFLTLGFLFAGFNKLRSKKA

>CORE_REP|Org4_Gene1307#

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>CORE_REP|Org86_Gene1313#

MSDDRIIDFNELKNKVKDSDVDKFEQYIYNLYFSVMDGKMSMAEFSRKIFDYMRDNNISQEKFMKIQKQFMERYGMDTEEVEKQLRNFGIDPSTAGFISNNTSSKVSTEDLESFKKSAGFYEKYGEKIQPKSCITTFIKNDLNDINVIIDQEKIMLCSDRKINLMDSELNEFLLEYKNMFNKKIKVVMCETTNKYDY

>CORE_REP|Org48_Gene1363#

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>CORE_REP|Org2_Gene2029#

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>CORE_REP|Org39_Gene1783#

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>CORE_REP|Org17_Gene740#

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>CORE_REP|Org62_Gene1392#

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>CORE_REP|Org29_Gene2775#

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>CORE_REP|Org46_Gene1974#

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>CORE_REP|Org59_Gene1302#

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>CORE_REP|Org89_Gene2282#

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>CORE_REP|Org40_Gene1766#

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>CORE_REP|Org62_Gene2876#

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>CORE_REP|Org12_Gene2142#

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>CORE_REP|Org54_Gene2665#

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>CORE_REP|Org36_Gene1490#

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>CORE_REP|Org18_Gene2069#

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>CORE_REP|Org51_Gene1058#

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>CORE_REP|Org53_Gene1921#

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>CORE_REP|Org69_Gene2329#

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>CORE_REP|Org18_Gene1429#

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>CORE_REP|Org96_Gene2282#

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>CORE_REP|Org30_Gene2579#

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>CORE_REP|Org82_Gene2161#

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>CORE_REP|Org30_Gene992#

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>CORE_REP|Org82_Gene2360#

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>CORE_REP|Org18_Gene1139#

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>CORE_REP|Org23_Gene1007#

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>CORE_REP|Org15_Gene1060#

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>CORE_REP|Org12_Gene3461#

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>CORE_REP|Org23_Gene1823#

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>CORE_REP|Org12_Gene2313#

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>CORE_REP|Org3_Gene1438#

MMNNELNTIILETLNNADITSNDIPSIDLYMDQIISLIDNKLSPNKRFESDKILTKTMINNYSKEGLIKPVKGKKYTKEQILQMIIIYSMKNTLTIQEIKRILHGVYEKDNFSEKDLVSCYEKFMLIKENQRKNIPDFIESNFENISINPENKDDLLIALLSLTSMADQLKNISEKLVDRYFPDITKK

>CORE_REP|Org18_Gene2056#

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>CORE_REP|Org27_Gene1673#

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>CORE_REP|Org35_Gene2369#

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>CORE_REP|Org57_Gene2372#

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>CORE_REP|Org18_Gene2277#

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>CORE_REP|Org18_Gene1621#

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>CORE_REP|Org48_Gene1031#

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>CORE_REP|Org21_Gene362#

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>CORE_REP|Org48_Gene1169#

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>CORE_REP|Org86_Gene2134#

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>CORE_REP|Org57_Gene1072#

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>CORE_REP|Org32_Gene2708#

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>CORE_REP|Org69_Gene966#

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>CORE_REP|Org77_Gene330#

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>CORE_REP|Org9_Gene1724#

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>CORE_REP|Org75_Gene910#

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>CORE_REP|Org50_Gene2900#

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>CORE_REP|Org10_Gene1012#

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>CORE_REP|Org67_Gene2534#

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>CORE_REP|Org11_Gene1578#

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>CORE_REP|Org18_Gene1722#

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>CORE_REP|Org85_Gene961#

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>CORE_REP|Org22_Gene1331#

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>CORE_REP|Org86_Gene1284#

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>CORE_REP|Org15_Gene1651#

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>CORE_REP|Org1_Gene2128#

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>CORE_REP|Org41_Gene1836#

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>CORE_REP|Org38_Gene1841#

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>CORE_REP|Org56_Gene2783#

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>CORE_REP|Org28_Gene1226#

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>CORE_REP|Org48_Gene1557#

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>CORE_REP|Org20_Gene2996#

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>CORE_REP|Org20_Gene2285#

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>CORE_REP|Org21_Gene1859#

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>CORE_REP|Org17_Gene1081#

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>CORE_REP|Org25_Gene2872#

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>CORE_REP|Org89_Gene997#

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>CORE_REP|Org33_Gene2615#

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>CORE_REP|Org36_Gene2518#

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>CORE_REP|Org41_Gene1851#

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>CORE_REP|Org37_Gene1067#

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>CORE_REP|Org54_Gene1134#

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>CORE_REP|Org70_Gene2126#

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>CORE_REP|Org79_Gene56#

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>CORE_REP|Org18_Gene1174#

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>CORE_REP|Org43_Gene1660#

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>CORE_REP|Org75_Gene584#

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>CORE_REP|Org89_Gene2420#

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>CORE_REP|Org4_Gene2093#

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>CORE_REP|Org18_Gene2097#

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>CORE_REP|Org79_Gene704#

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>CORE_REP|Org7_Gene2135#

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>CORE_REP|Org81_Gene2776#

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>CORE_REP|Org59_Gene2574#

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>CORE_REP|Org61_Gene2238#

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>CORE_REP|Org27_Gene1073#

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>CORE_REP|Org86_Gene2242#

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>CORE_REP|Org92_Gene874#

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>CORE_REP|Org83_Gene2264#

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>CORE_REP|Org4_Gene1924#

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>CORE_REP|Org63_Gene2397#

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>CORE_REP|Org69_Gene2793#

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>CORE_REP|Org97_Gene2596#

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>CORE_REP|Org72_Gene2527#

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TFGTTGKGMRFLDLGFGFYFTVPVFVYFITSLMSFVIADGFVKAIKIKEDNDLTIYA

>CORE_REP|Org66_Gene2418#

MLNFFKKNKSYKLHAVVSGNSINIEKVNDSVFSKKLMGDGVAIIPNSDVVVAPCNGKVTVLTESKHAFGMVSDEGVEILVHIGIDTVSLQGEGF
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>CORE_REP|Org92_Gene2448#

MDTKKYKDKLLKERENLTNLVEDMKDNTLFGDTTKHTSEKYSSGELSSYDNHIGDMGTDLYMQNMQNSLINHEEGRLYQIDLALSKIENGTY
GICDLCHNQIDLERLDILPDTSLCNDCAKKENNLLGDAMQNPDVEDSNFYSEDLTNLTDLNKNGILRD

>CORE_REP|Org16_Gene1452#

MFKSLKRTKVEKYIIDNKDSFYRIAYSYTKNEEDALDVVQEAMYKALYSVENIKEVNYIKTWFYKILVRTSIDFIRKNRKYNNMTDIDLIDETGEYD
KYTDLDLRRALEELPIEYKSIIILRFFEDLKIEEVAIILDENVNTVKTRLYTALKKLKLKIEE

>CORE_REP|Org92_Gene3171#

MNKKTLFQEVEGRLYNYKKLESQIRIKDIYIKKLENEFCGCKAQSYEEKTGPTYNISSSVENEVIKREEDLNRLKEDKKTLEIEKETIECALTSLNSFET
EFFNEMYMNNEKINMDYMSNAMHIDRSHCFRIRKRIVCKIIDMLYPKIKEFELPIFSWKA

>CORE_REP|Org10_Gene1718#

MNTIIIYSSKYGCTKDCANILKNKLSDNVTFVDINNNNNNKIELSKFDKIIIGSSIYVGSVSKKIQVLCNDNVELLNKKQVGIFLCCGFSEQADKYLK
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>CORE_REP|Org54_Gene1346#

MLSKAEIKYFNECASEILSSEKVQLMRTFPHHGNVSCLEHSLSVAYYSYLLCKKLHLRVDIQSVIRGALLHDFFLYDWHYKGDRKGLHGFTHPRE
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>CORE_REP|Org55_Gene2531#

MNLKRSNEKREEYRRMYSDKESFLSLIQNFTSVSIAKELTLKNIELETSFICEYKGKEVDIIYKVFSKSGKVSHYIVLEFQTEMDTEIVPRLKSYREQI
WKSFIMKKSLEEIEDKNFKLPKVIPVVLYSGPERLSRKKGILDIVESISEFSNNSSMKN

>CORE_REP|Org11_Gene1548#

MSKELVKDRVIKYLIEDLLVPQDMIDTNVELAEFEEGAEGILDIVVNVKDEEDYYAPVMIVQCLDEDVELEGEVLQKQIEFLEDVDNITMSGRLV
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>CORE_REP|Org95_Gene1853#

MVKKRLVAVVISLAMISVGNFSYAHSGGHNSSGGHHNKNKSELTRYYCGGHSAHQHNKGFCPYASTKENSGVTISSVHNEKNHKNYFAEKG
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>CORE_REP|Org18_Gene995#

MVKTNAMRILDSNKIDYKVMSYEVKSEHVDGVEVAHDIGRDVNEVYKTLVTQGVSKNIYVYVIPVHENLDLKKAAKVAKEKSVEMIHVKDINK
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>CORE_REP|Org95_Gene2572#

MTDMSMILHFLFSGVATAGFAVFFNAPLYLLLPAGVTGGIGWIVYVYLFNFTTNAVFAGFIAAALVSACSETLARKLKQPAIVFVIPGILPLIPGIG
LYNTMLSLIQKNYSLAMSKGTDALFLSAAIALGVLVVTSFVRTLNLLKIRKNFIPYRKSK

>CORE_REP|Org20_Gene1224#

MSLLSNKKVLIIGDRDGIPGPAIEECVKTVEGAEVVFSSTECFVUTAAGAMDLENQNRVKDAADKFGAENVVILLGAAEAEAAGLAAETVTAG
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>CORE_REP|Org42_Gene273#

MKKILILFFSIILSLGMVSCSSSGDYKNVSTSKIKKALKSSDLLIKESKIFDAKDFNYFNDVEEYIIQGFVINSSEKLSLEDIIVIKTDEVDKIYKTLENYKK
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>CORE_REP|Org62_Gene972#

MIKLVRVDHRLIHGQVAFTWTKFLSTDCILIASDELLKDELRMAGLKMAKPSNVKLVMKSIADSIKALNSGVTDKYNLLILCESVEDVYRLAKEVK
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>CORE_REP|Org21_Gene1942#

MKMLNGIIKLFYSEIVKTKINNLDSSGYSLRDECKEIRNITLKIDSVFFKLLKLAFGSILLMVAFNLNMVLGIGVFLVGVVYILYKRNMEEQVKEHIN
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>CORE_REP|Org42_Gene1035#

MITKFFSNILSVFLYFLLSLLGVAGIIFLCMIPMFLYDFSSDKVIALITRILYFSDYFVVILFLIFIINSTKYSPFILENVKRFKMMGCCLLVNTIIECVVGY
KSNTSLIMIFGDNSGGISPLMVISFIFALMCFVIAETFDKAIKIKKDNDLTI

>CORE_REP|Org26_Gene1356#

MFKEMRLKKREMTKEDTVEVLKNGEFGTFSTISENGYPYGVAVNYVYFNDSIYFHCARNGHKLDNISKNNKVSFLVVANESVIPDKFSTTYSSAI
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>CORE_REP|Org76_Gene1702#

MSISNVREYFKQFGKEDSILEFEQSSATVELAAEAAGVIPARIAKTLSFKIGDDAILIVTAGDAKIDNKKYKAEFNCKAKMLTPEEVLEFTGHAIGG
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>CORE_REP|Org49_Gene830#

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>CORE_REP|Org88_Gene1648#

MKKLVIILISIINVVSLTACKKSNESKYNNLNNKESGQTTIEMELDKNYDTSDSFVNARLFCVSNDIDVLETEISFQMDGDSGIVEIKDNKTDETL
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>CORE_REP|Org64_Gene2602#

MQCPYCNYKESKVIDSRHTDLKSIRRRRECESCKKRFTTYEKIETTPLMVIKKDNSREYFDREKIKYGLLKACEKRPVSIEEIESIVVHIENEINKCFIE
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>CORE_REP|Org44_Gene2850#

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>CORE_REP|Org51_Gene2686#

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>CORE_REP|Org41_Gene1716#

MKKNLEATIEEIVTKITDEHGFEMVDVEYVKEAGEYYLRVYIDKEEGISLNECELVSRELSPILDEKDPIKENYFLEVSSPGLDRALKKDRDFVRYQ
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>CORE_REP|Org62_Gene2381#

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>CORE_REP|Org95_Gene2461#

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>CORE_REP|Org95_Gene2164#

MEFINFVSDKVIDLKMDCKTKEDFFKEIHNKVFDLGFVKEEFGEKILARENVFPTGLNLGDYGVAIPHTDAEYIKEQFISVCTFNEPVVFSSMED
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>CORE_REP|Org75_Gene427#

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>CORE_REP|Org89_Gene2491#

MANTMDLLKDKLKETGFKITPQRRAIVEILLKHDHSHLSSEEIYDLVRVDCPEIGLATVYRTMQLLDEIGLISKLNLDDGCIRYEISLHKEDCHNHH
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>CORE_REP|Org97_Gene1694#

MIRTKVVELIATVCRENKPHKWVDENYTPYDKSGKVELMSIEDLNELISSSGRADFLYSSRLQKLLNEVYINQSRASYISGCGLFWSSYWDILEEK
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>CORE_REP|Org30_Gene1597#

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FVEVTRKVNSIIDNVEELFLNYNVDGDDLKTLNKELNDILNDIDYIEKHTKKI

>CORE_REP|Org25_Gene1310#

MGLRDKFAQSFARSKTMSGPEKKANEIMGKLLLKKAILPIVLMFVIIIAGAMLKINSWVTLGINLVIAVGAFFYIRNSSKKYQNFKPYVGNLISLEK
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>CORE_REP|Org1_Gene2413#

MGTNIFNKEYVFLNVDAKSKVEVLKFISKKAKDLNLAEDESLVYEGLMAREEQFTTNLGESIAIPHTKNDAIENPAVVVLKFNEDVVWNEGEDK
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>CORE_REP|Org4_Gene1134#

MKHLYEEVAYLKGLAEGLEISAESKEGKMIHKIVDALEVFADAIVTLDEEQEELQDFVESIDEDLADLEEDIADMEEDLYEEDDDEDDEDFSYIE
MECPNCGELVEIDEDLLYDDEVDVVCPDCKAVILSSEDDCDDDCTCGGCPSCDDRE

>CORE_REP|Org89_Gene1981#

MAIRKIRTFDDEILRKKSKYVENVDNKIREILNDMAETMYNTPNGGGLAACQVGVLKRLVVIDLGEGLIKLVNPEIIKQEGEQIVVEGCLSFPEV
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>CORE_REP|Org18_Gene1930#

MRYMESKFFNWYTQSLGGTFGIISCICAYLNGYMFVYTNSASKYFESIGFLGIISSYTLLPLCMLTLIFGVIYSYTPETSDKSIFNIPFFTLNKRLILITV
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>CORE_REP|Org78_Gene1419#

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>CORE_REP|Org61_Gene3559#

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SKAHNDANMLSLGERVLGKGLALEIVEAWINTDFEGDRHARRVNMIKSIEEKHNK

>CORE_REP|Org14_Gene3084#

MNYIVKDTISFLVKTFPKIYSSLYLEDLKKFAPDYNVNKTQLRALVFIKNYGVISMTDLCSKLNIEKGSLTSMVDDLTDKKYVTRKRDLVDRRKYLI
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>CORE_REP|Org76_Gene786#

MNINEIKELLKAIDSTNLEYVKLESSDLRLEVSKKAQSTSSPVLSVQQESVVDLSLEKPVVNDTPVTSNENLSVVVAPLMGTFYDSPSPDADSFVK
VGDVVEEGDTLCILEAMKLMNEITSEIKGEIIEVLVSNEELVEYNQPLFKIKPL

>CORE_REP|Org36_Gene1399#

MLTYLMKRQMHKKDDGMSKPMMITGAVITGVGAYAVYKMVKSHKSNSQMVNTNYYGNSDYDDYKYDEFDYDCDCRDTKQDYEYEELKK
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>CORE_REP|Org52_Gene2415#

MKLSTKGRYGLKAMFELALNQDNGPVSLKFIAKKQKISDQYLEQIFSSLKKSGLVKSVRGAQGGYLLSKNAEDITVGDILVVLEGPVALSDCVLD
EDVCENSNMCVTKIVWEKMKKGIEDVIDSITLKDMINDYNKNKLENDITNIKK

>CORE_REP|Org13_Gene2780#

MDFKNLQYESLSYIICNLQKNFKLYCEKCLKPYKLTNGLYFYLIYINKNRNCSLNDVSTEFEVDKAHTTRTISRLEQDGYIEKIQNPNDSRAFQLRV
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>CORE_REP|Org59_Gene1252#

MSENGLSKNINIVDLLLNADTENLERPSTIVELKRLSTIFGQEFKVMCRALTISKDEEIQNTCLKIDENMKTDIDLPEMQMLTIIEGVCDLDGKLLF
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>CORE_REP|Org46_Gene2957#

MSKNKFIYMNYYDNGYFKRGMAIYMVLALIILATIFIYSTTILYILCIITAVFLFKQGRDFSNKYEGKVYITLDNHSILINNQCIFSIKSKQSQKFNYKII
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>CORE_REP|Org9_Gene2340#

MNVDLISLGLESNDYESVIEELGSIMCKKEYVKETYINAVLERERTLPTGLDIGEMCVAIPHTDSKHVNESNVAVGILKNPVKFNSMIDPKDRLD
VELVFLLAVKNPDSQVKLLKDLMSVFQNIKLLKNIKNASTKEEVAKLLDFIEI

>CORE_REP|Org67_Gene2718#

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>CORE_REP|Org93_Gene1829#

MSLKQKLQEDLKSSMKNKDTVRKSVVTLIRASIKQYEVDNRVELDEDGIIDVIAKQLKQRRDALVEFEKAGREDLIKETEGEIEVLKEYLPQQLSE
EELEEIVKSTISEVGATSMKDMGKIMSVIQPKVKGRADGKLINKLVKQNLQ

>CORE_REP|Org46_Gene2065#

MDEMSFKKELLELTRDINMKFTTLLTKFYQPLGITAVQALILSELCEHGEKKISDLGKNLNMTNSNVSVICQRLEKNGFLNRIRDIEDQRIVKVKV
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>CORE_REP|Org76_Gene1404#

MLKYKEILETIIEILKKNFTESIFIDDESVQGSEGSCFFVSILSVICTPIMLNTNNKDIVISIKYLPKPQSKSIRMYEISDELNKLFNRNIKVTDRKLNITK
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>CORE_REP|Org74_Gene1091#

MKKNMLYVGIIYFICGILLVLLATFTEFSFEAFIWGLSGAALGPGVCMILQYMYWSKPERAVDYEEKIKNQRIEMNDERRIMLRDKAGRITNQI
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>CORE_REP|Org27_Gene1455#

MFKIKHFNDLSLDEFYEIAKSRYEVFACEQKIFSLNDYDDIDKSSYHIFLKENGLICAYARIIPKEYSSYNDVSIGRVLVLSSHRRKGLAKQMMDCAI
DFIKVNLHENNITLSAQTYIKNLYLSCGFKEISEVYDEAGIEHIKMRL

>CORE_REP|Org96_Gene2652#

MNQQGFIMEIVDDRTAKLKMQRHSACAACGKCATTNSAESKEILVEVDNTIGAKVGDHVEVSMDNMNVLKAAVMAYIIPLIALLVGTIGTYY
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>CORE_REP|Org90_Gene1014#

MKLNVRIADINNWHDLVSLSVDKSQLDYIESNALSIAESKFITAWVPVGIYDENSLIGFAMYGRLEDDRVWLDRFMIDSKYQGKGCGKASLDF
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>CORE_REP|Org68_Gene1232#

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NGEKILDNEILKFVSIISDKMDCLDIDNKDKLFTSLEESKNIIEQLF

>CORE_REP|Org18_Gene1063#

MNIIQYIFIERGFFMKKLDTESLEKMAKQKNIDKDKIEKMADSYKGKSENELMEELIKIGKNLDGRDEVVSKFKAFLDENQRKKLDNIMEKISDA
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>CORE_REP|Org23_Gene2888#

MEDKYIVHFISKTKASMIKFIENKLSKNGLGELIPTHGNILTALYENNGILTMKEIAAKIGKDKSTVTVLVNKLINLGYLERQKCTNDKRITYIKLTKK
ALLIEDTFNSISTQVKETAYHNITENEKQEFLRILKKINDNFKNAD

>CORE_REP|Org3_Gene1083#

MDFFSEIFNNGALGISLIACFLAQFIKIFTGKEKRIELSRILISGGMPSSHSSFVTSLATVVGIEKGFNSTDFAIITVLALIIMYDAAGVRRAVGKQATI
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>CORE_REP|Org83_Gene1616#

MAKVVSINISEKKGVIKVPVQCAELKINHGIVGDAHAGNWHRQISLLGKESIDKMKMKGFDQLKYGDFAENITTEGIEVFSLPIGTKLRIGQCEVEVTQIGKKCHNGCEIKKLTGDCVMPREGIFVQVLKEGIINVNDSIDVI

>CORE_REP|Org23_Gene1228#

MRATGSIQSLMETTLETIKGSIDANTIIGDPIKTDTTVVVPISKVTIGFGIGGGEYSKGYDDKDREIELKNEKSDTNFAGGSAGAISVQPVAFVVVESGETRIMSLDSNINLVDNILSITPRVLEKIQNISQSNKNQDKNNM

>CORE_REP|Org46_Gene1933#

MSKIYIVYWSGTGNTEKMANFIAEGVKSKGKTPEVLDVSLLKPSDLKEENKFALGCPSMGAEQLEEGYMEPFVSELESMVSGKQIGLFGSYGWGNCEWMREWEERMQNAGAVIIGGEGITAMEEPDEEAKDECIELGKMLAE

>CORE_REP|Org95_Gene1169#

MANMEARNVMSGTWGELWLDGNKVAEVKKFQAKMEFTKEDIIIAGQMGTDTKYIGYKGKGSITLYHVSSRMHKLIGEKIKRGSEPRFVAISKLNDPDSYGAERIAVKNIAFDDLTLADWEVGVKGEIEAPFTFTEYDFLDII

>CORE_REP|Org60_Gene2323#

MNNKLHELEKNLPETSCSFCTHLSFKGPSLDYRYDIKCVISDTKPDFRGCCEHFEPEYTELNTGDLDNLYINFLETCLKVNYNDYINSMYWKLFKERTLLENNFKCSICGSTENVDVYHVNKNLGRETSKDVVVKCDKCNCK

>CORE_REP|Org30_Gene1314#

MTKLWAIIFALLAGGSTALEAFINGELGKSTTALVATFISLTVGAIFFLASIIVTGDLKCLVSINGFNYKLLLGGVFGGLIIYFTVKAIPNLGVSNTLILTLVSQVLVGFFIDSVILGQETMHLYKYIGVVLLILGTFFIVN

>CORE_REP|Org8_Gene1239#

MNILFFLTPKSEVAYIYEDYTIRQALEKMEYHKYSAIPIISKDGKYVGTITEGDFLWTLKNDLNLDLKGLEDVPVTDINRKMDNSPVSINADIEDLVIKSLNQNFIPVIDDQDTFIGIIKRRDVIGYCYEIIRGYKNLANDN

>CORE_REP|Org53_Gene1160#

MLDGRIMGLDVGDKTIGVAVSDLMGLTAQGVKTIKRVGKKKDIEELKAIIKEKQVNKIVSGLPKNMNGTLGPQGEKVIKFCELVKAETGIDVEFWDERLSTVAAERSLLEADVSRQKRKKVIDMLAAVIILQGYLDFKINS

>CORE_REP|Org40_Gene956#

MKYVGLLLTSVGMFLLIAVNFYYNSITLDMQRIEDYVMETNLILEDVAEKESYVSNEKEDYISRLMHVKKGIENSKTSFLIERYKEYKIKSIESLIYTISEEKKDYLDEVDRYNKLGEKEINKLINKNFLEVTYLSITTYI

>CORE_REP|Org33_Gene1232#

MENKNSKCVMVIDENLPMGIISNTAAIMGITLGKHAPETVGPDVIDKTGNSHLGIIDIPVPILKGNKEIIKDLRKKLYTLEFNDLTVVDFSDVAQSCNLYEEFTQKIASVPEDELQYFGIAIYGNKKKVNKLTGSMPLLR

>CORE_REP|Org61_Gene2230#

MKSLFKFNKELCTACGACLLACIDQNDNDIDNGELFRCVFTIEEGESVEYFSLACIHCDEPKCLDICPKDCFKKEEGFVVLDNQNCIGCKLCEKACEYGALIYGNDGKANKCNGCIERYKCGMDSPCVMVCPTGALKFNK

>CORE_REP|Org68_Gene2346#

MSKVLNENNIFLGLDSVSKEEAITLAGRKLVENGYVKEEYIPAMLEREKVMTTYMGMGVAIPHGVNEAKKEILSSGIVILQFPNGIDFDGEKAYLLIGIAGVGDEHLEILSNIAVVLDDDLTERLKNSNDKQAFMEAFAN

>CORE_REP|Org96_Gene2161#

MNTFKTEVLLKYSAKDIFNIFTKSARLNFPNFNEKKAVGTFVQQKNNKRFKVEITNFEKNRVYEIKTSNKRESTITRYELVHIDLENTKLIFIESESKRNIFGKINSALVRVLFGKRQPEEFNKFIKKLEMELENNSVNL

>CORE_REP|Org48_Gene1896#

MNKKKNLIGMAISFLLIISIINPLQVEAETIIESSVYISSIQENCTYNNTKFKTIKSRSRHKISKSNKSKVKLKKRSIRTKKYGYQTINKYKIRNARRHNILTKLILLIIVIFIVIILVILIFIKRKKVLLKIIKRISFF

>CORE_REP|Org73_Gene1488#

MDTLGERIVYLRKAKNLKQYELEKMLGCDNLSKFERNIRKPNYEILKSIAEIFNVSVDWLLNGDNLSHKSDLICDSSSNYPLNSINSNEIKLLNNFRKLNDYDKAKIEGMIELKLHEYEKEKDLGKIEYNKNKDEKIDK

>CORE_REP|Org63_Gene2377#

MSLYKFIYDDKEYLLKEENCSALINDEENPVQGVSISKIIDILNEAEEVDFDVEYYQEACPLCLEGVKEKKKFFPFLEYHFYIFSRDGEYVISNISIDYKGLSFNKLSRANKVDNSYIVSVIICENCQDYIVQIENCIV

>CORE_REP|Org21_Gene434#

MTVIELIVSISIILLIVTLSFPKDNLENHKINLFARQLCSDIRYVRRINMFSNYNTYIYYINQGKHEGYVLRKDGKNIKSIMLPKNAKIARSIEIIKFKSDGSPQKASTIEIYNNRLRKTITITPVSGRVLLKEGKYET

>CORE_REP|Org71_Gene1853#

MDKISGKLTVLFEEPFWVGIFERQDGKKYEACRVVFGAEPKEVEVYEFILERFFSLDFGSIKLEKNVTKDKIGYKRMQRKVKKEQEKETIGTKAQNALKLQYEERKQDRKNLAKNRKEEEKERLFNLKQEKRKAKHKGH

>CORE_REP|Org63_Gene2021#

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>CORE_REP|Org93_Gene1163#

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>CORE_REP|Org44_Gene3415#

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>CORE_REP|Org97_Gene909#

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>CORE_REP|Org67_Gene2907#

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>CORE_REP|Org48_Gene1938#

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>CORE_REP|Org28_Gene1315#

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>CORE_REP|Org4_Gene2684#

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>CORE_REP|Org13_Gene631#

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>CORE_REP|Org17_Gene861#

MVLNLDFNSDKSIYVQIKEEITKAIASGELKINESLPSVRSMAENIGVNLHTVNKSYNELKEEGFLNIDRRKGAIVAQLPMKIDNTTRQKNKLDLE
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>CORE_REP|Org1_Gene2616#

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>CORE_REP|Org80_Gene1138#

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>CORE_REP|Org87_Gene1729#

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>CORE_REP|Org42_Gene1292#

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>CORE_REP|Org50_Gene1311#

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>CORE_REP|Org18_Gene2837#

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>CORE_REP|Org49_Gene1613#

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>CORE_REP|Org39_Gene3462#

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>CORE_REP|Org18_Gene1205#

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>CORE_REP|Org46_Gene2186#

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>CORE_REP|Org1_Gene1945#

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>CORE_REP|Org16_Gene2264#

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>CORE_REP|Org40_Gene1659#

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>CORE_REP|Org34_Gene1281#

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>CORE_REP|Org89_Gene1133#

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>CORE_REP|Org74_Gene1129#

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>CORE_REP|Org31_Gene1140#

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>CORE_REP|Org48_Gene1434#

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>CORE_REP|Org60_Gene1770#

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>CORE_REP|Org74_Gene1739#

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>CORE_REP|Org91_Gene1340#

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>CORE_REP|Org89_Gene2581#

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>CORE_REP|Org37_Gene1742#

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>CORE_REP|Org71_Gene2521#

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>CORE_REP|Org80_Gene2371#

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>CORE_REP|Org91_Gene1570#

MNFELDNTTPIYLQIVKYIKRQIVTGELKPGETIPSRREMALNLKVNLNTVQRAYKEMGDMNIINTFKNYQSSVTVDENILKNLKLELINESLSVFIEDMKAINVSKEEVLKIIEDKY

>CORE_REP|Org54_Gene2559#

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>CORE_REP|Org94_Gene2188#

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>CORE_REP|Org74_Gene1916#

MDNTITINISIIYVLLAILACIALVYLIIVLVKLHKILNNVGTMLNENTQNINTTLNNLPNVVETFGEVGENMKDVTEVVTEVTADFLVTKDSVKSNMDVIVDILTIIKNIFVDKK

>CORE_REP|Org84_Gene2478#

MSAKVTNQYGSIEIDNQVIAQVVYRAAMESYGLVGLAYKSKGIVELLKGENATKGVRVEEVEEDAIAIELYVIIQYGTNISTVANNIIDRVKYVVEKMTGVRVTRIDINVQGIRVK

>CORE_REP|Org87_Gene1097#

MNEMLRAIEQEQLKNEVPNFGPGDTVKVHVRIIEGKRERIQVFEGVVLKRQGGGARETFTVRKMSFNVGVERTFPVHSPKIEKIEVTRKGKVRRAKLNYLRGRVGKAAKIKEARNK

>CORE_REP|Org93_Gene1197#

MHENKKNLLDGSLAQYNDTAVPKIPVFAGNDITSEVYYFKPNQVLNAHRHPNGEQIFVFLKGEGKMKLGEHECDVKNGDTVFVPTGEWHEITNGSNEEMVAVQITKINAGAEYRG

>CORE_REP|Org95_Gene2094#

MIRKKSELQVEVKENLNGGIGKVKLENIIQNEELKGKGRLFKRVALPVGSSIGVHDHTTDFEVYYILKGKGKVFDNGEFVEVNEGDVVYTADGEKHSIENIGEEDLEFVALVLYM

>CORE_REP|Org11_Gene1455#

MSKSNDVLDIVFKITDGLEYEVAENSVVTILEKQDHKIQKFFRKLKARIPKYKKIELDEYSSFVFLQIDGQRTVREIGKNLEAKYGEESHPLYERLLVFLNHIEVNCHYIERLDI

>CORE_REP|Org82_Gene1678#

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>CORE_REP|Org29_Gene2579#

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>CORE_REP|Org62_Gene1272#

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>CORE_REP|Org67_Gene1253#

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>CORE_REP|Org74_Gene1875#

MKEENFINVEYEDKRFSINSKEVLYIEKQEYEVKIYTESGNYEVGENAPCIRKLLKEENFFKCSNSYIVNLDKCEFYLSNNCIFVNNNFIRILGSERKK
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>CORE_REP|Org1_Gene1468#

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>CORE_REP|Org37_Gene1921#

MFAVGFVVIIALAFFILSVLLFNGKASMLLAGYNSMSKKEKARYDKKKLCRSSSIVTFIVSIMLFIMAFLGYRIESGQMDEKKMVPFSIIFIIVILSSV
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>CORE_REP|Org45_Gene2936#

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>CORE_REP|Org88_Gene1578#

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>CORE_REP|Org39_Gene2479#

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>CORE_REP|Org78_Gene1483#

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>CORE_REP|Org39_Gene2343#

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>CORE_REP|Org49_Gene1500#

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>CORE_REP|Org17_Gene980#

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>CORE_REP|Org18_Gene2314#

MNDMARDVFSVKMTPLEAQKMVEKNLEADLVSVDIYNLENNKSIIVTIFEKYYARSNSDAGLVVICENTTGKTLVKITSTGSAIGLFQIDWGTGNNLIKRVKKILIDYII

>CORE_REP|Org81_Gene1703#

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>CORE_REP|Org92_Gene2661#

MERINCNVINCSHNNSHICYADKIFINGEKAHNDRHTCCSSFLDESIYSNLSSNVNNKNCEELVCTVKNCKYNKDGSLCTLDNILVAPETDRVNLYIETCCSSFECK

>CORE_REP|Org28_Gene1233#

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>CORE_REP|Org27_Gene1897#

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>CORE_REP|Org1_Gene2638#

MSSKYNVWTFNYEFLGLDSGDEKNNEVYYEIDLDEILNENYIDEDIDSGLDSDGNSILGELISEMDIDEDVSVDMTYQELEVDLEDLDSYLDEDIDSDIKGILDEI

>CORE_REP|Org39_Gene3812#

MDEKIIEISFNIIGYAGEGKGLAFEAIKEAKNGNIEKAKELLKESKEVINKAHRYQTELIQNEASGNKTEISVILIHAQDHLMNGMNFQQLAEEIVDLHLKLQDK

>CORE_REP|Org59_Gene1041#

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>CORE_REP|Org9_Gene2217#

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>CORE_REP|Org70_Gene2409#

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>CORE_REP|Org92_Gene1522#

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>CORE_REP|Org36_Gene3621#

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>CORE_REP|Org19_Gene2019#

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>CORE_REP|Org53_Gene2454#

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>CORE_REP|Org6_Gene1037#

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>CORE_REP|Org49_Gene1131#

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>CORE_REP|Org31_Gene1494#

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>CORE_REP|Org52_Gene1233#

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>CORE_REP|Org67_Gene2687#

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>CORE_REP|Org84_Gene2746#

MFNKVYEKKEFIVFQVKKGYVVYNTRKSFEEGHTHLKHFEAAKTAIDLAINKKIPRSKDGYYLTSLIRISDDGYYIDKLSELLYVREQKGKKEKYCNSGYQM

>CORE_REP|Org40_Gene2393#

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>CORE_REP|Org20_Gene1298#

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>CORE_REP|Org92_Gene1462#

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>CORE_REP|Org60_Gene1963#

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>CORE_REP|Org65_Gene1337#

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MILQINICTLGKINIGSIIFTEEVVLMDRLKRDMKNMKEDLKEGVKKTAYVMKNTAEDLKDDAQGAMVNLEIKKDEMMERYEQKKFSKELEKQMKNEMK

>CORE_REP|Org18_Gene1992#

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>CORE_REP|Org75_Gene2890#

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>CORE_REP|Org33_Gene1095#

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>CORE_REP|Org78_Gene2357#

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>CORE_REP|Org3_Gene1169#

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>CORE_REP|Org42_Gene2033#

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>CORE_REP|Org2_Gene2167#

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>CORE_REP|Org58_Gene1239#

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>CORE_REP|Org9_Gene1788#

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>CORE_REP|Org1_Gene1869#

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>CORE_REP|Org77_Gene1794#

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The essential and non-human homolog core proteins in the FASTA format

>CORE_REP|Org39_Gene1249#

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KSIDSYIEKSFENAKTTSYNSVESCLNAINEGKANLMVLSSYQFDELLRKGKSENLSVISVLDTSYGMRIGVSNKTNPILVSILNKSIDKITEEELSDCI
YSNTIDKPYKVPFGVIFKEYSIQIISFVCILFLIAIKYIIYNKKKKEDYLKRIAYTDSLTGADSIDKFKINSNKLFAKNNPEEYALFYMDVDKFKYINDMF
GYDMGNNTLIHISDTIASELKEDEIFARVSADHFVLLIKYKTDDDIKTRLNSIYNKVQIFSNPKINYYKLILDCGIYKISKSDNDINTIMDRANTARKT
IKGGHKNSFAFYDKEMHKKILKEKEIENSMVDALNNGEFVVYFQPKYRLSDYQIIGAEALVRWDNPQKGLIPPIEFIPVFERNGFIVNIDFYVFEE
VCKKIREWMDEGQEVVPISVNLSRMHFVNSNFIEKFKLIVDKYKIPTSLIELELTETAVLDNIEGLLDTMNNLKENGFVISMDDFGTGYSSLNLLK
ELPVDILKLDRAFFTEKDESNNEKIVISNVIKMAKELKMKVISEGVETISQVEFLKQIGCDMVQGYLFSKPMPVKEFEKIAFKKE

>CORE_REP|Org18_Gene1463#

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SAEGGIKKNKVISINKKYEKSFKCVSSDLVDMTLEQYFETFNIDFFDNREFKRLNLTQEKKAEIVSYNDTANCIVNFVMSDSEGEEHVEEVRVGD
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IYKKDETVEIIIKDTGVGIDKEKLNDIFNRFKQIENSGISNEFGSGIGLCLTKSLIEIQNGKIYIDSKVGEGTNVKVIFPIKEVVEEVYDNSNYNDNIEK
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ISVKDTGVGIPQDKLELIFEEFSQVDKTLSRNTEGSGIGLAIVKNLVSLHGGDIEVVSEVNKGTEFLISLPMKGFSSEHYTEDKRIYNIQEKIKIEFSDI
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>CORE_REP|Org36_Gene1812#

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KIYKKEQATRAKNNFFIKDNLVALREIALRKTAERVNKEVQMTRLSKGDVTVIPTSDTLLACISPSPSSAKVIRTASRISDSTFAKWIALYVETPNTA
RLPFDEQKQLQNNLKLAKKLGGEIIVLHGENIIEQILRIAKLRNVTKIVIGRNHSSNKRFSKRFKKDIVDKLIDEVDYIDIHIIPYKFASDVKYKPKKDK
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ITSTLTSKIQHEAETAAKREENTKMIYQIIKGFLRLSNKDDIVNKGIELLSLSLSRDVICYLNVDKHNKSKLYKKNTNNKDKNDLDSEDEKAVASWV
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EQVLINLIDNSLKYSKEDCKIEINVYEKDDYVWFEVSDNGPGISKELKKHIFDRFFTGEEGAKDSRKGVGLGLSICKSIIQAHKGEIMVENNKDKG
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ELYHHINQALRAHVIMKKDVDYVAKDGEIVIVDEFTGRLMFGRRYSEGLHQAIEAKEGLKIQRESKTLATVTFQNYFRMYKKLSGMTGTAKTEE
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KEIKNDFPQDPKEQLMLAIEAVFRSWNNPRAIVYRKLNDIAHNLGTAVNIQSMVFGNMGETSGTGVAFTRNPATGENKLFGEFLMNAQGE
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QLLHPKFEDNALKEAKVIAKGLPASPGAASGKVYFNADDVVKANEKGEKVVLVRLETSPEDIEGMVKAEGILTARGGMTSHAAVVARGMGKC
CVAGCGEIKVDEFNKEIRALDDVVIKEGEYISIDGSTGNVYLGDVKKTEVSLTGNFEKLMNWVDKHKCMMVRTNADNPRDARAAIEFGAEGI
GLCRTEHMFFDEARLPAVREMILSNTVEQREKALEKILPMQREDFVELFKVMDGKPVNIRLLDPPLHEFLPHDDETIEELSKSMGIKVSDIKKRIV
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TADEIAQEADFFSFGTNDLTQMAFGYSRDDAGKFLGQYVDEEILEKDPFQVLDQNGVGKLVKMGAKLGREVKPELKLGICGEHGGEPSSVEF
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VFVPQYAENALKINAGSGGYFVAILGLFAGVAAPLSGRLIDKFGAKKILLLGFSVSMIGSLYLVLIALKTNTVFSVCLSLMFMGLGMGFTMGTPL
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AGINQGIDGVKKGIAGIDKGIKGMEQGLKKQDKAIDELTTAYNKIPTTEKIPTNNENNSNEQNQDNASNSESDATNNDSTENKNNNSNDNKP
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GVELFTTQSQEEAVEIASILEEKNNERQMIEAKMYHEAEEMLKSNSRYNDDKVLVLAKEGWQHGIIGIVASKLTEKYYKPTILLGIENGEATGSA
RSIKGFNIFEALIKCKDLMTKFGGHEQAAGLSLDSDNVEILANEINKFADYNLTEDDMIENVNVEFELQENVINLNLVEELHKLEPFGLNNPNPR
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KAEEKLPKIVIIIDELADLMMASANDVEDYICRLAQMARAAGMHLIVATQRPSVDVITGVIKANIPSRIAFAVSSQTDSRTILDMGGAEKLLGKG
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LVFEDKVTTLEELTKALNNDWEGYEELRKLALDVPKYGNDNDYVDSLAIEVSDFYYTETRKYKDIFGSKFNSAFMGISNYVPTGKIVGATPCGRK
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WLPMYILSSLSLKIFSQNIRNTRWTNIYETIMFQSLMPAVILETFAISKNKFSVTNKNKLEENRMYKFLQGIPYFIYMVLSIIGILKMFVAIFKMSS
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AKIVNVVELNSKWKYAAYITHIEDSEIDNWMCIVHDRIPTLPMTISNQLGFFDDLQINVKKRIEKTRTLSRRSPRVNMNFQMDIKNIGKLRIVNF
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RSNGDIVLNPSSKNANSTKENLFSYIGRSDSISKSSINNMKSNIKNFKSGSLSYSMFGKGYYLSYAPIGINDWYLFSEVPKTAISEKSYAIIKLTLSAC
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FILLIACSTEDELLNRLSKINKEICNLSTTNSSKYKIVMSSGIYKINKKDDIKKIDLLIDRANIAAKSKKEKYEHSYSFFNEETRNRLYKEKRLEDNMNK
ALEKGEFIVYYQPKYSLNDVNEIEGAEALIRWNSPEFGFISPIDFVPLFEKNGFIVNIDMFVFEEVCKTLNKWINKGYTPVPISVNMSRVHLYRDN
FIENITDLISKYNISPEFIELELTESVVFDNLNILIDIMKKIKEIGFLISMDDFGSGYSSLNLLKDLSFDILKLDRGFLIETTDTKRGKIIISKIVEMAKAIDI
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DANKFERQFDLLLSIIDDGIICTNNDGIIQFYNHIARKILSINANEMIDSFVGDCIKDINFQNILTNKTPFFEKLIKINHIDINLEIKHIQLNVFDGFILK
MTKFSQLEKKQAKLRAQLVNSGNISKYTFDDILGSSIQTINTKKIANKMAQSNSSILIIGESGTGKELFAQSIHSASRRKDGPFVAVNCSTFQENLL
QSELFGYDEGAFTGAKKGGKIGLFELANNGTIFLDEIGEMDLNSQSKLLRVIQEKQVRRIGSNNVIDIDVRIIAATNRNLKELVSKNMFRRDLYFR
LNVLPLKIHPLRERAADIFEIFGSLKYDIPCNFILSEEVKEIFKMYRWEGNVRELRNLGEYFCYLGKDIIEICDLPEYILDTIDSNYSRTVCNKVSDNIK
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INRSNKLNS

>CORE_REP|Org65_Gene2693#

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SEYLTGTQGKDPGYDPLPFLIEEAHKRGMEFHAWFNPYRITMADESIDKLPANHPAKKNPSWVVKHGNKYYYDPGLPEVRKYIVDSIAEVVQ
NYDIDGVHFDDYFYPGVSFNDTATYQKYGKGQNKDDWRRENVNTLLRDVKASIKSIKPNVVFGVSPAGIWRNKSSDPTGSDTSGNESYVGTY
ADTRAWIKQGLIDYVVPQLYWPIGLKAADYSKLVAWWANEVKGTNVDLYIGQGIYKQGQSSYGGQNIAKEIVQQVTLNRKYSEIKGSMYFSA
KDIANSTSIQKDLKSLYSSSEEPVTPPSNVKVEKLRGDERYDTAVAISKKGWATNSDTVVLVNGYSIVDGITSTPLATSNDAPILLVNKDNIPTSTK
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NELKRLNPSKVILIGGNNSIGDKVESEIKDTLSNVSINRVGGSDRYSTSLMIAKELVKTNPVEKLYITSGTGEADSLSIASKAGEEKQPIVLVSKDNV
SDEVYNWISDLKVKDAYFIGGNLSISDSVINKLDKVITNDVSKNRIAGENREETNGKVIQKFYPNAEYSSMFVSKSNQLVDALTSGPLAAKLKSP
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>CORE_REP|Org95_Gene1329#

MNKHNFEVILNQLQINIYVTNIHTNEIIFMNKKMKEEYNILDPEGKVCWQVLYPEKNSTCSFCKVLELLKNDKKGVLIKWYEKCNKLNRVFENY
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PGEIVKNPLVYWKKIVHPEDWNRFYKSNTEIGKNQMDYHTVEFRAKNRSGEYIWLRCRGQLMRDEFGEPSIFAGIMTQLGKQNKIDSLTQLL
NYHEFMSVFEDKISNPMIEKLCIVLLDIDDFKNVNEMYDRDFGDNIIKTLAQSVQSILPDNAELYKLDGDEMGILVDNVEENEILTLYNQIQNMI
IHLQLWRKYGLNITISAGCVIYPKHGDTVKELYKCASYSLQYAKEHGKNRLVFFSQEILKNKMYSLEMMRDLKASINDDFRGFSLRFQPQVDTES
HKIIGVEVLLRWTNDKCKAISPLEFIPILEENDMINIVGAWVLRMALRTFRKWIDYYPFFKVSVNVSAVQILEDTFIEDIVKIIDDENFPYQNLVLEL
TESHTVQNMSILQFKFKALQDLGIYIAMDDFGTGYSSLEVLKFSPIDIVKIDRVFVKDILKSKFDATFIHFIVAICHDVGIKVCLEGVETQEEYDLVK
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>CORE_REP|Org18_Gene2588#

MLDLYKDVQYVKGIGPKKADKLNKLGIFTLKDLLYYFPRQFEDRNNLKKIAQLEDGEKVTIKAVISSINTFSPKEGMTLTKIDVKDETGSAKLVFFN
KSYIKNTFRPGDSILVFGKVKKKFNNLELTSCELEYLTNSPKNTCRFMPVYQLTYGVTNKEIMSIIRTVLEDKELIIQEYMPQRIIEKYRLCSIDFAVR
NIHSPSSKESLKIALYRIVFEELLILQLGLFVFKSGRNKEDGIKFETSKDLKKIISALPFKLTKAQNRALDEIIQDMNLEKIMNRLVQGDVGSGKTVV
ALLALANCVLNGYQGALMAPTEILAGQHYISLTESLKDFGINVGLLIGSLTKKQKDTVLEQIKNNEIDILIGTHALIEDKVEFNNIGLVITDEQHRFG
VMQRSKLSLKGANPDILVMTATPIPRTLALILYGDLDISIIDELPPGRQPIETIAIEKSKRDRAYNNLVRREVESGRQVYIVCPLVEESEAIEAKSAVE
LVEELRAEYFHDLRLGLLHGKMKSSEKDEVMRLFKNKEIDILVSTTVIEVGVNVPNATLMIIENAERFGLAQLHQLRGRVGRGSHKSYCVLIYDS
KTDVCRQRMAIMEETNDGFKISEKDLEIRGPGEFFGTRQHGLPELKVANLFKHIKILKLAQQEARYILGEDNNLQLKENMALKKEIIDKFKDTLK
EISLN

>CORE_REP|Org49_Gene2710#

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YKESADETAKIIRKLGLIHINLIPYYPGCDKSKCEIGIITGSRNSIPQNIKQIIDIGDKIIDINTVIEIFTKLNISIDKLHIIKEKYDEDTVSGYRYYTTMNKT
MKSFLEIIDEGIASIDKLGKFIYCNKVFSNLIGIDQNEIISNNFMDLFSDKVVKKIFFQEDEVNDEVVNLNNKKLIINKVNVYENNERIKSIISIKDISAI
QVLEDKIQNKFQAKGFVSKYTFESVVGESKIIKEKINIARKIAITDFSVLILGENGTGKEIFAQAIHNESLRKNKPFVAVNLSSLSDTLIESELFGYEEG
SFTGAIKGGKMGIFERAHTGTIFLDEIGDISLDVQQRLLRVLQEKEVMRMGGSKIIPIDVRIIAATNKDLKKKIKEGSFREDLYYRINVLHIEIPRLRE
RKEDISLISKYFLDEINSNKCFTEESMKALKLYEWPGNVRELKNLVYYIDTIVEEDRVDYEHLPEQFRFEKNNTLVNENFDSIILDFKQSNFFEESICI
LTSVETWNNKNILLGRNKLQEILKEKGIVLSVDQIRKRIDKLKSHGLLLSGVKKQGSFITDEGKNFISYIKFKGVI

>CORE_REP|Org82_Gene2537#

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TSLDNISKLKTILYMTIDEIGDGLIFFNTFNKVTFVNKSLLNMLELDEKLIKSPSLMEYMPKSFLDKITKNLNIDNMIIYIDEIDKKFILSKKPFYLYKNI
EGCLITLKDVNNIEILEQKIRSDSVKRGYVAKYKFNNIIGNSSIIKDCIKRAKKMALTDNPILITGETGTGKEAFTQSIHNHSNRKNKPFVAINCASL
PSELLESELFGYEDGSFTGAKKGGKKGLFELAHTGTIFLDEIGDMPHDLQVKLLRVLQEKEIRKIGGTSIIPIDVRILAATNKDLEKLIIENKFRMDLF
YRISMFTLDLPPLRKRLEDIPLLLESFLKELPYKNIKLDKSLLEALNSYTWMGNIRELRNCVEYMAYMGSNYLTINDLPQNISSKLNNNHMSSNM
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>CORE_REP|Org36_Gene176#

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VNDSDETTLETISLFYKIGVTNIRPIPYMNDNNYKNIKIAITPGVPEKVPSFISDIFDLGHRYIDISTFIEIINLLQIDSKEIQSNLVKYSEEIISLDTGIKD
KYKELFLKIEELDTILNLSKDGILFTSKDGEINTYNSKVKDILDINEDIYGKYIEDIFVDSLKVLLSEKEILDKVVVFNKKYINVNKKNIYNRDEKMGTY
YSLQEITYIKKLEQNLTKKLREKGQIAKYTFKDIKTNSPKMFECIDLAKKVSKSDLSILIRGESGTGKELIAQSIHNNSNRKNQPFIAVNCAAVPENL
LESQLFGYDKGTFTGGLKDGKQGLFELANNGTIFLDEIGDMPLELQTKLLRVLQEKQIMPVGSHNVINIDVRIISATNKNLEQMIDNSQFREDLY

YRLNTIPINIPPLRERKEDILIIMEDLINKKLIITPEAKKLIQNYMWKGNIRELQNVTSYLNIMCEDIVLEKDLPPNLRSSDNKNTSLKLKYSKNDILNI
LEILILNKESDVGIGRGLILKALLDKNLQITEGKIKKIFEYLKKEELIICSSGRYGSKITQKGEDFYNKLKYKGL

>CORE_REP|Org14_Gene669#

MILLQKKIGIIASDIELKERIEELYREDVENGTIIIDILNLDLMENQGRILVEKGAQAIIGRGGGYSLVIDTVNVPVIPMNMKSTDLLRAIEIAKKYSK
KVVLILGDNEVSFDYVGWRNVISTEITEEWFESKYEIRSKVVKYIDQKDEVVIVGGGLACSFARQYGIDSVFATASDESIREAVEYCKKLLDTLGEE
KFNNEVLRNILDGIKDGVIAIDSNGSIILYNESAKNMLKVERKCALNKYILDVFPKMEWMLDCLHEKEAVEDRKIRNINNLIVNTRTTLIKVDNST
YGVLGIIQDITKLQNLERKIRFDLNQKGLYARYTFDDFLFKDKLTKEFIEEAKKIGKSDYTTLLYGESGSGKEIIAHSIHNISKRKDRPFVAINCATIAE
NLLESELFGYEEGAFTGARKGGKRGLFELAHGGTLFLDEINSLSFNIQTKLLRVIEERQIMRIGSDYIIPLDIRIIAATNESLTEKIVMGTFRADLFYRL
SSLEINIPPLRDRREDIIPLFNNFVNEVLKDDGLNGINSIDENFVLTKDEIDKLYNYSWPGNVRELKTIAQKYVVTGKIKLRQDRNFKTKQSLSNSE
VDKFNSETTASAEVQDESINISKINDGKISIDIKEVNKYVEEKIISMLFAQGLSKNEVAQVLGISRTSLWKKYNKNI

>CORE_REP|Org18_Gene1724#

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FKPNNWWKESFVNSIDDSIKFFDLIPSKERANKFIFTDPIYTLSANILKDKKSQDINSYMDLKGKTVAIPEGDYSINFLKQKIQDINILLTPDIKTGV
NHLMSGKVDAVVGDEPVLRYYINNYGLSNKYSVLSNPIYTKKAVLAVPKQYEELVSILNKGIFKLQKNGVYKDLKKKWYSTYNEVDDILYERGIV
PSIYLFIGIILISIYVFYSYTYLLKIEIKRKTEQVIENKKTLEATFNSITDIIMLVDENNNIVESNKVLYDFMGEMSYKIADLISMIKGVIENTFSENTNKT
SEIEIHNKILKINTFPVEYKKNNTEYIVVLIKDITNDKIVEAKLLRENKMISIGQLASGVAHEIRNPLGIIRNNCYLLKDNVTMEEVNDCVKSIESNVD
RASNIITNLLNFARISDDNLEHINIRNFIENIVKLQYKMLQLKNVEIKIDCEHNLICYINGESLKHVFINLISNSIDAIHQDGKIIIYCYEKNHCLFIDFK
DNGEGIKEDALKDIFNPFYTTKPIGEGTGLGLYITYNEIKKNNGDISVESKLGVGTCFHIKIPLNKEVTI

>CORE_REP|Org48_Gene1112#

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PEQKLDLIIKQEENIDDFYRINIYRLIELCKYASSKYTRSKVRKLLPENFKYIIEELLHEHVKSEHKEEYYKSIVETIVDIGIAKEFIIAISTVIQKLVVDRLH
VIGDIYDRGPRPDIIVDKLIEHHCVDIQWGNHDILWMGAASGEKTCIANALRISARYANLDIVEDIYGINLLPLATFAIEMYKDDPCKEFIPKIND
QSVTTTEKSLMAKMHKAISIIQFKLEGEVIRRRPEFEMEHRLLLNMINYDEGTITLKGKTYKLKDTYLPTIDKKDPYKLTIEEKNVIDKLVSSFRGSE
KLQKHVSFLFSKGSIYLKANSNLLIHGCVPLNEDGSFMSMNIMGKEYKGKALMDRMESLAREGFFFKDKAEEKLYGMDIMWYLWTGKCSSLF
GKDDMTTFERYFIAEKETHKENKNPYFKLRENEMACKKLFEEFDLELDESHIINGHVPVESKNGESPIKANGKILVIDGGFSRAYQKTTGIAGYTLI
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>CORE_REP|Org86_Gene2665#

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LIVSTDASGREIPQGMEKYYEPVQGNGLVLSIDEVIQHYTEKAVQKAYELNNAKKVTAIAMNPKTGDILALASKPDYDPNDSRTPIYPYYQEELE
KYNDKDKIKGYYQMWRNPAVSDTYEPGSTFKLITSSSALEEGVIKDGEKFTCTGSVTVGGRKIKCWRHYRPHGTQEFKQAVQNSCNPVFVELG
SRLGVGKMYDYIEAFGLMDKTGIDLPGEAKGILYNEKNVGPVELATISFGQSISVTPIQLITAISSIANGGDLMQPRVVKSYTDNKGNITETVKPK
KVRSVISKETSKKMLEIAESVVTEGGGKIAYIPGYRLGGKTGTAQKVIDGKYAPGKYICSFVGIAPCDDPQIVVLAIVDEPTGVSAFGSTTAGPIVK
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>CORE_REP|Org45_Gene309#

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ESVASGFIFVLPAVILIGSQITFLEGLAVGVGGVLFGIGVAAIVHNYLIVEEHGKLMYPESMAISETLVASEAGGDSIKYMGIGFVISGFITVLTGSFL
NVANNVMSLVGSKFYKWKFDIEVNPLLLGIGFIVGLEVSLTMFAGSILSNFGIAPLIGYFTDMAKDGAMVWNNPAMPLNQMDVGAISSSYVK
YIGAGMMLCGGIIGAIKLIPTIIASIKETLKAKSSTGEGEEGSSIQMILLLGGVVIGFLAAFLISGGNIVMAIIGAIISLLLSLLFVIVAGRLTGTIGTSNL
PVSGMTIASLVIVTLVFVIMGWTDLEANKSLLLFGSFIVVAIAIAGGYTQSQKVTYIIGGSKNEMQRYFTIASIVGVIVVVGVILLLSDQLRATGDN
VQFALPQANLMSTLTSGIMSGSLPWVMIIVGVFMAIVLYALNLPIMTIAIGFYLPIATTSIILVGALIRLFVELVSKTEKEKEVKVSNGISLSSGLVA
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>CORE_REP|Org66_Gene2171#

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TFMAAESLNKMAENKGVSIKVETNGSAGVKNKLTKDEIENATCIIVAADKNVEMARFNGKKVIKTKVADGIHKAEELIDKAVNGDAPIYHGGD
GSHNESNEESESGFRKIYKHLMNGVSNMLPFVIGGGILIAIAFLLDDYTINPSNFGSNTPIAAFFKGIGDKAFGFMLPVLAGYIAYSISDRPAFVV
GFVGGALAGDGGSGFLGALLAGFIAGYLVEGLKKIFSVLPASLEGIKPVLLYPLLGTLLMGIIMTFLVIPPVTAINNAMVGFLNGLGGTSKIFLGLV
LGGMMAVDMGGPVNKAAYVFGVASLESGQFEIMAAVMAGGMVPPLAIALATTFFKNRFTKEERDSGKVNYVMGLSFVTEGAIPFAAGDPL
HVIPACVGGSAVAGALSMLFNAALRAPHGGVFVIPVVTHPFAYILAIAVGALVGMMLLALLKKPLNQEV

>CORE_REP|Org54_Gene2682#

MRESIDLEKESFFNRLFKKYKFRHLTLLILDICSVLVAFRMSLSLTGNLNAFTTNDIIISVCIYIVLHIVSFRLFKCYNTLWRYAGEEEIISIFVATLAYLIP
IYIINKLLGFDYPIMFYVLNTIFIIMFTSGARIAYRAIRIVMNKTYSRGKVSNILIIGAGDAGEMVIQELKRNSELKKVAVAIIDDDKDKIGRIIHNVKI
VGTTSDIKAVVEKYNVDEIIFSIANIEKRRKKEIIDICKNTNCKIKTIPGIYEIIDGKVDIKQIREVEIEDLLGREPIKTNLREISNYIEGKVILITGGGGSIG
SELCRQIAGFNPKELIIVDNYENNAYSIQQELLRKYKNKLDLKTVIASIREEKRMDEIFNKYKPEVVFHAAAHKHVPLMESSPGEAIKNNIFGTLNI
AGLSSKYRAKKFVLISTDKAVNPTNIMGATKRAAEMIIQTMNAESQTEFVAVRFGNVLGSNGSVIPLFKKQIEDGGPVTVTHPDIIRYFMTIPEA
VGLVIQAGAMAKGGEIFVLDMGEPVRILDLAKNLIKFSGFEPDVDIKIEFSGLRPGEKLYEELLMSEEGLLDTEHKKIFIGRPIDVDREKITKYLKLL
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>CORE_REP|Org51_Gene2854#

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VGDTISDVKEGVNAGMWSVAVIKGSSELGLTQEEVENMDKEELKAKMSIVSKKFKEAGAHFVIETMAELEDILIKIENETIKSDFVPENDYILLTP
GPLSTTKSVRASMLKDWCTWDVEYNNLVQDVRRRLVSLATQNTDKYTSVLMQGSGTFSVEAIIGSTISKDGKLLVIANGAYGKRMKDICNYLD
IEFVDCTFKDIEAVDLNVVENLLKENKDITHISMVHCETTTGRLNPIQEVGKLAKKYNKIYIVDAMSSFGGIEIDVEDFNIDFLVSSSNKCIQGVPG
FGFIIANKEELSKCKGIAKSLSLDVYAQWETMEKNNGKWRFTSPTHVVRAFYQALLELEEEGSVEKRYARYKENQFTIASRLKSLGFDTLVNDNA
QSPVITTFLYPKNAKFEFMEFYTYLKDNGFVIYPGKLTDIDTFRIGSIGEVYPTDMERLADVIEKFINR

>CORE_REP|Org44_Gene3221#

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KLYVSQSLKEQYWKRTHGIIRTCLEKSLIILQKLGVSPEMAHKEVGGIQSSISIDGRTNHAMEQLEVSWKFSTPLQAADNELLVRDVIEDVFTSH
GLEVTFKAKPIHGVAGSGGHTHVGVSAKLKDGSIKNLFAPKDLKEDYLSELGYGALMGLLYNYEVLNPIVTASNDGFNRLVPGFEAPVCIVTSLG
HSYEIPSRNRSVLVGLIRDMKNPKTVRFELRSPSPLSNTYLVIAGCYQTMLDGIKAAAKSGLSTKELEKELSKNVGEESFYLEKDRAYRDENDVFE
HYSLEERNARFGIPPATVYENMKNLEIYASKLKSLKQGDVFTDSIIESFKIGAIDKWQKKLKTRIIEEGIQKIRSIVKIHTKENMDALDEVVWNSISD
LKFNIMKDTLTRESLFTRVREAVENKDYQAASDLQIELKRSMEEIQQLYMQYKKNIY

>CORE_REP|Org5_Gene1668#

MFTGIVEEVGILRKITANGKSGKVTILSNKILDGTNLGDSIAVNGVCLTVSNLGKNEFTADVMMETIRSTNLGLLNANDKVNLERAMSLSSRFG
GHIVTGHVDGKGTICKFEKDENAVLVSIRPDKKLLSSMILKGSVAIDGVSLTISYLDDEIFKVSIIPHTKINTILLTKNVGDFVNLESDVIGKYVNNF
MANNYKELNSNSSNHKSNIDKDFLFKMVFKNNKGVNYMFNTIEEAIEDIKNGKMVIVVDDESRENEGDLLMAAEMATPESINFMATYGRGL
ICLPATEKKFKSLNIPLMVRENTDTFQTAFTVTIDGADTLTGISAYERAETVKLFCDENSTSKDFKTPGHIFPLIAKTGGVLVRDGHTEASVDLARL
AGFKEIGLICEIMKDDGTMARVDDLMIFKEKHNLKIITIKDLIEYRKINETTIEKVSSAFLPTKYGNFEIIGYRDTYSNEEHIALTYGNINIENTLVRLH
SECLTGDVFHSLKCDCGLQLESSMKKIVENGSGVLIYMKQEGRGIGLLNKIKAYKLQEEGYDTVEANLMLGFEEDMRDFYMAAQILKNLNIKSI
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>CORE_REP|Org36_Gene1073#

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MKPYFAVYSSFLQRAYDQVIHDVCITKKPVTFLIDRAGLVGNDGETHHGMFDLSYLNSIPNIVVMAPKDTREMELMMDLSLKLDCPLAIRYPR
GSSYYLDKGEYGEIVLGKYEVLDDGQDTVILCIGSMVKHALEAKEILSREGINPTIVNARFLKPIDEGMLKALLKNHKNVVTIEDNIVTGGFGSRIN
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>CORE_REP|Org62_Gene1531#

MKRFLRRIILVLFILLIFISFISIKLIHNVGDYGKLINYVGIVRGASQRLTKLEMNHKPNDELIEYIDEILQELITGHGNYGLVLTDCNKYNEDLLLLEKK
WEDLNSEIKKVRMKEPNNQLLSISEEFFSLANDTVFEIENFSKEKSNYLMTLIIIISIIGILACIILILQYSKKMIKLEKLNVDLKNIAYKDELTGVNTIEK
FKLDANQNICMHKDKKFAVFYIDFENFKYINDIFGYDYGDMILKRYANLMMNDIGKYEIFAREIADRFVALRCYIDKEDLVVRQRIVDSELINTT
NEIKNKHSITVVSGICCIEDVNEKLSIDGLINRANFAQKTVKNKPGTNYAFYNDSIRKKMIEENTIKSRIHEAIEKREFIVYLQPKVNLHNQKINCAE
ALVRWLTPDKGIISPAIFIPVLEKNFFIALVDKYVFEEVCKWIRKRLDENKPFVQISVNVSRIQFYNTKFVETYSNIQNKYRIPKNTIEIEFTESVAFE
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>CORE_REP|Org10_Gene2464#

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KYADLLKDMQVSSLCNIKIGECECSFENYECSMEYFNEVISNKKYRNVNIIQKYRASNNITKILIKTRNYPVAINNLAKSEVYLEKIKNHSLKEVEKF
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>CORE_REP|Org35_Gene1187#

MKKKAALATLAMLPLGVVNAHADGDIGIVTINYLNVRNEPTAESSIAFVAKKDDKVLIKDSSNGWYKIKAESGQEGWASSKYIAKSNSDSLRTS
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KSTPSPEFSTFSAQRTSSFVNASSSDIEYYLNPKNFTNTTKGMMQFLKINSYRDGISESSLNSYLNGLSSSVFKNQGAAFINAAKKYNIDVVYLVS
HAMWETAYGKSTLAQGQTLTSYKGQPLSKPVKVYNFFGIGAIDKSANVSGAEAAYSNGWTSVEATIDGSAKWISQNYVNSSKYNQNTIYKM
KWNYDYTWHQYATDVNWANGISGIMENLIGLYGGGSSLVFEVPQYK

>CORE_REP|Org88_Gene3147#

MLSKLKEFQQEMIKYTETVASVLDVDIEIVDDRLIRISGTGLYKSKINESVVTEGFIYDNVIQTGQELVVLDICDNQLCIECSHYMKCLNKVIIAVPI
KYNNRTIGVIGAISTDKTKKVEISAKIDNYLKFVNHICDLISMKIEEHEVSKNSSRKMDMMIEIIENVEKGVIILDINSKISYINNIALKKLDIDKNIIEN
IVNIVSVESSSNGHELLEIDIDNKIYNINAKIIPVYPYINQYDKIIIFDKTYINHKGHVKVNSGWGNSDIESIIGNSEAMLKVKERTKKLAKSNSTVLIT
GESGTGKELIARAIHAEGSRWNKPFIAINCAAIPENLLESELFGYIKGAFSGASSGGKVGKFELANEGVIFLDEIGDLSMPLQAKLLRVLQERKFAR
IGSNKLIDLDIRVIAATNKNLLKLVNEGKFRDDLYYRLNVIPINLPPLRERKDDIEAIMMKFASKYSLELGIQLNKIEENVMNMLINYNWPGNIREL
ENAVEYMMNLVGDDGIIYKDMLPLDILNYYNINGNICKNKDINIIFEDDIVGGIVENQERILSIKELELTYINKLLNKYGRDTKTKKKIAKDLGIGLA
TLYRKLEEEQS

>CORE_REP|Org88_Gene1297#

MNDIKDIIEEIKARCDIASIISEYMSIKQSGANYKGLCPFHGEKTPSFYINTSKQIYKCFGCGEGGDIINFVMKMENLDFMDAVKILANKCGIEINT
NMNEETRIKIEKSKKFQDIHTEAARFYLSNLLGSKNLGYEYLRIRGLDDKIIKKFGLGFSLDSWNSLMNTLISKGYKKQDLLECGLIAKNRDGTNCY
DKFRNRVMFPIFDYRGNIIGFGGRVLDDSLPKYLNSPDTLIFNKKQNLYGLNFARKNLESKTIVLVEGYMDLISLYQYGIKNVVATLGTALTEQQ
GLLIKRYADTAIISYDSDEAGIKATLRAIDILTKLGINVKVLDLKDAKDPDEFVRKYGLSDYKKAMDVSTHYIKYKIDHLKKEFNIQKDEERVKFAKE

ASKIIKQLTSPVEIDFYTKYLSNQIDINVESIKREVYGKNYNKPYNNKNQKKIEEKVIEKVEVRQDGKQLVEETLIKIMLEDKKIREIALLKVEESDFLL
KESKEILNYMIKNQELDKITIDKLKSLNISEEYLKELNSISLNSINLENTKEIEGIITNIRKNSLEEQINSLLREQQELENNNDMKEVDGRVMEIALKIV
EINKILKSL

>CORE_REP|Org24_Gene932#

MKCGKYKKYDKMQIVNRKWPDNEIFKAPIWCSVDLRDGNQSLPTPMSVNEKVRMFKMLIDTGFKEIEVGFPSASNTEYTFLRKLIDENMIPD
DVTIQVLTQSRAHLIEKTFESIRGCKKAIIHLYNSTSVLQRDVVFNMSKQEIIDIAVEGAKLFNEEVKKYPETEFTFEYSPESFTGTEMDYALEICEA
VIDVWKPTPQKKVIINLPSTVEMATPNVYADQIEWFCKNISCRDSIILSLHTHNDRGTCTAASELGLLAGADRLEGTLFGNGERTGNMDIVNVG
LNLYTQGIDPELDFSNIDKIIGIYEDCTKLMVHDRHPYAGNLVHCAFSGSHQDAIRKGMIAMKNRDNDYWEVPYLPIDPHDIGREYKEIIRINSQ
SGKGGAVYIMETDYGFMIPKNMHSDFGNVVKMESDRIGEELSSEAIFNLFKKEYIEVESPYKVKKYKIKSMDELNYENDDSNDTNMIEMTARIS
YMGNEQRIVGIGNGPVDSFNNALKQCGMKDYKFRYYWEHALEEGSHSRGVAYVGIEHNNEVYFGVSISENINTAAINALMNAINKSYIEEEIK
NGDDYDAENISQTC

>CORE_REP|Org45_Gene290#

MSILLKKAPKLAKHIITSFYINRDIDEVLKYLCENVTWIGPGEQEFLTSFNEIKNYFYAGQYEIPSCDINNDIFEIVSEYENRCMVLGKYTVRTKENA
QMILEVNQRCTFEIIEDREKLLVKHMHISNPYGEMQLDEYFPTKIGTQSYDYLQRLLKEKTEVIEMITNNINGGLKGSNDDSTYSFFYVNEGLPKI
LGYTYNEFMEMSGGSAVGAVYPPDLPKALEDCEQCFAKGPTYSSEYRIRKKDGTLMWVLDSGMKSLNSDGIVKINSIITDITQLKNIESELKLER
ERYRIALQNITDIMFEYDMENDNFIKYQRVEIDKKIELENFETKNYSKLLESGKIIHLDDIGKLLEVLRGNLHETIEIREINSLTKNEWRWIRVQCSVI
YDSDHNPIKTIGVLKDITEDKSKLESLINQAQRDPLTQLYNQRVSQNLIQEYLCSSDSKNNDALLIIDIDDFKTVNDTFGHLEGNEVLVAVSKILLH
NTYDKDIVARIGGDEFTIFIKSLTKDLIIKITNDILNDASKIKVKDNHKITLSIGIAFTDDSTKLYKDLFSKADKALYLSKADGKNCYSVYE

>CORE_REP|Org2_Gene2090#

MRNKKINIIFLTTIMFIMSTVMVFAEEDIDTIALANAEKFGILTLIPPLVAIILAFITKNVIISLLIGILSGSFIIKASGINVFATFIQAFLDLVDRALVSLA
DPWNAGIILQVLAIGGVINLVAKMGGAKAIAEALAKRAKSAKGTQLITWFLGLLVFFDDYANSLIVGPMMRPVADKMKISREKLAFIIDATAAP
VAGLAIISTWIGLEVGLIHDAFESISIDVDAFGIFLNTIPFRFYNILILAFIVISALLLKEFGPMRKAEIKSRSRKISIDLDEGVEELDDLAPKNGVKLSV
WNAIIPIGTLIIVALASFYYSGYTSIMGGDDKALIQLFTNSPYSFEAIKEAFSASDASRALFQSALVASLVAIIMAVVKKIFTISEAIDVWIDGMKSLV
ITGVILILAWSLSSVIKELGTAKFLIHLLSGSLPPFLLPSLIFGLGAIISFATGTAYGTMGILMPLAIPLAYSLNPDMSYVIVSTSAVLTGAIFGDHCSPI
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>CORE_REP|Org94_Gene2766#

MAYKGIGASPGVALGKALVVEHSELVIEKKSIDNVEAEIAKLEDAVAVSKEELVKVKEKASEELGAEEAEIFEAHLLVLEDPELIGSAIDKIKTESVN
AEYALNEIKEMFVSMFESMDNEYMKERAADIKDVTNRILRHILGIKVVDLSALSEEVVLIAHDLTPSDTATMNKKMVLGFLTDIGGRTSHTAIM
SRTLEIAAIVGLNDITSKVKDGDFVVFNGDTGEVIVNPDEETINKYTELKAKYEDERKALQLLKGKPSVTLDGKHVELAGNIGTPNDIEGLIKNDA
EGVGLYRTEFLYMDRDSFPTEEIQYEAYKAVLEGMDRKPIVIRTLDIGGDKELSYLSMEPEMNPFLGYRAIRLCLDRKDIFKTQLRALYRASVHGR
LRIMFPMISSLEELLQAKEVVKEVLAELDSEGVAYAKDVEIGMMIEVPSAAVISDVLAKHVDFFSIGTNDLIQYTCAVDRMNQKISYLYNQFNPA
VLRLIKTVIDNAHKEGKWAGMCGESAGDQKMIPILLGMGLDEFSMSPISILPARKLITSVKESDMKKLADDVLNMGTAEEIKSYIEKTFNI

>CORE_REP|Org18_Gene1567#

MGGTIFMVQIVIVLAIFMILVIPMGKYLYHIATNQKTFGDRLFDKVDNFIYKVCSIDKKKEMNWKQYALALLFTNAVMVFIGYIILRTQSMHIFN
PSGIKSMEQGLSFNTIISFMTNTNLQHYSGESGLSYFSQMTVIIYMMFTSAATGYAAAMAFVRGLVGKKKTLGNFYVDLIRITTRVLLPGALIIGL
ILVTQGVPQTFAGTETVTTIEGKLQDIARGPVAALESIKHLGTNGGGFFGSNSSHPFENPTIISNIVEILSMMILPGACVVAFGHMIKNKKQGWV
VFGAMSIIFLIGLVVCFKAESAGNPILSQLGLNQSMGSMEGKEVRFGIAQSSLFTTVTTSFTTGTVNNMHDTLTPLGGLVPLLNMMLNVVFGG
KGVGLMNMLMYAIIAVFLCGLMVGRTPEFLTKKIEGKEMKLIALLIILHPLLILMFSGLSVAIPAGLEGISNPGFHGLSQVLYEFASSAANNGSGF
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>CORE_REP|Org58_Gene1169#

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KKATKMNDLDIYKAVQEQLTRPIIQIQTKNIDINKSMKKELEKNGIMVEEKTMRYAKDGLLSHTIGYIKEDDKSGQSGIEKSMDSVLRNSNEKYI
SAFKAGDAGNEKSLNILKGSVKTVDNKDKDRHLKTTIDYNIQKKLEQILNKEENPTAAIISEASTGEILAMCSRPNFDQNDISKSLKGKNGEFENR
VIKATYPPGSVFKMVVLFSALENGVIDENYTYNCTGKTKVGNTNEILRCNKRDGHGFQNLRQAFSNSCNPAFLDIAMKLGKEKILKSAEKLHLF
EKVDIGLDEEKIREAPKNISIRNLAIGQENIEFTPLQINQMTQIIANNGTFKPLYLYKSLVDNNMNTIKTYKSSKKEELISPYVCTQVKEYMKSVSRI
GTAKDLKDIEGGCGVKTGTAQSSLNKKAIDHGWITGFYPEERPKYVITVLVEGTQKGNKSATPIFKEICESIK

>CORE_REP|Org72_Gene2695#

MIQYIDGKRLREMFISGANNLQNNKELVDKLNVFPVPDGDTGTNMSLTISYALKELAKVENDNISDIGKALSKGSLMGARGNSGVILSQIIRGIA
KSIEGKSKLSTEDLAKAFKNGSDTAYKAVIKPIEGTILTVVRESGEFAIKTAKKEKDVVKFLSMLVKESNSSLERTPDLLKNLKEAGVVDSGGKGLV
LIYEGMLASIKGNNIEIKNADLDTNISTSMDFAKSTTSTDNIKYCYCTEFILESSKVEDTKIRDIMMAYGDSLAVVGDDGVIKVHVHTNDPGNVL
QEALKYGQLLTIKIENMKLQHENTLLDVEEKKENDSEPLEEEKEFGFIATSMGEGLANIFKDFGVDHIIEGGQTMNPSTEDFMNAIKDINAKNIFI
FPNNSNIIMAANQAKELSDKNIIVIPTKNTPQGFAALVTFNGELSEDENKEAMMNALNSVKSGQVTFAVRDTVMNEIDVKEGNIIGIAEGNLL
SAGDYVDEVTSNLIEKLVDEDTAIITLFFGEDVTESQANELRTSLEEKFEDVDVELYYGGQPLYYYLISVE

>CORE_REP|Org19_Gene1156#

MLSIINSSNLVGIDSFLVKVEVDVSNGIPSFNIVGLPGKEIKEARERVKSAILNSGYKFPSTRIVVNLSPADIKKEGAFLDLSISIGLLRELIKKDENYIR
ESMFIGELSLDGKIRKVRGILPIIMGAKTQNIKRIFIPIENIKESLLVDEIDIIPIKSLKECVDFLNEEIKVDKVSIMSFLDDKSRKENGELEKDNSYIDCK
YTKINNEESKYDEDFKDVKGNYFVKRSAEIAAAGNHNMFMIGPPGSGKTMIAKRVRTILPDISIEEMIEVSKVYSILGMINESKGIIDKRPFRAPH
HTTTKQSLIGGGMDARPGEIALAHRGILFLDEIAEFDRKILETLRQPIEDGYVNISRVKYSAKYPCRVLLVAAMNPCPCGYYMSETECRCRSNEID
RYINKISGPLLDRFDIFVEVNSIKYSDFNSLKQEESSQKIKRRVENARKIQINRFKKDNIKNNSEIKAYNLFKYCKLEKEASKTAEMIFNKYNLSSRSY
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>CORE_REP|Org64_Gene2747#

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AIVIAIIGLLFTEQFVTIFAAGFRNDPAKFQAAILFTKIMISGVLFLSGSKIFSSFLQVNDSFVIPGLIGIPYNIIIIAAIALSAGKNVWILPAGALLAMAS
QLLFQLPFAFKKSYKYKPYINLKDESIKELVNLVLPMLVGVAVGQLNIFVDRLLATTLGDGKLSALNYANRLNEFVMALFVTSIITVIYPKLAKMSG
KDNKEGFISTIVKSSNCIILVVLPISIGAIILAEPLVRILFQRGKFDALSTDLTSIALRLYSLGLLACGVRDVLYRAFYSLSDTKTPMINGSIALIINIVLNLI
LIRPLGHAGIAISTSTSNIITVILLFISLKKKNGYFGGDKIIKTGLKSLVASGVMAVATLLIYNNLYAFMGSGTIKEIISVGAGVLGGASVYTVLIVLFKV
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>CORE_REP|Org94_Gene2771#

MNKNSMTKIYSLNKIIFIIIGILGIVLLTRHIEVDIKVLILILLTLFSINVFISYLKIKLYEDKINLGLINNSDKFINITKDENFLKHVQNYIISNEKENCVMA
CFDLCRLKLINDIYGYELGDEVLNNILSNLKYYFGKEAIYGKLKSDVFVLIIKLENREQKIPYLVNLIKNKIVILSQIDSFKMDINIEASIGIYKFNNNEID
IKKAIDNADMARLKSKGLKHIEYVEFDNAMEEEIQSIMKIERDLFLAIKNKEFVIHYQPKVDSSTGNIIGSEALIRWLHPSLGMVGPNKFIPIAEKN
GLINNIGRWLIQEVFITINKWISEGINVLPVSINLSRVELYKNDLVDFFKLMFNTYNIPKELIELEITETTALRDVKFISERLYEIKSLGMNISLDDFGV
GNSNFINLKGIPLDIIKIDRSLILDIVTNTKTKFMVKAIVNLSHDLNVTVICEGVEDMHQVKVLSELGCNFIQGYVFFKPLDEMNYKKLLTDGSYIN
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>CORE_REP|Org20_Gene1142#

MDNFKKILLNELPNFKEYSSKFLNGEINKMQYKGFSGGYGVYAQRDKKSFMIRLRVSAGVLSQYQLNKIYEIAIKHNLDKIHLTTRQAIQLHDLSI
NSIVDIMEEGIKNDIFTRGGGGNYPRNVGLSPLSGVDPSEVFDVTPYAVATDKYFIKNATTYHLPRKLKVSYSNCYTDTAHCSIQDLGFVATLKN
DEPYFRVFLGGGLGKQPKVALELDELIKPKDALYCVEGMIKFFMDYGNYENKNRARVRYMVESLGEELFLEKFKEYYKLEKENGSLELNIEEIDYS
KPGVKIDIQDSRLIPQKQDGLYTVYIHPVGGILLTKDLSTLLKELDNVENPMIRLGMTEGLYILNLNGNEAKRILEISKTISCNSQLEQSISCIGVPIC
QMGIQNSQKMLHEIIDYFRLQNNEEILNKAPKLYISGCLNSCGVHQVGSIGLCGKKKNVDGISTDTFELFVGGSFEIGKTRLGKSLGDFKASDIPE
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>CORE_REP|Org90_Gene1316#

MSKVAKATFYLMIVTIISKILGMGRELVLSSIYGTGLYTESYLTAMNIPNIIFAAIGTAIVTTFIPMYQDISSKQGEKQALKFLNNVLNIIVGICIVVAI
LGVIFSKQLVSIFAIGFEGERFLLTVKFTKILITGIIFIGITSVMSAFLQIKENFIVVGFGSIPYNIVIIISIMLSTVFGPYILPIGAVVAMVVQLLFYMFFV
KKTNYKYLYYLNFKDDSLIKLLALLSPVFIGVAVNQVNSLVDTTLASTLVKGSIPALTYSDRLNGFVTGTFTASIVSVMYPMLSKLSAENNQKKFTS
SVKSSINMIIISMIPISVASIFFATPVVRIIFERGAFDARATQMTATALIFYAVGMTAFGLRDILGKVFYSLQDTKTPMVNGIISVGVNIVLDLVLIKP
MAHGGLALATSSSSIACILLLFLNLKRKVGYFGQDKIIKATLKSVVASLIMGVLSYFTYKFIFGILGVGTFNEFVSLAISVIVGGGIYTLLMTIFKVEEV
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>CORE_REP|Org6_Gene2184#

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>CORE_REP|Org18_Gene1870#

MLKRVRCSYLKKNRLIAKNISIAFIVLFFFSVFTFFYVGNINRVLEYETNDIITVTIAGWIILSFLFLGIIIYILYSKANSQKTIEKVAYTDFVTGYSNWRKFELDVTNLLKKTSQNNKYAMVIFDIDKFKAINDIYGHKKGNLILKDIADTLNELTDINETFARVSADNFNILLTYNKKEDIINIIKKIMANNELVNLSFGIYEIKDKDLSVSVYSDRASLAKSSIKNNSDVNFAFFNDKLREKLLFEDKIEKEMEYALESGQFVMYLQPKYNIKLDKFCGSEALVRWQYTEKEVIYPGDFIPIFEKNGFIRKIDMYILEQACKEIRSLFDKGISPLPISVNFSRVDFFKKDFIENIVNICDRYKIPYSLIEIEITESSMFGDTDTLFNVSRNLQDIGFIVAMDDFGSGYSSVNMLKNIPLNVIKLDRGFFVDDKDVDKSQIVIKSIVSLIKQLGIRVVAEGIETRSQIEMLKKANCDIVQGYYFSKPLPIKEFEKLVYKI

>CORE_REP|Org62_Gene1723#

MYKEPKYRTILESTKEELNDLRNISLNDKYKPIFHIHPQHGLLNDPNGLAYYNGKYHVFYQWYPYDVTHGMKHWAYVSSDDFVNWNREDVALIPIESYESHGAYSGNSIEVDGKLHMYYTGNIKYSAEDRYAYQNLAIMDKDGKITKYENNPIVSEIPKGYTGHVRDPKVFKRKDKYFMLLGAQTSNKKGAIIVYESKNSIDWNFKGELNVKNIDEDFGYMWECPDYINIDGKDILIFSPQGLEPKGFNYQNIYNVVYAIGNMDLDNLTFEIDIMKEMEKGFDFYAPQTFIKDSQTILFAWAGMGEVLYPTDKNKWAHCLTVPRKLNIKNNKLLQMPVDELVKLRYDEISGQNTIKKNINIIENDENVYELNINIKNIDSNKFGLELFSSQDEGVKLEFNKVENTVTLDRSNFKKVFSVEYGTNRKEYINIDENTNIKVLADRSILEIFINNGEAVFTSRIFAKENSNQIKIYSDKIVCYKYTKFKLKQGIEL

>CORE_REP|Org29_Gene1330#

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>CORE_REP|Org62_Gene2690#

MKLNDIIQGLDIINVKGELNIDINNVQYDSRKVTKGTLFICIKGFVSDGHKYIKDAIEKGASAFLVEEDVEIKGCTFIKVKDTRKDMAKVADNFYNHPSQKFNVIGVTGTNGKTSITTILNEILTLNKNKVGLIGTIKIFDGEKDIVSNSTTPESIDLQYHFNNMLDNGCDYCAMEVSSHSLALNRVDETDFKLGIFTNLTPDHLDFHKDLEDYRKAKEKLFFKTTMANIINIDDEGGKKIYENIKGINVPCYTYGVDTNADFMARDIKSDSDGVSYRLITPSYEEVIFIPVPGMFTVYNTLAVIAACYVLGIPKPIYKEGLRLSNGVSGRFETVPNDKGISVIVDYAHTPDALENVLKTTQQFAEGKIISVFGCGGDRDTEKRPLMGAIGQKYSDLCIITSDNPRTEEPEAIIKDILEGIDKKKENYHVVVDREQAISEAISMAKKDDVVIITGKGHETYQIIGKVKHHFDDKEVANECLSKM

>CORE_REP|Org50_Gene1780#

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>CORE_REP|Org43_Gene1303#

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MFYTTGPAYVICVVLYTVIGFKYSNNTIDYVQINQIKDVLNSNFHIGLVAMIPIIFLLLLLLLQKPPIISILSSAIMGLIIAVFQEGEKIGDVLNYMLSG
FTIDTGFVYADKLLNRGGIMSMAETVLLVFVVFVIAGILQKTGFLEVLLQPLINKIGKSRTKLVGSTFIVSYFANAFSSSMMFTSVFVGTLMSPIYK
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>CORE_REP|Org46_Gene2479#

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NSNRANGPFITINCATISPQLLESELFGYTSGAFTGASTKGKVGLVELANGGTLFLDEIGDIPQNLQAKFLQLIQDRTFTPVGSLKNKNVDIRIISAT
NADLVSKVKEKKFREDLYYRLNVIEIKLPPLRERRDNLVEIIKYYFNRYSSDFNLNKTISKEAMETIANYRFPGNIRELQNIIQKILLTCTDNHITIHNL
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>CORE_REP|Org23_Gene2342#

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FLNNAINHGILGPIGIAEAKEAGKSIMFLLESNPGPGLGVLLAYWMFSRGSVKQSAPGAVIIHFFGGIHEIYFPYILMNPVLILATMAGGAAGILT
FSILGAGLVAAPSPGSIFALMALAPKGGLLPVLAGVAVATVVSFLVAAPFVKRASANQSEEDSTSLEEAKAKMSDMKSASKNSEKNIEEKQLEV
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>CORE_REP|Org41_Gene1867#

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NVNDDIESIITNSYDKYSELKSILRGIDKTYVDKLCLEENRDVFDLYRIESKIEKLLNKKVWLKSGGYLIIEKTEALTVIDVNTGKFIGTGKLDETVYRT
NLEAAKEIVRQLRIRDIAGIIIIDFIDMHKKKHQNEVLNILEEEFNKDKRKAEVLGMTKLGLVEVARRREKESIDKYYLMSCPCCDGEQTIKSVHYIL
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>CORE_REP|Org81_Gene1711#

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ADPIYNKLGLNKIKLNPKELEKKLGFLGEPITLGLFLGMFIGILGNMTRINTMEAWGEIMKVGISTSAVMAIFPKVASMFAQAFAPITEAARKIM
QKAGNREWYIAVNDAVGYGEPATLISGLILIPIMLVIAMVLPGNKVLPVVDLLAIPYMVQGLVAIHNGNIPKVLVSGIIWFGLGLYVCTSTAPLF
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>CORE_REP|Org18_Gene3090#

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GIVNKTGAIEAVIAHTVNKMKKFQFLIIPISMILFGLGGTTFGMSEETLPFYMIFIPLMTSMGYDSLTAVATVFIGATAGFGAATTNPFSVGIAQA
LSQIVPGSGIEFRVVMFIIYMAISIGFVMMYANKVKKDPKKSLVHDISLNQELMVNSDTNIKEFTKREAMVIAIFTIGMAIMIYGVLRLEWYITEI
AMIFTAIGIISGIASGLKQDEIVNSFISGAGDLITAGLCIAFARGIVIIAENGFIIDTILNSAANLLNGLPKTIFINLTFLIEGLIAFLIPSASGLASLTIPVLA
PLGDLVDVSRQMIVTAYQFGIGVTNLITPTSGVLMGALAVANIPWSKWVRFVIPLMVVLTILVMAFLTIGLYLGF

>CORE_REP|Org94_Gene1661#

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YTPKKYTPFQMVNNYKYIETKYVNFVLEKYLNKKHLNIIVGIPSRDISRIILTYSQNNIKKTLNKVIIITLVIDSVVALGVGYLFSRKLTKPISSVLWSIE
TMANGNYSLYLKDRGIYEEVFKNINMLADTLRVNEVERKENEELREEWLANITHDIKTPLASIQGYAEIINDKDYEFEEDEIQEYTEIIYNKSKYIK
DLVDDLNLSTRLKNDTIVLDKKKINLVSLVRNIIIDILNDNRYKNRNIEFESNEDLIEVYVDSILFRRAITNLIFNSIVHNSEGTLISVEIVKKDNIEIIIKD
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>CORE_REP|Org61_Gene2639#

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TMLVARVLQAMGSGSLMPLLQVIILYLCPEEKRGAAMSLVGITVGFAPAIGPTLSGWLVDSFGWHSLFLFLSPIAILDVILSFILLKNVGETQNLK
LDIPSIVLSSLGFGGLLIGFTNQGNYGWTNIATYLPILIGIMSLILFTLRQLKSKEPFLELRVFKNKPFLISTILIMIVYASMMSATLMIPLYVQSVRGF
SALSSGSLMLPGAILMVVLNPIAGRHLDKYGPHALSILGTGFLFLGTLSFAFLGRDTSLIHVSLMYCIRMIGISMVLMPLTTWGIKTLDRELISHAT
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>CORE_REP|Org14_Gene1#

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NIKMYFFVTIVSTITGIITGQLVDYFKLEEKLGLKNRRKSDKYDTSKNNSKENKEKHNHDEIILDTLAKSHGNTNRLAFIITHGKGYKIYIGIILIGFIF
MSLAHSGLNLPIIEKLHSLEEVIAVIGILFSIIYMWCFITISIDTTGDMRIREKANKAPIRETLAAGLIYLTPWKAGRVLVDPMCGSGTILIEAAMIGI
NMAPGLNREFISEKWRTLDKKIWWDVRKDAFNKIDNESKFKIYGYDIDEESIDIARENAEIAGVDEYIEFNVGDATQFKSEDEFGFIITNPPYGE
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>CORE_REP|Org2_Gene1975#

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VTSQALTAILTIGYYISGKSNLRFSKSNLKLDKKLIKAVFAIGMSPFAMQLAASLVQVISNIALKTHGGDLAIGAMATISSIAMVFLMPIFGINQGA
QPIIGFNYGAEKYDRVKKAYLGSLVVATIILCMGMVVVMLFPEAIIGIFNKDPELMNISVNGLRIYLLMLPIVGLSVTGTNFIQSIGKAKMAMLLS
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>CORE_REP|Org37_Gene2294#

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DVVIATGGMGMVKAAYSSGKPALGVGAGNVQCIIDRDVDIKEAVPKIIAGRIFDNGIICSGEQSVIVAEEMFDKIMDEFKNNKGFIVRDKVQK
EAFRNAMFVNKSMNKDAVGQSVHTIAKIAGVEIPEDTKIIVIEADGPGEEDIIAKEKMCPVISAYKYKSFEEGVAIAKANLNVEGKGHSVSIHSN
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>CORE_REP|Org18_Gene2460#

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GDMADKLSELEEEEREHIINLLNQENADYVKELLFYDEDSAGGTMTTGYISINKDMTALEAIDHMREEAEEAETIYYIYVVDDEEKLVGVLSLREL
IIARDANIVEDLMSENIISVYVDEDREEAVRLVSKYNLIAIPVVDRQEKLKGIITVDDIIDVMEEEATEDMYKFAGSSEHEREVAEKENPTLREQIIS
ALRGRLPWLIITLVGGLLASLILSNLDYIMNPVYAPLVFFIPVVIGMGGNIGTQSSSVTVITLSNKDLNFSNVVREGIVGIITGLLCSIITGIVIYFVMR
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>CORE_REP|Org85_Gene2194#

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GDRIGVDPLTYPGIKTAAKMLGVQLIPIKQEHNEISEEGLLYACKNENIKGLYIIPDYQNPTTHIMSQNGRKMIANIASKYNLIVIEDAIHSLLNET
HLNPVASYLPNQTIYITSLSKIIAPSLRLAYISTPKQYRESLSDALYNINLSQSYFLTEIAYRMITSGEADKLINARRKSARRRNKIINQYLSGYNLLGN
EECIFRWLILPEGIMAEKFEIQALKEGVQVYASERFAVGKEKPISAIRIAVCATESIEELKAGLSILKRLLEEKK

>CORE_REP|Org94_Gene2824#

MITGYGLLIAFVISIGILLVSIIKFKVNPFLALLITSIITGFMVRMPINEISTTISTGFGNTLGSIGIVIGLGIIFGNILSESRATESIAKGLLAKTGEKNSAL
AVTTAGFLISIPVFMDAAFVIMMPIIKYVSRVTKKSLMVFVCALGVGTIVGHALVIPTPGPLAVAANVNANVGSFILYSIIVAFPAALIGGWIYGK
RFEKYPAYAIDENDREKNLEQGKDSIKIEDDDSSKVPGFGISMFSLLFPILLILISNVFSMFLEKGSTMSGVLAFIGDKNIAILLGILVAIGFLKKYINK
PMGDVVIEAADSAGLILLITGSGGAFGSVINASGIGNFLVDTMSGLSISVVVLGFLLSALLRISQGSATVALVTTSSILGPTILATGMSPVLVGLAIC
AGGVGFSLPNDSGFWVLSRFSGLSVKDTLNSWTIGGTIAGVVAFIMVLLLSVINGIIPLPGL

>CORE_REP|Org13_Gene2861#

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SIKINNIHNIKIYPNSIGNRDKVSVMKVAYKSAKEFSNDISQVSVSYLDKDQKILIANTEGIYVEDRRIRTRLGISSIASKGNENQTGFEGPGGCKGF
EIFEEIDPEYYAKESARVAHTMLHAKNCPAGNMMVAIDNGFGGVIFHEACGHSLEATSVAKGNSVFADKLGQQIASTKITAIDDGTIPNYWGS
MNIDDEGNPTQKNILIENGILKSYMIDKLNGRRMGMNPTGSSRRQNYKFAPTSRMTNTYIAAGEDRPEDIIKSIPDGLYAKKMGGGSVNPVT
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>CORE_REP|Org7_Gene2173#

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TLLYQTESKDIIELGTVHPPYEQNTYIIDFIKNVLKQPEMDRFLQYMSPSGTYMQKKSIAKWIERNNVYTSEENILLSTGGQNAICATLLGLFKAG
DRIATDSLSFSGIKSIAKMIGIQLVPIPQENNEISIEYLESYCKNENIKGIYLIPDYHNPTTHTMSDLSRKKIAKIAKQYNIIIIEDAINSIFRDGIQTPIFS
LASDNTIYIFSTSKFLCAGLRVAFVVAPKRYIENLENALYNMNLMVSPFTAEIVHRLLYSPIIDKIIEEKRDAIIERNEVADKVLSDYNLIGDKNCSFR
WLLLPDELDGKSFEISAKNLGVQVYCAERFSVGNSTVPKAVRICVTAPKDVEELEKGLNIIKSLLKS


>CORE_REP|Org39_Gene2136#

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KFKRKKLTMEEIKEEVKILEKMGHKRLALEAGEDPKNCDINYILDCLDAIYSTYNENGNIRRVNVNIAATSVDEYKLLKEKGIGTYILFQETYHKPTF
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KKIVAITRLAVPFTGIIMSTRETAEMRNELLKYGVSQISAGSLTGVGGYKAYEDGDNTEQFEVGDHRSPVEVLKELITDGYIPSYCTACYRKGRTG
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>CORE_REP|Org73_Gene2599#

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FILIFIRVIQAIGTSTLYPSGVALIQNNIKERQSSALAVLTIFASTTAGLGPTLGGLLLDLGGWHAIFLVNIPVVLVSICLGYFLFPKEVKEKKSIKETLK
NVLSRLDIIGILLFSIAMIFILLFLLSMKESFNLEQLVFGIILMCLFIWHELRTKLPFIDIKLFVSNPKLSKVYLQFIILNFFNYILFFGLPSYFQDALHYSA
KSTGLFMLFMSGIGIFISPLTGKWIDKSGTRFPLVTSSIFMFISAVLLSVVFIHIPVIGKGIILSLAGISYGVGNVALQSSMFEESPRDSIGTASGLFQT
SRYLGSILATVLLGMVFEVNITSEQFQILGYVMVVLGTISFLLNFILKKELRNVE


>CORE_REP|Org82_Gene2492#

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SKYYKEKFDIPFIGVTGSVGKTTTRDMIYSAISAKLNILKNEKNLNNHFGVPLTLFNLNKEHECAVIEMGMSGFNEIKYLVDIVNPKIAVISNIGLS
HVEKLGSQEGILKAKMEITSNFDETNTLIVNGDDKFLSTLKEKEHVYKLKTFGFNKNNDIYCESYTMEEDSLTFICVINGKKEEIFIPTIGEHNIYNA
MSAILVGLCLNISLDYIKKGLKNFKGTKMRLDIIKNEKLTIINDSYNASPDSMDAALKILGRYKGRRVAILGDILEMGEISEYGHRLVGKSSMNNT
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>CORE_REP|Org93_Gene1653#

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AVFVALVVFGGLKSISNVATKIVPFMAVIYVVICGIILISFWNKIPETFMLIIKSAFTPTAATGGFLGATMSLAIRNGIARGVFSNESGLGSAPIAAA
AAKTEWPAEQGLISMTGTFIDTIIICTLTGFSLVISGVWCSDLNGAVMTQAAFNGAIPTFGPILLTVSLTLFAFTTILGWSYYGERCFEFLFGVKG
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>CORE_REP|Org19_Gene876#

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MSNSFSVLVILAILLTIGFKIGKEPLLWMFGASESTIRYSMDYLNIYLIGTVFVQISMGMNTFINTQGFATTGMMTVAIGALINIILDPIFIFGFNM
GVKGAALATIIAQGVSAIWVLMFLFGKKSILKIKKKYMIPKASIILPVLGLGISPFIMQSTESLVLIALNSKLQMYGGDLAVGSMAIMSSIMQILML
PNMGVTQGAQPIISYNYGSGQLDRVKKTFKLCLLSCFTYSTILWLLLMIFPAFFVSIFNKNPQLLSMTSWSIKIYFAGAFMFGIQIACQQTFLALG
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>CORE_REP|Org27_Gene2060#

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MSYVFLGACLSVAAKDGLAALFGAQIAAGVIVFFVGFGVKKIRHIFTPIVSGTIIACMGLGLFATAIKNLAGGEGTQTFGSPINFTVGVIVAFVIIM
INKYGKGLVKNSSILIGILVGYAISLVLGLVDFSAVQGAAIVSLPTPAAFGLEFRPELIVMFTIIYIIGIADMMGACTIATVGAMDREVTDEELASVV
LGNSITSIISSLFAALPTGVFSQNTVIVSMNKVTSRFVIALGALVLLLAGISPALGAIMTTIPSCVVGGATLVVFSSIAMSGFSIMSMDGFTEENNLI
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>CORE_REP|Org18_Gene1417#

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NYIENLPRTAVDDIEMPDMYFGFYNHVIVIDHLVQKTYIATPNIDIELEEKIIDDIEQRILKEEKKGIDSICYEEKEVTSIRLKSNFTKEEFKNAVQSV
REYIRQGDIYQANLTQRFSGETELTSFELYRDLRRFSPAPFGAFLNFEDAHILSNSPERFIRCVNKRIETRPIKGTRPRGKDKEEDLRLQQELRNSE
KDRAELLMIVDLERNDIGRISKTGSVKVPELFVIEPYANVNHLVSTVVGELKDDKDATDVIKATFPGGSITGAPKIRAMEIIDELEPTQRNVYTGSI
GYIGFNGDMDFNIAIRTIIKNDKKVYFQVGGGMTWDSDPDEEYQETLDKAKSIMKALRGYYEE

>CORE_REP|Org95_Gene1227#

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NLVSIIILSIIILAITFFNLDRLALFLGATESTIGMVKDYLGIIIFFNGFFIVSYSLEVIIKTDGFPILATVGVIISALTNIILDYLFVIEFGWGVKGAGIATGL
SQVFSTIFFLIHFLRKNSTLNFSKFRIDFKTLRKIVFIGFPDSTTELSCGIVVLLFNLSLTKYIGENALIYYSVINYINTLVLMTMMGITQGMQPLTSFY
YGAGNIDNVKKLLKMGIKATIIASVAVFAICMAFSGPIVSLFIHPEETMLFNEGVRVFKIFSISFLLVGINVIISGFFVSVEKPSISTVISLGRGLVIVVL
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>CORE_REP|Org63_Gene2662#

MDLKGKKVLLVGLAKTGISTIKHLDKLGASIIVNDIKDENKLRNILDELESINDIKYILGHHPEDVDDIDMVVVSPGVPLDLPFILKLKNSGKYIIGEV
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KIDLEVIRDVLMTFKGVEHRQEFVRNLDNVIYVNDSKGTNPDSTIKAIQSYDRPIILIAGGMDKGSNFDELLETAKSYVKSLVLLGETASNIENCA
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>CORE_REP|Org46_Gene1302#

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EDNPFMAGAFHGVGEADRIINVGVSGPGVVKRALEKVKGEPFDVVSETVKKTAFKITRVGQLVAKEASSRLNVPFGIIDLSLAPTPAIGDSVANI
LEEMGLEVVGTHGTTAALALLNDAVKKGGVMACSHVGGLSGAFIPVSEDAGMIDAVIKGALSIDKLEAMTAICSVGLDMIAVPGNTTAGTLG
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>CORE_REP|Org6_Gene2794#

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RANSIEEIKPCEISKLGVDNALSKVGGKSIPSGKYKTILLNEAMVSLLSTFSGIFNADSAQKGLSLLKNREGDMIASPIVTIVDDPLLENGMASTPF
DDEGVATFKKEVVLNGKLITLLHNLKTANKAGVKTTGNGIKSSYSSPISIYPTNFYIDKGDKSLDEIIKDIDEGLMVTSFAGLHSGANSVTGDFSLA
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>CORE_REP|Org19_Gene2030#

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>CORE_REP|Org22_Gene1525#

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VLGIIYFLSNKSTLKLRKPKTDFRLIRDTMINGSSEMVTELSTGITTFLFNVVALKLAGENGLAALTIVLYAHFLMTSVYLGFAAGVSPLISYNFGAE
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>CORE_REP|Org83_Gene1650#

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SENLLESELFGHEKGSFTGAVDSRKGRFELSNKGTLFLDEIGDIPLNVQVKLLRTLEDKSIERIGSNKSIKVDFRLICAMNKEPKVEISNGNIREDFF

YRISTITITIPPLRKRREDLATLIEFFLNKYQIEHDKKIHSIDKEVKDFLLNYNYPGNIRELKNIINRLVVLSEEGNLSKDNLNLISNNVYIDDKISIKPLR
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>CORE_REP|Org76_Gene847#

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>CORE_REP|Org57_Gene2857#

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HVLAGAFFDAFVYLGGSGMVLGLIVALLIAGRRRKEMIVLGGPPAIFNIGEPLIFGLPIVLNPIFMIPFVLAPVICSAVSYLAIDFGLVAPVILPKIPW
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>CORE_REP|Org58_Gene1641#

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KRLCHGAPFYVLGPLVTDIAPGYDHITSAIGGALACAKGVDFLCYVTPAEHLRLPNLDDMKEGIIAAKIAAHAGDIAKNVKGAREWDNKMSKA
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>CORE_REP|Org18_Gene1107#

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SSEGTSSQNNSTSSGTTISGNGKVNVSSRLNVRSGAGTNYSLVGKANNGDVVKLLEQSNGWYKIKLSNGVTGWASSQYISKTSEDVGTNNSS
NSNSTNNSDKKPSSEESIEGKNGKVTSAVSLNVRSGPGTSYSIIGKLNGGDVVELKAKSNGWYKVKLSSGTIGWVSASYISETNEDTKEKPNSSS
NQNSQSNSNSKPSFTGNSDKSTAKGSTIVDFAYTLIGIPYQWGASGPDKFDCSGFTQYVFKHSVGVSIPRVSREQANFGSAISMGNYAPGDLV
YFDTDGDGTTNHVGIYVGNSKFIHCSGTQTNPNKVKVDNLTSSYWSKVLLGARRFV

>CORE_REP|Org48_Gene1183#

MGKTKDIIVFGFALFAMFFGAGNLIFPPYLGIITGPEWLIAFLGFTFADAGLALLAVMATAKFDGNVVEMFKRCGMKLGILIGCADILCIGPFLAI
PRTGATTYEMGIMPLFGTSIPVLLFCILFFAISYVLTIKPSKVVDIVGQFLTPALLIALAFIIIKGIISPLGDIVDKPMIPNVFAEGIGQGYQTMDAFAA
IALASVLIVSLNDKGYSTISDKLKMIGKAGVLACGGLALVYGGLCFLGATVSTMYGTDAVQSQVIVNITEGLLGNVGKVILAVVVSLACLTTSIGLT
SATGQYFSRLTKGKLSYEKIVLAVSVFSAVVASFGVGTIIKIASPILSIVYPPSIVLIILAFFNEKIKNDNVYKGAVYMSLLVSILTVISSYGVAVPVVNS
LPLHSLGFNWVVPVIIAGIIGNFIPSKSQSNTLGTN

>CORE_REP|Org50_Gene2566#

MKRNLSLLLICLLIFTSFLGRSNISFADNEPAIVAKHAVLMDYETGKILYNKDGNSKLYPASTTKVWTACLVLKEVKDLNQVIEIKDLPQIDGSSMY
LKEGESFTVKQLLDALLVHSANDAAFVLARYVGGGNVQKFIDLMNSEAKKIGATNTHFNNPHGLPDPNHYTTAHDMALIAREAMNNDTFRQ
IVKTKSLKFEATKAYPYERYFVNTNKFLTSHDKITYKGQPINIKYDIVDGIKTGYTDAAGKCLLSSAVKDGRRVIVAVFNSTNADLYLDSRILIDYGF
DNFKCATIVDKEKYTDTKKVLFTKQHELIYEPKNSYKIFLEKNESKGNYDTKTELNKIDLPIKKGAKVGTLNVYNNGKLENSIDLIAKNNLDSSLPFL
TENNVLMTFVKIIAGILILLVLFIITSNIKKKKKIKKARGKRNMKK

>CORE_REP|Org21_Gene996#

MEEEKINYALEQIPENQKRGWVAMFSVLVAIGVDLSSVILGAELAQSMPMKQAILSVIVGSFFSAILYTTCSLVGSSTSLSTSMITKYVFGEAGAK
IFSLVIGVSLLGWFGVQVGFFAQNAQIIIKDIFNLDVSMQILSLIGGLLMMSTAIYGYKAMEKLSVYSVPFLLVLMMLTIFLAFRANGISVDDNM
KSTMTFAGGVSLSMSIIIVGAIVSPDISRWAKSRRDCALSSFLGIQFGNAFMIIVSIVLVKCMGTSDIMRIFITLGIAIPGIIVLTLAQWTTNTSNVY
SASLSIALVLKKAPEKVLTIVLGIIATLLAVFGIYEGFIGFLNLLGIVIAPVGGVYTAEYYIVKQELKGFDKGVLYKPIVKRSIVSWIIGILITYLSTYGFITL
TTIAPLDGFIAGFVVQSIIGKVLCSTKNKQEIDKAV

>CORE_REP|Org49_Gene2497#

MEKIVNDILKEEVYYEKLQNGLDVYFMPKRGFMKKYAILATNYGSNDLEFVPLGEDKKIRVNEGIAHFLEHKMFEQPDGGDAFDKFSKLGVNA
NAFTNFTMTAYLFSATENFYESLEHLIDYVQTPYFTDENVEKEKGIIAQEIKMYNDDPDWNVYFNCLKAMYVNYPARIDIAGTVDSIYKITKEEL
YKCYNTFYNPGNMALFVVGDLDVEKVIDVTKKSNNYKVDKLSKSIERFYPEEPKSVKEKEVIEKFPISMPMFNIGFKDSNVGLKGKELLRKEIVTD
ILVGMLFKKGSKLYEDLYMQGLINDNFGAGFSSQVDYAFSIIAGDSKEPKKVKKIILDYIEKSKKEGLSKEEFDRTKKKKIGSFIKCFDSINFIGNSFIS
YVFKDINLLDYLDVIKDITFEEVEERLKEHFKEEYCVISIVEPK

>CORE_REP|Org18_Gene2736#

MSKQMRDIFIVGFALFSMFFGAGNLMFPPFLGMESGKDWLIPLIGFVVADAGIAMLVIIATARCKGSMDDVLRRAGKGLARVMSVAALACL
ALLVIPRTCATTYEMGIMPIFGDHGPVAKAVFSIIFFGLTLAFTIRSSKVIDIIGKYLTPALLLVLFVLIVKGIISPAGPMSPEHMIDKNLFGEGISQGY
QTMDALGAASMATIMLMSIIAKGYTSDKDQIGMTIKAGFVACVFLAVVYGGLTYLGATVSTLYDTSIPQASLLVEITSILLYGQVGKVILGVIVAL
ACLTTSTGLTASISTYFEGISKASYKQLVIGICVASMLISNLGVDSIIAISVPILQTIYPVLLAIVVMELAGKHIKNDNAFKGAAYVTLVISLLSAINGM
TGAVPFIQSLPLAGLGFNWVIPAILGGIVGNFIKSNKQVA

>CORE_REP|Org38_Gene801#

MLNETKELLKDYYGIDDDTFKLSQEIMEEIKDKFEEIKEIREYNQYKVLKAMQESKLSDMHFNWTTGYGYNDIGREKIEEIYSKVFNTEDALVRPI
IVNGTHALTLCIQGIVRPGDEILSVTGRPYDTLEGVIGIREEKGSLKEYGVTYDDVDFLEDGNLDLEGIKNKINDRTKLVMIQRSKGYSWRKSLSIS
DIKEAIEVIKSVKPEAIVMVDNCYGEFLDTKEPTDVGADVMAGSLIKNPGGGLALTGGYIAGRKDLIELISYRMTSPGIGKECGLTFGTTRNVLQ
GFFLAPYIVSQAVMGAIFCSRAFEKLGYDVLPKYDDLRSDIIQCIRLNNADEVISFCEGIQEAAPVDSYVKPVPWDMPGYESEVIMAAGAFIQGS
SIELSADAPIRPPYNVYFQGGLTFDHSKMGTLKAIEFIKKLKK

>CORE_REP|Org85_Gene2013#

MRRIFDKWEKLSIKYKLFSITTSLLIALALIIYLILYFLLPSYYHEYKIESLQESLKSLVDSSIHFDTYTLEERLYYMAKDQNLAILLKDNQGKIVYGKNEV
VILRYSKYMINSLEDEYRTSIPIYTKDAKDGPYTLELVMPLQPIDEANEVIRKLMPYIISIAILIAIIGAYIYSIVITKPLINIIESEREQEYRRKDFVATISH
ELKTPITIISGQIEGMIYSVGKYKDRDTYLKKSYECTQELKDLVNEMIEVSKSEILEKDLKLVSINISELLNRLVKRQVFLIEEKHMKTILKIEENLEVKA
DQERITKAINNIINNAIKYSPEESEIIIRLYDKNKRISKKNSNQRVVLEIENTGVTIEKRYLEEIFNPFYRIEKSRSRKTGGSGLGLYIVSQIFKSHGFDY
SIKNKENSVIFTVEFKN

>CORE_REP|Org97_Gene2113#

MNEQTRISLERAAELKSKIDDYIQARKTINRGLEKEEEINKRKQKILSILNGTEEDWNNYKWQLSNRITDVDTLSKIITLTKKEKEYIKEVGTQFRW
AISPYYLSLIDPEDICDPIKLLSIPTHIELEDEQEDLDPMGEEYTNPAGCITRRYPDRLIINVTNECAMYCRHCQRRRNIGQQDSHKSKAIIQESIDYI
RENEEIRDVLVTGGDALTLKDDYLEWILSQLKEIPHVDYVRLGTRTLVTMPQRITDEFCNMLKKYHPIYINTHFNHPMEITKESKEACEKLANAG
VPLGNQAVLLNGINNDKFVMRCLNQELLKIRVKPYYIFQSKHVKGTKHFNTSVDDGLEIMEYLRGYTSGMAIPTYIVNAPKGGGKTPLLPQYLV
SKGTDYVMLRTWEGKVIKMEDEPAVDIKKLIKEQAQD

>CORE_REP|Org47_Gene974#

MKRIKTSSMKEKVDEKILREQVSSIIEDIRNNKDIALKKYNEKFDRNTRDEFRITKEEIKEAYKHVDDEFINNLKIAAKNIKEFAKAQKSSFENSFEK
EIYPGVILGQTNIPIESCLAYVPGGQYPLFSTALMLIIPAKVAGVKRIVACSPTMKNTEKINPKTLVAMDIAGADEIYATGGVQAIAAFTYGTEKIK
PVDIIVGPGNKFVTEAKRQCYGQVGIDFVAGPSEVLIIADETSKPVYIAADLLAQCEHDLNARGILLTNSLEIAEEVEKNIETMLKDLPTKDIAYSS
WKNNGEIILVDDMEEAIKISNFYAPEHLEIAVNKCDDIFDRLTNYGSLFIGNLSAEVFGDYVSGTNHTLPTLKASRYTGGVWVGTFIKTCTKQIFN
EEAIESLAPVAEKLAKEEGLYAHAKAAEVRFKK

>CORE_REP|Org61_Gene2620#

MAIKKKVINSSGASTTGGNNVGKSTPSSPTQSKGNGKWKEISKHIMTGISYMIPVLVMGGLIGALSQLIPYAILGLDPSVGIVDAMNSGEFTGF
KLSLLNIAQLMSNFGFTLFGFAIPLFAAFCANSIGGKTALIAGFIGGYIANKPVGVPQFVDGQWTEVVPVASGFLGAILIAFIIGYFVKWLNKSIKV
SHNWLAFKTTFLIPLIASLACMVLMIFIITPFGGLINESMKNFLTAAGAAGEYVYATALAAATAFDLGGPINKAAGFVALGLTTENVLPITARTIAI

VVPPIGLGLTTLLDKRIVGRRVYDRQFYQAGKTSIFLSFMGISEGAIPFALERPGFVIPLNIVGSVIGAITGIILGAIQWFPESAIWAWPLVDNLFGY
IIGIAVGAIFIAVGNIFYRNKLIKDGKLVVDYID

>CORE_REP|Org26_Gene2105#

MGRRTTRVSRLGKEKKRSVLIVLAALVLIMGGFTYFFNSKFLYNGKIAKNVYIEGVNVSDMTKAEALKAITDKYTPEDLNLAYDGKKYTISPKDID
LKYDTEDVVKDAYESTKKGSYFQNLKKYIDIRVNKANMKIKAEYDEAKLSSKVSSIADSINVKMKNASISVGSGGLSYTDSAVGREFDLAANKESI
YNMIKNKEHKTLELKVNLQKPDITTEQVKTVNSVIGQYSTTYSQAVEGRSYNVGLSARKTSDVLLMPGEEFSYNKLTGPSNKANGYKDAPVIVY
GKLEQSAGGGVCQTSSTVYNAALLSGMEITQVTNHSSASTYVPKGRDATVSDGGLNLKFKNPYKHPVYIKNYAGGGSVSSVIYGNSGDKPNISI
EVKQTGQNKYSTYRIFKDSSGKVIKKEHISNSSYKELKK

>CORE_REP|Org29_Gene1788#

MSKVIVVGGGASGMMAALSASKNNNEVILVERNGELGRKLRATGGGRCNFTNNREIEDFFDKVVSNKKFLYSSFYTFTNKDLISYFESRNLEYK
IEKENDHKVYTKNDKSIEVIEVLNKDLLNHNVKIMYNKKVIDIITEEIALKDDSNKDKSKYLIKGIILDNGDKILGDKVIISTGGVSYSKTGSDGSMY
KILKKHGHTLNKLYPALVPLTIEEKWIKDLQGISMKNVEISCKIKKRKISKSGDMLFAHFGITGPCVLIMSSYINKIIEKEKVELNIDFLPNLSTDEISSI
IRAFPNKNVLNNLKQILPQNFLREIFSLLSLVDKKASDLSKADEIRIIEYIKNMKLTCNGTTGINTGMVTSGGISVKEINSSTMESKLVKNLFFTGEV
IDIDAETGGYNLQIAFSTGYLAGISV

>CORE_REP|Org14_Gene3214#

MKIVFLYNPEVKKFLSKYVTLIFVIIIISIGFSVINVSLTKDMIVRNNQAIIGTLSSKYPNLESEIVDIITQGKSMENTDYGKKILSKYNYDKSIRINSEPII
SKLVLDTIKINIILVCIIFILIFVLVVRYFKSIYNDLSDMTKYVYYSSEGKSFDMKNKNQEGQIGLLKTELLKMTTILNEKVELLKTEKIFLNNTISDISHQ
LKTPMTSLIMLNDLLYNDIPYEVKIDFLNKIKNQLNRMDWLIKSMLKLSKVEAKVINFKKDKVKFSELIHRAMQSMKIPMEIKNQKLTIEGSDNI
SYIGDIDWSVEALVNIIKNCVEHTPEFGNITITYKENPLFSELIIKDDGEGIHKKDIPHVFKRFYRGRSSSKEDSVGIGLAMSKSIIESQNGDIYVNSE
KGKGTEFHIIFHKMYDSD

>CORE_REP|Org12_Gene1026#

MATIKPFKAIRPNKYIVDKVAALPYDVMNSKEARRIAEGNPYSFLHIDKSEIDLDENIDLYDEKVYLKARENLDEFRKQEILVKDDKECIYIYKQIM
DGRAQVGIVACISVDESLNGTIKKHEYTRPEKEIDRTKHIKYCDANTGTILVTYKHQRVIDDIINDFMDNNEPLYDFITDDKIEHTVWKIDNDDII
DNLVDKFEKLDYLYIADGHHRTASAENVAKEMRAKNPNYTGKEEFNYFIAMIAPDENLMVLDYNRVIKDLNGLSEEEFINKIKENFELEEIEGKE
KYKPDKKGTFGMYLGDKWYKMKANKNLLEIEDPVDSLDISILQDYVIDAILGIDNPRVDKRIDFIGGIRGLEELEKRVNEDMKVAFAMYPTSIED
LIRVADANKIMPAKSTWFEPKVRCGLFLHEINE

>CORE_REP|Org46_Gene2737#

MELNKVELLAPAGDLERLKIAITYGADAVYIGGEIFGMRSAAKNFSKEDMAEGVAFAHERGKKVFVTVNIIPHNEDFLQLEDYLLELEEIGIDAVI
IADPGVLSVIKKVIPNMEIHLSTQANTTNYLSANFWYEHGIKRVVVARELSFDEISEIRAKTPLDMDIEAFMHGAMCISYSGRCLISNYMTGRDA
NKGSCAQSCRWQYHLVEEKRPGEYFPIYEDERGTFFFNSKDLCMIEYIPELIKSGITSLKIEGRMKTAYYVATVVRAYRMAIDEFYKDPENWKFN
PMWMEELKKGSHRHFTSGFYLNKPTTEDQNYQSASYVRNYDFIGIVRETEDEDGLIVVEQRNKMCVGDEIEVMGPYKETMFTKIEAMYNEE
GEAIESAPHPRQIVKLKLSVKVGKDYMLRKVIEEKVEE

>CORE_REP|Org1_Gene1708#

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FSIAISTMVLAGVGVNLDVSIITVAPIGLYIGRKLNYSKLSILLAMLGGGKAGNIISPNPNTIAVADNFSVNLSSVMMANIIPAIIGVVITVILASILIN
KGNKVQSYEILEQREDLPSLFKSLCGPIIAIFLLFLGNVSPIVIDPMIALPIGGIVTLIVTGNLNNSREYLAFGLSKMQGVCILLLGTGTIAGIIQMSEL
QQSTIGALQFLNMPQFLLAPVSGILMSLATASSTAGATIASSTFHDAIINGGLSPISGASIVNAGSSVFEQLPHGSLFHTSSGSINMDIGERFKLIP
YEALIGIVMTIISTSIQLVL

>CORE_REP|Org10_Gene510#

MEDEILKGKIKQLTILALIFIFITPVFAFADTPPVPNSSRAALLIDQETKRILFEKNIDEKMPLASLSKMMTFLLAIEAVDKNQVKETDMVKIDKSTA
SVGGSTCKLKDGDEISLGELMQGLMLVSGNDAAIAIAKHIGKTEKNFVNMMNKKAEEIGMIDTYYFNPNGLPIYTDPEHKEPPIENMSTAHDI
VTLGKYMYDHYENQVTRITTMQVYNDTKKDFTHYNTNPLLVSVPGVDGIKTGYTDNAGYCLAFSMMVPKDAKNERNHRLIGVVLGDGNKK
NRISSSATLLKYGKDNFHSKKIAHKGDIIETPCVDGIDDFKITVKVDKDLYGVVSDNENINPKVVFKNMNYPIHKGDIVGVAKYYNDSGKFVGSV
DVKSESNIGCIPLKDKIKIKVAKINKKLEIKNSVCFKA

>CORE_REP|Org4_Gene2664#

MQEREELVLNPVPKEERVGWLAPLFNMLGSNIAISELMVGGTLILGMTLSNMIITSIIGNLILVAIIMIQGYIGYKEGLNTYVLAKGAFGEIGGKYLISLLLGITSFGWFGVQAGVAGLSVQKIFPSVNLTLVTVILGLFMVVFALYGFKAMAKFNYLVIPPLMILMVWGVFKAFSTYGVEAIYNYTPQTTMSMVEGLNIVVGLVIVGAIISPDQLRYTRRVKDIWIISFLGLGIISLFQQVAAGVMSMGAPTWDITEVLANLGFGWVAFVILILASWSTNVSNAYSGGLALKTIFPNVKRNVLTLVAGLIGTIIAATGIIFKFQSFLSFLGIAVPAIAGIMWCEYYFIQGRTYKHREGINWIAVISWLIGFAASYYSSKINFLIPPINGIVVSMVIYYILMKCFGIKDK

>CORE_REP|Org52_Gene1914#

MINKNVFTSTKNHLIKMYIIVVGSFLIIFSIFIYSYFRGLTYSGIDSEINDELEYIVSQFKRTSFLNPIRLKDPKDMVYVYEDGRISYYTQNEYFDELLPDRRLDKKNSFFKYTENGYTFRELNVDVGRYQIQIIRNIDSEMNSLRQLTSVLIIGILISVIITYFVAVYLTRKALIPIETAWKNQAKFIQDASHELRTPITIVSSKLESMLKSPESTVNDEVETIATAMKETRRLKKMITDLLSLTKEDSIVKVNLEEIDLEKLLEEISEDYIDIAEFQEKRFVFNSKLKNKVIITDKNKLRQLILIFIDNAFKYTKLGDEISLELKEDIEDEVTLLISDTGIGIKKEEIPLIFDRFFRSENVRNKDLEGSGIGLSIARMISLNLSIDINVTSDVDIGTTFELSIPKKLK

>CORE_REP|Org29_Gene1424#

MSLLKNSLANLKGHKLRVFVALLWIIIGITSVILVSSIGNGFQKEIKKSVNNVNPNKTTISFESADNTGLTDDMSIFLKPFNAKDLEELSFVEGVERIAPSRDGFNLDSVYSSQASFDKKTTYVDVGPVKKDSKINLICGRDFSLDDEKRKVILLTLQSTSEIFENPEDALGHGININGTIFEIIGVLDDSQQNQAGGFFGGYQDMQFTTSLVPKKAFDTLMSQNSYSNEIYQLDLVSSKGYNVNEVANNVIAKLYEMHPGINGSYTTPDPTEQTAYLESINSNVNKYVSIITVVAMFVGGIGVMNIMYVSVMERQREIGIRRAIGAKPRSILFQFLVEAVFITVCGGILGTIVGFAATNYVSKYIGFEAIPSLNSLFYAIVATILTGVVFGLIPAFKASKLDPIKAIYK

>CORE_REP|Org18_Gene2684#

MMKVLLSGGGTGGHVYPAIAIANKIRDEHPDAEIIFVGTEKGIESEIVPKYGFELKTVTVQGFKRKIDFDNVKRVFKLFKGLEQSRKIVKKFKPDIVIGTGGYVSGPVLFNASMGKIPAIIHEQNSFPGVTNKILSKTVTKVLTSFEDSHKRFPEAAEDKLVFTGNPVRKEILLSRKNIARKNLSISDEKRMVLCYGGSGGSRKINDAMRLVIKNMVNEDIAFIFATGKSYYDEFMGSISDINLKPYQKVVPYLEDMANALAASDLVIGSAGAISLAEITALGKPSIIIPKAYTAENHQEYNAKSIEKQGAGIAILEKNLTPESLNTAVFKLLGDRELLVDMANASKTIGKPEAIDLIYDEIMKVYNSTQKSTSKKTKKEKVIKEVKEIKKETTPSIEGQAKVIGIKKR

>CORE_REP|Org57_Gene2615#

MKKVVIIGGGPAGMIAASTACEKGYDVTLIEKNHKLGKKLAITGKGRCNITNACEIEELIENVPTNGKFLYSAFYTFTNDDVISMFNNLGVKTKTERGKRVFPESDKAFDIVNALERQLKSKKVNILLNSKVEKIISKNNKIEKVILNDKKEIKCDSVVVATGGLSYPLTGSTGDGYKFAISQGHTIIDTKPSLIGIEVQESFTKDLEKLSLRNVEIRVFNSKQKKVYSDFGELEFTRFGLDGPIIKSASCRMKDTRKENYTILLDLKPALDEEKLDKRVQKDFQKYTNKKFEKALDDLLPKKLIPIIINLSEINANTVVHQISREQRKNLVHLLKNLKFTVKRYRPIEEAIITSGGVKVNEINSSTMESKLVEGLFFAGEVIDIDAYTGGFNLQIAFSTGYLAGFNC

>CORE_REP|Org66_Gene913#

MKQKVVERFLKYVSFDTTSNSQCENCPSSEGQRVLAKYIVEELKTMGVDDVSLDENSYIMATLKGNTDGVDTIGFISHLDTIEDVSGKDIKPRIIENYDGKDIVLNEALNVITYVKDSPELEEFKGDDLIVTDGTTLLGSDDKAGIAEIVTAIEYLINHPEIKHGDIKIGFTPDEEIGRGADLFDVEKFGAKYAYTLDGGIVGELECENFNAANATITIHGRNVHPGSAKNKMVNAIHIAAEISEMFPADERPETTEGYEGFWHLNSIGGNVENVSMAYIIRDHCKEKFENRKSIMIENIEKINKKYDNRVELDLKDSYYNMKEKIEPVMFIVDIAKEAMEELGIKPRLVPVRGGTDGARLSFNGLPCPNIFTGGLNFHGKNECIPVSSMEKATKLIVRIAEKYAERV

>CORE_REP|Org88_Gene1163#

MSILVQKFGGTSVESYEKMNEVCKIVKAYKKNDEELQLVLVVSAMGRKGAPYATDTLINLCSAVNDEPSKRELDLIMSCGEIISGTILANLLNAQGIDSVFFTGQQAGIITSDEYSNAKIKYINPKKIKRALDDGKVVVIAGFQGVTDDGEITTLGRGGSDTSAVAIGKALECETVEIYTDVDGIMTADPRVEPNAKVLSFIDYEEVFQMADKGAKVIHPRAVQLAKSGNITLAIKNTMNPTFEGTKIGSLCRHLEDNIEYEQERDFKVAVANKDSVAQVKIKSAEEVFTEVLNEIEKKFITIDMINFFISEKAFVVEDADIKSLKEILDKFELDYEVNRDCAKVTLICSRIADEMSGIMSKVVRGLSKAGVSLLQTSDSNMTISCLVSEEDMHTAVHAIHQQFYLK

>CORE_REP|Org70_Gene1218#

MSTKNITDKTKNKKDVGALIGAAFIMATSAIGPGFLTQTAQFTQDFGPNFSFVILITTILFIGAQVNVWRVIGVSGLRGQDIANKIIPGLGYLVAFLVALGGLAFNIGNVGGAALGMNVMFNMNMTLGTVLSGLIAIFVFMSKNSNSLVDKITKFLALGMIIIVGYVAISNHPPVGEAVSRMVKPENPKGLIFPIITLLGGSVGGYITFAGGHRLIDGGITGEENIKEITKSSLLGILVATMMRVLLFLAILAVVSKGLQLDPENPAASAFKFSAGAIGYKFFGLVLWSAAITSVIGAAYTSVSFLKTLNPFIDKYEKYFIIAFIAISTLIMAFIGKPATLLILAGALNGLILPITLGIMLIASKRKDIVGDYKHPTWLLIFGLIVVLISAYTGITSLSSLGALFA

>CORE_REP|Org32_Gene174#

MQQALKLKYQTKELGKDFVIESCNSIKPWLINIRRELHKIPELALEENLTKQKVISYLKEIGIDYMEFTKHNGIMAYILKESADKTICIRADMDALPI
EEENNIPYKSIHSGKMHACGHDAHTTMLLGACKVLHSIKDKLNVNVKFLFQPAEEGFGGAKFLVEDGCLENPKADYIFGLHVMPHIETGLIETK
YDTLNASVDTIKISIKGKRAHGAYPENGIDAIVTASQIVTSLQTIISRNLEPNNAVVLTIGKIYGGDAHNVICEDVKLEGTLRTLNSKTRNFMIDKIA
KIVGDTASAFGCVGTLHVSDENYPAVINEKELVDTVISNTKELLGEEKFILRPNPSLGGEDFSFYTEHCKGAFFHLGCKNEEKGLISPLHTSSFNIDE
DCLPIGVMMHVMNTLYFN

>CORE_REP|Org7_Gene1542#

MENKVKIGVLGYGVVGSGLIDIIDNNKEKRSIEIVGILVNNLEKHKDKKYSNIITNNIDDIFNKDIDILVEVMGGLEPSLSYIKKALNNKIHVVTANK
DLLAECGDELAKLASENKVSIKFEASVAGGIPVLKPIIESLEGNNIDSINAILNGTTNFILSKMYDENLSYDMALRQAQELGFAEANPESDVLGYD
AARKLSILSTLAYDNRVYWKDVYLEGITDIDEKDIEYAKKLNCKIKLIGQSKYENDKVSAFVRPVLVEKDNILARIDNEFNAVIVNGDSVGEVSFVG
KGAGSLATGSAVYSDVIDIIDNRVSSIDSFTKDKIQVNKIVREKCGALLRFKKCNKDEILNIVENCLVKFDILNDDDELAIMVYADSEYEINNSLCLI
KDKGYCEKMNKMLKIS

>CORE_REP|Org38_Gene748#

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LENESLPAGIVSSITGFKSFKISVNGKSGHAGTLPMNMRLDAGCCACECVLAIEKVAKTTADLVATVGKMNFYPSSSNVVPERAEFTLDVRSCS
QEILDNSVEKIFNEISHICENRKLNYTSELAFENVPVPCSNKITKIIEKSFIDLNLNPFYIYSGAGHDAQEMDNITDIGMVFIRCAGGVSHNPNESV
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>CORE_REP|Org7_Gene2623#

MNNKKYYPTAIALYFSYFLLGIGISILGQYKPEFSSMWGAKTLSDGTLDVSIVLAVIAALGLGRLISYPFAGPISDKYGRKVSGLIGNFLHAIFFVGIV
FSPNFYIAYVFAIIGGAANSFLDTCVTPSCMEIFASLGTIANMFTKFTIALAQFLLPFIIGFVAANSISFKVIFIVTAILIVVDAILIAVLPFPPANNVID
NKGKTVKSEKMKFTPTSIALVCIGFTCTSTFVLWLNCNQELGKLYGMADPTKIQSFYSMGVICAVLITSLLIKKYIKPIRILVIYPIIALLMLLIVYFVQ
TPTICMLGGFVIGYSAAGGVLQLTTSTANEMFPTNKGKITSIVMIASSIANYVILNIAGIITKSGGVNGPKYVVLFNVAITFVGILLALFVNMRYEK
EKVYDYDV

>CORE_REP|Org44_Gene2527#

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TTLGFITTDANIDGVLLKEALKIAVDKSFNRVSVDGDTSTNDMVMILANGKAKNDRINKKDEHYQVFLSALTYVCIELAKLVAKDGEGCTKLIEC
YINGALSEEHAVKLAKTVISSSLVKTAVFGADANWGRILCALGYAGEEIDMEKVDIIFESMKGYIEVCKNGNGLDFNEEKAKKILEDDEISILVDL
NMGNARGNAWGCDLSYDYVRINGSYRN

>CORE_REP|Org74_Gene2696#

MKKTIMSLQHLLAMFGATVLVPILTGFNPSVAIFCAGVGTLIFHFCTEGKVPAFLGSSFAFIPVILAAKEAYGGDLAYAQGGIIVAGLIYIIMSIIVK
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FSLGAIVIISPVVLAVFMEHIGDMTTNGAVVGKNFIENPGLNRTLLGDGFATIVAGCLGGPANTTYGENTAVLAITKNYDPSILRRTAIFAILLACV
GKFGGFLQSIPGSVMGGISIMLFSMITYVGLKTIRDSSCVESKINILIIAVILLIGLGTTYLSNKGISVGIPITSTVKITGLSLAAIVGIVLNRILNNQDFK
VEEE

>CORE_REP|Org29_Gene940#

MRFIHTSDWHLGKSLEGHSRIEEQAKFCEEFIKIVESNEIDMVIIAGDVYDTSNPPAQAEKLFYQTVSRLANNGQRCVLIISGNHDNPERLSAITP
LAHEQGILIYGYPLSATIEAKYKGFEITYATQGCTKLNINGENIVIATLPYPSEKRLNEVFSSEDEFEKQKNYSEKVGDIFRSLEENFRSDTINIAVSHI
FVIGGESTESERPIQLGGSFLVERKDLPEKAQYTALGHLHKQQKASERLNAYYSGSPLQYSKDERAYTKGAYIVDIKAGEKPIIEDVYFNNYKPIEV
FKCNGIEEALDICEQNQDREIWSYFEINTDEIISQNEIKKMKELLKDIIEIKPIITSCYEQESVDIKEKSMAELFREFYSFSKGVEPKGELMDLFLDIISE
EGESADETN

>CORE_REP|Org35_Gene1079#

MKLRALDISEANSYIKRILINDPILSNLKVKGEISNFKVHSSGNVYLSLKDETSKLNCVIFKSNFNRNLKLDNGVKIIANGYISVYERDGAYQLYINEI
EIEGIGNLHIEFNRLKEKLNKEGLFDPKYKIPIPKMPNSIGVITSPTGAVIRDIINVIKRRYPKVNIKLYPVMVQGDKSAEEICEAIRFFNHMKNVDT
LIVGRGGGSIEELWSFNDEMVAREVFNSQIPIISAVGHETDFTICDFVSDMRAPTPSAAAEIATPSLDDINYKLGNIKSRMSKSLTNQIELDQYRL

ETVFNKINNYLDSYTIKDKVIQLDKIYDKIIFGIENNLKLEDEKLVKIGALLHNLSPLATMDRGYSITQKNGKVINSIKGLKIKDSIDIVLKDGNLECMI
DKIENKEG

>CORE_REP|Org38_Gene120#

MKTSILIALIEKTSLIVVLFLLITKLKIFKQIFQKEEYSFNDLVCIALVFTFLAIFGTYSGINYMGSIVNTRIISIVSGGILFGPMVGITAGVFSGIHRYFM
DIGGITSVPCLLSSILAGVLSGFLYKRIPKQHRVMYGILVGMISESFTILLIYLISYPHSLAIQIIGGIYLPLIVGQIGIGFVISIVEGIEKDKKDIEARNKAE
IKALQRQINPHFLFNSLNTIASFIRFSPDKARELIINLSTYLRYNLEYSDNLIDINKEIEQVKSFVEIEKARFGELLTVSYDIEDVNIKIPSLIIQPLVENAII
HGILESGRAGVVKISIKKLPYSLENTVRISIEDNGIGISEEIINNVYQDNMPENKIGLYNVHLRLKLMYGRGLNIRRIDNGTLIVFYVKE

>CORE_REP|Org78_Gene1879#

MELWKRNLFVCWIGMFFSSIGMSQIAPILPLYIKQLGVTDVSLIQQYSGIIFGCTFVVAAFFSPI*GKAADKYGRKSMLLRASIGMGIVIFTMAFV
QNVYQLLGLRILQGVFTGYATACTTLIATQTDKNHSGWALGTLATASTTGSLIGPTVGGYIESILGLKSTFIITGGLLFVSFIISILFVVDNFKPKEIKE
SISIPKEQLNILPNKFLIASIFVTTFITQLALYSIEPIVTIYISQLTNFASNVALIAGLTFSASGLANLLAAQKLGKMSDKIGPQKVLLISLLWAGIIFIPQA
FVKTAWQLMLLRFLLGLSVAGLNPSVNSLLKKIAPEEYVGKIFGYNASAQYIGCSSGAFLGGQISAHLGIRTVFFSTSLLLFRNALWMYKFTGLFI
KDKTK

>CORE_REP|Org69_Gene1011#

MKILVLNCGSSSLKYQLIDMNNEEVLCIGLVERIGIEGSILKHEKAGRDDKYVVEQPMKDHKDAIALVLEAVAHPEFGAVKEMKEIDAVGHRVV
HAGEKFATSVVITPEVEDALKECIDLAPLHNPANIMGIDACKAILPDVPMVAVFDTAFHQTMPKSSYLYGLPHELYTKYGVRRYGFHGTSHNYV
SQRAAEILGKDIKDLKIVTCHLGNGASIAAVDGGKCVDTSMGFTPLEGLIMGTRCGDIDPAILPFLMRKEGLDADGLDKLMNKESGVYGMTGI
SSDFRDIEDAAKNGDERAQATLEAYVKKVQKYIGAYAAEMNGLDVVVFTAGVGENGKAIRADIASNMEFLGMKLDKEANDVRGKETVISTA
DSKVKMLLIPTNEELMIARDTLRLVK

>CORE_REP|Org36_Gene1022#

MSKVFEVKKDIYFTGVVDEGLKVFDIIMETEFGTTYNSYLIKDEKTVLFDTVKANFKDEFLSNLSEVTDIAKIDYVVIHHTEPDHAGSLKYLLDINP
NIEVYCTKAAKLYLDGQINRPFNCHVIKDGEILNIGKRNLRFITAPFLHWVDTMFTYIEEDKTLLTCDAFGCHFASVDAEVVNSEDYLKSAKHYY
DCIVKPFAKHVLSAVDKVVGLNIEFDTILTSHGPMLTKDPMAAVKRYVEWSTEAVNTTNQNQVSIFYLSAYSNTLEMAKKIKEGLDKEGAKAEL
YDLEDMTLTEMHDTLVVSKVILLGSPTINKTMVKPMWDLFSVIDPMANQGKIAGVFGSFGWSGEGITMAETLLKSMSFKMPVESLKKKFFPS
EETLKECMAFGAEFAKLVK

>CORE_REP|Org52_Gene1563#

MSIIVQKYGGSSVADTEKIKSIAENIIERRKENPQMVIVVSAMGKSTDEYITLAKELSNEPSKRELDALMSTGEMISASLLSIALNALGCKAISYNA
YQLNIKTSGLHGKSQIDDINVNRIKNSLDEGNVVIVTGFQGINEDGDVTTLGRGGSDTSAVALAVKLNGKCEIYTDVDGIYFTDPRKYSKASKLD
EIEYEEMLELASLGAQVMHSRSIELAQKYGVEIYVGRTCGTEKGTYIRGGKDMKLEDKVITGLATSDDDSSITIKDFKAENISSLFEDIATIGISVD
MISQTAPILDKISVSFTVPKEELGECKKIVSKYTDEEHVVIDNNITKFSLVGLGMKNTSGVAAKVFKIFNENGIMIKLITTSEIRITCAINSDDKQVAI
EKIAEVFNI

>CORE_REP|Org43_Gene1184#

MRKLIYFITPFIIGVVFLFGLDKFLDSKTDELLREKNLLPIMDDTLSDIKDKGVTANNHFLREKDIMILGSSELSNSTKQHPKYYFNTNRSKNKVFAI
GRAYTQTLQDAAILGSMNPNIDNKKVVLLISMQWFMEKDGVTSHHYQSRFSPIQFYRFLDNPKISKQNKIEYAKKSSKLLWGSDEYKAEALYA
KLYEPKTLLEKAEKVLLEPYFQGRKYCIALKEKGILYKRLIKLDKKRATKRKSPINWSHERKKAIEDAKKRVGKNPLNIDNYYYKQHFKDGIDQYKG
RDKDVNLLTSKEFESYKLMLNVCTDLGIKPVVVLIPSMDKFYNLTGISEKERNQYYDKAQNIAESKGFEVLNLKDKGSDKYYLRDVMHLGTKGW
VDVCERLFKIFKEQ

>CORE_REP|Org76_Gene334#

MNFNQKRIAASIMATAIIMPTMGNLAYANESEVESVSIESRTITGNAVNFRKGPGTNHESMGKLYKGDKVEYVGKEGSWVKVKYNGNTGYV
HGNYVAINSLGSSNESSDTSVKSTKVVTAKGLNFRTGPSTSSSKISTLGYGTEVGYISESNGWSKISSNGRVGYVSSKYLGTSVNDSTNENVENSS
NDLVKGTKVVTAKSLNVRTGPGTSHSKIATLSYGTEVGSISESGGWTKVSYGNQTGYVSSQYLAEKGSVDTSIPSYSTNSPSQGADSVISFAKTL
LGKPYVWGAEGPNSFDCSGFTQYVMKKSAGVSIPRVSRDQSKYGTYVNRGDLRSGDLVFFDTQGSNNGSVSHVGIYIGNGDMIHASSGSSK
KVTISNINSSYYSSRYVNARRVL

>CORE_REP|Org56_Gene2763#

MHELILISEKYKEDILDFFTDIHMHPELSFKEFRTTKAIKDLLVSLDIEILDLGMETGVVGLLKGKYDGPTVALRGDIDALPIYEEVDIEYKSRYDGIM
HACGHDIHTSCLVGCAYVLSHIRDSLHGNVKFIFQPAEEVNKGAKMLVERGVMENPKVDAIFGLHNHPDIPCGKIGVKLGGLMAAVDTIKIEV
NGFGGHGGIPNRTIDPIVASSAIIMGIQTIVSRNISPLESAVISIGTINGGTANNVISEKVDMTGTCRSFSNEVRKKISENLENIVCEIARGYQATAK
LDYLFDLPAVINSKEMYTIACKSVCDLYSEDAIVDPIPSTGGEDFSIFMEKAPGFFYWLGVGNKEQDCIYQWHNPKFKADKNSILVGTNVLCQS
VINYMDKLKNKI

>CORE_REP|Org70_Gene1064#

MSRVIWIVIDSVGIGALPDAENFGDSKDVSTLGNIFREYPDINIPNMRKLGIGNIDGVDFFESIKTPIGCFGKCKEMSQGKDTTTGHWEMTGIIV
DKPFKTFEHGFSKEIIDEFEKKTGRKVVGNKPASGTVIIDEYGEHQIKTGDVIVYTSADSVFQIAANEEVIPLEELYNMCKIAREIMMGDNAVAR
VIARPFIGKKKGEFVRTSNRRDYSLDPFEPTVLDNIKESGLDVLAVGKIEDIFNGKGITDAIHTKSNMDGVDETLNYMKQDNKGLIYSNLVDFDS
KYGHRRDPEGYKKALEEFDSRLPEIMANMREDDILIINADHGNDPTYKGTDHTREYIPVMIYGNKIKKGFNLGVKDTFADIGATVADILNVKLP
KHGSSFKKDLF

>CORE_REP|Org18_Gene1426#

MSVENKSNKKELKKVTAKTLIEKGKKQGSLTLAEIMEAFSETELDKDQVENLYETLGNLGIEITETKNYKADIDFSVADDDLSIGHLDEDAEAISH
DDSSAIEIETVDLSLPKGISIDDPVRMYLKEIGKIPLLKPHEEVEFARRMHEGDEIAKQRLVEANLRLVVSIAKRYVGRGMLFLDLIQEGNLGLIKA
VEKFDYTKGYKFSTYATWWIRQAITRAIADQARTIRIPVHMVETINKLIRVSRQLLQELGRDPKPEEIAKEMEMTEDKVREIMKIAQDPVSLETPI
GEEEDSHLGDFIPDDDAPAPAEAAAYSLLKEQIEDVLGSLNDREQKVLKLRFGLEDGRARTLEEVGKEFDVTRERIRQIEAKALRKLRHPSRSKKL
RDYLD

>CORE_REP|Org71_Gene2296#

MKINWNTKYTTIAIYTFIIAASSIIFYLVSSQIDVFSNNLDAIFTTLQPFIIGFAIAYLLNFILKFYEDRIFIKSEKLKKLKQSSKRGLGLLLTYATAAVILYL
FMYFVLPQVIESIVGLANDIPMYVNNATKLIDKLMTDLNLDEQYFNLAVDKWNEFVTYIIKFVTDLIPILGSMLKNVASSIWNIVLGLIVSVYLLID
KEKFYGLSKKITYAVFTEKQAARILELTHRSNYTFGRFLGGKILDSFIIGILTFVILTLVKMPYTLLISVIIGITNIIPFFGPLFGAIPSTLIVLFVSPIKAFW
LLLIILIIQQIDGNIIGPKILGDSIGISAFWILFSLLVAGKLLGFIGMVIGVPMFAVIYSIIKDTVESKLDKKGLPTDTSDYM

>CORE_REP|Org27_Gene973#

MDIKEITKSYKDYVIKLRREFHENPEKSMEEVRTSKRVKEELDKIGIPYVSAGGTGVIATIKGANPGKTVALRGDMDALQVVECTDVEYKSKNEG
LMHACGHDGHTSMLLGAAKVLNDIKDSINGTVKLFFQPGEEVGKGARAMIQDGAMEGVDSVFGIHLWTDVESGTISVEEGPRMASADFFKI
TVKGRGGHGSLPHQGVDAVLASSAIVMNLQSMVSREVSPLEPLVVSVGVLNSGTRFNVIASEAILEGTIRLFNPELRKQIPGILERIAKSTAEAYR
ADAELEYGYLTPAVINDKECSKIATDAAIKLFGEDCITLFEKVTGAEDLAEFMNIAPGALAFVGARNESKGACYPHHHGCFNIDEDALEIGTALYV
QYAVDFLNK

>CORE_REP|Org33_Gene1231#

MKKLASTALAILIALTPLSFSFANNKENADANQLNISSKSAILMDVGSGQILYEKDAHKKLPPASVTKVMTMLLIVEALDSGKIKLDDEVQVSETA
SSMGGSQIFLEPGETQKVDTLLKGIAVASANDACVAMAEHLAGSVEGFVDRMNAKAKELNMNDTHFANTNGLPVANHYTSAHDIALMSRE
LLKHEMISKYLTTWMDKVVVGKKQVTVGLANTNKLIKHYQGATGVKTGFTQEAKYCLSASAKRGNTHLVAATLGAETSPERFNDASSLLTYGF
ANYESVKLCSKGDNIATLTLDKADENKVKLVAKEDLNALIKKGSSKEFEKKIEIVKNPKMPIKKGTVLGKIKICKDKKVIGEVELINTKDINKASYLQ
MLQRIIDNMI

>CORE_REP|Org31_Gene2820#

MKLMGYLRENGQFGIRNHVLIIPTSVCSSETATRIASLVPGAIAIPHQHGCCQIGSDIELTAKTLIGFGKNPNVAAVLVVGLGCDGIQAKELASEI
ATTGKKVDYVVIQECGGTLKTVSKGAEIVSKMAREVSKEVRVEFGMSEITLALECGGSDPTSGIASNPSIGVASNLLVDEGGSSILSETTEVIGAE
HLLATRFEDEEMKDKFLKFVSDVEKRAIAMGEDLRSGQPTPGNKAGGLSTIEEKSLGCMYKAGNKPFKGALEYADIVPPDKKGLYFMDTPGQ
DIDSITGMVAGGAQIVIFSTGRGTPTGSPISPVIKITGNSDTYNKMPDNIDINAGRIITDGAKIADIGQEIFNEIIEVCNGKHTKAESLGHREFGIYR
ISSTF

>CORE_REP|Org18_Gene2679#

MMLNFDVELEECAQIKVIGVGGGGNNAVNRMVEAQLKGVEFISVNTDKQALYTSKAEYKVQIGEKLTRGLGAGANPEVGKRAAEESKDEIVK
LLQGADMVFVTAGMGGGTGTGAAPVVAGLAKEMGILTVGVVTKPFAFEGKIRMKNAEGGIAELKSKVDTLITIPNDRLLQIVQKNTSMLDAF
AVADDVLKQGIQSISDLIAVEGLINLDFADVTTIMKDKGLAHMGIGSASGETRAIDAARQAIQSPLLETSIQGAKGVLLNVTGGPNLGLFEVNEA
STLVMESCDPEANVIFGASIKEDLGDEIMITVIATGFEGLQNGALDLDTKPKSSIRSSLNTTVKQAVKEIEEEVIAEEKIEPPKKASIIEEDDDESMEI
PTFLRRRR

>CORE_REP|Org94_Gene2126#

MKKISILGSTGSIGKQTLDVVRDNRDKFEIVAISANSNIELLLEQIVEFKPKYVTVFEENKALKLKEMLPKNIEIEVLAGMEGLKIISSLDEVDVLLTA
VVGMIGLVPTLCAIKKGIDIALANKETLVTAGELVMKEAEKYNVNILPVDSEHSAIFQCLNGENKKNIEKIILTASGGPFRGKKKGELVNITKNEAL
KHPNWSMGRKISIDSSTLMNKGLEVIEARWLFGVEQENIDVVVHPQSIIHSMVQYTDSSIIAQLGCPDMRLPIQYALTYPDRMESSFERMNFS
KFSTLTFEEPDLETFPCLKLAYECLKMGGTYSSVLNSANEVLVSEFLEDKIGFYDIPYYIEKTLEVHSSISEPTLEEILETDRWSRSYVANLIKK

>CORE_REP|Org67_Gene2443#

MKKAIQFGAGNIGRGFIGGLLVKSGYYVVFADVNEDILNSINKDKKYTIHIRDVECIDEVIDNISAVSSIKEEIIDEIVQAEIITTAVGPLVLTKIASTIA
KGIKARKEKGLTSNLNIIACENAIYASSSLKEEVLKYLNKEEVEYLEMYVGFPNCSVDRIVPPGKNENPLDVTVENFYEWNVEKQGFKGEIPTIVG
MNLADNLMAYIERKLFTLNTGHAITAYIGYLKGYKTIEESIKDKFICDIVKSAMVESGEGLIKKYNFDSEVHYKYIDKILNRFKNPYLNDDVLRVGR
EPLRKLSDKDRLIKPLMTAKSYGLSVDNLILGIGAALHYNNSEDTQSVELQELIKSIGVKKAVAKIANISNDEELLNNIEKSYIFMKNL

>CORE_REP|Org12_Gene2962#

MIFSQYGDYFYLYILLLTSIPAVILGLMGKNIKYYGMLASLFMIFLIVGIDVQLKYLVIFIILEVIIVKGYEYVRRKTKNKYIYWGFLFASMLPIIINKISP
VTSFGIIGFIGISYLNFRTIQMVIEIYDGAIKEVKISKMLYFMLFFPTLSSGPIDRSRRFEQDLEKQISRKEYIEEYLLPGIKNIVMGVGYKFVIAFLINT
YWVSRIPKDMSFINILSYMYAYSLYLFFDFAGYSLFAIGTGYIFGIQVPINFDKPFISKDMKEFWTRWHISLSRWFGDYIFSRFVMSSMRKKRFKK
RTTAAHVAQMITMITMGFWHGLTWYYVAYGVYQGLALVLTDIYQRKSKFYKKHKKDKWFERVQIFITFHIVCFGLLIFSGYLA

>CORE_REP|Org45_Gene11#

MQLNRRCTYCEFCESKRKRYLLYEKAIELAKNGEGFVNPNPLVGCVIVKDDYIIGKGYHEKFGSNHAEVNAINSAKQSLKDSTLYVNLEPCSHYG
KTPPCVDKIIQNKIKRVVISTLDPNPLVCGNGVKKLRDNNIDVTVGTLEEEARDLNEVFFYYIKNKRPLCIVKSAVSLDGKIATKSLESKWISNESSR
YLTHKYRNKYQSIMVGINTVLNDNPLLTCRLNQEKVSHPTRIVIDTHLKLPLNSNLVKDKTSKTIVFTCCKESKKLSMLKENNVETIISPSKNNLVD
LEFVMYKLGELNIDSVLVEGGATLNDSLFRNRLVDKVKLFLSPKIIGGKDAPTFVSGEGINHLSDSTQLAINNVTLIDGDILIESDVLN

>CORE_REP|Org72_Gene2785#

MPKENLKKQIDIRMKTEFDGVVFYTTMLLVFVGIVMVFSASFIQSSFKHNDAYYFLKKNVIYAVLGFIVMIITSRIDYSFWKKNATAIGAIAVVLL
LLVLTPLGIEANGAKRWLGIGALTFQPAEIAKFATIILTAKLIEKNYDKIKSLTKGVVPLLVVPGIFFALIILQPNLSTAGTVILVTFVMIFVAGMDMK
IVFAMIGSGAALFAALVIAEPYRLSRVTSFLDPFQDPLGKGYQVIQGLYALGSGGLFGLGLGKSKQKYFYIPEPQNDFIFAIIGEELGLIGCIIVIMLF
VVLVYRCVRIALKTSNVFACMVVIGIGAQIGIQAALNIAVATSSMPATGVALPFISYGGTSLTIFMGAVGIVLNISKHVKIN

>CORE_REP|Org26_Gene1036#

MKKININYKSTIKLIKQLDWKLIVTVLAIFIFGLVILSSATHANSTGSYNQLIKQGLAFVLGIGMIIVILFFDYNLLGRYYKALYIISLILLAIVLLPGIGTV
KGGARSWINLGPLDLQTSEIVKLTFVLSYAKILESKKDKLNTLKEVMPVVVYSLPFIGLLIAQPDLGTGIVFCCMIFAMLFTAGLSSKLIKRGIIILLVS
MPLMYLMMADHQKVRIEAFLNPEDVTLKGNYQVMQSLIAIGSGGVTGKGLYNGSQNQEDFLPVQDSDFIFAVVGEELGVIGMAVLIILFMIF
LLRLLAIARDAKDFYGTLIVVGVMGMFGYQIIQNIGMTVALIPVTGVTLPFVSYGGSSLLTSLANLGLVLNVCMRRKKINF

>CORE_REP|Org81_Gene2994#

MNDIKVMTVFGTRPEAIKVAPLIKELEKRENIKSIVCVTAQHREMLDQVIETFNINVDYDLDIMEKGQSLNDITCKILNKLPLILNKENPNIILVHG
DTTTTLATSLTAFYNKTLVGHIEAGLRTYDKYSPFPEELNRQLTGIIADMHFAPTNLAKKNLISEGKPNNNIFVTGNTAIDALKMTIKENYNHPIID
EIGNDRMILLTSHRRENLGKPMKNIFRAIKRIVDDFEDVQIVYPIHLNPKIRTIADEIFGKFPKKIHIIEPLDVADFHNFLNKSYMIMTDSGGIQEEA
PSLGKPVLVLRDKTERTEGIEAKTLKLVGTNEDRIYNSVSDLLINKDNYVQMSKASNPYGDGNASKYIVDIIIKKFNCKYLN

>CORE_REP|Org94_Gene1709#

MIAVKKAYKFRLYPNKKQQELINKTFGCCRFVYNKYLAKRIDVYKNNKETFTYKQCSSDLTNLKKELKWLKEPDKFSLQNALKDLDNAYKKFFKE
KAGFPKFKSKKINRFSYKTNFTNGNIMYCGQHIKLPKLGMVKVRDKQVPKGRILNATISKEPSGRYYVSLCCTDVDIEAFENENTNNHIGLDLGI
KEFCISSCGEFIENPKYLKKSLNKLAKLQSELSRKTIGSLNRNKARLKVARLQEHIANQRKDFLQKLSTKLIKENDIICIEDLQVKNMIKNHKLSRSIS
DVSWSEFIRQLEYKANWHGRQIVKVGKFFASSQICNKCGYKNEEVKNLNIREWICPSCNETHDRDINASINILKEGLRLITIQNK

>CORE_REP|Org87_Gene1052#

MRVEAPIKVDRKTKKLAKRVESGEIAVINHIDIDEVAANSLVEAKIKLVINAAPSISGRYPNKGPGILTENNILIIDNVGEELFEELKEGETIEVVDGK
IYRKGKFLGAGEVLDKYEVSYQIKAAYENLAVELDRFIDNTIDYAKKEKGFILGEVEIPKVKTNYANKHVLIVVRGQDYKEDLSTMLSYIEEVKPVL

VGVDGGADALIEFGYTPDVIVGDMDSVSDEALKKASEIVVHAYTDGRAPGLKRVEELGLDAVVFPAPGTSEDIAMLIAYEYKAELIVAVGTHSN
MIDFLEKGRKGMASTFLVRLKIGSKLIDAKGVNLLYRSKLKIKYIWALIATALFPVLVVASLSPGVQQFIQLMQLKFRVLLQM

>CORE_REP|Org69_Gene1184#

MKDDKTILILTAQFGAGHISAAKAVKESIIEKYSNYNVVIQNFINASIPMMNKPMVKLYENNTKYTPGLYNYYYYFKKSFDSRHDFSHKLYTPKLS
EYIADINPDLIISTFPLAAACVNNFKIKNPDINIPTLTVITDVVDSMEWVFENTDLYFVPSPEIKNRFFQKGINPDSIKVTGVPVDKRFQIESKEICC
DKYRLLLLGGGRGLFDIDEDFMHWIDEFIEEHSDSIEITIVTGKNKKLYDNLTHKKPLKNIKVLGFVNDMYNLIRECDLMLTKPGGATIFEAIQSQ
TPVLVKMPKVGQEIENAKFIIDKGLGMIYSDDLDLKNIFYRLVSNEFDSIINFMKKNLEEFKTVIHPEKIADYISELIDKHYS

>CORE_REP|Org26_Gene3286#

MNIKSAFIRKRGGKFYVYVEYIEETTGKIKQKSYGSYEKKKDAEKHLIEIKSTINNNKFITPSKTTLVERCYKYIMSNEKKWSPYTTVNRKSWVKNYI
EPFFKDTILIDVNPSLLQIFIDKNFDGSAPSTAKVRYNFLSSVLKEAYRLKEISENPCDFVKLPAQNVTYEIEIYNREETLLLIEKLKDSLIEIPILLMLLL
GLRIGEVAGLRWSDVDLDNSIININQILIYANSKITFKEPKTAKSKRTLSVPKELIEKLKIEKVKQNKIKLQGTLENENNLVCLNTNLKPWIPTALSKT
FHNFIKRNNLRNIRVHDLRHTNASLLLLGGTNMKVVSERLGHTDIKITMNRYSHVLEEMDKEASDNLSKLLFK

>CORE_REP|Org29_Gene2365#

MKIIVIKIVIIVKIIIAITTNKIKLKILGGLIQLIIQKKFTIADGNFERELFGNFDENVKLIEKTLNIDVILREGNIILIGEEKNVDSALKLMNELHQTVSNG
KHLDKQSISYSLSLLLEGSEQKIKELEGTIVITQRGKAVQPKTLGQKEYIKLIENNDITFGVGPAGTGKTYLAVAMAVKAFKRDEVSRIILTRPAVEA
GESLGFLPGDLKDKVDPYLRPLYDALFEMLGADKFNKYLERGTIEVAPLAFMRGRTLDNSFIILDEAQNTTSEQMKMFLTRLGFGSKAVVTGDV
TQTDLPQNKKSGLIQATEILKGVPGIGSIMLTDRDVVRHELVQRIIRAYEKHDKREEFKKEERKKVKMQEKTFKRK

>CORE_REP|Org16_Gene1985#

MNAFIRKRNKNYVVYLEFEDEKTGKRKQKNMGTFDKKREASKRLNEVKESLYNDGFLVPSEITVSEFLLDFLNKYSENISLATYNNYVSICKNYIN
PSIGKYKIQDLHPVHIQNYIDKLSYKLNPQSIKIHINILKLAIKRAYRLKLIKENVMDSIEAPRYKKFKNEIYDREQMIKLLDLAKNTEMELPINLAIGL
GLRISEVLGLTWDNIDFEENTITVNKITSRINGSVILKEPKTESSVRKISSPKELMSLLKEYKIKQNKNLLKSSIRNNNNLLFFNKKCEPIAEDVMSKK
FKRFLEKNELPHIRFHDLRHSHVTLLINSKVPIKVISERVGHSNISTTLSVYSHVLKEMDKEASDKISESLFNAN

>CORE_REP|Org18_Gene1237#

MDFMEKRDTYLWLKSIGGITTKTIEIIENEIVNIEDIFDFSEKEIYNLKNISLNIRKNIVKYRGHAYLENIKELLYKKAIKYICKYDKEYPENLKNIYNAP
KLLFYKGDIGLVNNNFNIAIVGSRKPTAYGINCAKTISCQLSQYGVNIVSGLAIGIDAYSHIGCMSGKSKTIAVLGSGVDNPLPKQNLHLSNKILEN
GGLLLSEYNINSTVAPYHFSNRNRIISGLSDGVVVVEAAIKSGALITVDFALEHGKNVFAIPGNINSQMSRGCHKIIKEGAKLIENIDDILNEYNIFN
IIDKKINQKYDNISLNAKSKQIIEAIKREGNLHIDSICDYTGIEIKYVNSIINELVLNELVVEMNNKTYSLNV

>CORE_REP|Org76_Gene168#

MSKKNKSLLSELKGHLMTGISYMLPLVIGSSLVVAIPKLTALAMGITSLDAYKNVSGFYHILYLMEQVGWTGIGLLNTVLAGFIAFSIGEKPAMG
AGFIGGLIASNTNAGFLGAVIAGFFAGYVCKFLKKKIKISGSASGMMPLIIMPLITVGLTGFLMSVVLAGPLGNINTSLNAWVAEMCQNGTNSV
VLALILGAMIGFDLGGPVNKAAWMAGNALLLEGIYLPAILVNCAIVIPPLGYGLATFIRKSKFSNALAETGKGNIVMGIIGITEGAIPFTLTNPLKL
VPVNMIGCALGVGLSALLGVHAIMPPVGGLYGFISIGSGWAYLVGAIFGALVIAILSTTLVDFNEDETTENTEFDEIELDIM

>CORE_REP|Org56_Gene1672#

MSFYDVIEKYRDFDFDGYLNNVTDNDVLRSLSKDKLEDFDILNLLSKTAVKHLEDMAQKAHKLSVQYFGKTVCLYTPMYIANYCVNQCVYCSY
NIKSGIKRKKLTMDEIREEGEAISKEGFKHLLVLTGESSFHSSVEYIGEAIEILREKFPSIGIEVYPMEVEEYKYIVDKGVEGLTVYQETYDEEIYKRVH
IKGPKSNYEFRLDAPERGAKAGMRTLSIGALLGLNDFRKETFFTILHGKYLKTKYPHIELSYSTPRMRPFKGCFEELVDISDTDLVQAMVCMRLFD
PHAAINISTRENLEMRSHIIPLGVTKLSAGVSTDVGGHSQDEHDTAQFKINDESTVKDVEKMLNSIGYQHVFKDWERF

>CORE_REP|Org35_Gene2739#

MKVLILTGKFGMGHYSASNSLSEDIKAKFDNSEITIKDIFEYIMPNYSDKMYKTFSILVNRGSSLYNLFYKCAENGKKDIKFTFSDYFLNKLDTLLHE
VQPTVVISTFPFCSQLVSRYKEKYNSNLPLITCITDISSHSEWISKNTDCYLVASKSTKEELVFKGIDESKIKVNGIPVKKEFKRIEHVNHSTKKNILIM
GGGLGLLPKSEQFYKELNSLEGVKTTVITGNNKKMYYKLYGRYENIEVVGYTNEVYKYMKDSDLIISKPGGITLFETIYSELPILAFNPFLQQEIDN
ASFILNNEIGRILGKNKKYYVDEIKDLIYDDATLKEMSSNMKELKKQFDNNTLENILFSLDEQGACRECM

>CORE_REP|Org63_Gene2841#

MYCNLLKPIKIGNLELKNRVSFAPTSMGLKLEEKIKKFSDIAKSGVALITLGDVSIRPSFHKIAISLSDEDGVMKYKKIVDEIHNSGAKVSAQLFCSD
YDVNLIKDTMKMGITSHDEIKKIMNDGVKDYITNMPKEEIKNIINLFKVTALNAKKAGFDMIQIHGDRLVGSFSSSIFNNRNDEYGGTCENRSR
FASEIISSIRNEVKDIPIDYKFAIRQENPHYGNAGVLLSEVEYFVKKFESLGINSFHVTLANHSKLEDTIPTNNHPYFKDEGCFLYLADEVKKHTNLP
VCGVGKLSSPDFIESIISNNRVDMISMSRQLLADSNWLQKVKDGRVDEIKKCCYCNKKCADALQTHSQFGCILD

>CORE_REP|Org9_Gene2310#

MQDKKIYLNIVLTVVVSYILIKVIDNYKYFFGVISLLMSLLTPFIIAFVLAYIFNPLVKFLESKLNFKRIYSLLLTYGVLIVILISFILFTVPSIVNSLADLVA
QIPTYIDKTEQFLFDLGKSLQSVDPNTLKEYGDKIMSVMPKFSNLLIGSLGGIFSTTFSVGKFIVQFLLGFIICFYILLEKEKFLLFTKKVVYISLGKKYG
DFIIELCQSLNLNIGKYFTGKILDSFIVGVLSGIGLYFLKSEYALLFGTLMGVMNMVPYFGPVIGMAPVVIINLFSNPTIALTSLIYLIIIQQVEVTFIEP
KIVGGQLGLSPFFTILAVTVGGGFFGIPGMILSAPVMGVIKIYFCEFVNRRHDKIQME

>CORE_REP|Org96_Gene2580#

MSTNHGANLYSLSSKYGFSKEEFMDFSSNINPFGTSSLAKQYIVNNIDMVSMYPDPDYIDLKTSISNYCKCSIDNIVLGSGATELISSFIHTINPKQ
ALLLSPAYSEYEKELSKINCSIEKYFAKEEDNFHINLENLIKTINAKDYDLVVICNPSNPTGFAFTKVEVREILKNTDSFLMIDETYVEFTDTDTYSCT
QLVDDYSNLFVIRGTSKFFSTPGIRLGYGLISNTNVKNEINKNLDLWNINIIASKMGEIMFSDLDFISNTISLMNTERDYLLKELKNIKSLDIYNTKG
NFILCKIKTKELTAKSLREQLLPQKIIIRDCCSFEGLDEYFFRVCILKPNENKLLISSLKAIFILKTY

>CORE_REP|Org92_Gene1881#

MIIISKENIKYYLIVVFIGILFFKFINTPSDFISSIEGFLKFFSPFLLAILLALLLNPLVMLFEIKFKAHRLLAIFLSYIFIGFILAFAIRLLIPSIANTLNRLINEM
PMYTDYIDSFIEKNMSNIYFLKTLIPHIQHSLDNLLKEASNFVGKIPKNFLIYTLSISSMLFNMTMGFILSIYIIYDKEKIALGFKRFLYSSTARNKADN
IIEFFRTTHDIFYDYLLGRILDSLIIGIIAFLGFQFVIRIENALFLASIIFLGNIIPYFGPFIGAIPPIAMTILYSPQKTIWVIAFLFILQQLDGNFIEPKVMG
NQVGIGAIWVISAILVGQSLFGFIGVFLSVPIAAVVKTYVDKYIDNRLQ

>CORE_REP|Org5_Gene1807#

MSGIWGNNLKVSIFGESHGNAIGINIDGLPSGIELDLDKIDKEMKRRAPGKNSISTSRNESDIPEILSGYFNGRTTGTPLCAIIRNSDTRSKDYGEL
KNLMRPGHADFTGNVRYSGFNDYRGGGHFSGRITAPLVFCGAICKQILSQKGIEIGAHIKKIKNIEDMSFDYVNISKQQLSNLQTLELPLLDLSKE
EAMKNTIIDAKNQRDSVGGIIECAVVGINVGLGNPFFDSVESTLSHLLFSVPAVKGVEFGLGFELADMYGSQSNDEMYYEGNQVKSKTNNNG
GIIGGITTGMPIIFKVAIKPTPSISRQQNTVNIKDKKDDILYIKGRHDPCIVQRAIPVIEAVTAIGIFDLMKGR

>CORE_REP|Org51_Gene1144#

MNFKENRLKIAVLIIVILIILAGIFVFIQIGPYDKNNKKDVIIDVPSGASVGKISDILYENKLIKNELLFKLLVKVSNKAPSIKSGTYLLNQSYSNNDIISLL
VSGKIYQDGIKVTIPEGATSKEIIAMLVSKNLGDKATFENLIKKPQEFYDKFPYLKEDGITSLEGFLYPETYYFNSKKQSEEDILSEMLKVFDSKYTDK
FKKKQKELNMTLQEVMEMASIIEKEAVLDKDRPIIASVFYNRLKVGMPLQSDATIQYIFEERKKIVTYDDLKIDSPYNSYKNKGLPPTPISNPGIES
IEAALYPDKTDYLYFVAKIDGGNNYSTNYQDHLKYVKEYKEARDKQSKDTKATNKENTKR

>CORE_REP|Org58_Gene2738#

MKVYNVIMAGGGGTRFWPLSRQEVPKQLINLSGEDALINETINRIDSLAKKDDLFIVTNEKQLEALKDIVKDKCLDSNILPEPCARNTAAAIGFA
AFNIMKKYGDGVMCVYPADHYIKDEKEFKSILEKAIYIAENNDKLVTIGITPTFPSTGYGYINFNRENTIEDVAYEVVEFVEKPNYEIAKEYVNSKK
YVWNSGMFVWKVSKILEDFKRYLPKVYEKLEDISKYLGTKEEMEKIKEIYPTIQSISIDYGIMERSNDVIVVPGDFGWNDVGSWDSLGAIYPTDD
EGNIKRGENITIDTKNSIIYSDDKLISTIGISDLIVVSTNDAVMVCRKDKAQDVKKIVEQLKEEDRQEYM

>CORE_REP|Org56_Gene2044#

MIIKELIIRDLVAKVPIIQGGMGVGISRSSLAGAVAKLGGVGVISGVQIGYDEEDFETNTINANLRAIKKHISKAKEISNGGIIGINFMVAMKEYET
YVKEAVKAGVDLIISGAGLPNKLPSLVKGSNVKIAPIVSTAKAANVILKMWDRKEKTTADLIVVEGPKAGGHLGYSNEELDNIDSIDYDKEFVEIL
KVANTYGEKFGRNIPVVAAGGITSSSDVKKYIDMGASGVQVGTRFVATYECDAHENFKMAYINASEEDVHIVKSPVGLPGRAIRNKFIEEVKIN
RPEIKKCYNCLIPCNPKETPYCISQALINAVKGDVENSLLFCGNDAYKIDKLSTVEDVINELISEL

>CORE_REP|Org52_Gene1117#

MNKKKITFIFVILILALILFSFFRSSSQNTKYSKTSYYLGTVNEVTVFNVKESKSDKILNECDSILRYIDNKMSTHIPGSDVSKINDNAGKKFVRVSDD
TFFVVKEAIQYSKLSDGYFDITIGPLSNLWAIGTDKAKVPSDSEIQKLLPLIDYKNIILDEKNKSIKLTKENMKIDLGAIAKGYAADKIVAYLKSEDVK

KGLVNLGGNIFTLEDGKNDKPFKIGIQDPTSKNGESIGNIETTNKSVVTSGIYERFIEKDGKIYHHMLNPFTGYPFENNLSSVTIISDKSINCDALST
STFGLGLEKGMDLINKIDNVDAIFITKDKKVYLTKGIKDNFKLTDKSFSIEKLNKQ

>CORE_REP|Org18_Gene2133#

MSYERRKTREVSVGTVKIGGENPISIQSMTNTDTRDADATIAQIKRLEEAGCDIVRVAVPDIKAAKNIAKIKSSVNIPIIADIHFDYKLALEAIEQGV
DGIRINPGNIGSIERVKMVVEKCKERNLKIRIGVNGGSLEKELLKKYGSATAEALVESAMGHIKILEDLDFHNIVISLKSSDIYKTVDAYELISKKVDY
PLHIGITESGSVHKGTIKSSIGVGALLLKGIGDTVRISLTGDPVEEVIVGKQILRSLGLLNDKIKVISCPTCGRCNIDLISVVNEVEEKIGSMEKNITVA
IMGCAVNGPGEAREADIGIAGGKGEGLLFKKGEIVRMIDGNKLVDELLEEIEKL

>CORE_REP|Org39_Gene1501#

MREKESIRELRGYEPNHVNCKVKLDANEGSKRLFKYLIKEISDSDIDLNLYPEDSYSNLKESIIDYINISGVNKKNLLVGNGSSEIIDLIIHTFVDKDEV
ILSFSPSFSMYSIYSQINGSKFIGVESDENLVINIDSVIEKVKENNPKIVIVCNPNNPTGTILKREEIIKLLDSTNSLVVLDEAYMDFGEESMLSDVFK
YDNLIVLRTLSKAFGLAGIRTGYMLSNSSLINSVEKVRPPYNLNSLSDFIATRALRNKDVVKAYIKEVKEEREVLYKEMIGMGIKAYKSQANFILFY
SEIENLSQKLIDRGVLIRKFGGKLENYYRVTIGDKEENSMFVGAIRDILKKEK

>CORE_REP|Org87_Gene2187#

MKKMWKGNHAIAEAALRGGCEFYAGYPITPQTEVMEFLSHRMSELGRTFIQSENEMAAIYMVYGAYASGMRSMTSSSGPGISLKQEGISYL
CANHYPCVIVNVQRWGPGLGSLDSAQTDYLRDTRGGGNGDYHLIVYAPNSIQETVDLMYNSFDVAEKYRVPVEILTEAALGQMMEPVEFPE
FKKREEDLGWTYDGSNRDHAKVADNQKPTFCMEKRMRISENEQQWEDYQIEDAEYVFVAFGIPSRTTMNAVRRLREQGEKVGIIRPITVWP
FPYKAFEKVSKDVKGFISVESTDTGQLVEDVALASKKVCKENVPVYGLFSGNHIPKTLQVMDTYSKIKSGEIKEVF

>CORE_REP|Org88_Gene1169#

MSVDQEKLKALNEALGKIEKDFGKGSVMKLGEATSMSIDVISTGAIGLDIAIGIGGLPRGRIVEVYGPESSGKTTVALSCVASAQKDGGIAAFIDA
EHALDPVYAKALGVDVDNLIISQPDTGEQALEIAEALIRSGAIDIIVIDSVAALVPKAEIDGDMGDSHVGLQARLMSQALRKLTGSIKKSNCVAIFI
NQLREKVGIMFGNPETTTGGRALKFYSSVRLDVRKIDTIKQGDKVIGSRTRVKVVKNKVAPPFKQAEFDIMYGEGISKIGDLLDIAADVDIVKKS
GSWYSYNDTKLGQGRENVKKFLEDNLDLTNEIDEKVRAFYNLNEEHEEAGNSVSKEIVEE

>CORE_REP|Org78_Gene2222#

MSNKNKYHKNKKKYWEEMKMARMYYEKDVDLEVLKNKKVAVLGYGSQGHAHAQNLRDNGVHVMIGLYDGSKSAQKAKEDGFEVKSVAE
ATKESDLTMMLMPDEKQKKVYEESVKDNLKEGQTLAFAHGFNIHYNQVQPPEFVDVVMVAPKGPGHLVRNVFTKGSGVPALFAVYQDHTK
KATETVLAYAKGIGATRAGVLETTFKEETETDLFGEQSVLCGGISELIKLGYKTLVDAGYQKEVAYFECLHEMKLIVDLIYEGGFERMRYSISDTAE
YGDYVSGKRVITDAAKQGMQNVLEDIQNGKFAKAWIKENEEGRENFLKTREEEYNTEIAEVGRNLRSMMSFLK

>CORE_REP|Org96_Gene2359#

MNYKDIIRNVKEKNFEKMYLFYGREYYLIENAIKAFKDSLNEGMLDFNLDIIDGKEIVLNQLISSIETLPFMDDRKIVIIKDFELLKGKKKNFTDSDE
KYLIEHLDNIPDTTTIVFVVYGDVDKRKSLVKKIGNNGIVFDCDKLSDMDLFKWIKKSFALNDVIIDNSQIMYFIEQEGYRDKSSEKTLSDLENEIN
KISSFVGKGNNVTNDVIDKLSQKKVENDIFKLIDYIGEQNASNAMKILNDMIQEGESVLGIFSMIARQFKIIMQVRQLQLDGYSTKLIADKLKMH
QFVVGKALKQTKNFSDDIIVEILNYILESDYKIKTGLIRDTLAVEMLVSRYCKREAI

>CORE_REP|Org1_Gene1963#

MNKIKVGIIGATGYVGAELIRLLMNHDKVEVTAIGSNSYVGKNIVDIYPSIGYKNNMICIENEKVIDMCDVVFTALPHGVSEKFVIKAIKSKKKVI
DLGADFRIKDEEVYSKWYGVSFIDKILHKKAVYGLSEIYKEDIKDADIIANPGCYPTSISLPLMPLLSSKLIKNNNIIIDSKSGLTGAGRELSISSHFTE
VNENITAYKIGKHRHTPEIEQNLSESCKEKVSVVFTPNLIPVNRGILSTIYCTKEDNISINDIHRKLTDYYEFKEFIEVLPLDKVASLKNVRFSNKCVIS
LHENGDTLIICSAIDNMIKGAAGQAIQNMNIIFGIEENTGLKNIAPSF

>CORE_REP|Org47_Gene1973#

MEKKKIVLKNFTEDELKEFMKTIDEKPFRGSQIFSWIYKGAKTFEDMNNIPKSLRNKLEEISCIGHIDIELKLESKVDNTKKYLFLLDDGNIIETVM
MDYDSRVTVCVSNQVGCRMGCNFCASTMDGLIRNLEPWEILDQVIKIQEDTGKRVSNLVLMGSGEPLDNFENTKQFLKIINEKNGLNIGYRHI
TLSTCGIVPKMYELADLEIAINLALSLHSPYDEERRKIMPVANAYSIKEILDACRYYIKKTNRRVTFEYSLIKGVNDSEKEAKALAKLLKGMLCHVNL
IPINKVEEREYEKPDKAFIYKFRDSLEKNNIPATVRMSMGSDISGACGQLRRKYK

>CORE_REP|Org95_Gene2649#

MKTSDFKFDLPQELIAQVPIEDRASSRLMVLDKETGNIEHKVFRDIIEYLNPGDCLVLNNTRVIPARLIGEKLETGGKIEFLLLKRTEEDTWQALVK
PGKRAKVGTKFSFGNGKLIGEVVDLSDEGSRIIKFHYDGIFEEILDELGNMPLPPYITARLDEKERYQTVYSKHNGSAAAPTAGLHFTEELLNKIKE
KGVDIAFVTLHVGLGTFRPVKVEDVLNHKMHSEYYMVSQEAADKINRAKENGKNVICVGTTSCRTIESACNEDGKMKETSGWTEIFIYPGYKF
KVLDKLITNFHLPESTLIMLVSAICGKDNVLNAYNEAVKERYRFFSFGDAMIIK

>CORE_REP|Org27_Gene1040#

MKIVIDGMGGDNAPKSNVEGAVNAIKEYQVDLIITGDKDLLEKEFSNYEFDRNKLEIVHTTEIIENEDKPVKAIRSKKDSSMVVALNLVKEGKAD
AIISAGNTGALLAGGLFVVGRIKGIDRPCLCSAIPNVKRGMTLIADCGANADCKPKNLVEFAAMSNIYSRKVLGLENPKVALANVGLEEGKGND
LVKRSYEEIKKLDLNFIGNVEAREVINAYTDIIICDGFTGNILLKSAEGVALSVMSLIKETFMASTKSKIGALLIKDDLRKLKSFIDYSEYGGAPLLGLN
GGVIKAHGSSDAKAIKNAINQGIKFSKGKVVEDINQFISKYNEENKNNEDE

>CORE_REP|Org56_Gene2385#

MELNERKLNILKAIVKDYIETAEAIGSRTISKRHDLGVSAATIRNEMADLEELGYLIQPHTSAGRVPSEKGYKLYVNSLMSKSELDDNDKILIEQC
MNHNINHIKELIHETSKLLSQLTNYTTVAVTKSLINQSVIKHIQLVAMNDNNILLIVVTDKGDLKKANLTTNVYLDQSKLNLISDNLTRKLLGKSIT
DLDDNLIAFIKYEISEYSGLIDELLNALNSNMKEEDFSLSLNGATNIFSYPEFNDVLKAKSFLNMLEKKETIADIIKSKGIQKDNLNIIIGSDNDCELA
QDCSIVTATYNVDRDLVGRISFIGPTRMDYARIYSIINYMSLLINRK

>CORE_REP|Org82_Gene1721#

MIVVLKMGADKNEVKKLIEAIGREGVEVNPIDGTELTVLGLVGDTSKIDAKRIEANKIVEKVMHVVEPFKKANRKFHPEPSIINVNGMEIGSKKI
AMIAGPCSVETEDQIVSIAKDVKKSGAGFLRGGAFKPRTSPYAFQGLKYDGLDLLKKAKEKTGLPIVTEIMSTQDIDIFEENVDVIQVGARNMQ
NFDLLKELGKTNKTILLKRGLSATIEEWLMSAEYIMAGGNENVVLCERGIRTFETYTRNTLDLSAILAVKKLSHLPVIVDPSHAAGKSWMVDSLS
KAAIAVGADGLIIEVHNDPAHALCDGKQSIKPNEYDELISELKTIASAVGREI

>CORE_REP|Org54_Gene2802#

MTKLSKKNITYLLILVSIVVLVFGIVLSITIGAKDMNLSTVIDSLIKMEDGINMRIVKDVRLPRAIAAALVGGFLAVSGAIMQGITRNPIAEPSVIGIT
QGATFAISISLVLQKKLPQLIHGSFSVMMFAFIGASISGLFIYFISSKSRGRVNNVKLALAGVALGTLLISLASAISMYFNLSQQLSFWISGGLVGVK
WEGIKLLFVAGGIGFILAIIMAPRITILSLGEEVAIGLGQKTNFVRFICIVLVILMTGASVSVSGNIIFIGLIVPQIAKGIVGSDYKYIIPSSLVLGAVLLV
YTDILSRMINPPYETPVGSITALIGVPIFIYLVRKGEK

>CORE_REP|Org73_Gene2904#

MSTIIPKDYKSSLNVIDTQIAIKKLKDFFEMRLSNELNLIRVSSPLFVLPETGANDNLNGEKAVSFDIPFMNKNAEIVQSLAKWKRLALKKYGFEV
GSGLYTDMNAIRKNEELDNIHSLYVDQWDWELVIDKSSRNEKTLKDVVKRLYGVFKDTEIFVCSMYEGIKEILPEEITFITSQELEDMYPELSPKE
REDKIVKEKKAVFITQIGKTLISGEKHDGRSPDYDDWELNGDILFYNPVLDSALELSSMGIRVDEESLDRQLKLAGCEERKEFDYHKMLLNGELP
YTIGGGIGQSRICMYFLQKAHIGEVQVGVWPQDMIQNCSSAGIELL

>CORE_REP|Org48_Gene1100#

MNTKAGILGVGSYLPEQSYDNFHFEKIMDTSDEWISTRTGIKERRFAKESEATSDLASKAALKAIECAKLNVEDIELIILATITPDMSLPSTACIVQ
DAIGAVNATAFDISAACSGFVYGVTIAKQFVETGCYKNVLVIGAETCSKFLNYDDRTTAVLFGDGAGAAVIGPVSEGGILSTHMGSDGKGKDCL
KVPAGGSRLKASKETVEANLHTIEMAGSDVFKFAVRKMAETSLRALEKANLNTTDIDYLVPHQANIRIIQASSKRLELDMKKVYVNIDKYGNMS
AASIPVALDEAYREGKIKKGDNVVLVGFGGGLTWGASVVKWTL

>CORE_REP|Org50_Gene1894#

MKKITINDIANLAGVSKSTVSRYLNNKDISDSTKEKIKTIIDEYGYEPNAFAQSLRAKKTYFIGIITPCLDSFVKSKIMMAIDEELKELKYTSLIINTSRK
IRSEIDSISKLASLKVDGIILIGTEITKEHKNVIEKLDIPIVVVGQKVDGINSIVNDDYGAGYKMGQYIANKGYKNIVYLGVDESDISVGLNRKNGVL
NGLKDKGYDAKVFYTDFDQETSIQRSGEMLESENPDIIICATDNIAIATMKEINKRGKNIPRDISVAGFGGYDILSIISPKLTTIKFENKNAGKVAA
NTIVNLIQERKEPLLKEIKFELIEGESTINKN

>CORE_REP|Org23_Gene1323#

MGFKVELGGFQTLIQDRGRVGYGQYGVSGCGAMDEYAHRVGNILVGNSEDEASLEVLMLGPTITFDEYTQIAVTGGDLGAKINGKEIQNWR
SYQINPGDVLSFRGVKSGARAYVSIAGGIDVPLAMGSKSTYTRAKIGGFEGRALKKGDYINTFIQEKDFTINKKLSSKYIPTYSSEIVLRIVKGPQFD
AFSNGEVEKFLSNKYKVTNEIDRMGCRLDGESIKHLNGADIISDGISYGAIQVPGHGKPIIMLSDRQTSGGYTKIGNVISVDLYKLAQAKPNDVV
KFELVDIYEAHRLLREQEDKIQDIYKSMKNIRVVKAKVLNDIAV

>CORE_REP|Org8_Gene1196#

MKIMMNNMDSIINYIYEGDYFIVTSHISPDGDNVGSTLSMYYTLKNLGKNVYYVLDDEAPLNLRFLVEGVKIYKSNEFNMKNYSLIALDCGDK
MRICVSDEIKNNASKLICIDHHASNDSYGDLNYVDIDASSTCELVYNLLVRFQQTKDINIINEDIATCLYTGLVTDTGNFSYSNVHASSFEMAKNL
LVLGAQKNTIIQNIYQSNSSDYYKLLGEALKGLEIFDSKVSSIVLTQDMMNRNNISFNDVDGITTYTRDIKGIEVGILFKEKKQNEIKVSFRSKNYV
DVSEIAKLFGGGGHVRAAGCTIRDSIDNAKKMVLEAVLKSI

>CORE_REP|Org91_Gene1013#

MENKLIVSSSPHVRSNEDTSYIMKQVIIALLPAAVAGVYFFRLNALSAMFFCILGTVGTEFLYQKFTKQKSTIGDFSAVVTGLLLAFNVPASLPW
WMCLVGGIFAILVVKMVFGGIGCNFVNPALAARAFLLASFPVAMTAWTQPGVNWIGKNLDAVTTATPLSFLKNGAAGLADLSSNGISLADM
MIGNIGGCIGETSAILLLLGGVYLMYKGIINYVIPVFYIATVFILTFLLGGFNITFAIYQLFAGGLMLGGFFMLTDYTTSPMTKKGQIIYAVLAGLITT
VIRMYGGYPEGVSYSILLVNCLAPLIDKFVRNRVFGEVAK

>CORE_REP|Org18_Gene1114#

MKMVILTAVLVLGIMGLIFGIVLDFASKKFAVEVDERVEAILGVLPGANCGGCGFPGCGGLANAIVEGNAPVNGCPVGGADVGAKVGEIMGI
SAEAGEKQVAKVICKGTCSSAKDKYEYEGISDCRAANVLNSGAKMCKFGCLGLGTCKDACKFDAISIVDGIAVIDEEKCVNCGKCKEVCPKGIIIT
KPESQEVVVECNSKEFGKAVKEKCTAGCIGCGMCVKACKFDAIIFEDKIAKIDPNKCVGCMQCVAKCPTKVISGDITKKKKVTIDQELCVGCTVC
KKQCKFDAIEGELKEKHKVDADKCVGCHLCMEKCPKKAIKIL

>CORE_REP|Org85_Gene1579#

MEKRKVIIDCDPGIDDSLAILLALNSPELEVIGITTCCGNVPANIGAENALKTLQMCSSLNIPVYIGEEAPLKRKLVTAQDTHGEDGIGENFYQKV
VGAKAKNGAVDFIINTLHNHEKVSIIALAPLTNIAKALIKDRKAFENLDEFVSMGGAFRIHGNCSPVAEFNYWVDPHGADYVYKNLSKKIHMV
GLDVTRKIVLTPNTIEFINRLDKKMAKYITEITRFYIDFHWEQEGIIGCVINDPLAVAYFIDRSICKGFESYVEVVEDGIAMGQSIVDSFNFYKKNPN
AIVLNEVDEKKFMYMFLKRLFKGYEDLIDSVEGVI

>CORE_REP|Org73_Gene1768#

MNKKAAIVAAVAIIIGLVTVFALGGSKKNESKTSEDSNNTIKITHNLGETDVKLNPKKVVVFDYSALDTMDALGVAENLVGLPKASLPASLEKYK
DEKYADLGGLKEPDLEGIKSANPDLIIINGRQEDFYEQLSKIAPTISTSKDDKKYLESVKNNIDKIAKIFGVEEKANQEFSKIEKKIEILNKKVTDKNL
NALTIMVNEGNLSVFGEESRFSILYNSFGFENKDKNIKESSHGQNITFEYIAKQNPEVMFVIDRGIATGSDVKESSTAKSVLNNDIIKSMDAYKN
DNIIYLDSPTWYVNDGGLTSLNKMIDDASKAVN

>CORE_REP|Org44_Gene1774#

MSKLKKFVILLAFLVVIFPISVYGYFYYKLSAIHDSSISSDLLDNNDHKNEDGIINILLMGTDARPNEDSSRSDAMMILTIDNKHNDIKLTSLARDSY
VDIPGHGKQKLTHAYAYGQADLLIQTIEENFNIDIQNYACVNFESFMYIIDAIGGVEVTIEKGEIRELNKFIPETYKWNKSDDKGSIQYIRNAGKQ
TLNGYQALSFARIRHNDTAFARDGRQRQIIQAIIKKTETLPVTKYPGLLDAVLPYVKTNMKPNAILSLGAQVLKMGDLNIKQFEFPIDDEIHSTG
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>CORE_REP|Org63_Gene2683#

MLKLILNRVKVLIPMLILISILSFGLLELAPGDPADAYINPLMSAQDIENIRVNMGLDKPVYIRYLNWLKNTLNGNLGISYINHMPVTEQIMEKM
GNTFILMGTSLIFSILVAIPLGIFLAVNKNSITSKVSSIFNYIGVSIPSFWIGMILISIFSVKLNIFPSGGMHTIGNDSIEDLVKHLVLPVITLGLYNTAIF
TNYVEAGVNEQLKKQYVVTARAKGLSEKVILFKHVLKNSLTSLVTILGMSIQKLVTGAFVTEVVFSWPGMGRLMIDSIFSRDYTVIMAITMLSAL
FLILGNLVADILYLLIDPKIKSSKGGF

>CORE_REP|Org40_Gene2370#

MNNWIEVTIKTTTEAVEPITNILYEQGAGGAVIEDPKDFLFQKKNELDWDYVEEEVFKKNEEDDVLIKTYVSEEKNVMEFVEIIKQKVLGLKDFG
IDIGEGSVSLDQVNEADWANAWKAYYKPTKVGQRVVVKPTWEDYAMQDGDLIIELDPGMAFGTGTHETTSMCIRELEKYVNKDSKVFDIGC

GSGILAIAAAKLGAKEVVAVDLDEVAVKVAKENVLENKVEKSVSVMHGNLTDVIKDKADVIVANIIADIIKILAKDVQNFMKEDAIFISSGIILDKVEEVKESLIENGFEIVEVQKLGEWSAIVSKLKK

>CORE_REP|Org93_Gene1876#

MEPLFLKPIFMDRIWGGTALKDKFNYEIDSPTTGECWAISSHKNGDCLIENGKYKGKKLSELWNKNRELFGNTPGDKFPLLTKILDANDNLSVQVHPNDEYAKKNENGELGKTECWYVIDCSDDAEIIIGHNAKSHKEFVNMVNNNEWDKLLRKVNIKKGDFFYVPSGTIHAICKGTLILETQQNSDTTYRVYDYDRTDNSGNKRELHVQKSIDVTNVPHINFDTDYKIVSTSDFKCTTFVSNEFFSVYKLDVFGKCNFTHNTPFSLYSVLDGNGKLIHNSVEYNLKKGMHFILPNDFGDFSFEGNLEIICSHI

>CORE_REP|Org72_Gene2043#

MIENNSEKIKVLENDIKQLITISKANNIDLSDKINSLNEKLEKLKEDAFSHLSAYEKVTLSRDIKRPTTLEYIEHICSNFLELHGDRLFKDDPSIVGGIGQIGKFNVTIVGHQKGRDTKENIKRNFGMPHPEGYRKALRLMKQAEKFNRPIITFIDTSGAFCGLEAEERGQGEAIARNLLEMSKLSVPVITFVIGEGGSGGALGIGVGNDVCMLEHSVYSVISPEGLSSILFKDSSKAKEACDVMKLTSNDLYDLKIIDKIIKEPLGGAQKDVDAVSKEIKAYILERLNHYKDMDKEEIIAQRYNKFRNIGKCL

>CORE_REP|Org4_Gene2815#

MKKIKSLAIFISIITTLVLVTACSDKNTEDKDKSETRVVQSVKGEVKIPSNPKKIVDISGSSEELLLAGYKPVATANVDSYETDKLPSYIREELKGVKIVGHSMMDTMDMEAILEVNPDLIIMSQRQEKIYDQLKEIAPVVMMKDYANDWRSKLTDVSKLFDKEEEAKSWLQKYDEKATKLGKEVIEKNGEKTYLPVLASSGQFMVFSDGGIGTLINDDMKLARPKNMPKQDGITLPMVSMEGLTDIDADHIVVIATEADKKDLENSAIWSQIRAVKDGNVTILDAAPFFSQSYNPIGKELLLESVKNELTK

>CORE_REP|Org77_Gene552#

MIRYYKTIDSKLEKLSFFEDGCWINLVEPNHSEINEISNLLNIDVESIESALDEEERSRIDVEDNHTLILIDIPVDESDSNSSHYTTIPLGIILTEEAIVTVCDAQTKILNDFIVGHIKDFFTFKKTRFLLQILHKNAAYYLHYLRKINKMTIIIEREIYKSMKNKELVQLLELEKSLVYFSTSLKSNELVLNKMVRTAGIKKYPDDEDLLEDVIVENRQALDMAKIYGDILSRIMDAFSAIISNNQNNVMQILTVVTLIFSIPTIISGFFGMNVINMPFSDDPNGFWIILLISAIICIVITFFMSRNKLL

>CORE_REP|Org70_Gene2380#

MYYIGVDIGGTGIQAGVVDNYGKIIFRSECKTVIEKGFEGILNDIKIMIYKLLEDNKLTMSDIKSIGFGVPGFINKEGLVTCVNLKWNKKAFNKELKRRFPDVEIHGENDATVAALGEAKFGSMKGANVGVLYTLGTGVGGGIVINQKVFSGAHGLGSEIGHQIIGENYFNCNCGNNGCVETFCSATAIIKYSQKLIEEGEKSRILDLAEGNLENVNAKMVFDAYRENDLVAIKVINRFKEYLAKTFANTINSLDPEIISIGGGISKSSDIILDGIEDLVRKFVLYKTEDIATITCATLGSDAGIIGAAFL

>CORE_REP|Org22_Gene1177#

MNKICKILNIKYPVIQGGMAWVATASLASAVSNAGGLGIIAAGNAPKEAIKKEIVECKKLTDKPFGVNVMLMSPFVDDIIDLIIEEKVQVITTGAGNPAKYMDRLKEAGTKVIPVVPTIALAQRMEKLGATAVIAEGTEGGGHIGELTTMVLVPQVADAVNIPVIAAGGIVDGRGIAASFALGASAVQVGTRFICSEECSVHSNYKNLVLKAKDRDAIVTGRSTGHPVRTLKNKLSKEFLKMEQNGATPEELDKKGTGALRFATVDGDIEKGSFMAGQSAAMVKEITPCKEIIEAMVNQAREIMPAIEL

>CORE_REP|Org66_Gene1170#

MVIIKSIKEIANIKESVITIGNFDGVHKGHQVLIGKTVEHAKKENIQSIVFTFANHPVNYFRPNSTKNIISNDDKIKLLEDLGIDIVVIIPFDEYMTKIPAKDFVDEILVKKLKAKKIVIGHDFTFARAKEGNVNLLKSLEHEFGFEVEVIKPIKINDVRVSSTYIRSLVSQGDMANVKEYLGRNYKLEGCVIHSKHLGRTIGFPTANIDLKNNMLVPKRGIYASIVHIGDETYFGATNVGYNPTVNGKTLSIETNILEFDRDIYGENIIVEFLERIRDERKFNSIDDLKNQLYNDTNYVYENYVCKNK

>CORE_REP|Org60_Gene2521#

MENLVREFEENSRRKKTKLNIKPYMYILPLGIILVAFYVIPIIMSIYFSFTKYNIISPATFIGLENYKKLFTDETLKVSIINTIKFTVVVVPCQTILSLILAVWITGKGNSKIASFAKGAIFIPVLSSMVLIGMVWRALLNGEGSIIYQVLGAFGIESSKLLGDSKTALPTLMFISMWKNIGYFMVIYISAIMNLPKHCYEVAKVDGATKLQEFIKITVPLLKPTTIMVVFLGSIWSLQVFDLVYTVTGGGPGISTMSIVMHAFNLNFKNFNSGYAMTVANVLFLLIAVVSILQNKLVKRDNSDF

>CORE_REP|Org17_Gene3504#

MIYTVTLNPSIDYIVKLNELKTGSTNRVNEEYVYPGGKGINVSRILKELGNDNISLGFISGFTGEYIIRTLEEKNLKTDFIKIKNGFSRINVKIKESEETE
INGQGPNIDDEDIDILYKKLDKLNQDDILILAGSIPSTLDEKLYENIMARLEKKNIKVVVDATKNLLLNVLKYKPFLIKPNNDELEELFGVKLNSIED
MVKYARRLKEMGAINVLVSMGKDGALLITEEDEVLISDVPKGKVKNSVGAGDSMVAGFISGYLNTGKYDYALKLGAASGSATAFSYDLAKREY
IDKLVNEISVKQF

>CORE_REP|Org72_Gene2503#

MDKDLTYQIKELKKEKNAIILAHFYQPPEIQELADAVGDSYYLSEIARDCKEEVVVFCGVRFMGESAKILSPEKTVLMPVSNAGCAMADMVDEE
GVIKLKQQYPNALVVCYINSTAKVKSHCDVSVTSSSAIKILENIDNKEIIFLPDKNLGGYIAEQFPDKNFIFWDGYCKYHNNIRAEEIIELKDKYKNA
EVLVHPECKKEIRDLGDYVGSTSGIIKYATNSKNKDFIIATEEGILHELKKNNPNKNFYIPGGKILCTDMKKTTLENLYSTLKNMENEVIVEDEIME
KALNSLLNMHKLAEG

>CORE_REP|Org85_Gene1827#

MFILAFIICTVVIFIVSTKINQKRYDELSLMLNQILEGKEVTYPDTKDTRASKISHQVKKIKDMIEIEVEQSKLEKEAIKGLISNMSHQLKTPLSNITIY
CELLENINISTLQKKEFLQKMKNETFKIDWLLQSLFKMTKLEDGVIEFEVEELLIKDTLIQSISTIFNKAEAKNIRVNLEPFSDIKLVHNKKWIIEAIVN
VLENAIKYSPSDSTITISVIKMELYTKITIKDEGIGIDSRELNDIFKRFYRSKNVANQNGTGIGLYLTRLILEKENGNIIVESKLGSGCCFSIFLQNCKSL
N

>CORE_REP|Org79_Gene52#

MVDIIVIGAGPAGLTSAIYAMRAGLSVTVFEKNIYGGQVASTSEVENYPAVQKISGVEFSNNIYNQAVAQGVDIQFDEVEEINLEGKIKIVKTSSA
EHKAKAVILANGVERRKLGCVGEQEFTGRGVSYCATCDGAFFKDKEVAIVGGGNTALEDALFLANNCTKVYLIHRRDSFRGEEVLEKSVKARKN
IEILYSHGVEKIEGEKTVSKIEVKNLKTEEKRTIDVSGIFIAIGLKPNNKMFENVLDLDEGGYIISDESCTTSVEGVYVAGDSRTKFLRQIITAASDGAI
AAVQAANYINVE

>CORE_REP|Org33_Gene1037#

MDFKQLEVFVAVAKHQSFSKAARELFLTQPTVSAHIQNLERELETVLINRSNKVITLTKSGEILYEHAIYILNNCKRAIYDIKEYSGKIEGIIDIACSSI
PETYILPDFMKSFSMSYPDVKFSISHYDSQYAISEILNERISFGLVGSKINNPQIEYLDLLDDELVLITPSDFKIDNKNNCIDIGELAYLNFIMRKEGS
GTRNLILNTLSKNNFPVSKLNVIAHVESNEAIKEMVRLGLGVSFISYISAIDYLNAGKIKCYKIKDVDFTRKFFFIYSKKKTFSPLEDKFLNRLCEYFEII
I

>CORE_REP|Org63_Gene2774#

MKKKLLDGKITLIICKSVKIYTKKGEEMSKGNNNNNSRNKSKKTSHLNRKKRKLNKKKLAVLICFTVLFLFIAFKATQGVVALVKSMDKSNKTSQ
QQNVNSEQFDFGNEEENKKKKYTVFIDPGHGGNDKGTESKTSNRYEKDLNLQIAKKLANKLSKQKDIQVVVSRTDDTYISLKDRAILANNSSAD
VLVSIHLNAEKNGNTATGIETWYRNKATDGSKELAQAVQSTIVSYVKVRDRGIVENNFEVLRESNMPAILIECGFLTTPSEEQKIINEKYQDQLA
EGIVQGVLSYLDSKGNK

>CORE_REP|Org53_Gene987#

MSKKGRVVKVQHFSVNDGDGIRTTIFLEGCKLKCKWCSNPDSWSNIVKLGVMKDKCVSCNRCIDVCPQNISSLFDRAQINNKCDLCGECIKVC
LKDAICIMTEEMSVEEIVEEVEKDFIFFFESNGGITFSGGEPTLQIDFLRELVDIFYDKGINIAIETCGYFDWNKVNDVFEKIDHIFVDIKSMDDNIH
KEYTGVSNKIILDNICRLSKLNKSMVIRVPIIYGVNDSEENIRNTALFVKQNVPGGKMELLPYHKFGIDKYKALGLEDYIYEFDEICNNHMLKLKEI
VELTGVKIIEYK

>CORE_REP|Org89_Gene2365#

MKIAVIMGGISSEREVSLNSGKEIYNNLDKNKYEVVKVIIDDKKDIFTKIPEDIDFAILALHGKFGEDGCIQSILETMDIPYSGCGPLCSGMCMDK
NITKKMLRDSNLPTAPWVLVKSVDEIDYDEIDNIGYPVFIKPNSGGSSVATFFIHSKDEVGEAVRKGLEVDEFVMIEKYIPGGEYTSFILNGEVFP
TISIKSDSGFFDYEAKYSVEKGAKEEVVYLDEELQKRVNEISETCWKIFNCKAYVRVDMIISEGIPYVLELNTLPGMTQTSLIPRSAAARGIKYSELL
DKLIEYSLN

>CORE_REP|Org27_Gene2092#

MLEIIVPATSANIGPGFDCLGIALNIYNKFYVEEIESGLEIEGCEDAYKNENNLVYTSMKYFFDRVKPEKIPAGIKIKIQSEVPICRGLGSSASCIVAG
VIAANALSGANLDKNQLLNIASEIEGHPDNVAPAILGNMIVSVTDNENIHYDIIKIPEELKFCAMIPNFKLSTEKARGVLPKEIPYSDGVFNVSRVA

LLISALLNKNFDLLKVACQDKLHQDYRGTLIENYNDIVEKSEQLNSIGVFLSGAGPTIMSLIKENDDSFVDNMKNYLQKLKSDWEIKELCCDSNGAVLNII

>CORE_REP|Org73_Gene3005#

MASLIKQRKYNRNILLEYIKLMRPKQYIKNGFVLAALIFSNNILNPSLALKSILSFIAFCMISSSAYILNDILDIEKDKMHPKKCKRPLASGSIGKKGAISLGIVLVLSSILLSLLIHKNLCVIILLYLFNNIMYSLKLKNIILIDVFSIAIGFILRVCAGSIAINVSLSSWIILCTFFLSLYLGFGKRKKEIILLKEDASNHRKILKEYDEENLNQMMSISLSATIVCYSLYSANNIYNSNMIFTTVFVVYGVLRYNYIVNIGDEGNPTDVVLNDKSLKFCVLFWVIACIGILST

>CORE_REP|Org45_Gene3308#

MALILPKGLPVINKLLDEGIDVIYKEDFKKKLTYEENIDTKIAILNLMPIKIDTELDLLRRIDKTGFNVSVEFIKISTRESKRSCNEYVKEFYKTFDEAKGEYFDGFIITGAPVEQMEFEEVDYWNELEEIMDYSKSKTKSTLYICWAAQASLYKYYNVKKLPLSQKCFGVFKHKVDKNSKIVDGFENEFFAPHSRHTTVNIEALKENKELSIVSHSKEAGPYIITNSRDVFVMGHSEYDKYTLDKEYKRDINRGDKISIPQNYYINDDPSEEPTVKWKKHSELLFRNWIKNYLIQ

>CORE_REP|Org18_Gene1469#

MIMDTKKENNYENYICVGSSNVSNAMKMYLKEIEEYKMLSAGEEVELAKEIINSSSVAKEKFINSNYRLVVSIAKRYKRDSIDMLDLIQAGNIGLIKAVEKYDYKKGYKFSTYATWWIKQSITRYIDDCENTIRIPIHLHQRINFVKKKKQELLNVLLREPTIDEIADACGLEVDKVLELLRRDKNVVSLDTPLKEDEDSSLVEFIPSDADFKDVVIHEVEQHNLKEKIEELLTGLGEQEQQVLRMRFGIDDDDPKTLEQIGKVFGVTRERIRQIEAKAIRKLRHPSKLKQLKHFY

>CORE_REP|Org18_Gene1671#

MSIMRYDIAIIGSGPAGLSAAINAKIRNKTIIMFGNDNLSNKLVKAPSIDNYLGFYDISGDELKDKFKSHIDSMDISIENKRINNIYAMGEYFTMMSGNDMYEATTVILATGVEYTRPIKGEEEFLGRGVGYCATCDAPLYRNKKVAVIGYNEESKEEANFLSELTSKTYFIPMYKKDNLMRSSDNLDDSIEVIHDRPVQIDGDKLVNKVSFKENHIEVDGVFVIKDSTAPSALVPGIEIDGIHIKVDNNMKTSIDGCFAAGDCVGKPYSYIKAAGQGQIAALNAVYYLDKLKRA

>CORE_REP|Org20_Gene994#

MLEGKIIKGISGFYYVDTYNGIYECKARGIFRKQKITPLVGDRVKISIVDENEKKGILEEIDSRDTELIRPPIANVDKALIVFAIKNPKPNLSLLDRFIVLAEKENLETVIILTKADLDDNDTLETVKNIYELSGYKVIPVSNITKLNIDKVKEELKENVVVFAGPSGVGKSSLLNEIDENFKLQTGVVSDKIKRGKHTTRHAELLKLEFGGMVADTPGFSSLALEDIEEVELKDYFIEFDKFNDCKFGSKCIHENEPNCAIKEAVTNGEISKERYDSYIQLLHEIRQNNSRRY

>CORE_REP|Org72_Gene2726#

MAISMTGFGRGEYKDDNYYFLVECKTINHKYSDINIRLPRKISFLEDKVRNLVKNYVKRGRVDLYIKFDLLGKEDVNLNFDEGLASQYIDILKEIKNKFDIIDDISVMNVAKFPDIVKIEEKEEDEDLLWSMLNQAVEDALIKLREMRSEEGKKLAEDIAMRCDLLKNHIEEIEKYSSSVVEDYREKLNLRISELLDDPSIIDENRLAQEVAIYADKSSITEEIVRFKSHIGQLKNTIFKDDSIGRKIDFLIQEMNRETNTIGSKSSDINITNLVVEVKSELEKIREQIQNIE

>CORE_REP|Org66_Gene2694#

MNLYHLRYFVTLAHLEHYTKAAENLSITQPSLSHAISLLENELGVALFEKEGRNIVLTKYGKIFLKDVEKSLEILDSSVKSLKITGTGEGQIDLAFLRTLGTDFIPDIVHKFLKSNPAKSIDFKFHTGVTTDIIQGLKERKYDIAFCSKLEKEKGIEFIPVAKQDLVLIVPYSHPLAAKDTIDLKETIPYPQIVFNQRSGLRYIIDDMFKKINQQPNIVYEVEEDQVIAGLVAKNFGIAVVPNMNMLSFTKVKVIQIIHPSWERNFYLAFIKDRYLPPAIKNFKNFVIKNAQL

>CORE_REP|Org18_Gene2252#

MRTTDMKGIYSALLVSFDKEGNINEKGLRQIIRHNIDVCKVDGLYVGGSTGENFMLSTDEKKRIFEIAKDEVKEEIKLIAQVGSVNLKEAVELAKFTTDLGYDAISAVTPFYYKFDFEEIKHYYNTIINSVDNRLIIYSIPFLTGVDMSLDQFGELFENEKIIGVKFTAADFYLLERMRKTFPNKLIFAGFDEMMLPATVLGVDGAIGSTFNVNGVRARQIFELTKNEKISEALEVQHVTNDLITDILGNGLYQTIKLLLEEQGVEAGYCRQPMKEATDEMKSRAKEIYRKYF

>CORE_REP|Org67_Gene2731#

MYGESKKLSIDNNIFLQYCLIILGMILSTLGINLYLAPAKLLSGGVAGICVILYKLFGINQGISSFLMNIPIFIIARKYFDNKFLLISFVNMLLFSLALGLTQDIAKYFPIDDTMLQCIYGGALTGIGMGLTFKARATAGGLDIIAAIMKRKYDIPMKNTFLFINFFVVCAGAFLFGAKLVMYTLITMYIISFTMDIGKDCFDRKKSILLISNKYDEISKVIMNKMGRGVTFLEAEGAYTQNKKKMIYCIISANEIGKFKDLIYDMDSEAFISVNNVEEVKGGGFKDKFL

>CORE_REP|Org77_Gene475#

MEETNEMKDSKHLISNIQSQYTRLSKGQKLIAQYILNNYDKVAFMTACKLGETVGVSESTVVRFANALGYSGYPKLQAALQELIKNKLTTVQRVEMAHDYSDDFAILNKVLKSDIDNIRSTLEEIDERAFKEASNKLLRARKIYILGMRSSFVVAQYLGFYLDIILDNVHIIRMDMGDAFEQIVRINEEDVIVAISFPRYSKKSYQIVNYAKEKGAHVISLTDSLFAPVASLADNTLLVKSNMASFVDSLVPALSISNALAISVGMKEKEDIKQHFDDLEQIWKRYSVYE

>CORE_REP|Org10_Gene2425#

MNINYLYYFQTVCKYKNMTKAAESIHISQPSITLAIKELEKELGFELFYRIGNKIELTPEGKIFLDKSKHFIKQFEDFQCDALDLGKKRKASLKIGIPTVLGTFLLSKILPRFNVIYPDIELKIFEVPTFVGAKMIEESTLDFCIGIIDSDIYDDIDSKTIYKTELYLVTNPKNELAKHPIISNYMLKNVPFVILSEGSYHYKIITKRLEKAKPNIILHSNQLSTIRYLLENDLASTILYKEIFQNTENLCSIPLERAITANIGVLWRRNQYISHSMKLFIEYMASIHIN

>CORE_REP|Org56_Gene2657#

MDLLHLKYFQTVARMEHITKASHKLNIAQPALSKTISSLEKELGVQLFDRKGRYIVLNEYGRLFLKRVDSILDLVESSKKELQDTSLENSGEVKILSPAAANVLPSLLSNFRKLYPNITFNVSHTLPSSYKKSDFDLYISSSFTKLNSENSITLTCEEILLGVSINHPLSLKDEVYLSEVSDENFIVITKGENYREVIDILCESANFKPKIAFESDSPYTIYALIKSLQGVGFICGKSWGLSQDPEIKLLHIKDIEFKRYLNLSWFSENYESKAVLLFKNFLINYFKNI

>CORE_REP|Org95_Gene1253#

MSEVKNTLQKHPVLRYSTMLFGMLMTSIGINGFLRPAHLLSGGATGIATSINYLTNINVGLLTFLINIPIFILGFIYLEKEFCISSLVNMIVFSLLLGATQEISNIIPIHDILLQSVYGGILSGLGVGVVFRTRSSQGGTDIIAAILKIKKNIEMKDTALAINGLIVLTGSFLFGLDLALYTLIGLFLNAYSMSFIKDAMNYQKSVMVMSNEVDLIAEDIMKSLVRGVTFLDAEGAYTHQKKKIIYTIVSSNEIPKIKDIALKYDKKAFISVNDVTEVKGRGFKAKDL

>CORE_REP|Org65_Gene2631#

MEISGRTGLFALIGTPVGHSKSPVMYNYSFKKLDLDYRYLAFDITIDKVKEALLAIKTFNIKGANVTMPCKSAVTEYMDELSPAARIIGACNTIVNDNGKLVGHITDGVGYVRNLKENGVEVKGKKITIMGAGGAATAIQVQCALDGAREISIFNPKDDFYKRAEQTVENIKKDVPECVVNLYDLEDTNKLYEEIESSDILTNATLIGMKPYDNETNIKDTSVLRKDLVVTDVVYNPKKTKMIEDAEANGCKAIGGLGMLLYQGAEAFNLYTGLEMPVEEVNELCFK

>CORE_REP|Org21_Gene594#

MLGIIAPSGPLRNTSLEEIKFNLESYGYEVKFSESCSLNYKGYLAGNDDIRARDIEDMFLDKDVDIIMCLRGGYGTTRILDKINYDIIKQNPKPFIGFSDITGLNLAFYKNCGLLPYHGIMAANVGKWDKFTYKSLVNALEFKDELYLENPKEEKIYTVCEGKAEGIIMGGNLSLIIATMGTKYEIDAKDKILFIEEIGEPQYKLDRMLTQLYSSGKLEECNGIIFGDFKDCIEENDLMELLIEFANKVNKPSIYNLQSGHCIPMITIPLGRMCELDATEKIVKLKK

>CORE_REP|Org18_Gene1829#

MMLLKKDRITFSEILILIVGCILMAISLNLFFNPHAIAAGGITGLGVVLNSLFGVELWIVNLLLNVPLFIFAYKILSKKDCFKTVLGIIFLTIALKLTANMATLDITNDMYLAIISGSILMGVGQGLIFRINGSTGGTDLMALLLNKYFPTFSIPVLMGIVDCVVVVLSGIVNRQVEIALYSTVALYILVKVSDLLIEGFNYSKSFTIISDLSKDISKKIMEDLDRGATILKGEGAYTGENKNVLLVVVEKKEVVELKKLVKNVDPNAFIIITDIHEALGNGFKKIE

>CORE_REP|Org43_Gene2026#

MINIEKANTLIEALPYIEKHQGKTIVVKYGGSAMKKDGLKESVMEDLVLMSYVGINIVLVHGGGAEINKMLAKVDIESKFVNGLRYTDEETMEIVKMVLAGKVNKDLVNKIHTKGGKAVGLCGIDNNMILCDPYKNYELGFVGEIKKVNVELIESCLKSGYISVIATIGVGDDGETYNINGDTAASAIAKELNADKLILLTDVPGLLREPDEEKSLITEVILEDVDKLFKEGIITGGMIPKIQGCVDALNNGVNRVHILDGRVPHSIITELFTDSGIGTLIRKENE

>CORE_REP|Org82_Gene2233#

MSELSGKGCEIIVPFEERLPVRDIEKSIIKKYRKNLWSKFMKSIRDYKLVEEGDKIAVAISGGKDSILMAKMFQELKKHGQVNFDVEFIAMDPGYHANIRQLLIDNCEYLNIPIHLFDSRIFEIADEIAKDYPCYMCARMRRGALYSKAEELGCNKLALGHHYDDVIETTMLNLLCAGNFKTMLPKLNSTNFEGIKIIRPLYYIREEHIIRFIQNSGIWPLNCACMVAAKKTGNKRYEIKDLIKSLESNFKNVEKSIFKAAENVNLDSVLGWQKDGEKHSFLENFE

>CORE_REP|Org18_Gene1941#

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>CORE_REP|Org88_Gene1902#

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YKEKVDSYKEKTKESEAVVTGYGRINGIKTVICVMNPDFMMGSMGSIVGEKITYSIEYAAENNLPIIICSASGGARMQEGMVSLMQMAKTSQ
ALSKLEEKSLPYISVLTDPTTGGVTASFAMLGDIIISEPNTLIGFAGPRVIEQTINQKLPEGFQTSEFLLEKGFIDMIVDRRKMKEVLYQILAMHKK

>CORE_REP|Org59_Gene1409#

MLVKEIKLLRNIIKDWRKHGYSIGLVTTMGFLHEGHQSLIKKAVKENDKVVVSVFVNPTQFGPNEDFNSYPRDIDKDFKYCMDSGATVVFNPS
PEEMYLKGNCTTINVSGLTDFLCGAKRPVHFGGVCLVVSKFLNIVTPDKAYFGEKDAQQLAVIKRMVKDLNIDTEIIGCPIIRENDGLAKSSRNTY
LSEEERKSALILNKSLSLAKEKLVKGNLNPENIKELITAKINSEHLAKIDYVEIVDSETLQPVKQIEHSILVAIAVFIGKTRLIDNFTFKLNI

>CORE_REP|Org4_Gene2335#

MLVKNLIIYAVSDSVGETAQQVAKACMSQFYVNETYEIKRFPYMINKGVLLETLENAKAENALIVYTLVDEELCSIVERYCEREGLSCIDLMTDIL
REISKRTGRKPKREAGIIRKLDESYFKRVEAIEFAVKYDDGKDPRGVLQADIILVGISRTSKTPLSMYLANKNIKVANVPLVPEIPIPKEVFEIDTKKII
GLTNSPEKLNEIRTQRLKALGLSSKANYANLERILQELDYSEEIMKRIGCPVINVSNKAIEETAGIILDIMKENGLKIYKEIEI

>CORE_REP|Org81_Gene1297#

MIIQQIYNNNVVLVLDENIKKELILTGCGIGFQKKKGQEIDKSKIERTFVIQDESFLDKISKLASQVDEKFFEISTEIIAYAEENLNTKLYEYIYVALTD
HIAFAIKRYHENITIKNDLLHEIKRIHKKEYEIGKWAVDYINKEFDVKFPVDEAGFIAMHIVNSNYKGSSKESLLITKIVKDILNIIRYYYRVEFKEDDI
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>CORE_REP|Org25_Gene1039#

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ENAKNKEFDANSINAVKSSLMGPVSGIGDSFFWGTLKLIAAGVGIALASQGNIMGPILFLLIINVPHFIIRYICLDKGFKYGTQFFKDVSGSSIVSK
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>CORE_REP|Org11_Gene1255#

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KITQSAINLGADYYIVKPFDFVVFINRIRELVSNRVTQVEPKPRPVQETQMTRSDFVKNVGNIENVGNIETEITNIIHEIGVPAHIKGYLYLREAIK
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>CORE_REP|Org68_Gene892#

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>CORE_REP|Org85_Gene1752#

MNIVIVGLGVIGGSFAKALKKAGYENVFGVDVDLETLKKAEKAKIIKKGCTTGKELFKKADLIILSIYPRLVVDFLNNNKNFFKKGTIITDTTGIKETL
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>CORE_REP|Org14_Gene3586#

MNIKIAKNAGFCFGVKRAMKMAWDEVEKSDSGIYALGPLIHNKQAVAKYEEKGLKTVNEIDTIPNHENMIIRSHGVPENIYKEAKNKKLKIVDT
TCPFVKKIHTVVSEYHNKGYEIIVIGDMKHPEVIGINGWCENSAIIIKTLEQMENMEFDNSKKYCLVAQTTINPELYISIVNKLSDKLEEIVFNDTIC
SATKTRQESAKELAKEVDCMIVIGGKHSSNTQKLVNVCEELVPTFAIETKDELDVNMLKKYKNLGITAGASTPNWIIEEVVTFLENL

>CORE_REP|Org34_Gene878#

MKRKSFLAYPYVVWSAIFVIIPLILVVFFSFTKESGGGYAFTLENYKEVIDPIYIKVFGRSILLAGGATLICLVVGYPVAYIISKARVSRRGSLILLFILP
MWMNFLLRTYAWVAILGKNGLLNTFLGWFGIQPLAILYTNFAILLGMVYNFLPFMVLPIYTALSKMDNDLINAAHDLGANNMTVFRKIIFPLS
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>CORE_REP|Org65_Gene3658#

MKNTIQTFKNAKSEGKKLSMLTAYDYSMAKIMDECNINGLLIGDSLGMVVKGEENTLSVTIDEIIYHTKAVKNGAKNALIVSDMPFLSYHVSIE
DAVKNAGRLVKEGGAHAVKLEGGANVIKQIESIVNAQIPVMGHLGLTPQSVNSFGGFKVQGITSEAAKQLIEDAKLIEKAGAFSIVLEGVPAKIS
EIITNSISIPTIGIGAGINCDGQILIYQDMLGIFEDFVPKFVKQYANVGDIMKDSIKNYILEVETGAFPQEKHSFSIKESELEKLYED

>CORE_REP|Org59_Gene2609#

MKFWKLHGIGNDFIAIDGRFDQINPSDYTALAKKVCHRRFSVGADGLLVVKDSKVADVEMVYYNSDGSRAAMCGNGLRCFCKFVYDNCIVK
KESFTVDTLDGIKDIKINLTNREINSIRVNMGKGSFIAKDVPVLTNKERFVQESIKVLDRELKVTSMLMGVPHTVVIVDELDVDDVCKYGKEIEN
NKIFPEKTNVNFVKVEDKYNIHVYTWERGCGYTLGCGTGMTASAIVCNLLNMVESSVNVTSQGGTVKIDVGDFSYMTGPAVKICEGILEV

>CORE_REP|Org52_Gene2358#

METFSLLEIFKAVILGIVQGITEWLPVSSTGHMILVDEFIKLNFSNTFISTFLVVIQFGSILAVLVIFFRKLNPFDSAKNIKQKKETVRLWLKVIIAVIPS
GVIGILFEDDIDRLFFNSTVVAIALIVYGIIMIGLEKRNKKPKYKDFSQVTYKLALCIGLFQCLALIPGTSRSGSTIIGAVLLGTSRYVAAEFSFFLAIPT
MLGASALKLLKAGFGFTGFEWLILGVGSVVAFVVSIVVIKFFMDYIKKHDFKVFGYYRIVLGIVVLAYFFLL

>CORE_REP|Org12_Gene2351#

MIKKEISNFRGSSDYVVSPELMASVNVAIALEKPLLIKGEPGTGKTMLAQAISNELKKDLVIWNIKSTTKAQEGLYVYDTVQRLYDSQFGGEGVD
DISKYIKYGKLGEAFSSNQQVILLIDEIDKADLEFPNDLLWELDKMEFYINETKETVRAKQRPIVIITSNAEKELPDAFLRRCIFHYIEFPDRDMMEE
IVKVHFDKVEEHLLEQVMTTFYWIRSLKDIQKKPSTSELIDWIQALTLSGMPIEKIEKEVPFAGILLKNNEDIESMQRHL

>CORE_REP|Org83_Gene1695#

MEVNFVKEKEKLDKLKKMLLELGSVVVAYSGGVDSNFLLKVAKDTLGENVVAVTIHAMMHSSREIEEAKQYTQNFGVKHIILNIENFDLKEFKE
NGIDRCYHCKKYIFSKIKEVAKEHNIKYIVDGTNIDDLGDYRPGLKALSELGVISPLKDSGLKKEEIRSLSKILGLKTFNKPSFACLASRIPYGVEITDE
NLRIIEKSEEYLSNLGFSQFRVRMHGDIARIEVGQEELGKFFENNNFNKVDTKLKIFGFKYVTLDMSGYKMGSMNLNV

>CORE_REP|Org57_Gene2439#

MRVVKIFNNNALSTVTNDRKEAILLGLGIGFNKRPGDKVNEDKIEKIYYVQDHMQTKFLELLKNVSPEVMDASQQIISLIPGNEGKFNNKGILSL
VEHISFAIDRMKNNVFLPNLMLLDIKMMYSKEFELGVKALEIIYRVCHIHLPEDEAGYIALHFVNLQSNDNLAYDTLKFVKGSIDLIKECYGLELDE
SSLSTLRFRTHLKFLAQRIFKNEICQDDKMIEMYDYLINNHPKNKEYLEKLNVYIEKEFRYKLDKPEKIYLLLHLTKIL

>CORE_REP|Org57_Gene1082#

MKKRIDLLLVEQGYFESRERAKKAIMAGLVFVDNQRCDKAGTEVKEDCSIEVKGNPIPYVSRGGLKLEKAMKNFDLTIDGKVCMDIGASTGGF
TDCMLKNGAIKVFSIDVGYGQLAWKLRQDDRVVCMERTNIRNVTIEYTKQFADFASIDVSFISLKLVLPKAKELVRHDGEVVALIKPQFEAGRE
KVGKKGVVREKSTHIEVIKMISDFSVENGFEILGLDFSPIKGPEGNIEYLIHLRNGNEGYEFDGETYNNKIVEVVEASHNLDK

>CORE_REP|Org53_Gene2600#

MFTSILKKLKKDKSFAFACITLSIIIILIITSFILNIDSNAIDTTSKLQEPSLKHIFGTDELGRDYFSRALYGGRISLSVGILSMLISVVFGTAVGVISGYIGG
KLDQFLMRLVDMLMSIPSFLVLIVLNTYLTPKVSTIILIIGFLSWMEVSRIVRGETLKIKENEYCLAAKATGIKTRNILLRHIVLNLKETIVVAGSLNIA
NAILTESALSFLGLGIQLPLASWGNMLQDAQRHIFDKLYLAVFPGLLIFLTVMSLTIISKKFSSNT

>CORE_REP|Org33_Gene1887#

MNFFGLVGEKLSHSVSPQIHKRVFEILNIESAYKNFEISKEDISKLDGAIKLLGIQGVNVTVPYKERIMKYLDFISPEAKRIGAVNTILLRENMLYGY
NTDYFGLDSMFKMANIDVQGKVAVILGTGGASKAALTYFIDSGIEKLYVSTRKKDDKKLLNSKAILIDYEELKHIKGDIILNATPVGMYPNVGISP
VSKSIIQNFDILIDLIYNPGETEFLRIGNSMGKKTCDGLYMLVGQAIKSQEIWQDTKIDNSILDVIYNELKLEFL

>CORE_REP|Org67_Gene2668#

MKTARRLLSDGLLLFIACASLVPFIYMLIISLKITYNSYSLDISFSTVTLQNYIDIFTKKGFAQYFFNTAIVSFSGVLLNLVFSTLAGYSFAKMDFKGSD
KLFLFMIMTLIIPSQVTMIPLYIIMKHLGWINSYLALIMPIPTAFGVFIMRQAILGVPKELLESAKIDGCSDFRILIQIVLPLIKPALITLAIFTFMGAW
NEFMWPLIATTKDAMRTLTVGLSTLKTFQITNYGQMMAGATITFLPPFIFYLILQSKFVEGVSLSGIKG

>CORE_REP|Org69_Gene1655#

MKNILKKVGIFTIMLGLLGGVVGCSKPDNEKDKDASKESKKEVVVGFDNTFVPMGFLDEKGNTVGFDVDLAKETFKRLGMEVKFQPIDWSM
KETELNDSKTVDVLWNGYSITDERKKIVSYTEPYLQNKQIIVTLSDSKINSKADLKDKEVGTQQGSTALDAVEKDKDFMNSLKGGAPVLYDTYD
KALRDLEIGRTSAVVGDEVLIRYYMGQKGEDKYKVLKDDFGLEDYVVATSKENPELCEKINETLKEMKKDGTFDKIYDKWFK

>CORE_REP|Org18_Gene1421#

MSLIVFDYGKRTYIMGILNVTPDSFSDGGDFNNLDIAIQHAKDMVDQGADIIDLGGESTRPGHSYVDSDEELRRVIPVIKKLKQELDIPISIDTYK
ADVAEEALKLGVTMVNDVWGLRKDKNMASVIGKYDAEVCIMHNQDGTNYDKDIMESIKDFFKVSIEMAMSYGVKKEKIVLDPGVGFGKDF
EQNIEVLRRLNELKDLGYPILLGTSRKSVIGKVLPVEPKKRLEGTIATTVLGIRDGVDIVRVHDVYENLMAARMTDAIYRK

>CORE_REP|Org13_Gene1645#

MKFKKLLCLLLCLVLTLAVVGCSKAKDDKKIVVGATLVPGGELLEELKPLIKEKGYTLEVKNFDDYILPNEALNNGEIDANLFQHEPYLKEAVKAKG
YKIMAGKKLYVCPAILYSYKIKSVDEFKKGDTIAISNNPSSCSKNLRYLESIGLLTLPKGDGLVSPKDIIENPKGIQFKELDIAQIPSSLPDVTAAFIDTT
YAVPAGLDAKKNGIYTAPINDEYANLLAFRTEDKDSEKIKVLQDVLTSDKARSLIEEKYKGIVIPTF

>CORE_REP|Org78_Gene2970#

MNIVVCLKQVPDTNEVKINKETGTLIRDGVPSIINPDDRNALEEALKMKDELGAVIKVISMGPPQAKSALKEALAMGADEAYLISDRAFGGSDT
WATSTIIAAAIEKVGKYDVIFCGRQAIDGDTAQVGPEVAEFLGIPQVTYAKEVKVQDDKLLVTRYTETGDYLIEAKMPVLLTAIKELNNPRYPSVK
GILEAYNNGDAKITVLTLADLDVDTTQIGLKGSPTNVYKSFVPVKDKHNEIIEGINKKEKAEKLIEILFDLKLV

>CORE_REP|Org83_Gene1388#

MKLKKLLSVALVSAIAISAVGCSNKEDKKILVGASSNPHAKILEVAKPLLKEKGYDLEVKIFDDYVLPNTALDEGSLDANFFQHIPFLEETVKEKGY
KLTYTSKVHIEPMGFYSEKVKALDEIKDGAVIAVPNDATNGARALKLLAKNKLIEVKDGELITKKDITKNPKNIQIKEMNAEQLPTVLKDVDGAVI
NSNYALTANLNPTKDAIVIESSDSPYVNIIACRENNKDSDKIKALSEAMNSKEVKKFIQDEYKGSIVPAF

>CORE_REP|Org24_Gene2359#

MKNKFFTTLLTGFFAIVFLFIVSPLLMLIIKGISYVPICLKSVEVQYAITLSIKTSLISTIVCLLLAIPVAYFLHITKLPFKKLIIQIINLPMSLPHLVSGIALLL
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AMIAGSTRMKTEIIPTSIYLNMSTGDIDIAIGIAVILIFISLTCLMLFEIFFNREVDKN

>CORE_REP|Org22_Gene2952#

MIKLIATDLDGTLLDEKSEINPEFYKVFKKLRERGIMFSAASGRQYQNLIKKFEDIKDDMMFISENGTLVVYKGKEILSNPLNKELVNEIIETTRSIK
GKKIVMSGKKYAYIESKDEAFIQEVSTYYAKFKVVEDLTKVEGDILKIAVFDFKGAEHNNNIYFEKFSDRAQVCISGVEWLDLTAKGANKGSAIKK
VQKMLDIKYEETMVFGDQLNDVEMMKSAYHSYAMENANEHLKQIARFRAKRNTENGVVDKIKEVIKIG

>CORE_REP|Org85_Gene1168#

MASEVLQKTRKINKTLQTSGGSSVSFDLLAGALGDVLSSNVYVVSAKGKVLGLHLNDAQDSSVIEDEYTKQKKFSDEYTQNVLKIDETLENLNG
EKILEIFPEEHGRLQKYTTVVPILGSGQRLGTLVLSRYSNSFNDDDLVIAEYSATVVGLEILRAIGEELEEEMRKKAVVQMAIGTLSYSELEAVEHIF
AELDGKEGLLVASKIADRVGITRSVIVNALRKFESAGVIESRSLGMKGTHIRILNDKLTDELKKLKNNQ

>CORE_REP|Org64_Gene2604#

MQVNKVEICGVNTSELPVLKNKQMKELLLQIKNGDEEARQQFVRGNLRLVLSVIKKFNNRGENIDDLFQIGCIGLIKAIDNFDLSQNVRFSTYA
VPMIIGEIRRYLRDNNPIRVSRSLKDIAYKALQVRERLIRTNSKEPTVSEIAKELELEVESVVMALDAIQDPISLFDPVYQDNGDAIFVMDQVQDK
KDTDENWLQEISLKEAIKKLNSREKLVLDLRFYKGRTQIEVADEIGISQAQVSRIEKNALKNMRKYV

>CORE_REP|Org28_Gene2625#

MRAIIVEDEFPARKELRYFIENKSGIEVVSEFTNGIEVLDFIQENKIDVIFLDINIPHLDGMLLAKTLNQFKSRPKIVFITAYESYAVDAFSLDVFDYIL
KPYSEERIISMLNKLEKSEMSDIELSNVNSNLYKYKKEAVNQEIEEITHKISLWKGDKLVVIDIDDIYYCEANERQTFIYTEKEKFILKEGISEVENLIN
DKTFFRTHRSYIVNLTKVKEIIPWFNNTYILKLKNSDYEVTVSRSKVKEFRLLMHI

>CORE_REP|Org28_Gene1975#

MKNLEIIDKVKDSIYPIATFLFILILWQSMVGVLEVPQYILPTPVDIINVFFKDYQNLSMHAVVTIGEAILGFIVAIIISLVIGILMDFVSIIKKCLYPIM
LVTQMIPTIIIAPLFMIWFGFGTMPKVLMVMLTCFFPILISFVDGIENIDKDYLNLFKTMDSNKVNTFIHLKFPMAMDKFFSGLKISATYAVMAA
TVAEWLGGTKGLGVYMLRSKSAYALDKVFASTILVVIFSLMFVGIVQAVKKVVIRHRLID

>CORE_REP|Org23_Gene1723#

MDKLVLGGHEFNSRLLVGTGKYGSNNILPEVIKESGSEIITMALRRVDLDNKQENILTYIPKEMTILPNTSGATNAEEAVRIARISRKMGCGDFIKI
EVISDTRYLLPDNEETIKATKILADEGFIVLPYMTPDLYAGRRLIEANAAAVMPLGAPIGSNRGLQMKEMIRIMIDELDIPIIVDAGIGKPSQAME
AMEMGADAVLVNTAIASAGDPVQMARAFKLAVEGGREAYIAKTGNVSEFANASSPLTGFLGNL

>CORE_REP|Org8_Gene2346#

MGEIINALDRALDIILLLYHEKREMGITEISKAMGVYKSTVHRTLVTLENKGFVIQNAENGKYWLGINLYAIGMVVGEKMSLTEIVKPYTKKLNQ
EFNEVVNVSILEERAQDSPRSIIIHKEYGSNQLLSVNPSVGSSSECYCSAVGKCLMAFNDSIDFEKYRKTPIHKYTEHTIDNWDDMMLFLAKIKE
QGYAIDDEELEHGLTCIGAPILDKNNKAIAAISLSGPTIRMREGDFEYKIKRVIETAKSISELFR

>CORE_REP|Org36_Gene2165#

MKRKVQVKNITIGEGRPKICVPIIGKNKKDIIKEAKELKDACLDIIEWRVDFFENVENIKEVKEVLYELRSYIHDIPLLFTFRSVVEGGEKLISRDYYTT
LNKEISNTGLVDLIDVELFMGDEVIDEVVNFAHKKEVKVIISNHDFNKTPKKEEIVSRLCRMQELGADLPKIAVMPQNEKDVLVLLEATNEMFKI
YADRPIITMSMSGMGVISRLCGEIFGSALTFGAAKSVSAPGQISFKELNSVLNLLHKSIN

>CORE_REP|Org73_Gene1372#

MQDKSVREIKEIIETLEVEKYMEYIELLRVDERKSVQVLAIKLAKKLDNIRKEEERLETINIFENEGYDKGYLYIGGIDEAGRGPLAGPVVASVVVFK
KDTKIEGVNDSKKLSEAKRDELFEVIKEEALDYGIGIVNNEEIDEFNILNATYMAMKKAINCLKKAPDYLLVDAATIPGIDITQNPIVKGDSKSISIA
AASILAKVTRDSIMYQYDRVYPEYGFKSHKGYGTKEHYEAIEKYGITPIHRKSFLKNIL

>CORE_REP|Org41_Gene806#

MFAEERIQAILNILKKEGRVTVKELSSKFNVTEDCIRKDLKNIEKISSIRRIYGGAVLARETLENQDTKDRKEINIPTKKIIAEKAFNLIEDRETIFLDIST
INILLAKLLAESNKKVTLVTNMLDILNVVTSRPNNLNIISTGGLLNLSLDGFVGTPTIEFISKYKFDKTFMGSCGVDVFNSSLTTFEIEDGLTKKAIIN
SSKKVFIVMEDKKFKFDGNFKFAHLEDISSIITEKTPTPDIVDILSEFNVNVL

>CORE_REP|Org18_Gene1530#

MLTRRIIPCLDVRNGRVVKGKKFKDIVDVDSPEVLGKFYSDCGADELVFYDITASNEERKTSLEFVTKVAENINIPFCVGGGVNKLEDFTDILRKG
ADKVSINSSAVKNPELIREASLKFGAQCVVLSIDAKKNEEGSWSVYVKGGREKTNLDAIEWAVKGVELGAGEIVVNSMDEDGMKNGYDIELLS
KITSLVNVPVIASGGAGKKEDFYEAVNKSNVDGILAASVFHFGEIKINDLKKYLKDMGVEVRL

>CORE_REP|Org52_Gene1151#

MDRFFVEKNNINLQDKTCTIEGEDVKHISKVLRCKLGEKLEICDKNNNEYICEIMNIDKSIVNLEILEKVDINRESELKVRLYQGLPKAPKMEMILQ
KLTEVGVEEIILVQTKRSVVKVDDKKEDKKFERWERIIYEAAKQSKRGKIPKLRGVLSFKEALEDMKKNNVNICPYENERTVSIKHALKKCDSNID
SVGIFIGPEGGFSEEEIEQIQKNNCNVVSLGPRILRTETASVVASTIALYELSDLGGEK

>CORE_REP|Org86_Gene1966#

MFSVIFLCIGGFLAAFVDSIAGGGGLISMPVLMAIGVPVHLAIGTNKFAASAGCISSAYRYSKSGKINNDLLKKLVPFTIIGSVLGVRCVLSISEEILN
VLVVVMILIVAIYTFISKNLGQEDNFEAVNKKNLRLGMLMALIMGFYDGFFGPGTGTFLTFGFIKIYGYDFLHASANTKILNLTSNITSLLLFMING
QVDYKIAIVFALVMIMGAYVGAKVAIKKGSKMIKPIFLVMALFMVVKLVYQTLV

>CORE_REP|Org86_Gene2784#

MNEPLVSIITPVYNSEEFLSETIKSIQNQTYKNWQLLLVDDCSKDNSSEIIKSFRKEDARIKYIKLEKNSGAAVSRNVGIKNAEGRFIAFVDSDDLW
DSRKLEIQIEYMLKENVGFSFTSYRYMRQDGSKTNKVARAPKKIDYEGLLRNTIIGCSTVVIDKEIVGEFSMPLVRRGQDTATWLQLLKKEKYAY
GIQEDLVNYRLVGNSISSNKIKALKRTWNTYRNVENLSLPKSLYVFCFYVFNAIKKRV

>CORE_REP|Org29_Gene2697#

MKKNLVSIITPMYNSEKFIEATIKSVLNQTYQEWEMLIIDDCSTDNSPNIVKSYMQQDSRIKCIKTETNKGVSNARNLALSKATGQFIAFLDSDD
QWNSSKLEKQVNFMLENDYVISFTSYELMDENDKKLNKVIKVPPNVDYKRLLKGNILGCLTVVIDKSKLDFEIRMSGVRHEDYVLWLSILKKGHI
AHGINEVLALYRKSSNSLSGNKIKAAMWTWNIYRNIEKIPLYKAIYYFINYGINGIKKS

>CORE_REP|Org16_Gene2574#

MDRVAFTLFGIDIMWYGILMACGMILGTLIAIKEAKRVGIKDDDVLNIAIIAIPVGLICARIYYVVFNWSYYAQNMSQIFNFRGGGLAIHGGLIG
GILAGYIYTKIKNINFLKMADTVILGMPLAQAIGRWGNFINGEAHGGATNLPWGIMVDGVKVHPTFLYESIWDFGIFIVLLLFRKNKKYEGQVI
VTYITLYSIGRFFIEGLRTDSLMLGPLRMAQVISLIGVIGGIIAHVYLSKKNKHNISEE

>CORE_REP|Org57_Gene1789#

MIIMLSPAKNMKNIEVFDRDLSLPCFIDNTKEIVENIKTFGIEDFKNKMKINEKLAVLNKNRFESIKFDRLGNPAILTYDGIQYKNIEAENFTRKDE
EFANSCIRIISGLYGVVKPYDSIYEYRLEMQTKLRVGEFKNLYEYWGNRIYKELIKEKTAIINLSSNEYSKSIEKFIKDSDTYITCTFKVNKNGILKVEST
QAKKARGMMTKYIVKNRIRDIEELKKFNLEGYKYKENLSNNSEYIFVKE

>CORE_REP|Org24_Gene2241#

MATEKLTPSVVSIPNKFCPGCGHGIVNRIIAEVIEEHGYEKNHVLTLGVGCVCNMNFSWNGDKMQTAHGRASSTAIGVKVALPDTLVMTYQ
GDGDAYVIGLSETLNTAYRNHNVTVFVINNNNFAMTGGQMSWTTMPGQVTTTSVNGRDIKTTGSPLKVPEMVANFFDVAYVARGSVHSP
KEIINLKKYIKNAIEAQLNGEGYSLVEILAPCPTNWGVSLEKSIKWMEEEIVPYYALGEFKQRDGE

>CORE_REP|Org47_Gene1188#

MRNIKMIVAYDGSRYKGYQKLGDNNMTIQEKLENVLSKMTNETVEIIGSGRTDMGAHARGQVVNFRTNCMDSLDKIQKYLYEYLPEDIVVK
AVEEVDERFHSRYNVKSKTYMYRIDNNKYHNPFIRKYATHVSKKLDLDRMRKASEYLVGEHDFTSFASSKSKKKSNVREIYSINIKEDDNIIEIYVE
GNGFLYNMVRIIVGALIDVGLKRRAPQDIKYMLESRDRCQSSDTAPAKGLCLWKVRY

>CORE_REP|Org24_Gene952#

MKIVNKSSNIPLHTQLSSIIREMIETGELKEGDAIMPERELCNIQNVSRMTVNKTIVGLVTEGLLYRVQGKGTFVAKQKKKYQFSNVKGFTDVM
KEKGVNIKTDILSFEMELPDDLVKRKLGISDNTTNIYKIVRLRYTDGEPFGLEIVYLSEEMCKGLTKGILDNSSLYRVLNEKYGYKIQKAEQVMEPVI
LSDEESKLLETDEGALALKLHRNSYNREGSPIEYTISIFRTDKYQYEIVLSE

>CORE_REP|Org18_Gene1810#

MVNIILNWRFYFMKEKILILEDEIGIRSFVSINLKREGYEIVEAGTGREAIEKMTTEKDITIALLDVMLPDISGIEVCKFIRENFDQVGIIMLTAKAQE
DDKIEGFISGADDYIIKPFSIKELLVRVSALLRRVAKDDSSVKSSEIVSPPFILDIDKRKLFKNGKEIELTPTEFSIVKYLISNAKQSLSRDQILDEVWGT
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>CORE_REP|Org18_Gene1020#

MYAPIFALVLFSFNDSKSMARWNGFTWKWYGQLLQNESIMSALYYTIVIAILASVISTIVGTISAIGIHKMRGKSKKLILNVNYLPILNTEIVTAVA
LMSLFVFVKMEFGFTTMLLAHIMFCLPYVILSVLPKMKQLPDNIEDAAMDLGATPIYALRKVILPQIKPGIVSGFLIAFTMSIDDFIISFFNAGNG
VSNLSIEIYGMARRGIKPEINALSTIMFAVVLGLLLLANKKESIVRGIK

>CORE_REP|Org74_Gene1718#

MENRVLIIDDEVEILKLLETVLKKEGLNNIYTAKTKKEGLELFKSINPDLIVLDIMLPDGEGYDICKEIRKTSNSPIIFLSAKTEELDKLLGLAIGGDDYV
TKPFSPKEVAFRVKAHLRRLSYFSDAQNESKNLNNNEEKIISFGPYILNESRAELIKDGKSIGLFAKELKILSLFAHNQNQIISKEKLWDKVWGEDY
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>CORE_REP|Org6_Gene1990#

MELSNIIEKNEIITVVGAGGKTSFINYFANFYRDKLKVLLTTTTKIYVPNDYDNIIITIDGTVIPSICHGITVCGSYINNENKLVSIDSSILDEIVDQFDL
VLIEGDGSKRKKLKGWNAKEPVVYHKTTKTIGILDITSFGMNINEENIHRVEIFKKIANLDTSSINSSSTVSIENLKNIVLNPNGLFKNYSGKRVLFI
NKVENEKYKNLAIKLIENIKEYESEIEIFYGSVKQKFCVRY

>CORE_REP|Org45_Gene2586#

MNSYNILVVEDEKEIADAIEIYLLNQGYNVFKGYNGLEGLKVIENQEIHLAIIDIMMPKMDGITLTMKLRENHNFPVIMLSAKSEEVDKIMGLNI
GADDYVTKPFKPLELLARVNSQLRRYTKYLNMVENKEQKVDDDDGVFAIGGLELNENTKEVSVDGKHIKATPIEFKILSLLMRNAGRVFSADEI
YERVWNDNAVNTDTVMVHVRNIREKIEVDPKNPKYLKVVWGVGYKIEKIQR

>CORE_REP|Org58_Gene1491#

MIIFPAIDIKDNKCVRLTQGEFDKVNVYYDNPLEVAYKWKNEGAEYIHIVDLNGARSEFGVNTKIIEDIANNIDIPIQVGGGVRDKEKVKSLINAG
VTRVILGSIAIENLNLVEELVNEYKEKIVVSIDAKDGKVAVRGWEVVSNVDSLTLCKQLEKIGVQTIVYTDISKDGMLQGPNFDIYERIAKETSLNV
IASGGVTSIEDVKRLKAMNLYGAIIGKALYDKKIDFKEAQQLCLLGE

>CORE_REP|Org46_Gene2958#

MKKSIMDVHCHTLISGHAHSTFKENVEEASNKNIKYLGISDHGPNMPGGPHPFYFYNLHLLPREVQGVKILRGIEGNIMDYHGNLDVQEDML
QHLDYIIASLHRPCIASGTKEENTNAILKVMDKPKVKIIGHPDDSRYPLDYEPIVKKAKDKNILLEINNSSLSSNSHRTGTWENVSHMLTLCKTYG
VRVILGTDSHICYSIGKFENAEKVLKSVDFPDELVINYHEDEIIGFFDINF

>CORE_REP|Org17_Gene1030#

MKYNIQLQVYEGPLDLLYDLITKHKIDIKDISIIDITKQYLNYLKMLDKMDLEITSEFITMASKLLEIKSKYLLYKQKDEEEDPRIELMEKLEEYRKFKV
ASQDIKENITYVNERFYRNKEEIIIDDNVDLEDISIEAIKNILPYIFKVKTSQIENANDEKLDKIVRKKIISVEEKILYIRDIIKDKIEVTFTNIIKSYENDEII
ATFLSILELIKEKEIVVVQDIFFDDILIRKSSEC

>CORE_REP|Org32_Gene1458#

MTSWKKKTVYKCLIAVALFCGIVLISNFSKVSALMMDTNGNVLIKHGSREKKLIAITFDDGPHPKETSQVLDVLKKYNVKATFFIAGKHAKWYKE
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KIINKVQNGDIILLHDYATNDTVEALDMFIPKMIEKGFKFVTVSELIK

>CORE_REP|Org34_Gene1893#

MRINKYIASCGIASRRKAEEIILEGRIKVNGSIVKELFFNVDEEKDIVEFDNKKVKPSENYIYIVLNKPEGYITTVKDQFNRPSVIDILKDVKERVYPIG
RLDYETSGLLILTNDGDLTYKLTHPKHEIDKTYVASVKGIISGDEIRKFETGLKIEDYTTAPAKIKVTKENKEKNYSVCEITIHEGRNRQVRKMCKAI
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>CORE_REP|Org10_Gene1187#

MFNSIASKKVYEQVIEQIQYKILNGELKKGDKLLSERELSEQMNVSRTSIREAIRVLETMGVIESRQGEGNFICTNIEKTLIEPLSMIFKLNNGTLED
ILELRIILEIEIAKLASKRITSSEVIELKHIIDEMRVETNKKDNNRVLVLLDQKFHSKLATLSKNYLIQSLFMTASKLFDGFIEDAREKIIAEPFNENILLK
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>CORE_REP|Org31_Gene2712#

MMNIKNKKHILKKFIAMVLIAGVVTVEAGAITASAAEPTNSPMSATVDQCDFLNVRSGASANDAVVGKINTGDKVEVLELHSNGWIKIKSVDNVTGWVNGDYLTIQGGNVDAKVQNVLNLAFKQQGKPYKWGATGPNSFDCSGFTSYVYKNGAGVNLPRVSRSQATVGKKVSRAELKPGDLVFFGSGGSINHVGLYVGDSKFIHSPQTGDVVKVTSMAPGTNYAKRLITATRVLQ

>CORE_REP|Org54_Gene2394#

MENNFTTRTSFLVGDDGIEKLNNSNIIVFGVGGVGSFTVEALARAGVGNITIVDFDDVDITNINRQIPALHSTVGRYKVDVMEERILDINPNINIKKIRSLYNKDTSDEILTERYDYVVDAIDMVSSKIHLIETCEKKGLKIISSMGMGNKLDPTKIVVTDIHKTSTCPLAKVMRKELRDRGIKKLKVVYSTEQPIELKKKVMNGRKVTPGSVSFVPSVGGLIIASVIVNELLGQ

>CORE_REP|Org77_Gene971#

MNNILLLEDDKSLNRGISFKLKKEGYNVFSAFSIEEAKSIFAKEEICLIISDIGLPDGSGFDFCEEVRKKSDVYIIMLTALDEEVDIVTGYDLGADDYITKPFSLMVLISKVNALMKRVNTVKNYTLLVCDDLFFYYIENKLIVRADNKEEEIILSKTETKLLKYLMENSMQTLTKEQLLESLWDSSGNFVDDNTIAVNIRRLRQKVEKNPSAPKYIKTVRGVGYIWGERSIKKC

>CORE_REP|Org18_Gene1116#

MIYLKKSFNSTIKVKEMAPEERPREKMLAKGVKSLSNAELLAILLRTGNKNKNAIELANYIINRDIQGIRHLEDMTIEELCNIDGIGLSKSTQIKAALELGSRVASFKPIKYKIRNPWDIQRYYMDSLRYLKKEVFKAVLLNTKNEIISDVDVSIGTLSSSLVHPREVFKEAIRRSASKIIVMHNHPSGSVEPSREDKNITSRLIKCGEIIGIEIIDHIIIGDGLYFSFKENMII

>CORE_REP|Org7_Gene907#

MSKLIYIADDEDNIRNLVKTFLKNEGHDVMDFKTGDELLEQFNIKECDLVILDIMMPGSSGFEVCTKLREKSTVPIIMLTARDTDIDYITGITLGSDDYFTKPFSPMSLVMRVKSIFRRIEFEKKQNYDKYSNSIDMELKFGDVIINKKNKIVTSKNVNIDLTPNEYNLLTYLFENIDRAVSRDELLNKIWGYDIEVETRAADDTVKRLRKKILDTNILIETVWGFGFRLKEKS

>CORE_REP|Org55_Gene486#

MEIKPLVLIVEDDKPICKFIKVSLETQNYRCVETDNGGTAISLIHSLDPDLIILDLGLPDIDGIEVIGRVRACAKTNKIIVVSAREHERDKVEALDGGADDYLTKPFSVTELLARVRVALRNKAQQDNINNDAPKSFEVKNLKIDYENHIVSINGEEIHLTPIEYKIIELMSKYSGRVLTHKFIIDKVWGNYYESENQSLRVFMASIRRKIEKNPAQPEYILTEVGVGYRMADE

>CORE_REP|Org80_Gene2105#

MDKPMYKRVLLKLSGEALAGEKGFGINNDVVNDIAIAIKKIQEIGVEVAVVVGGGNFWRGRTSEGMDRTTADYIGMLATVMNAMALQDALENIDVATRVQTAIDMRQIAEPYIRRRAVRHLEKERVVIFGAGTGNPYFTTDTTAALRAAEMEAEVILLAKNVDAVYDKDPKVHADAKKFTELSYMEVIQKELKVMDSTATSLCMDNKIPIKVFELTTENIIRAVKGENIGTTVK

>CORE_REP|Org49_Gene2732#

MKEPIYKVIENHVRELINSDSLKEGDLIPSEKQLSEEFNVTRMTVRSALNNLVKEGYITRQRGVGSIVLANNIYDNISSVSGFTKEMESKGYKVSNILVSLEIVQADEELSGKLNISLEENVWEIKRVRLANDARVSYMITYMPVKLFPNLNKTHCENSLYNFVEEVCAYKIAMSEREVQAVISNKECMDNLKLEEPEPLLYISQICKLQNSEIFEYSHTYHYGYTLTLNAVVE

>CORE_REP|Org16_Gene2414#

MKKKVKFISFFVLFILIISSIIVYKSLIFKDDIYVVSKKNLPNEKTHVVENEIKGEDNNHNKVTKDIDKNFQNNKITIYISGAVNRPGIVTIESDKRLYDAVELLGGTTKEADLNGVNLSVRLEDEQHYIIPKIGEATSVTSNDDSNKPNQKNESRGEPKNKSNKNISNESKVNINVATIEELDSLPGVGEATANKILQHREENGQFSSIEEIKNVNGIGDKKYENIKDLICVD

>CORE_REP|Org15_Gene2509#

MYPVYGGFWGFDPTMVVLIPAILLTIYAQFKVSSTTNKYLRVNTRRGYTGEQTARRVLDSNGLYDVKIEMVRGHLSDHYDPRRKAVRLSEDVYYGTSITSVAVAAHECGHAIQHAKGYAPLQIRSSLVPVVNFASSISWFLIFLGFIMAGPFLKIGILLFSASVLFQIITLPVEFNASSRAIVQLGNLGIIDESESRQSRRVLSAAALTYVAAALVSILQLLRLLLIAQRRND

>CORE_REP|Org18_Gene2759#

MYVVGLIIVVALIFLVHSIIPTYYNKLLNKEVLKNMAGENEIALTFDDGPDKRYTEKLLDVLKENDIQAMFFVVAKNAEKEPEIIKRMLRENHIVGL
HSLEHRNAWLYSYSYVKKDFIESTNIMKNLGVDVNYYRPPWGHTNIFSNSFVKKYNLKMTLWDVMAEDWEKDSTVDIIINKLMSRTKENSIIC
LHDAGENSGGAVGAPERTIEALKIAIPKLKASGLKFVTPERM

>CORE_REP|Org18_Gene2640#

MNVIGIIGAMDEEVSILVDLMDIRETIKKASLEFYKGILEGKNVVLVKCGIGKVNSALCAQILISEFKVDAIVNTGVAGALNEKLDVNDIVISTDAI
QYDVDTTAFGDPKGVIPRMKTSVFKADERLIDAAYKSSVEEVKTHKVLKGRVVTGDKFINSKELKEELVNDFGGYCGEMEGGAIAHVCYLNNT
PFVIIRAMSDKADGSADVTYDVFVHDAANNSKDIVLNMLKSI

>CORE_REP|Org95_Gene1194#

METRYLISGDKAVVAEFGNEISEDINKKVISFMRAIEISNLKGIVTEMVPTYRSLMISYNPLEIDFDSLIENLKKIEDNLESIVLPKPKIHEIPVCYDEV
FGIDIKNVASYNNLTVDEVIKIHTSREYLIYMLGFTPGFPYLGGMDERIATPRLEVPRTKIYGGSVGIAGSQTGVYPIDSPGGWQIIGRTPLKLYDE
NREEQILLRAGDFIKFVPITLDEFIEIEKNNLSI

>CORE_REP|Org34_Gene2492#

MNTKVLVIDDEMHIVELLKFNLEVSNYEVSYSYDGFDGFIKAKEIKPDLILLDWMLPNISGIEVLRKIRSDKDLKNIPVIMLTAKNMENDKVEGLE
IGADDYITKPFSIKELLARISSVLRRYNLTSLGEENNILTTGNLKLDLSKHEVTKGSEKIELTLKEFELLKLLIQNKGKVLSRNYLLDKIWGYEYYGETR
TVDVHIRYLRKKIEDEDKSEKYIETIRGVGYKID

>CORE_REP|Org46_Gene2434#

MKLTDRLLKIASLVSDGKKIADIGTDHGYIPVYLLKEGRVPFAVLADVNKGPLDNAHKEVIQNNLLDKVDLRLGSGIEILEIGEVEEVIIAGMGGILI
SELLEAKKEVAHNVEKLILQPMQAQEELRYYLLNNGYEILEEVLVREDFRIYEIIVAKYTGKNTIIEDEIYYEVGIKLLENKDSLFKDFIEKKIKTYSSIVS
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>CORE_REP|Org53_Gene1818#

MEKILVVEDDSILNKTLSYNLIEDGYIITSKFTAKSALKSIFECEFDLIILDINLPDKSGFELCNEIKGNYNIPIIFLTANDMECDMIKGYELGALDYITK
PFNINIFKQKVKAFLNHLTIKTKQDYYRDGYLEINFSELSANINGNQIIFTPLEYRTLKLLTENPKSILTRKVLLEKLWDIDANFVDEHTLTSVISRIRS
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>CORE_REP|Org51_Gene2784#

MSGYTNDECEIPKIKSYPGADKEIASEIDYSIVKGTVLFDLYQRIMDLVLSIIGLVIGLPLIAIFGILIKIEDKGPITYKQERLGKCGRRFYIYKLRSMRT
DAEKFGAQWAEKDDPRITKVGKFIRKTRIDEIPQLFNILKGDMGLIGPRPERPNFTVQFNEEIPGFINRLAIKPGLTGWAQVNGGYEITPEEKLK
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>CORE_REP|Org93_Gene2412#

MYRILLVEDDIDLSKEIALALEKWGFKVGLIDDFEVVLDEFIDRKPDVVLLDVNLPLYNGFYWCEKIRAISNVPLIFLSSRDSDMDLIMGINNGAD
DYITKPFSIEILVTKINGIIRRVYNYSDSNSILYCEDLMFDVGKGIIKHKYKDKSIELTKNEIKILTLLLKNKNRVVSRESLMMTLWDNDEFVTDNALT
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>CORE_REP|Org42_Gene967#

MQLILDTGNVEEIKELCTCLPIDGVTTNPSIVSKEKKNFKQLINEIGEIIGEDMPIHAQVLSTKYEEILEEALYISSLRKNIYVKIPVTQDGLRAIKDLH
RKGVKITATAIFTAHQGFLAAKAGANYIAPYVNRLDNISGDGVAMVSELIKIIDTYKMDTKVLAASFKNAQQVIELMQHGVHSATVPYDICKS
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>CORE_REP|Org28_Gene2247#

MLDKVKGRLIVSCQALENEPLHSPFIMGRMAKAAMEGGAVGIRAQGVEDIIEIKKVTGLPVIGIIKRNYEDSDIYITPTKKEVDELLTTGCEMIAL
DATNRVRPNNEDLKELIKYIKENGVLVMADISNYDEAIKAQEYGVDCVSTTLSGYTPYTKTLEGPDFVLMERLVKDLEIPVIAEGKVNTPQDLKK
VFELGVHSSVVGSAITRPQLITEKFVKAIEINL

>CORE_REP|Org27_Gene1678#

MKVLIVEDNKILLESVVEELSKHFETEKCEDGEEALYLINQNIYDLVILDLMLPNINGFDILKKMRINNIDTPVLILTAKETLDDKVEAFTIGANDYLT
KPFYMEELVARVYAILRTNGKIKERNGLEFKSLYLDTLEKRVYIEKEEIKLQNKQFNLLEYFVLNKGSILLKEQIYDRIWGIDSDATIEIVEVYVSNLR
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>CORE_REP|Org68_Gene1930#

MNLLIIEDDINLNEGLFYAFENDGFNVFKAYTKQEGLNIFNSKNIDFIILDCNLPDGDGFDVCQIIREKSDIPIIMLTARDSEIDEVKGLEIGLDDYIT
KPFSLSVLKARVKVAIRKKSNNKVIYSNGIKLDQKLLKVYKNKECLELSSVEYKLLSYLIENKGQILLKEQILHHIWDSEENYVDDNIVSVNIRRLRVK
VEDDPSNPKYIKTAYGMGYLWNEVE

>CORE_REP|Org49_Gene1942#

MNSSILVIEDDSNIQELISEFLSAEGYQVDTANDGLEGIQKFKQGSYDLVILDIMMPNLDGYGVCKMIRKSSSVPIIFLTALNDEGDQLKGFDLEC
DDYITKPFSFNLLIKRVEAILRRSNKTINDKFIVFEKLKLDLNTYIAEIDGEPIELTLKEFNILKALIEKYPQVITREGLLDSIWGYDYYGDTRIVDAHIK
NIRKKISLPYIKTVKGIGYTLEKDI

>CORE_REP|Org89_Gene2194#

MNNKCNDIYTDEVDEFIRSIKFDDKGLVPVVVQEVVSKDVLMLAYMNKEAIKKTLKDKVACYFSRSRQELWVKGETSGNTQKVVKMSYDCD
VDTILLFVEQTGVACHTGNYSCFYRDLFDDTAKMELEVQTNILKELYDLINERKNNPVEGSYTNYLFEKGIDKILKKVGEESSEVIIASKNTDKSELI
YEISDLVYHTLVLMIEKGVEIDEIKKELLKRRK

>CORE_REP|Org33_Gene1438#

MNSLIDFLTTLFPNALLQTLYMVIVPTIVATILGFILAIILVVTKPDGLKPNSTINSALGFIVNIFRSFPFMILIVAMIPITRLIVGTSIGETAAIVPITIGA
APFIARIIESSLNEVDKGLIEAAKSFGATKRQIVFKVMIKEAMPSIVSGITLSIISILGYTAMAGAVGAGGLGNIALIYGYQRFDTAVMVYTVIALIIL
VQIIQGVGNLAYKKLK

>CORE_REP|Org42_Gene1324#

MGNLVIAVDGPAGAGKSTIAKIVAKKLNINYIDTGAMYRAVTYKCLKSGVDVNNEKEVIQIAENSDIDFKDNSIYLDKEVINEEIRTIEVSNNVSN
VAKIKEVRQLMVQVQRKIGMKSSVILDGRDIGSYVFPNADYKFFLVATPEERGNRRYKELCDKGYNTTLKAVIEDIIRRDEIDSNREFAPLVKAN
DALEIDTTGKTIEEVVEEVISKINL

>CORE_REP|Org81_Gene2772#

MNKIKVLIVDDEKLIRKGLKIILSSYNDLEIVGDASNGYEALEFCKTNDVDIVLMDIRMKVCDGVLGTRLIKEYNNSITLLILTTFNDDEYIKDAMKF
GASGYLLKDSSDKVLHEGIRSSFFGNIVLDKSVAEKIMTSEKTIKQEYLYDMYNLTEKEISIIRLIANGLNNKEISQELFLSEGTIKNNITNILAKLELR
DRTQLAIFAFKNKIVIE

>CORE_REP|Org52_Gene1097#

MKKKICVAIIFALFIVFVEMFIDSSSEGSKIMTAELSKYRKGVNVLSINNIIVANKKYSLPKDYSPQESSEARDAFYKMNKDAQKSGLNLKAFSTYR
SYEYQDRLFKSYVKEHGEKEANRFSAKPGESEHQTGLAFDIGGDDQSCWANKKFNNTKEAKWLYENAYKYGFILRYPEGKENITGYMYESWH
YRYVGTEHSKNFAMNNLTLEEYLHIN

>CORE_REP|Org92_Gene1777#

MRRRRKKGADEKLLSYTKYVLRDDIDKLKGKWNLKFRNDNPIHVEFGTGKGKFITTLAKQNPDINYIAMELKEEVLLKAVEKADASNLNNILFL
WGDVSNILDYFEAKELSRIYINFCDPWPKNRWSKRRLTHSGFLEMYNRVLEDDGEIHFKTDNEKLFEFSLNEIAANNWLLKNISLDLGNSEYEN
NVTTEYEDKFMSQGMRIFRCEAKKRN

>CORE_REP|Org31_Gene1803#

MYLDLTEKQVLILEFIKSQIILKGYPPAVREICTAVGLRSTSTVHSHLNKLEKLGYIRKDPTKPRAIEVLERSKVNDVSGANQEIIELPLVGQITAGEPI
LAQQNIEEYIPFPASLVKGSNNFVLRVKGESMINAGILDEDYVVVDKKNTALNSQIVVALINGESATVKRFFKEGNLIRLQPENDFMEPIMLNDS
EVEIVGIVTGVFRVIK

>CORE_REP|Org86_Gene1933#

MKVFDLTHVTHNDMPVYAEPNRPDIKKVAIIEENGYQETLISVFSHNGTHMDSPRHMYTKGETLDKLDIENFVGKAYVLELEKGNENIELEYLK
KYEDEIKNSDFIIFKSGWSKFWDKKQYYVGYPTLTKEAANYIANTNIKGIGIDMLSVDRYDTSVFEVHHILFEKGKIIIENLTNLENVPEKFLFIAAP
FKYNDADGAPVRAIAIVE

>CORE_REP|Org17_Gene716#

MIDKESLKKCLRLYLITDSEMLEGRDFYKCIEDAISSGITTVQLREKNTCGREFLRKAMKLREITKRYGVKFIINDRVDIALICDADGVHVGQSDID
VREVRKLIGNDKILGVSARTLEEAICAKNDGADYLGIGSIFSTSTKLDAKSASFETVKEIKEKVDMPFVLIGGINLDNIDKLKCLDSDGYAIISAILKA
EDISKEVEKWTLKI

>CORE_REP|Org44_Gene2913#

MSINLSKGDKIDLKKSNPGLSNILVGLGWDPVQQSGGGFFKSLFGGGQADIDCDASVFMLNQEGKLSGIKDLIYFGNLKSACKSVLHTGDNLT
GEGAGDDEQILVNLDKVPSNIHKLLFVVNIYNCVDRKQHFGMIENAYIRVEDQGNKKEIAKYNLSDNYSEKTTLIVGAIYRKDGSWQFKAIGEG
TKDAGLKEVMQNLDRIECAYGI

>CORE_REP|Org67_Gene1541#

MDYLTIALAKGRIEGESFKKFKKMGLGDSIDTDTRKLIFKDEENKIIYIHVKPSDVVTYVEKGVADLGIAGKDTILENETDVYEIYDLGFGKCKFAV
AGLKGDSIYREDEYLKVATKYPNIAKKYFKEKGQKIEIIKLNGSVELAPIVGLSDVIVDIVETGNTLKANGLEILEDICNISARIISNRASYRFKYEQIQ
NIIRLFEELDN

>CORE_REP|Org30_Gene2599#

MEIFSYIIIAVVAYLLGNISTSYIVAKRIAGVDIRTQGSGNAGSTNVLRTLGKRAGAMTFLGDVLKGVMAVLISEFAARLVGIDTLLAGYLAVICVV
AGHNWPAVLGFRGGKGVATSLGAMLAVNPVITLMCLAVFILVVAITKYVSLGSVVGIGCSPIFMIMVKNKAGLIVALFLTASVIYNHRANIKRLL
NGTERKIGQKKE

>CORE_REP|Org72_Gene1897#

MLQGLEIVIAMFCITLIVSIPLGIGVAFLRLSKNKLVSGITQCYILIMRGTPLLLQMIVIFYGLPLLGIVFDRFTAGVVAFFLNYAAYFAEIFRGGIQSI
DRGQYEASKVLGFDKFTMYKRVIFPQVFKRILAPISNEVITLVKDTSLVYILGLNDILRISQIAMNREASLLPLFEAGAIYLIFVAILTKGFELLEKKYS
YYR

>CORE_REP|Org75_Gene481#

MNIIVDYGLGNIDSVSRGFRKAGIETKISSDIDEIKQADSLILPGVGAFRDSISALDKLGLIPIIKEHVSKGKFMIGICLGMQLLYEKSYEYGEYEGLG
LIKGSIDKLDISLKVPHMGWNNLKFNKANDDILKYINEDDYVYFVHSYYANSSNEELIAFSEYEKKIPAIVRKGNVYGIQFHPEKSGEVGLNILRAY
GEMIK

>CORE_REP|Org35_Gene2821#

MYSYIKGTVEEIYIDSIVVENNGIGYKINVSSNTIMNLQVGEATKIYTKLIVREDDMSLCGFVSREELKMFELLTSVSKIGPKVALSILSFASSAQLG
AYILSEDIGKLSKAPGVGKKTAERIVLELKDKVDKNNIEFEPTLLSQKPTLISQDESVDALVALGYTLSESKEAVQKCKKDGMNTEAIIKKALTYIMS
KSLK

>CORE_REP|Org66_Gene987#

MNLAKVFKNGLIDENPTFVQVIGMCPTLAVTTSAINGIGMGLSTAAVLICANLVISLIRKITPDKIRIPIFIVVIATFVTIVGMLLKAYVPALDKALGI
YIPLIVVNCLILARAESFAFKTGAMPSIVDGVGQGLGFTVALTIIGAVRELLGNGSLFGMTLFGASFQPVLIFILPPGAFLTLGFLFAGFNKLRSKKA

>CORE_REP|Org2_Gene2029#

MFKKINKDIEYIMKNDPAARSKIEVFLLYPSVHAMIMHRMAHALYKKKKLFTARLISQISRFMTGIEIHPGAKMGEGILIDHGMGVVIGETAEVGNRVTIYQGATLGATGKDTGKRHPTVGDDVLIGAGTKILGPLNIGSNSKIGANSVVVKDVPNGATVVGIPAKIVKIRNLEPVKKNKKEVSYEYDELDNVYYI

>CORE_REP|Org40_Gene1766#

MGITLAKGQKVSLTKSNPGLKKVIVGLGWDINKYDGGFDFDLDASAFLTGTDGKVTNDGDFIFYNNLKHASGAVEYMGDNRTGVGDGDDEQINVDLSKIPQNIAKISFSVTINEAITRRQNFGQVENSYIRIYNEETNEELIKYELGEDFSIETAIVVAELYRHNGEWKFNALGSGFEDGLAGLCKNFGVNIG

>CORE_REP|Org36_Gene1490#

MRIWKVERNTLETQILVELNIDGSGKAEIDTGIGFLDHMLTLMSFHGKFDLKVICKGDTYVDDHHSVEDIGIAIGEAFKNALGDKKGIRRYSNIYIPMDESLSMVAIDISNRPYLVFNAKFDTQMIGSMSTQCFKEFFRAFVNESRVTLHINLLYGENDHHKIESIFKAFARALKEGSEIVSNEIASSKGVL

>CORE_REP|Org51_Gene1058#

MNLILLFLSIVLVNNVITSQFLGICPFLGVSKKVDTAVGMGVAVTFVLTLASIITYFIQILLVKTGTGFLQTIAFILVIASIVQFVEMVIQKMSPSLYQALGVYLPLITTNCAVLGIALVNVQKSYNLVETIINGFGAGAGFTLAIVIFAGIRERLELADIPEAFKGFPITLISAGLMSIAFLGFTGLIKL

>CORE_REP|Org82_Gene2360#

MNLENINQRLNQMLPVGRLSHSRNVAKCAEKLCEIYGCDKEKAYLAGMIHDCAKYLSDKEIEDYVNKYEIYLDPIEDGNRSLSHSVIGAYICEYEFEVEDEDIINAIKYHTTGREDMSLLEKIIYIADLIEEGRKFPVVDTLRELAYGGKLDEALLTSFNNTLMFVINKKEEIHPRTVMARNYLIKEKLL

>CORE_REP|Org23_Gene1823#

MSVSLQKGQRVSLVKDNNPVKNLVVGLGWDMNKLGKKNYDLDAFAIALTNQDKMNVRGDLVYFGNLKHPSKAIIHTGDNLTGKGEGDDEQIIVNLEDIPEYVHKIVFGVSIYKAKKRDQDFGQMNNSFIRLIDSNSKQELFKYNLQEDFSGKVTVLAGEIYRRNEEWKFNALGIGQNEELRELINTYK

>CORE_REP|Org48_Gene1169#

MVSAGDFRKGVTFEKDGQPCLVVDFQHVKPGKGAAFVRTKYKNLKTGAIREESFNPSEKFPKAVIDTRQMQYLYNDGELYYFMDQENFEQIPLNYDQVEDAIKFLKENEVATIRFYQGQPFQVEAPNFAELEVTDTEPGIKGDTASNVTKAATVETGAVVQVPLFINTGDKVKIDTRTGEYLSRV

>CORE_REP|Org86_Gene2134#

MKLEIHKQLEEKMNGTIDALKFEFGTIRAGRANAQMLDKIRVDYYGTPTPINQIGAISVPEPRILMISPWDKSAMHEIEKAIANSDLGLNPSNDGEVIRLSVPALTEERRKELAKKASKAAEEFKVRIRNERRDANEKIKKMEKGGELTEDELKKAQDEVQKMTDKFIKEIDTLLSKKEKDIMEV

>CORE_REP|Org32_Gene2708#

MRVISGKARGLKLNTPKNEDVRPTTDRVKESLFNMINSYIMESEVLDLFAGTGSLGIECLSRGAKSCTFVDISKESIDIVKSNIKKARVESESIILNLDFKTAIDKLKLQNSKFDIIFMDPPYYKNMFIEAIEKIDNSNLLNEDGIIVVEHDTNDLFPDKICKLEKTRDKKYGNTTLTFYKMEA

>CORE_REP|Org9_Gene1724#

MSINTVIAKNLNRLRNERNLSLGQLAELSGVSKVMLSQIEKGDSNPTVNTIWKIASGLNVPYTAILEQPQNETFIVSKTDIDVQVSENKDYRLYCYYPNTPTRNFELFQMELEEGHSYTSVGHSEKSQEYIMIIEGQLKLEVNDSIYQLRENDSICFSAESIHTYHNQGEKTLKAVIINYYPV

>CORE_REP|Org75_Gene910#

MDNKFPNVGENLRLLRQEMGISLDKASKMTGVSKAMLGQIERGESSPTVSTLWKISSGFKINFTTLLNENTNTYEVIKKEEVEPIVEQKGNMKL
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>CORE_REP|Org10_Gene1012#

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>CORE_REP|Org22_Gene1331#

MNLPNKLTLFRIFLIPVFVLIMLLNVPNKFLIACIIFIIASITDALDGKIARKYNLVTDFGKFMDPLADKLLVISALTCMIEDHLVSSWMVIIIVARELT
VSILRAIAAADGKVIAAGNSGKLKTITQMVSIVFLLLGAQFENVLILNIGEILILIATLLTLYSGWEYLYKNKELFMSSK

>CORE_REP|Org1_Gene2128#

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NTSAIDENVTLREDISVVKINCQELAQKVNNPKAANIVVLGALIAKTGLLEKELALKTMCDFFEEKGKGKFNVQNEAAFMEGYNNAI

>CORE_REP|Org28_Gene1226#

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KQPITKVEIEDIRGVKCDKVLQTLFENELIREAGRLNKIGKPIIYKTTDEFLKLLNIESLEELPPIENYQEVATSE

>CORE_REP|Org20_Gene2996#

MGEAVKKEVVEWIKVIVIALVLAFAITRFIVPTIVKGESMYPTLVERDYLIVNRIAYKVGEPKYKDIIVFKTDLTEENGKKKDLVKRVIGVPGDHVKI
QDSKVYVNDKLLDETSYIHNNRTDGDIDIVVPEGKLFAMGDNREKSLDSRYDEVGLVDEHTILGKVLVRLYPFSKIGTID

>CORE_REP|Org79_Gene761#

MIILGIDPGIAIVGYGIIEYKNSKFKVIDYGAVTTPAHMNISRRLELVYKGIDTIVKNYNIDEVGMEELFFNKNVKTAITVAQARGVTMLACAHNG
KPVYEYTPLQVKQGVVGYGRADKAQVQQMVTSFLSLKKVPKPDDVADALAVAICHAHSNKLEKTLKNIGGKYV

>CORE_REP|Org43_Gene1660#

MKEYVVVDLETTGLDPYKGCEIIEIGITEIKNEQIVKNYSRLIKPKGIISSFITELTHISNEMVENEEPLELVLPRFRKYIGDRTIIAHNAKFDLKFLNYY
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>CORE_REP|Org75_Gene584#

MNKAYLGIGTNMGDRFDNLSRACELLKNSDSIYKVKESSLYETKPWGYTEQADFLNMCVEIETEFEPYELLEYCQEIERELHRERIVHWGPRTID
VDVLFFNDVVSTDERLTIPHPRIQDRAFVLIPLMDLNEKLIINEKTIKEHLNLLSAEEREEVKELVGYERKPI

>CORE_REP|Org79_Gene704#

MIRDYLEDKPLIDESVFVAKSADVIGNVKIGKDSSIWYNAVVRGDEGPITIGENTNIQDCSIVHGDTETIIGNNVTVGHRSIVHGCKISDNVLIGM
GSIILDNAEIGEYTLIGAGTLITSNKKFPPGVLIMGSPGKVVRELTEEDKRYIDESYEWYLEAAQNQKY

>CORE_REP|Org59_Gene2574#

MENKPRKAIFAGSFDPITNGHLDIICRASKLFDELQIGVLNNPNKKGLFSFDERVKLIEKSTSHLNNIKVVTFDGLLINYCQENGIGALVRGVRSG
ADVDYELQMAHMNRELNPDIETIILPSCTKYSFISSSLIKEVLLFDADIKNLVPKIVLEELKKKTSGGN

>CORE_REP|Org66_Gene2418#

MLNFFKKNKSYKLHAVVSGNSINIEKVNDSVFSKKLMGDGVAIIPNSDVVVAPCNGKVTVLTESKHAFGMVSDEGVEILVHIGIDTVSLQGEGF
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>CORE_REP|Org76_Gene1702#

MSISNVREYFKQFGKEDSILEFEQSSATVELAAEAAGVIPARIAKTLSFKIGDDAILIVTAGDAKIDNKKYKAEFNCKAKMLTPEEVLEFTGHAIGG
VCPFGLKNSIKVYLDDSMKRFDTVFPACGSSNSAIELTCEEMEKFSKSEKWVDVCKNW

>CORE_REP|Org64_Gene2602#

MQCPYCNYKESKVIDSRHTDLKSIRRRRECESCKKRFTTYEKIETTPLMVIKKDNSREYFDREKIKYGLLKACEKRPVSIEEIESIVVHIENEINKCFIE
EIETKKIGEMVMDKLKELDEVAYVRFASVYRQFKDINTFVNELKSILIEKGDK

>CORE_REP|Org44_Gene2850#

MIYEGKLIGKDLKIGIINSRFNEFITSKLLSGAEDCLLRHDVSTKNIEIVWVPGAFEIPLVAQKMAKSGKYDAIICLGCVIRGATSHYDYVCSEVSKG
IAKVSLDNELPVIFGIVTTENIEQAIERAGTKAGNKGYDCAMNALEMANLFKSLN

>CORE_REP|Org41_Gene1716#

MKKNLEATIEEIVTKITDEHGFEMVDVEYVKEAGEYYLRVYIDKEEGISLNECELVSRELSPILDEKDPIKENYFLEVSSPGLDRALKKDRDFVRYQ
GRDVDLKLYKPLNGCKQFEGELVGLTEDNNIKIIVNGKEIEFNRKDVAIVRLAIKF

>CORE_REP|Org89_Gene2491#

MANTMDLLKDKLKETGFKITPQRRAIVEILLKHDHSHLSSEEIYDLVRVDCPEIGLATVYRTMQLLDEIGLISKLNLDDGCIRYEISLHKEDCHNHH
HLICKNCGKIMEAKEDLLDNIEKEIQSLYKFKILDHDVKFYGLCDECNGVSDSEE

>CORE_REP|Org89_Gene1981#

MAIRKIRTFDDEILRKKSKYVENVDNKIREILNDMAETMYNTPNGGGLAACQVGVLKRLVVIDLGEGLIKLVNPEIIKQEGEQIVVEGCLSFPEV
WGKLKRPKKVTVQALNEYGEKIEIKGSGFMAKCLCHEIDHLNGIVFTDKIIEHVKL

>CORE_REP|Org61_Gene3559#

MKIGLGCDHGGYNLKKEIISYLEGKGIECVDYGTNNATDSVDYPVYGEIVANSVINKEVDYGILCCGTGIGISLAANKVPGIRCAVVSDVFSAKM
SKAHNDANMLSLGERVLGKGLALEIVEAWINTDFEGDRHARRVNMIKSIEEKHNK

>CORE_REP|Org76_Gene786#

MNINEIKELLKAIDSTNLEYVKLESSDLRLEVSKKAQSTSSPVLSVQQESVVDLSLEKPVVNDTPVTSNENLSVVVAPLMGTFYDSPSPDADSFVK
VGDVVEEGDTLCILEAMKLMNEITSEIKGEIIEVLVSNEELVEYNQPLFKIKPL

>CORE_REP|Org52_Gene2415#

MKLSTKGRYGLKAMFELALNQDNGPVSLKFIAKKQKISDQYLEQIFSSLKKSGLVKSVRGAQGGYLLSKNAEDITVGDILVVLEGPVALSDCVLDEDVCENSNMCVTKIVWEKMKKGIEDVIDSITLKDMINDYNKNKLENDITNIKK

>CORE_REP|Org93_Gene1829#

MSLKQKLQEDLKSSMKNKDTVRKSVVTLIRASIKQYEVDNRVELDEDGIIDVIAKQLKQRRDALVEFEKAGREDLIKETEGEIEVLKEYLPQQLSEEELEEIVKSTISEVGATSMKDMGKIMSVIQPKVKGRADGKLINKLVKQNLQ

>CORE_REP|Org3_Gene1083#

MDFFSEIFNNGALGISLIACFLAQFIKIFTGKEKRIELSRILISGGMPSSHSSFVTSLATVVGIEKGFNSTDFAIITVLALIIMYDAAGVRRAVGKQATILNQMVADIQHGKHIEQKKLKELIGHTPLEVWFGALLGIVTALILM

>CORE_REP|Org53_Gene1160#

MLDGRIMGLDVGDKTIGVAVSDLMGLTAQGVKTIKRVGKKKDIEELKAIIKEKQVNKIVSGLPKNMNGTLGPQGEKVIKFCELVKAETGIDVEFWDERLSTVAAERSLLEADVSRQKRKKVIDMLAAVIILQGYLDFKINS

>CORE_REP|Org68_Gene2346#

MSKVLNENNIFLGLDSVSKEEAITLAGRKLVENGYVKEEYIPAMLEREKVMTTYMGMGVAIPHGVNEAKKEILSSGIVILQFPNGIDFDGEKAYLLIGIAGVGDEHLEILSNIAVVLDDDLTERLKNSNDKQAFMEAFAN

>CORE_REP|Org44_Gene3415#

MNIALVAHDQMKNTMVGFCIGYESILKKYGLYATGTTGKRIMDETELNINRLASGPLGGDQQIGSLIVTQEIDLVIFLRDPLTSQAHETDIQALIRLCDVYHVPIATNLASAEIFIKALDRGELSWREVRKSKSQRV

>CORE_REP|Org91_Gene1340#

MDKILLSNLGFYGYHGVLKEENFLGQKFFVDMELYIDSREAGLSDDINKSVSYAEVYNVVKDITENKQFNLLEALAENIAEEVLNKFILINGVMVRVRKPEAPVNGIYDYFGVEIRRTRDE

>CORE_REP|Org37_Gene1742#

MIKLYGYTKCSTVKKAKNWLKENNLEFEDIDMVQNPPSKEELKSIYKTSGYDIKKFFNTSGMKYRELGLKDIVKTESDDKLLEILVSDGMLIKRPLLLDGKNVLLGFKEDVWKSTLLKED

>CORE_REP|Org87_Gene1097#

MNEMLRAIEQEQLKNEVPNFGPGDTVKVHVRIIEGKRERIQVFEGVVLKRQGGGARETFTVRKMSFNVGVERTFPVHSPKIEKIEVTRKGKVRRAKLNYLRGRVGKAAKIKEARNK

>CORE_REP|Org70_Gene2409#

MNKKLVALCACPMGLAHTFMAAEAIEQAAKALGYEAKVETQGADGVQNELTRDDILGATMIIHAVAITPEGMERFDGCEVYEVELQEAIKNAEGVIKEIEEDLGI

>CORE_REP|Org36_Gene3621#

MIKIMLACSAGMSTSLLVTKMESAAKENGIESQIWAIPESTIQNEIEKCDVLLLGPQVRYVLPKAQEIAKPYNIPVEVINMMHYGTVNGEAVLNRAIELNNTK

>CORE_REP|Org6_Gene1037#

MYAIVKTGGKQYKVSEGDVLFVEKLEANAGDVVTLNEVLACSKDGELKLGSPVVEGASVQAKVVEQGKAKKVIVFKYKAKKDYRRKQGHRQSYTKIVVEKINA

>CORE_REP|Org92_Gene1462#

MIRILLVCVGGMSSTLLVNKMEKDAKKRNIDCKIWAVGEGDIKSELDNFDILLLGPQLRFMLDDVKSIVGDRAPVSIIDMVNYGTCNGHAVLNSVLEILK

>CORE_REP|Org33_Gene1095#

MLNMNLQLLASKKGVGSSKNGRDSISKRLGVKRFDGQLVTAGSIIVRQRGTKIHPGTNVGKGSDDTLFALVDGTVKFERKDKKRKKVSIYPVAIAE

Sequences with virulence associated factors in the FASTA format

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>CORE_REP|Org40_Gene2650#(WP_009893719.1|sigma 54-interacting transcriptional regulator)

MKQMELAIVSLKKDAGEIYENQIRQFLGDNLKINLYSFEEGNLKFFKEKLILLSAYLKYDEIVKLSHYDAQIIVPKLTFEKNSIDMISKLEKDKIIYVYN
LSKDMAIETISLIHRLGIDNINILPCYPEIEFTPTDAVILTPGEKILPKFKNCEVVDLKYRIIDLSCIVEIATKTKLKHLIKDDLIKKYVEKIIPTSYSTGELLL
DANKFERQFDLLLSIIDDGIICTNNDGIIQFYNHIARKILSINANEMIDSFVGDCIKDINFQNILTNKTPFFEKLIKINHIDINLEIKHIQLNVFDGFILK
MTKFSQLEKKQAKLRAQLVNSGNISKYTFDDILGSSIQTINTKKIANKMAQSNSSILIIGESGTGKELFAQSIHSASRRKDGPFVAVNCSTFQENLL
QSELFGYDEGAFTGAKKGGKIGLFELANNGTIFLDEIGEMDLNSQSKLLRVIQEKQVRRIGSNNVIDIDVRIIAATNRNLKELVSKNMFRRDLYFR
LNVLPLKIHPLRERAADIFEIFGSLKYDIPCNFILSEEVKEIFKMYRWEGNVRELRNLGEYFCYLGKDIIEICDLPEYILDTIDSNYSRTVCNKVSDNIK
KYQFNIGKDKNIMKYDYNFKRSLDEYIFILDNLKKAYDLKERIGRKSLCKIALEENRFLTEQQIRNMLLELQDFGLVDILVGRGGSIITSKGVEFLKN
INRSNKLNS

>CORE_REP|Org95_Gene1329#(WP_009896470.1|	c-di-GMP phosphodiesterase PdcA)

MNKHNFEVILNQLQINIYVTNIHTNEIIFMNKKMKEEYNILDPEGKVCWQVLYPEKNSTCSFCKVLELLKNDKKGVLIKWYEKCNKLNRVFENY
DSLITWQDGTVVHMHQSIDIANSTSLNKPIKINEFHEISNNKEEKGVFNFSRDNFDYNSTLLYDALIRGTDEYIYICNMKTGVFRYSPSQVELFDL
PGEIVKNPLVYWKKIVHPEDWNRFYKSNTEIGKNQMDYHTVEFRAKNRSGEYIWLRCRGQLMRDEFGEPSIFAGIMTQLGKQNKIDSLTQLL
NYHEFMSVFEDKISNPMIEKLCIVLLDIDDFKNVNEMYDRDFGDNIIKTLAQSVQSILPDNAELYKLDGDEMGILVDNVEENEILTLYNQIQNMI
IHLQLWRKYGLNITISAGCVIYPKHGDTVKELYKCASYSLQYAKEHGKNRLVFFSQEILKNKMYSLEMMRDLKASINDDFRGFSLRFQPQVDTES
HKIIGVEVLLRWTNDKCKAISPLEFIPILEENDMINIVGAWVLRMALRTFRKWIDYYPFFKVSVNVSAVQILEDTFIEDIVKIIDDENFPYQNLVLEL
TESHTVQNMSILQFKFKALQDLGIYIAMDDFGTGYSSLEVLKFSPIDIVKIDRVFVKDILKSKFDATFIHFIVAICHDVGIKVCLEGVETQEEYDLVK
QIKPDYIQGYLFGKPQTATEIFDLLKLDN

>CORE_REP|Org49_Gene2710#(WP_003422726.1sigma 54-interacting transcriptional regulator)

MKKHNILFVSTDDKINIDISKQLENIFGEFCSIDNLIYVNRINIELSSYELVVCSDNDIKEYIHNNIDKNIPIVIIHRTINIENINQIISIENDSDVMVIDA
YKESADETAKIIRKLGLIHINLIPYYPGCDKSKCEIGIITGSRNSIPQNIKQIIDIGDKIIDINTVIEIFTKLNISIDKLHIIKEKYDEDTVSGYRYYTTMNKT
MKSFLEIIDEGIASIDKLGKFIYCNKVFSNLIGIDQNEIISNNFMDLFSDKVVKKIFFQEDEVNDEVVNLNNKKLIINKVNVYENNERIKSIISIKDISAI
QVLEDKIQNKFQAKGFVSKYTFESVVGESKIIKEKINIARKIAITDFSVLILGENGTGKEIFAQAIHNESLRKNKPFVAVNLSSLSDTLIESELFGYEEG
SFTGAIKGGKMGIFERAHTGTIFLDEIGDISLDVQQRLLRVLQEKEVMRMGGSKIIPIDVRIIAATNKDLKKKIKEGSFREDLYYRINVLHIEIPRLRE
RKEDISLISKYFLDEINSNKCFTEESMKALKLYEWPGNVRELKNLVYYIDTIVEEDRVDYEHLPEQFRFEKNNTLVNENFDSIILDFKQSNFFEESICI
LTSVETWNNKNILLGRNKLQEILKEKGIVLSVDQIRKRIDKLKSHGLLLSGVKKQGSFITDEGKNFISYIKFKGVI

>CORE_REP|Org82_Gene2537#( MBH7044485.1|sigma 54-interacting transcriptional regulator)

MDKKKLILITYDKLNSDHYKEELTNFFGDEIIIETQNILDGIKENLEGEVVLSLSPLTSNFLIKHFKEDIEIIHGTKALSKLGYEKMMKLPPGTKSLLMT
TNKTSAFEMATYLYKIGINHIDFVPTYPDCDEIYDLDTAITPGQIRFIPKYIKNIVDLGWRKISLDTYMSLLVVLKLKNEKFIEKLYKLSKETLSHDFLN
TSLDNISKLKTILYMTIDEIGDGLIFFNTFNKVTFVNKSLLNMLELDEKLIKSPSLMEYMPKSFLDKITKNLNIDNMIIYIDEIDKKFILSKKPFYLYKNI
EGCLITLKDVNNIEILEQKIRSDSVKRGYVAKYKFNNIIGNSSIIKDCIKRAKKMALTDNPILITGETGTGKEAFTQSIHNHSNRKNKPFVAINCASL
PSELLESELFGYEDGSFTGAKKGGKKGLFELAHTGTIFLDEIGDMPHDLQVKLLRVLQEKEIRKIGGTSIIPIDVRILAATNKDLEKLIIENKFRMDLF
YRISMFTLDLPPLRKRLEDIPLLLESFLKELPYKNIKLDKSLLEALNSYTWMGNIRELRNCVEYMAYMGSNYLTINDLPQNISSKLNNNHMSSNM
SIFNDLNQYDKNICISILKSLHMKPMGRTKLMKFMEYNVTEYEVRNMLEYLTRNGYLISSKGRKGSSITEKGIKIIENNII

>CORE_REP|Org36_Gene176#( WP_009895253.1|sigma 54-interacting transcriptional regulator )

MKKSVALVNDSRKDLIDFLENNLKLVFGDSININRYFINEINDNDIINDDVILVMSVERLDKIINNILDKKKVIVVRRTFREDKIYNLLSLPQGTNVLI
VNDSDETTLETISLFYKIGVTNIRPIPYMNDNNYKNIKIAITPGVPEKVPSFISDIFDLGHRYIDISTFIEIINLLQIDSKEIQSNLVKYSEEIISLDTGIKD
KYKELFLKIEELDTILNLSKDGILFTSKDGEINTYNSKVKDILDINEDIYGKYIEDIFVDSLKVLLSEKEILDKVVVFNKKYINVNKKNIYNRDEKMGTY
YSLQEITYIKKLEQNLTKKLREKGQIAKYTFKDIKTNSPKMFECIDLAKKVSKSDLSILIRGESGTGKELIAQSIHNNSNRKNQPFIAVNCAAVPENL
LESQLFGYDKGTFTGGLKDGKQGLFELANNGTIFLDEIGDMPLELQTKLLRVLQEKQIMPVGSHNVINIDVRIISATNKNLEQMIDNSQFREDLY
YRLNTIPINIPPLRERKEDILIIMEDLINKKLIITPEAKKLIQNYMWKGNIRELQNVTSYLNIMCEDIVLEKDLPPNLRSSDNKNTSLKLKYSKNDILNI
LEILILNKESDVGIGRGLILKALLDKNLQITEGKIKKIFEYLKKEELIICSSGRYGSKITQKGEDFYNKLKYKGL

>CORE_REP|Org14_Gene669# (WP_003416780.1|sigma 54-interacting transcriptional regulator)

MILLQKKIGIIASDIELKERIEELYREDVENGTIIIDILNLDLMENQGRILVEKGAQAIIGRGGGYSLVIDTVNVPVIPMNMKSTDLLRAIEIAKKYSK
KVVLILGDNEVSFDYVGWRNVISTEITEEWFESKYEIRSKVVKYIDQKDEVVIVGGGLACSFARQYGIDSVFATASDESIREAVEYCKKLLDTLGEE
KFNNEVLRNILDGIKDGVIAIDSNGSIILYNESAKNMLKVERKCALNKYILDVFPKMEWMLDCLHEKEAVEDRKIRNINNLIVNTRTTLIKVDNST
YGVLGIIQDITKLQNLERKIRFDLNQKGLYARYTFDDFLFKDKLTKEFIEEAKKIGKSDYTTLLYGESGSGKEIIAHSIHNISKRKDRPFVAINCATIAE
NLLESELFGYEEGAFTGARKGGKRGLFELAHGGTLFLDEINSLSFNIQTKLLRVIEERQIMRIGSDYIIPLDIRIIAATNESLTEKIVMGTFRADLFYRL
SSLEINIPPLRDRREDIIPLFNNFVNEVLKDDGLNGINSIDENFVLTKDEIDKLYNYSWPGNVRELKTIAQKYVVTGKIKLRQDRNFKTKQSLSNSE
VDKFNSETTASAEVQDESINISKINDGKISIDIKEVNKYVEEKIISMLFAQGLSKNEVAQVLGISRTSLWKKYNKNI
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>CORE_REP|Org18_Gene1724#(WP_009896876.1|transporter substrate-binding domain-containing protein)

MNKKKIVIIGIIYSFLVVFSLTNMYVNMEYNLNVFEYIKKSLPFTEEEKKWLEKHKNLIYSSDQSSPPLRYKGKEDGQYKGIIVDLINSLSIQIGRDFY
FKPNNWWKESFVNSIDDSIKFFDLIPSKERANKFIFTDPIYTLSANILKDKKSQDINSYMDLKGKTVAIPEGDYSINFLKQKIQDINILLTPDIKTGV
NHLMSGKVDAVVGDEPVLRYYINNYGLSNKYSVLSNPIYTKKAVLAVPKQYEELVSILNKGIFKLQKNGVYKDLKKKWYSTYNEVDDILYERGIV
PSIYLFIGIILISIYVFYSYTYLLKIEIKRKTEQVIENKKTLEATFNSITDIIMLVDENNNIVESNKVLYDFMGEMSYKIADLISMIKGVIENTFSENTNKT
SEIEIHNKILKINTFPVEYKKNNTEYIVVLIKDITNDKIVEAKLLRENKMISIGQLASGVAHEIRNPLGIIRNNCYLLKDNVTMEEVNDCVKSIESNVD
RASNIITNLLNFARISDDNLEHINIRNFIENIVKLQYKMLQLKNVEIKIDCEHNLICYINGESLKHVFINLISNSIDAIHQDGKIIIYCYEKNHCLFIDFK
DNGEGIKEDALKDIFNPFYTTKPIGEGTGLGLYITYNEIKKNNGDISVESKLGVGTCFHIKIPLNKEVTI

>CORE_REP|Org51_Gene2854#(WP_021388183.1|2-aminoethylphosphonate--pyruvate transaminase)

MKKIYGEKIKAVVFDWAGTTVDYGCFAPLNVFIEIFKRRGIDVTMEEARKPMGKLKIDHIREMCEMDRIKNLWSDKFGKVPTEDDVNELYAEF
EPMLFETLEDYTTPIPHVVETIEKLRKNGLKIGSTTGYTREMMNIVEPNAAKKGYSPDFLVTPSEVSQGRPYPWMCYKNAEALGVSPMSSMVK
VGDTISDVKEGVNAGMWSVAVIKGSSELGLTQEEVENMDKEELKAKMSIVSKKFKEAGAHFVIETMAELEDILIKIENETIKSDFVPENDYILLTP
GPLSTTKSVRASMLKDWCTWDVEYNNLVQDVRRRLVSLATQNTDKYTSVLMQGSGTFSVEAIIGSTISKDGKLLVIANGAYGKRMKDICNYLD
IEFVDCTFKDIEAVDLNVVENLLKENKDITHISMVHCETTTGRLNPIQEVGKLAKKYNKIYIVDAMSSFGGIEIDVEDFNIDFLVSSSNKCIQGVPG
FGFIIANKEELSKCKGIAKSLSLDVYAQWETMEKNNGKWRFTSPTHVVRAFYQALLELEEEGSVEKRYARYKENQFTIASRLKSLGFDTLVNDNA
QSPVITTFLYPKNAKFEFMEFYTYLKDNGFVIYPGKLTDIDTFRIGSIGEVYPTDMERLADVIEKFINR

>CORE_REP|Org62_Gene1531#(WP_003420306.1|GGDEF domain-containing phosphodiesterase)

MKRFLRRIILVLFILLIFISFISIKLIHNVGDYGKLINYVGIVRGASQRLTKLEMNHKPNDELIEYIDEILQELITGHGNYGLVLTDCNKYNEDLLLLEKK
WEDLNSEIKKVRMKEPNNQLLSISEEFFSLANDTVFEIENFSKEKSNYLMTLIIIISIIGILACIILILQYSKKMIKLEKLNVDLKNIAYKDELTGVNTIEK
FKLDANQNICMHKDKKFAVFYIDFENFKYINDIFGYDYGDMILKRYANLMMNDIGKYEIFAREIADRFVALRCYIDKEDLVVRQRIVDSELINTT
NEIKNKHSITVVSGICCIEDVNEKLSIDGLINRANFAQKTVKNKPGTNYAFYNDSIRKKMIEENTIKSRIHEAIEKREFIVYLQPKVNLHNQKINCAE
ALVRWLTPDKGIISPAIFIPVLEKNFFIALVDKYVFEEVCKWIRKRLDENKPFVQISVNVSRIQFYNTKFVETYSNIQNKYRIPKNTIEIEFTESVAFE
NQNHLLEIIHDLHENGFTCSLDDFGKGYSSLSVLKDLPFDALKLDSMFFKASLDKDKEKIVIKNIVHMLKELNITTVAEGIEYEEQVEFLRDIGCDL
VQGFVFYKPMPILEFEEILDKEFVYNS

>CORE_REP|Org88_Gene3147#(|EFH15286.1| Sigma-54 interaction domain protein)

MLSKLKEFQQEMIKYTETVASVLDVDIEIVDDRLIRISGTGLYKSKINESVVTEGFIYDNVIQTGQELVVLDICDNQLCIECSHYMKCLNKVIIAVPI
KYNNRTIGVIGAISTDKTKKVEISAKIDNYLKFVNHICDLISMKIEEHEVSKNSSRKMDMMIEIIENVEKGVIILDINSKISYINNIALKKLDIDKNIIEN
IVNIVSVESSSNGHELLEIDIDNKIYNINAKIIPVYPYINQYDKIIIFDKTYINHKGHVKVNSGWGNSDIESIIGNSEAMLKVKERTKKLAKSNSTVLIT
GESGTGKELIARAIHAEGSRWNKPFIAINCAAIPENLLESELFGYIKGAFSGASSGGKVGKFELANEGVIFLDEIGDLSMPLQAKLLRVLQERKFAR
IGSNKLIDLDIRVIAATNKNLLKLVNEGKFRDDLYYRLNVIPINLPPLRERKDDIEAIMMKFASKYSLELGIQLNKIEENVMNMLINYNWPGNIREL
ENAVEYMMNLVGDDGIIYKDMLPLDILNYYNINGNICKNKDINIIFEDDIVGGIVENQERILSIKELELTYINKLLNKYGRDTKTKKKIAKDLGIGLA
TLYRKLEEEQS

>CORE_REP|Org45_Gene290#(WP_003419837.1|sensor domain-containing diguanylate cyclise)

MSILLKKAPKLAKHIITSFYINRDIDEVLKYLCENVTWIGPGEQEFLTSFNEIKNYFYAGQYEIPSCDINNDIFEIVSEYENRCMVLGKYTVRTKENA
QMILEVNQRCTFEIIEDREKLLVKHMHISNPYGEMQLDEYFPTKIGTQSYDYLQRLLKEKTEVIEMITNNINGGLKGSNDDSTYSFFYVNEGLPKI
LGYTYNEFMEMSGGSAVGAVYPPDLPKALEDCEQCFAKGPTYSSEYRIRKKDGTLMWVLDSGMKSLNSDGIVKINSIITDITQLKNIESELKLER
ERYRIALQNITDIMFEYDMENDNFIKYQRVEIDKKIELENFETKNYSKLLESGKIIHLDDIGKLLEVLRGNLHETIEIREINSLTKNEWRWIRVQCSVI
YDSDHNPIKTIGVLKDITEDKSKLESLINQAQRDPLTQLYNQRVSQNLIQEYLCSSDSKNNDALLIIDIDDFKTVNDTFGHLEGNEVLVAVSKILLH
NTYDKDIVARIGGDEFTIFIKSLTKDLIIKITNDILNDASKIKVKDNHKITLSIGIAFTDDSTKLYKDLFSKADKALYLSKADGKNCYSVYE

>CORE_REP|Org72_Gene2695#(WP_065986483.1| DAK2 domain-containing protein)

MIQYIDGKRLREMFISGANNLQNNKELVDKLNVFPVPDGDTGTNMSLTISYALKELAKVENDNISDIGKALSKGSLMGARGNSGVILSQIIRGIA
KSIEGKSKLSTEDLAKAFKNGSDTAYKAVIKPIEGTILTVVRESGEFAIKTAKKEKDVVKFLSMLVKESNSSLERTPDLLKNLKEAGVVDSGGKGLV
LIYEGMLASIKGNNIEIKNADLDTNISTSMDFAKSTTSTDNIKYCYCTEFILESSKVEDTKIRDIMMAYGDSLAVVGDDGVIKVHVHTNDPGNVL
QEALKYGQLLTIKIENMKLQHENTLLDVEEKKENDSEPLEEEKEFGFIATSMGEGLANIFKDFGVDHIIEGGQTMNPSTEDFMNAIKDINAKNIFI
FPNNSNIIMAANQAKELSDKNIIVIPTKNTPQGFAALVTFNGELSEDENKEAMMNALNSVKSGQVTFAVRDTVMNEIDVKEGNIIGIAEGNLL
SAGDYVDEVTSNLIEKLVDEDTAIITLFFGEDVTESQANELRTSLEEKFEDVDVELYYGGQPLYYYLISVE

>CORE_REP|Org18_Gene1870#(WP_011861348.1|bifunctional diguanylate cyclase/ phosphodiesterase)

MLKRVRCSYLKKNRLIAKNISIAFIVLFFFSVFTFFYVGNINRVLEYETNDIITVTIAGWIILSFLFLGIIIYILYSKANSQKTIEKVAYTDFVTGYSNWRK
FELDVTNLLKKTSQNNKYAMVIFDIDKFKAINDIYGHKKGNLILKDIADTLNELTDINETFARVSADNFNILLTYNKKEDIINIIKKIMANNELVNLS
FGIYEIKDKDLSVSVYSDRASLAKSSIKNNSDVNFAFFNDKLREKLLFEDKIEKEMEYALESGQFVMYLQPKYNIKLDKFCGSEALVRWQYTEKEV
IYPGDFIPIFEKNGFIRKIDMYILEQACKEIRSLFDKGISPLPISVNFSRVDFFKKDFIENIVNICDRYKIPYSLIEIEITESSMFGDTDTLFNVSRNLQDI

GFIVAMDDFGSGYSSVNMLKNIPLNVIKLDRGFFVDDKDVDKSQIVIKSIVSLIKQLGIRVVAEGIETRSQIEMLKKANCDIVQGYYFSKPLPIKEF
EKLVYKI

>CORE_REP|Org46_Gene2479#(WP_003419821.1 sigma 54-interacting transcriptional regulator)

MNLNLELDLEFYKKILEASHDEICVSDDKGIIIYCNKAFEENYGLKKEDILGKNVSFLEDSGYSTKSPIPVVLKTKSKFSLEQDTQTGKKLIITATPIFD
ENGNLEFTVENCRDITELNNIKNKLEDTKKQVKKYKSEVETLYRTALRIEDTVIMDGIVMRPIINTVNHVSKTDVSVLLLGESGTGKSSLARYIHH
NSNRANGPFITINCATISPQLLESELFGYTSGAFTGASTKGKVGLVELANGGTLFLDEIGDIPQNLQAKFLQLIQDRTFTPVGSLKNKNVDIRIISAT
NADLVSKVKEKKFREDLYYRLNVIEIKLPPLRERRDNLVEIIKYYFNRYSSDFNLNKTISKEAMETIANYRFPGNIRELQNIIQKILLTCTDNHITIHNL
PNILTKNINITNNGNKTHISQINKVITPDSKSINYKNKNFDTLIKEYEKNIILDAYEKFGSSYKVAKHLEISQSKANRLIRKYTNT

>CORE_REP|Org94_Gene1661#(WP_231305334.1| HAMP domain-containing histidine kinase)

MKWKITRNFIFTIVFVAISVVIINIISILYVISTNSFFKVVDSGNNPEEFARSFEKDLYEKDGEFKLSKIGAEKLEKSNSWIQVLNDLGEEVYGVNVPK
YTPKKYTPFQMVNNYKYIETKYVNFVLEKYLNKKHLNIIVGIPSRDISRIILTYSQNNIKKTLNKVIIITLVIDSVVALGVGYLFSRKLTKPISSVLWSIE
TMANGNYSLYLKDRGIYEEVFKNINMLADTLRVNEVERKENEELREEWLANITHDIKTPLASIQGYAEIINDKDYEFEEDEIQEYTEIIYNKSKYIK
DLVDDLNLSTRLKNDTIVLDKKKINLVSLVRNIIIDILNDNRYKNRNIEFESNEDLIEVYVDSILFRRAITNLIFNSIVHNSEGTLISVEIVKKDNIEIIIKD
NGIGISKSDLKHIFKKYYRGTNTGEMHKGSGLGMAISKEIIEIHKGKIYVSSEIGIGTKIIIEIKQN

>CORE_REP|Org37_Gene2294#(WP_004454646.1| aldehyde dehydrogenase family protein)

MEKAVENFEDLSKEYINGYIERARKAQREFECYTQEQVDKIVKIVGKVVYYNAEYLAKLAVEETGMGVYEDKVAKNKSKAKVIYNNLKDKKSVG
IIDIDRETGITKVAKPVGVVAAITPCTNPIVTPMSNAMFALKGRNAIIITPHHKAIGCSTKTVEMINEELEKIGAPENLIQILDQQSRENTRNLISSA
DVVIATGGMGMVKAAYSSGKPALGVGAGNVQCIIDRDVDIKEAVPKIIAGRIFDNGIICSGEQSVIVAEEMFDKIMDEFKNNKGFIVRDKVQK
EAFRNAMFVNKSMNKDAVGQSVHTIAKIAGVEIPEDTKIIVIEADGPGEEDIIAKEKMCPVISAYKYKSFEEGVAIAKANLNVEGKGHSVSIHSN
TVKNIEYAGENIEVSRFVINQCCATSAGGSFFNGLAPTNTLGCGSWGNNSISENLDYKHLINISRIAYYMPENEVPTDEELWG

>CORE_REP|Org85_Gene2194#(WP_003423198.1|PLP-dependent aminotransferase family protein)

MPINSFENYPMNWKPKRPSKGQILYKALAEQLEQDINNGFLLPGTKLPPQRELADFLDVNVSTISRAFKICEKKGLISGVTGSGTFVSYDTRSNL
FLMSSNNKITFIEMGTMNPDFTLEEMNTLFKHIVKEIDFKTIFQYGQRDGAKWQKEAIAKLIYKAGLETTADSLLPASGGQNAIVAILAGLFQH
GDRIGVDPLTYPGIKTAAKMLGVQLIPIKQEHNEISEEGLLYACKNENIKGLYIIPDYQNPTTHIMSQNGRKMIANIASKYNLIVIEDAIHSLLNET
HLNPVASYLPNQTIYITSLSKIIAPSLRLAYISTPKQYRESLSDALYNINLSQSYFLTEIAYRMITSGEADKLINARRKSARRRNKIINQYLSGYNLLGN
EECIFRWLILPEGIMAEKFEIQALKEGVQVYASERFAVGKEKPISAIRIAVCATESIEELKAGLSILKRLLEEKK

>CORE_REP|Org18_Gene1417#(|ARC14034.1| aminodeoxychorismate synthase component)

MCNMIREINTKLNSFEIFTIFRNEHDSFILDSAMDKEKLGRYSFISSQPFKVLKYKDTDENPLEVLKEELHKYRVVNDTNLPFVGGAVGYLSYDLG
NYIENLPRTAVDDIEMPDMYFGFYNHVIVIDHLVQKTYIATPNIDIELEEKIIDDIEQRILKEEKKGIDSICYEEKEVTSIRLKSNFTKEEFKNAVQSV
REYIRQGDIYQANLTQRFSGETELTSFELYRDLRRFSPAPFGAFLNFEDAHILSNSPERFIRCVNKRIETRPIKGTRPRGKDKEEDLRLQQELRNSE
KDRAELLMIVDLERNDIGRISKTGSVKVPELFVIEPYANVNHLVSTVVGELKDDKDATDVIKATFPGGSITGAPKIRAMEIIDELEPTQRNVYTGSI
GYIGFNGDMDFNIAIRTIIKNDKKVYFQVGGGMTWDSDPDEEYQETLDKAKSIMKALRGYYEE

>CORE_REP|Org83_Gene1650#(WP_003423653.1|sigma-54 dependent transcriptional regulator)

MKILIVDDELEYGVVMKKILQKKGYLVDVTLSGEEAINIIKKDKNYDLVLSDVMMKNMDGVQLLDRIKAINKDIEVILVTGYGSIENAVDAMKK
GALSYFIKSNPIENLLEEVEKVKTSKTSVSLQKNNLEFTLESKNRDFNDVIKIAKKAACKDVNILILGESGVGKDILARYIHSISPRKNEIFVPVNCCSF
SENLLESELFGHEKGSFTGAVDSRKGRFELSNKGTLFLDEIGDIPLNVQVKLLRTLEDKSIERIGSNKSIKVDFRLICAMNKEPKVEISNGNIREDFF
YRISTITITIPPLRKRREDLATLIEFFLNKYQIEHDKKIHSIDKEVKDFLLNYNYPGNIRELKNIINRLVVLSEEGNLSKDNLNLISNNVYIDDKISIKPLR
EIRKEFECEYIEKVLSLCGNNISNTAKKLEISRRQLTNKIAEYNIK

>CORE_REP|Org50_Gene2566#(HBH1461641.1|TPA: D-alanyl-D-alanine carboxypeptidase)

MKRNLSLLLICLLIFTSFLGRSNISFADNEPAIVAKHAVLMDYETGKILYNKDGNSKLYPASTTKVWTACLVLKEVKDLNQVIEIKDLPQIDGSSMY
LKEGESFTVKQLLDALLVHSANDAAFVLARYVGGGNVQKFIDLMNSEAKKIGATNTHFNNPHGLPDPNHYTTAHDMALIAREAMNNDTFRQ
IVKTKSLKFEATKAYPYERYFVNTNKFLTSHDKITYKGQPINIKYDIVDGIKTGYTDAAGKCLLSSAVKDGRRVIVAVFNSTNADLYLDSRILIDYGF
DNFKCATIVDKEKYTDTKKVLFTKQHELIYEPKNSYKIFLEKNESKGNYDTKTELNKIDLPIKKGAKVGTLNVYNNGKLENSIDLIAKNNLDSSLPFL
TENNVLMTFVKIIAGILILLVLFIITSNIKKKKKIKKARGKRNMKK

>CORE_REP|Org85_Gene2013#(WP_003424453.1| HAMP domain-containing histidine kinase)

MRRIFDKWEKLSIKYKLFSITTSLLIALALIIYLILYFLLPSYYHEYKIESLQESLKSLVDSSIHFDTYTLEERLYYMAKDQNLAILLKDNQGKIVYGKNEV
VILRYSKYMINSLEDEYRTSIPIYTKDAKDGPYTLELVMPLQPIDEANEVIRKLMPYIISIAILIAIIGAYIYSIVITKPLINIIESEREQEYRRKDFVATISH
ELKTPITIISGQIEGMIYSVGKYKDRDTYLKKSYECTQELKDLVNEMIEVSKSEILEKDLKLVSINISELLNRLVKRQVFLIEEKHMKTILKIEENLEVKA

DQERITKAINNIINNAIKYSPEESEIIIRLYDKNKRISKKNSNQRVVLEIENTGVTIEKRYLEEIFNPFYRIEKSRSRKTGGSGLGLYIVSQIFKSHGFDY
SIKNKENSVIFTVEFKN

>CORE_REP|Org14_Gene3214#(WP_003419909.1| HAMP domain-containing histidine kinase)

MKIVFLYNPEVKKFLSKYVTLIFVIIIISIGFSVINVSLTKDMIVRNNQAIIGTLSSKYPNLESEIVDIITQGKSMENTDYGKKILSKYNYDKSIRINSEPII
SKLVLDTIKINIILVCIIFILIFVLVVRYFKSIYNDLSDMTKYVYYSSEGKSFDMKNKNQEGQIGLLKTELLKMTTILNEKVELLKTEKIFLNNTISDISHQ
LKTPMTSLIMLNDLLYNDIPYEVKIDFLNKIKNQLNRMDWLIKSMLKLSKVEAKVINFKKDKVKFSELIHRAMQSMKIPMEIKNQKLTIEGSDNI
SYIGDIDWSVEALVNIIKNCVEHTPEFGNITITYKENPLFSELIIKDDGEGIHKKDIPHVFKRFYRGRSSSKEDSVGIGLAMSKSIIESQNGDIYVNSE
KGKGTEFHIIFHKMYDSD

>CORE_REP|Org10_Gene510#(WP_165476817.1|D-alanyl-D-alanine carboxypeptidase)

MEDEILKGKIKQLTILALIFIFITPVFAFADTPPVPNSSRAALLIDQETKRILFEKNIDEKMPLASLSKMMTFLLAIEAVDKNQVKETDMVKIDKSTA
SVGGSTCKLKDGDEISLGELMQGLMLVSGNDAAIAIAKHIGKTEKNFVNMMNKKAEEIGMIDTYYFNPNGLPIYTDPEHKEPPIENMSTAHDI
VTLGKYMYDHYENQVTRITTMQVYNDTKKDFTHYNTNPLLVSVPGVDGIKTGYTDNAGYCLAFSMMVPKDAKNERNHRLIGVVLGDGNKK
NRISSSATLLKYGKDNFHSKKIAHKGDIIETPCVDGIDDFKITVKVDKDLYGVVSDNENINPKVVFKNMNYPIHKGDIVGVAKYYNDSGKFVGSV
DVKSESNIGCIPLKDKIKIKVAKINKKLEIKNSVCFKA

>CORE_REP|Org52_Gene1914#(WP_009902721.1| HAMP domain-containing histidine kinase)

MINKNVFTSTKNHLIKMYIIVVGSFLIIFSIFIYSYFRGLTYSGIDSEINDELEYIVSQFKRTSFLNPIRLKDPKDMVYVYEDGRISYYTQNEYFDELLP
DRRLDKKNSFFKYTENGYTFRELNVDVGRYQIQIIRNIDSEMNSLRQLTSVLIIGILISVIITYFVAVYLTRKALIPIETAWKNQAKFIQDASHELRTPI
TIVSSKLESMLKSPESTVNDEVETIATAMKETRRLKKMITDLLSLTKEDSIVKVNLEEIDLEKLLEEISEDYIDIAEFQEKRFVFNSKLKNKVIITDKNK
LRQLILIFIDNAFKYTKLGDEISLELKEDIEDEVTLLISDTGIGIKKEEIPLIFDRFFRSENVRNKDLEGSGIGLSIARMISLNLSIDINVTSDVDIGTTFEL
SIPKKLK

>CORE_REP|Org18_Gene2684#(WP_074033631.1| undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase)

MMKVLLSGGGTGGHVYPAIAIANKIRDEHPDAEIIFVGTEKGIESEIVPKYGFELKTVTVQGFKRKIDFDNVKRVFKLFKGLEQSRKIVKKFKPDIV
IGTGGYVSGPVLFNASMGKIPAIIHEQNSFPGVTNKILSKTVTKVLTSFEDSHKRFPEAAEDKLVFTGNPVRKEILLSRKNIARKNLSISDEKRMVL
CYGGSGGSRKINDAMRLVIKNMVNEDIAFIFATGKSYYDEFMGSISDINLKPYQKVVPYLEDMANALAASDLVIGSAGAISLAEITALGKPSIIIPK
AYTAENHQEYNAKSIEKQGAGIAILEKNLTPESLNTAVFKLLGDRELLVDMANASKTIGKPEAIDLIYDEIMKVYNSTQKSTSKKTKKEKVIKEVKE
IKKETTPSIEGQAKVIGIKKR

>CORE_REP|Org38_Gene748#(|WP_009893396.1| M20 family metallo-hydrolase)

MLGKKCMDYLQTLGKISSTTNGLTRLILTQEHKKSIDLISSWMEGLNLDIEIDDIGNVIGTYKSSFPNAPTLVVASHQDSVKCGGIFDGMLGIIVP
LVGLEEAKHNNRSYPFNIKLIAFAEEEGTRFETSLMGSKVFAGTFKEELLKSVDENGITLEEAVTKFGFNTKNLTNLHPRKDVDAYLEFHIEQGPV
LENESLPAGIVSSITGFKSFKISVNGKSGHAGTLPMNMRLDAGCCACECVLAIEKVAKTTADLVATVGKMNFYPSSSNVVPERAEFTLDVRSCS
QEILDNSVEKIFNEISHICENRKLNYTSELAFENVPVPCSNKITKIIEKSFIDLNLNPFYIYSGAGHDAQEMDNITDIGMVFIRCAGGVSHNPNESV
SVDDLDTAVKIFLKILDNLDLK

>CORE_REP|Org43_Gene1184#(WP_003422743.1|D-alanyl-lipoteichoic acid biosynthesis protein DltD)

MRKLIYFITPFIIGVVFLFGLDKFLDSKTDELLREKNLLPIMDDTLSDIKDKGVTANNHFLREKDIMILGSSELSNSTKQHPKYYFNTNRSKNKVFAI
GRAYTQTLQDAAILGSMNPNIDNKKVVLLISMQWFMEKDGVTSHHYQSRFSPIQFYRFLDNPKISKQNKIEYAKKSSKLLWGSDEYKAEALYA
KLYEPKTLLEKAEKVLLEPYFQGRKYCIALKEKGILYKRLIKLDKKRATKRKSPINWSHERKKAIEDAKKRVGKNPLNIDNYYYKQHFKDGIDQYKG
RDKDVNLLTSKEFESYKLMLNVCTDLGIKPVVVLIPSMDKFYNLTGISEKERNQYYDKAQNIAESKGFEVLNLKDKGSDKYYLRDVMHLGTKGW
VDVCERLFKIFKEQ

>CORE_REP|Org18_Gene1426#(WP_011861220.1|RNA polymerase sigma factor RpoD)

MSVENKSNKKELKKVTAKTLIEKGKKQGSLTLAEIMEAFSETELDKDQVENLYETLGNLGIEITETKNYKADIDFSVADDDLSIGHLDEDAEAISH
DDSSAIEIETVDLSLPKGISIDDPVRMYLKEIGKIPLLKPHEEVEFARRMHEGDEIAKQRLVEANLRLVVSIAKRYVGRGMLFLDLIQEGNLGLIKA
VEKFDYTKGYKFSTYATWWIRQAITRAIADQARTIRIPVHMVETINKLIRVSRQLLQELGRDPKPEEIAKEMEMTEDKVREIMKIAQDPVSLETPI
GEEEDSHLGDFIPDDDAPAPAEAAAYSLLKEQIEDVLGSLNDREQKVLKLRFGLEDGRARTLEEVGKEFDVTRERIRQIEAKALRKLRHPSRSKKL
RDYLD

>CORE_REP|Org81_Gene2994#(WP_095903575.1|UDP-N-acetylglucosamine 2-epimeras)

MNDIKVMTVFGTRPEAIKVAPLIKELEKRENIKSIVCVTAQHREMLDQVIETFNINVDYDLDIMEKGQSLNDITCKILNKLPLILNKENPNIILVHG
DTTTTLATSLTAFYNKTLVGHIEAGLRTYDKYSPFPEELNRQLTGIIADMHFAPTNLAKKNLISEGKPNNNIFVTGNTAIDALKMTIKENYNHPIID

EIGNDRMILLTSHRRENLGKPMKNIFRAIKRIVDDFEDVQIVYPIHLNPKIRTIADEIFGKFPKKIHIIEPLDVADFHNFLNKSYMIMTDSGGIQEEAPSLGKPVLVLRDKTERTEGIEAKTLKLVGTNEDRIYNSVSDLLINKDNYVQMSKASNPYGDGNASKYIVDIIIKKFNCKYLN

>CORE_REP|Org96_Gene2580#(|WP_021364696.1|aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme)

MSTNHGANLYSLSSKYGFSKEEFMDFSSNINPFGTSSLAKQYIVNNIDMVSMYPDPDYIDLKTSISNYCKCSIDNIVLGSGATELISSFIHTINPKQALLLSPAYSEYEKELSKINCSIEKYFAKEEDNFHINLENLIKTINAKDYDLVVICNPSNPTGFAFTKVEVREILKNTDSFLMIDETYVEFTDTDTYSCTQLVDDYSNLFVIRGTSKFFSTPGIRLGYGLISNTNVKNEINKNLDLWNINIIASKMGEIMFSDLDFISNTISLMNTERDYLLKELKNIKSLDIYNTKGNFILCKIKTKELTAKSLREQLLPQKIIIRDCCSFEGLDEYFFRVCILKPNENKLLISSLKAIFILKTY

>CORE_REP|Org51_Gene1144#(WP_003428368.1|endolytic transglycosylase MltG)

MNFKENRLKIAVLIIVILIILAGIFVFIQIGPYDKNNKKDVIIDVPSGASVGKISDILYENKLIKNELLFKLLVKVSNKAPSIKSGTYLLNQSYSNNDIISLLVSGKIYQDGIKVTIPEGATSKEIIAMLVSKNLGDKATFENLIKKPQEFYDKFPYLKEDGITSLEGFLYPETYYFNSKKQSEEDILSEMLKVFDSKYTDKFKKKQKELNMTLQEVMEMASIIEKEAVLDKDRPIIASVFYNRLKVGMPLQSDATIQYIFEERKKIVTYDDLKIDSPYNSYKNKGLPPTPISNPGIESIEAALYPDKTDYLYFVAKIDGGNNYSTNYQDHLKYVKEYKEARDKQSKDTKATNKENTKR

>CORE_REP|Org58_Gene2738#(WP_003426511.1|		mannose-1-phosphate guanylyltransferase)

MKVYNVIMAGGGGTRFWPLSRQEVPKQLINLSGEDALINETINRIDSLAKKDDLFIVTNEKQLEALKDIVKDKCLDSNILPEPCARNTAAAIGFAAFNIMKKYGDGVMCVYPADHYIKDEKEFKSILEKAIYIAENNDKLVTIGITPTFPSTGYGYINFNRENTIEDVAYEVVEFVEKPNYEIAKEYVNSKKYVWNSGMFVWKVSKILEDFKRYLPKVYEKLEDISKYLGTKEEMEKIKEIYPTIQSISIDYGIMERSNDVIVVPGDFGWNDVGSWDSLGAIYPTDDEGNIKRGENITIDTKNSIIYSDDKLISTIGISDLIVVSTNDAVMVCRKDKAQDVKKIVEQLKEEDRQEYM

>CORE_REP|Org39_Gene1501#(WP_003433486.1|		histidinol-phosphate transaminase)

MREKESIRELRGYEPNHVNCKVKLDANEGSKRLFKYLIKEISDSDIDLNLYPEDSYSNLKESIIDYINISGVNKKNLLVGNGSSEIIDLIIHTFVDKDEVILSFSPSFSMYSIYSQINGSKFIGVESDENLVINIDSVIEKVKENNPKIVIVCNPNNPTGTILKREEIIKLLDSTNSLVVLDEAYMDFGEESMLSDVFKYDNLIVLRTLSKAFGLAGIRTGYMLSNSSLINSVEKVRPPYNLNSLSDFIATRALRNKDVVKAYIKEVKEEREVLYKEMIGMGIKAYKSQANFILFYSEIENLSQKLIDRGVLIRKFGGKLENYYRVTIGDKEENSMFVGAIRDILKKEK

>CORE_REP|Org82_Gene1721#(WP_003428627.1|		3-deoxy-7-phosphoheptulonate synthase)

MIVVLKMGADKNEVKKLIEAIGREGVEVNPIDGTELTVLGLVGDTSKIDAKRIEANKIVEKVMHVVEPFKKANRKFHPEPSIINVNGMEIGSKKIAMIAGPCSVETEDQIVSIAKDVKKSGAGFLRGGAFKPRTSPYAFQGLKYDGLDLLKKAKEKTGLPIVTEIMSTQDIDIFEENVDVIQVGARNMQNFDLLKELGKTNKTILLKRGLSATIEEWLMSAEYIMAGGNENVVLCERGIRTFETYTRNTLDLSAILAVKKLSHLPVIVDPSHAAGKSWMVDSLSKAAIAVGADGLIIEVHNDPAHALCDGKQSIKPNEYDELISELKTIASAVGREI

>CORE_REP|Org50_Gene1894#(WP_003430307.1|		LacI family DNA-binding transcriptional regulator)

MKKITINDIANLAGVSKSTVSRYLNNKDISDSTKEKIKTIIDEYGYEPNAFAQSLRAKKTYFIGIITPCLDSFVKSKIMMAIDEELKELKYTSLIINTSRKIRSEIDSISKLASLKVDGIILIGTEITKEHKNVIEKLDIPIVVVGQKVDGINSIVNDDYGAGYKMGQYIANKGYKNIVYLGVDESDISVGLNRKNGVLNGLKDKGYDAKVFYTDFDQETSIQRSGEMLESENPDIIICATDNIAIATMKEINKRGKNIPRDISVAGFGGYDILSIISPKLTTIKFENKNAGKVAANTIVNLIQERKEPLLKEIKFELIEGESTINKN

>CORE_REP|Org73_Gene1768# (WP_077709045.1|siderophore ABC transporter substrate-binding protein)

MNKKAAIVAAVAIIIGLVTVFALGGSKKNESKTSEDSNNTIKITHNLGETDVKLNPKKVVVFDYSALDTMDALGVAENLVGLPKASLPASLEKYKDEKYADLGGLKEPDLEGIKSANPDLIIINGRQEDFYEQLSKIAPTISTSKDDKKYLESVKNNIDKIAKIFGVEEKANQEFSKIEKKIEILNKKVTDKNLNALTIMVNEGNLSVFGEESRFSILYNSFGFENKDKNIKESSHGQNITFEYIAKQNPEVMFVIDRGIATGSDVKESSTAKSVLNNDIIKSMDAYKNDNIIYLDSPTWYVNDGGLTSLNKMIDDASKAVN

>CORE_REP|Org44_Gene1774#(WP_003422877.1|		LCP family protein)

MSKLKKFVILLAFLVVIFPISVYGYFYYKLSAIHDSSISSDLLDNNDHKNEDGIINILLMGTDARPNEDSSRSDAMMILTIDNKHNDIKLTSLARDSYVDIPGHGKQKLTHAYAYGQADLLIQTIEENFNIDIQNYACVNFESFMYIIDAIGGVEVTIEKGEIRELNKFIPETYKWNKSDDKGSIQYIRNAGKQTLNGYQALSFARIRHNDTAFARDGRQRQIIQAIIKKTETLPVTKYPGLLDAVLPYVKTNMKPNAILSLGAQVLKMGDLNIKQFEFPIDDEIHSTGGIYGKAGWVLRFDPDTLDILHDFIFNDIEFKQ

>CORE_REP|Org4_Gene2815#(|WP_009891198.1|		ABC transporter substrate-binding protein)

MKKIKSLAIFISIITTLVLVTACSDKNTEDKDKSETRVVQSVKGEVKIPSNPKKIVDISGSSEELLLAGYKPVATANVDSYETDKLPSYIREELKGVKIVGHSMMDTMDMEAILEVNPDLIIMSQRQEKIYDQLKEIAPVVMMKDYANDWRSKLTDVSKLFDKEEEAKSWLQKYDEKATKLGKEVIEKNGE

KTYLPVLASSGQFMVFSDGGIGTLINDDMKLARPKNMPKQDGITLPMVSMEGLTDIDADHIVVIATEADKKDLENSAIWSQIRAVKDGNVTIL
DAAPFFSQSYNPIGKELLLESVKNELTK

>CORE_REP|Org85_Gene1827#(WP_003424113.1| HAMP domain-containing histidine kinase)

MFILAFIICTVVIFIVSTKINQKRYDELSLMLNQILEGKEVTYPDTKDTRASKISHQVKKIKDMIEIEVEQSKLEKEAIKGLISNMSHQLKTPLSNITIY
CELLENINISTLQKKEFLQKMKNETFKIDWLLQSLFKMTKLEDGVIEFEVEELLIKDTLIQSISTIFNKAEAKNIRVNLEPFSDIKLVHNKKWIIEAIVN
VLENAIKYSPSDSTITISVIKMELYTKITIKDEGIGIDSRELNDIFKRFYRSKNVANQNGTGIGLYLTRLILEKENGNIIVESKLGSGCCFSIFLQNCKSL
N

>CORE_REP|Org33_Gene1037#(WP_003438004.1|selenium metabolism-associated LysR family transcriptional regulator

MDFKQLEVFVAVAKHQSFSKAARELFLTQPTVSAHIQNLERELETVLINRSNKVITLTKSGEILYEHAIYILNNCKRAIYDIKEYSGKIEGIIDIACSSI
PETYILPDFMKSFSMSYPDVKFSISHYDSQYAISEILNERISFGLVGSKINNPQIEYLDLLDDELVLITPSDFKIDNKNNCIDIGELAYLNFIMRKEGS
GTRNLILNTLSKNNFPVSKLNVIAHVESNEAIKEMVRLGLGVSFISYISAIDYLNAGKIKCYKIKDVDFTRKFFFIYSKKKTFSPLEDKFLNRLCEYFEII
I

>CORE_REP|Org63_Gene2774#(WP_003426478.1| N-acetylmuramoyl-L-alanine amidase)

MKKKLLDGKITLIICKSVKIYTKKGEEMSKGNNNNNSRNKSKKTSHLNRKKRKLNKKKLAVLICFTVLFLFIAFKATQGVVALVKSMDKSNKTSQ
QQNVNSEQFDFGNEEENKKKKYTVFIDPGHGGNDKGTESKTSNRYEKDLNLQIAKKLANKLSKQKDIQVVVSRTDDTYISLKDRAILANNSSAD
VLVSIHLNAEKNGNTATGIETWYRNKATDGSKELAQAVQSTIVSYVKVRDRGIVENNFEVLRESNMPAILIECGFLTTPSEEQKIINEKYQDQLA
EGIVQGVLSYLDSKGNK

>CORE_REP|Org53_Gene987#(WP_021362441.1| glycyl-radical enzyme activating protein)

MSKKGRVVKVQHFSVNDGDGIRTTIFLEGCKLKCKWCSNPDSWSNIVKLGVMKDKCVSCNRCIDVCPQNISSLFDRAQINNKCDLCGECIKVC
LKDAICIMTEEMSVEEIVEEVEKDFIFFFESNGGITFSGGEPTLQIDFLRELVDIFYDKGINIAIETCGYFDWNKVNDVFEKIDHIFVDIKSMDDNIH
KEYTGVSNKIILDNICRLSKLNKSMVIRVPIIYGVNDSEENIRNTALFVKQNVPGGKMELLPYHKFGIDKYKALGLEDYIYEFDEICNNHMLKLKEI
VELTGVKIIEYK

>CORE_REP|Org89_Gene2365#(WP_003419800.1|D-alanine--D-alanine ligase)

MKIAVIMGGISSEREVSLNSGKEIYNNLDKNKYEVVKVIIDDKKDIFTKIPEDIDFAILALHGKFGEDGCIQSILETMDIPYSGCGPLCSGMCMDK
NITKKMLRDSNLPTAPWVLVKSVDEIDYDEIDNIGYPVFIKPNSGGSSVATFFIHSKDEVGEAVRKGLEVDEFVMIEKYIPGGEYTSFILNGEVFP
TISIKSDSGFFDYEAKYSVEKGAKEEVVYLDEELQKRVNEISETCWKIFNCKAYVRVDMIISEGIPYVLELNTLPGMTQTSLIPRSAAARGIKYSELL
DKLIEYSLN

>CORE_REP|Org18_Gene1469#(WP_011861237.1|sigma-70 family RNA polymerase sigma factor)

MIMDTKKENNYENYICVGSSNVSNAMKMYLKEIEEYKMLSAGEEVELAKEIINSSSVAKEKFINSNYRLVVSIAKRYKRDSIDMLDLIQAGNIGLI
KAVEKYDYKKGYKFSTYATWWIKQSITRYIDDCENTIRIPIHLHQRINFVKKKKQELLNVLLREPTIDEIADACGLEVDKVLELLRRDKNVVSLDTP
LKEDEDSSLVEFIPSDADFKDVVIHEVEQHNLKEKIEELLTGLGEQEQQVLRMRFGIDDDDPKTLEQIGKVFGVTRERIRQIEAKAIRKLRHPSKLK
QLKHFY

>CORE_REP|Org72_Gene2726#(WP_003416240.1| YicC family protein)

MAISMTGFGRGEYKDDNYYFLVECKTINHKYSDINIRLPRKISFLEDKVRNLVKNYVKRGRVDLYIKFDLLGKEDVNLNFDEGLASQYIDILKEIKN
KFDIIDDISVMNVAKFPDIVKIEEKEEDEDLLWSMLNQAVEDALIKLREMRSEEGKKLAEDIAMRCDLLKNHIEEIEKYSSSVVEDYREKLNLRISE
LLDDPSIIDENRLAQEVAIYADKSSITEEIVRFKSHIGQLKNTIFKDDSIGRKIDFLIQEMNRETNTIGSKSSDINITNLVVEVKSELEKIREQIQNIE

>CORE_REP|Org66_Gene2694#(WP_009890955.1| LysR family transcriptional regulator

MNLYHLRYFVTLAHLEHYTKAAENLSITQPSLSHAISLLENELGVALFEKEGRNIVLTKYGKIFLKDVEKSLEILDSSVKSLKITGTGEGQIDLAFLRTL
GTDFIPDIVHKFLKSNPAKSIDFKFHTGVTTDIIQGLKERKYDIAFCSKLEKEKGIEFIPVAKQDLVLIVPYSHPLAAKDTIDLKETIPYPQIVFNQRSG
LRYIIDDMFKKINQQPNIVYEVEEDQVIAGLVAKNFGIAVVPNMNMLSFTKVKVIQIIHPSWERNFYLAFIKDRYLPPAIKNFKNFVIKNAQL

>CORE_REP|Org10_Gene2425#(WP_009893591.1| LysR family transcriptional regulator

MNINYLYYFQTVCKYKNMTKAAESIHISQPSITLAIKELEKELGFELFYRIGNKIELTPEGKIFLDKSKHFIKQFEDFQCDALDLGKKRKASLKIGIPTV
LGTFLLSKILPRFNVIYPDIELKIFEVPTFVGAKMIEESTLDFCIGIIDSDIYDDIDSKTIYKTELYLVTNPKNELAKHPIISNYMLKNVPFVILSEGSYHY
KIITKRLEKAKPNIILHSNQLSTIRYLLENDLASTILYKEIFQNTENLCSIPLERAITANIGVLWRRNQYISHSMKLFIEYMASIHIN

>CORE_REP|Org56_Gene2657#(WP_236875716.1| LysR family transcriptional regulator)

MDLLHLKYFQTVARMEHITKASHKLNIAQPALSKTISSLEKELGVQLFDRKGRYIVLNEYGRLFLKRVDSILDLVESSKKELQDTSLENSGEVKILSP
AAANVLPSLLSNFRKLYPNITFNVSHTLPSSYKKSDFDLYISSSFTKLNSENSITLTCEEILLGVSINHPLSLKDEVYLSEVSDENFIVITKGENYREVIDI
LCESANFKPKIAFESDSPYTIYALIKSLQGVGFICGKSWGLSQDPEIKLLHIKDIEFKRYLNLSWFSENYESKAVLLFKNFLINYFKNI

>CORE_REP|Org59_Gene1409#(WP_118822203.1| pantoate--beta-alanine ligase)

MLVKEIKLLRNIIKDWRKHGYSIGLVTTMGFLHEGHQSLIKKAVKENDKVVVSVFVNPTQFGPNEDFNSYPRDIDKDFKYCMDSGATVVFNPS
PEEMYLKGNCTTINVSGLTDFLCGAKRPVHFGGVCLVVSKFLNIVTPDKAYFGEKDAQQLAVIKRMVKDLNIDTEIIGCPIIRENDGLAKSSRNTY
LSEEERKSALILNKSLSLAKEKLVKGNLNPENIKELITAKINSEHLAKIDYVEIVDSETLQPVKQIEHSILVAIAVFIGKTRLIDNFTFKLNI

>CORE_REP|Org11_Gene1255#(|WP_045136015.1| sporulation transcription factor Spo0A)

MGGFLVEKIKIVLADDNKDFCQVLKEYLSNEDDIDILGIAKDGIEALDLVKKTQPDLLILDVIMPHLDGLGVIEKLNTMDIPKMPKIIVLSAVGQD
KITQSAINLGADYYIVKPFDFVVFINRIRELVSNRVTQVEPKPRPVQETQMTRSDFVKNVGNIENVGNIETEITNIIHEIGVPAHIKGYLYLREAIK
MVIDNVELLGAVTKELYPSIAKKFNTTPSRVERAIRHAIEVAWSRGKVDTINQLFGYTVHNTKGKPTNSEFIAMIADKLRLEHSMVK

>CORE_REP|Org12_Gene2351#(WP_003433818.1| MoxR family ATPase)

MIKKEISNFRGSSDYVVSPELMASVNVAIALEKPLLIKGEPGTGKTMLAQAISNELKKDLVIWNIKSTTKAQEGLYVYDTVQRLYDSQFGGEGVD
DISKYIKYGKLGEAFSSNQQVILLIDEIDKADLEFPNDLLWELDKMEFYINETKETVRAKQRPIVIITSNAEKELPDAFLRRCIFHYIEFPDRDMMEE
IVKVHFDKVEEHLLEQVMTTFYWIRSLKDIQKKPSTSELIDWIQALTLSGMPIEKIEKEVPFAGILLKNNEDIESMQRHL

>CORE_REP|Org83_Gene1695#(WP_003423767.1| ATP-dependent sacrificial sulfur transferase LarE)

MEVNFVKEKEKLDKLKKMLLELGSVVVAYSGGVDSNFLLKVAKDTLGENVVAVTIHAMMHSSREIEEAKQYTQNFGVKHIILNIENFDLKEFKE
NGIDRCYHCKKYIFSKIKEVAKEHNIKYIVDGTNIDDLGDYRPGLKALSELGVISPLKDSGLKKEEIRSLSKILGLKTFNKPSFACLASRIPYGVEITDE
NLRIIEKSEEYLSNLGFSQFRVRMHGDIARIEVGQEELGKFFENNNFNKVDTKLKIFGFKYVTLDMSGYKMGSMNLNV

>CORE_REP|Org69_Gene1655#(|WP_003423750.1| amino acid ABC transporter substrate-binding protein)

MKNILKKVGIFTIMLGLLGGVVGCSKPDNEKDKDASKESKKEVVVGFDNTFVPMGFLDEKGNTVGFDVDLAKETFKRLGMEVKFQPIDWSM
KETELNDSKTVDVLWNGYSITDERKKIVSYTEPYLQNKQIIVTLSDSKINSKADLKDKEVGTQQGSTALDAVEKDKDFMNSLKGGAPVLYDTYD
KALRDLEIGRTSAVVGDEVLIRYYMGQKGEDKYKVLKDDFGLEDYVVATSKENPELCEKINETLKEMKKDGTFDKIYDKWFK

>CORE_REP|Org13_Gene1645#(HBF8615296.1| TPA: methionine-binding protein)

MKFKKLLCLLLCLVLTLAVVGCSKAKDDKKIVVGATLVPGGELLEELKPLIKEKGYTLEVKNFDDYILPNEALNNGEIDANLFQHEPYLKEAVKAKG
YKIMAGKKLYVCPAILYSYKIKSVDEFKKGDTIAISNNPSSCSKNLRYLESIGLLTLPKGDGLVSPKDIIENPKGIQFKELDIAQIPSSLPDVTAAFIDTT
YAVPAGLDAKKNGIYTAPINDEYANLLAFRTEDKDSEKIKVLQDVLTSDKARSLIEEKYKGIVIPTF

>CORE_REP|Org83_Gene1388#(WP_003419958.1|MetQ/NlpA family ABC transporter substrate-binding protein

MKLKKLLSVALVSAIAISAVGCSNKEDKKILVGASSNPHAKILEVAKPLLKEKGYDLEVKIFDDYVLPNTALDEGSLDANFFQHIPFLEETVKEKGY
KLTYTSKVHIEPMGFYSEKVKALDEIKDGAVIAVPNDATNGARALKLLAKNKLIEVKDGELITKKDITKNPKNIQIKEMNAEQLPTVLKDVDGAVI
NSNYALTANLNPTKDAIVIESSDSPYVNIIACRENNKDSDKIKALSEAMNSKEVKKFIQDEYKGSIVPAF

>CORE_REP|Org22_Gene2952#(WP_003426481.1| Cof-type HAD-IIB family hydrolase

MIKLIATDLDGTLLDEKSEINPEFYKVFKKLRERGIMFSAASGRQYQNLIKKFEDIKDDMMFISENGTLVVYKGKEILSNPLNKELVNEIIETTRSIK
GKKIVMSGKKYAYIESKDEAFIQEVSTYYAKFKVVEDLTKVEGDILKIAVFDFKGAEHNNNIYFEKFSDRAQVCISGVEWLDLTAKGANKGSAIKK
VQKMLDIKYEETMVFGDQLNDVEMMKSAYHSYAMENANEHLKQIARFRAKRNTENGVVDKIKEVIKIG

>CORE_REP|Org64_Gene2604#(WP_003416101.1| RNA polymerase sporulation sigma factor SigG

MQVNKVEICGVNTSELPVLKNKQMKELLLQIKNGDEEARQQFVRGNLRLVLSVIKKFNNRGENIDDLFQIGCIGLIKAIDNFDLSQNVRFSTYA
VPMIIGEIRRYLRDNNPIRVSRSLKDIAYKALQVRERLIRTNSKEPTVSEIAKELELEVESVVMALDAIQDPISLFDPVYQDNGDAIFVMDQVQDK
KDTDENWLQEISLKEAIKKLNSREKLVLDLRFYKGRTQIEVADEIGISQAQVSRIEKNALKNMRKYV

>CORE_REP|Org28_Gene2625#(WP_009897796.1| response regulator transcription factor

MRAIIVEDEFPARKELRYFIENKSGIEVVSEFTNGIEVLDFIQENKIDVIFLDINIPHLDGMLLAKTLNQFKSRPKIVFITAYESYAVDAFSLDVFDYIL
KPYSEERIISMLNKLEKSEMSDIELSNVNSNLYKYKKEAVNQEIEEITHKISLWKGDKLVVIDIDDIYYCEANERQTFIYTEKEKFILKEGISEVENLIN
DKTFFRTHRSYIVNLTKVKEIIPWFNNTYILKLKNSDYEVTVSRSKVKEFRLLMHI

>CORE_REP|Org8_Gene2346#(WP_167653455.1| IclR family transcriptional regulator

MGEIINALDRALDIILLLYHEKREMGITEISKAMGVYKSTVHRTLVTLENKGFVIQNAENGKYWLGINLYAIGMVVGEKMSLTEIVKPYTKKLNQ
EFNEVVNVSILEERAQDSPRSIIIHKEYGSNQLLSVNPSVGSSSECYCSAVGKCLMAFNDSIDFEKYRKTPIHKYTEHTIDNWDDMMLFLAKIKE
QGYAIDDEELEHGLTCIGAPILDKNNKAIAAISLSGPTIRMREGDFEYKIKRVIETAKSISELFR

>CORE_REP|Org18_Gene1530#(WP_003436672.1| imidazole glycerol phosphate synthase subunit HisF)

MLTRRIIPCLDVRNGRVVKGKKFKDIVDVDSPEVLGKFYSDCGADELVFYDITASNEERKTSLEFVTKVAENINIPFCVGGGVNKLEDFTDILRKG
ADKVSINSSAVKNPELIREASLKFGAQCVVLSIDAKKNEEGSWSVYVKGGREKTNLDAIEWAVKGVELGAGEIVVNSMDEDGMKNGYDIELLS
KITSLVNVPVIASGGAGKKEDFYEAVNKSNVDGILAASVFHFGEIKINDLKKYLKDMGVEVRL

>CORE_REP|Org52_Gene1151#(WP_003430913.1|16S rRNA (uracil(1498)-N(3))-methyltransferase)

MDRFFVEKNNINLQDKTCTIEGEDVKHISKVLRCKLGEKLEICDKNNNEYICEIMNIDKSIVNLEILEKVDINRESELKVRLYQGLPKAPKMEMILQ
KLTEVGVEEIILVQTKRSVVKVDDKKEDKKFERWERIIYEAAKQSKRGKIPKLRGVLSFKEALEDMKKNNVNICPYENERTVSIKHALKKCDSNID
SVGIFIGPEGGFSEEEIEQIQKNNCNVVSLGPRILRTETASVVASTIALYELSDLGGEK

>CORE_REP|Org86_Gene2784#(WP_003426498.1| glycosyltransferase)

MNEPLVSIITPVYNSEEFLSETIKSIQNQTYKNWQLLLVDDCSKDNSSEIIKSFRKEDARIKYIKLEKNSGAAVSRNVGIKNAEGRFIAFVDSDDLW
DSRKLEIQIEYMLKENVGFSFTSYRYMRQDGSKTNKVARAPKKIDYEGLLRNTIIGCSTVVIDKEIVGEFSMPLVRRGQDTATWLQLLKKEKYAY
GIQEDLVNYRLVGNSISSNKIKALKRTWNTYRNVENLSLPKSLYVFCFYVFNAIKKRV

>CORE_REP|Org29_Gene2697#(WP_003426502.1| glycosyltransferase)

MKKNLVSIITPMYNSEKFIEATIKSVLNQTYQEWEMLIIDDCSTDNSPNIVKSYMQQDSRIKCIKTETNKGVSNARNLALSKATGQFIAFLDSDD
QWNSSKLEKQVNFMLENDYVISFTSYELMDENDKKLNKVIKVPPNVDYKRLLKGNILGCLTVVIDKSKLDFEIRMSGVRHEDYVLWLSILKKGHI
AHGINEVLALYRKSSNSLSGNKIKAAMWTWNIYRNIEKIPLYKAIYYFINYGINGIKKS

>CORE_REP|Org18_Gene1810#(WP_003430276.1| response regulator transcription factor)

MVNIILNWRFYFMKEKILILEDEIGIRSFVSINLKREGYEIVEAGTGREAIEKMTTEKDITIALLDVMLPDISGIEVCKFIRENFDQVGIIMLTAKAQE
DDKIEGFISGADDYIIKPFSIKELLVRVSALLRRVAKDDSSVKSSEIVSPPFILDIDKRKLFKNGKEIELTPTEFSIVKYLISNAKQSLSRDQILDEVWGT
NYLYDFKIVDVNIRRIRNKIEDDPSKPKYIQTIWGYGYCFRKEE

>CORE_REP|Org74_Gene1718#(WP_021364494.1| response regulator transcription factor)

MENRVLIIDDEVEILKLLETVLKKEGLNNIYTAKTKKEGLELFKSINPDLIVLDIMLPDGEGYDICKEIRKTSNSPIIFLSAKTEELDKLLGLAIGGDDYV
TKPFSPKEVAFRVKAHLRRLSYFSDAQNESKNLNNNEEKIISFGPYILNESRAELIKDGKSIGLFAKELKILSLFAHNQNQIISKEKLWDKVWGEDY
VGFDNTIMVHIRKIREKLEDNPSKPEYILTIKGLGYKLAVKED

>CORE_REP|Org45_Gene2586#(WP_009905981.1| response regulator transcription factor)

MNSYNILVVEDEKEIADAIEIYLLNQGYNVFKGYNGLEGLKVIENQEIHLAIIDIMMPKMDGITLTMKLRENHNFPVIMLSAKSEEVDKIMGLNI
GADDYVTKPFKPLELLARVNSQLRRYTKYLNMVENKEQKVDDDDGVFAIGGLELNENTKEVSVDGKHIKATPIEFKILSLLMRNAGRVFSADEI
YERVWNDNAVNTDTVMVHVRNIREKIEVDPKNPKYLKVVWGVGYKIEKIQR

>CORE_REP|Org58_Gene1491# (WP_003436675.1| 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerise)

MIIFPAIDIKDNKCVRLTQGEFDKVNVYYDNPLEVAYKWKNEGAEYIHIVDLNGARSEFGVNTKIIEDIANNIDIPIQVGGGVRDKEKVKSLINAG
VTRVILGSIAIENLNLVEELVNEYKEKIVVSIDAKDGKVAVRGWEVVSNVDSLTLCKQLEKIGVQTIVYTDISKDGMLQGPNFDIYERIAKETSLNV
IASGGVTSIEDVKRLKAMNLYGAIIGKALYDKKIDFKEAQQLCLLGE

>CORE_REP|Org32_Gene1458#(WP_003438625.1| polysaccharide deacetylase family protein)

MTSWKKKTVYKCLIAVALFCGIVLISNFSKVSALMMDTNGNVLIKHGSREKKLIAITFDDGPHPKETSQVLDVLKKYNVKATFFIAGKHAKWYKE
PLVRASKEGHEIGNHTFNHPDISNLSSSQIEEEIVKCEDILKEVTGKKPTLFRPPFGSYREKDLIEIAKKHDYKVVLWTGVDVKDWKNPGANSIAD
KIINKVQNGDIILLHDYATNDTVEALDMFIPKMIEKGFKFVTVSELIK

>CORE_REP|Org31_Gene2712#(WP_003431770.1| NlpC/P60 family protein)

MMNIKNKKHILKKFIAMVLIAGVVTVEAGAITASAAEPTNSPMSATVDQCDFLNVRSGASANDAVVGKINTGDKVEVLELHSNGWIKIKSVD
NVTGWVNGDYLTIQGGNVDAKVQNVLNLAFKQQGKPYKWGATGPNSFDCSGFTSYVYKNGAGVNLPRVSRSQATVGKKVSRAELKPGDL
VFFGSGGSINHVGLYVGDSKFIHSPQTGDVVKVTSMAPGTNYAKRLITATRVLQ

>CORE_REP|Org77_Gene971#(WP_009905963.1| response regulator transcription factor)

MNNILLLEDDKSLNRGISFKLKKEGYNVFSAFSIEEAKSIFAKEEICLIISDIGLPDGSGFDFCEEVRKKSDVYIIMLTALDEEVDIVTGYDLGADDYIT
KPFSLMVLISKVNALMKRVNTVKNYTLLVCDDLFFYYIENKLIVRADNKEEEIILSKTETKLLKYLMENSMQTLTKEQLLESLWDSSGNFVDDNTI
AVNIRRLRQKVEKNPSAPKYIKTVRGVGYIWGERSIKKC

>CORE_REP|Org7_Gene907# (WP_009888771.1| response regulator transcription factor)

MSKLIYIADDEDNIRNLVKTFLKNEGHDVMDFKTGDELLEQFNIKECDLVILDIMMPGSSGFEVCTKLREKSTVPIIMLTARDTDIDYITGITLGSD
DYFTKPFSPMSLVMRVKSIFRRIEFEKKQNYDKYSNSIDMELKFGDVIINKKNKIVTSKNVNIDLTPNEYNLLTYLFENIDRAVSRDELLNKIWGYD
IEVETRAADDTVKRLRKKILDTNILIETVWGFGFRLKEKS

>CORE_REP|Org55_Gene486# (WP_003439080.1| response regulator transcription factor)

MEIKPLVLIVEDDKPICKFIKVSLETQNYRCVETDNGGTAISLIHSLDPDLIILDLGLPDIDGIEVIGRVRACAKTNKIIVVSAREHERDKVEALDGGA
DDYLTKPFSVTELLARVRVALRNKAQQDNINNDAPKSFEVKNLKIDYENHIVSINGEEIHLTPIEYKIIELMSKYSGRVLTHKFIIDKVWGNYYESE
NQSLRVFMASIRRKIEKNPAQPEYILTEVGVGYRMADE

>CORE_REP|Org18_Gene2759# (WP_009890976.1| polysaccharide deacetylase family protein)

MYVVGLIIVVALIFLVHSIIPTYYNKLLNKEVLKNMAGENEIALTFDDGPDKRYTEKLLDVLKENDIQAMFFVVAKNAEKEPEIIKRMLRENHIVGL
HSLEHRNAWLYSYSYVKKDFIESTNIMKNLGVDVNYYRPPWGHTNIFSNSFVKKYNLKMTLWDVMAEDWEKDSTVDIIINKLMSRTKENSIIC
LHDAGENSGGAVGAPERTIEALKIAIPKLKASGLKFVTPERM

>CORE_REP|Org34_Gene2492#(WP_003416112.1| response regulator transcription factor)

MNTKVLVIDDEMHIVELLKFNLEVSNYEVSYSYDGFDGFIKAKEIKPDLILLDWMLPNISGIEVLRKIRSDKDLKNIPVIMLTAKNMENDKVEGLE
IGADDYITKPFSIKELLARISSVLRRYNLTSLGEENNILTTGNLKLDLSKHEVTKGSEKIELTLKEFELLKLLIQNKGKVLSRNYLLDKIWGYEYYGETR
TVDVHIRYLRKKIEDEDKSEKYIETIRGVGYKID

>CORE_REP|Org53_Gene1818# (WP_003435302.1| response regulator transcription factor)

MEKILVVEDDSILNKTLSYNLIEDGYIITSKFTAKSALKSIFECEFDLIILDINLPDKSGFELCNEIKGNYNIPIIFLTANDMECDMIKGYELGALDYITK
PFNINIFKQKVKAFLNHLTIKTKQDYYRDGYLEINFSELSANINGNQIIFTPLEYRTLKLLTENPKSILTRKVLLEKLWDIDANFVDEHTLTSVISRIRS
KIEKDNLKYIKTVYGMGYMWLGERNEF

>CORE_REP|Org51_Gene2784#(Select seq gb|EFH05628.1| bacterial sugar transferase)

MSGYTNDECEIPKIKSYPGADKEIASEIDYSIVKGTVLFDLYQRIMDLVLSIIGLVIGLPLIAIFGILIKIEDKGPITYKQERLGKCGRRFYIYKLRSMRT
DAEKFGAQWAEKDDPRITKVGKFIRKTRIDEIPQLFNILKGDMGLIGPRPERPNFTVQFNEEIPGFINRLAIKPGLTGWAQVNGGYEITPEEKLK
EDIYYIKNRSILLDFKILFKTVKVVLTGDGAR

>CORE_REP|Org93_Gene2412#(EQE32499.1| transcriptional regulatory family protein

MYRILLVEDDIDLSKEIALALEKWGFKVGLIDDFEVVLDEFIDRKPDVVLLDVNLPLYNGFYWCEKIRAISNVPLIFLSSRDSDMDLIMGINNGAD
DYITKPFSIEILVTKINGIIRRVYNYSDSNSILYCEDLMFDVGKGIIKHKYKDKSIELTKNEIKILTLLLKNKNRVVSRESLMMTLWDNDEFVTDNALT
VNMNRLRSKVKELGFDDFIKTKKGIGYIIQC

>CORE_REP|Org28_Gene2247#(WP_021359412.1| N-acetylmannosamine-6-phosphate 2-epimerase

MLDKVKGRLIVSCQALENEPLHSPFIMGRMAKAAMEGGAVGIRAQGVEDIIEIKKVTGLPVIGIIKRNYEDSDIYITPTKKEVDELLTTGCEMIAL
DATNRVRPNNEDLKELIKYIKENGVLVMADISNYDEAIKAQEYGVDCVSTTLSGYTPYTKTLEGPDFVLMERLVKDLEIPVIAEGKVNTPQDLKK
VFELGVHSSVVGSAITRPQLITEKFVKAIEINL

>CORE_REP|Org27_Gene1678# (|WP_004454472.1| response regulator transcription factor [

MKVLIVEDNKILLESVVEELSKHFETEKCEDGEEALYLINQNIYDLVILDLMLPNINGFDILKKMRINNIDTPVLILTAKETLDDKVEAFTIGANDYLT
KPFYMEELVARVYAILRTNGKIKERNGLEFKSLYLDTLEKRVYIEKEEIKLQNKQFNLLEYFVLNKGSILLKEQIYDRIWGIDSDATIEIVEVYVSNLR
KKLSKYGYDKYIKTKRKVGYIFDDK

>CORE_REP|Org68_Gene1930#(|WP_009897090.1| response regulator transcription factor

MNLLIIEDDINLNEGLFYAFENDGFNVFKAYTKQEGLNIFNSKNIDFIILDCNLPDGDGFDVCQIIREKSDIPIIMLTARDSEIDEVKGLEIGLDDYIT
KPFSLSVLKARVKVAIRKKSNNKVIYSNGIKLDQKLLKVYKNKECLELSSVEYKLLSYLIENKGQILLKEQILHHIWDSEENYVDDNIVSVNIRRLRVK
VEDDPSNPKYIKTAYGMGYLWNEVE

>CORE_REP|Org49_Gene1942#(WP_003424455.1| response regulator transcription factor)

MNSSILVIEDDSNIQELISEFLSAEGYQVDTANDGLEGIQKFKQGSYDLVILDIMMPNLDGYGVCKMIRKSSSVPIIFLTALNDEGDQLKGFDLEC
DDYITKPFSFNLLIKRVEAILRRSNKTINDKFIVFEKLKLDLNTYIAEIDGEPIELTLKEFNILKALIEKYPQVITREGLLDSIWGYDYYGDTRIVDAHIK
NIRKKISLPYIKTVKGIGYTLEKDI

>CORE_REP|Org89_Gene2194#(WP_003420108.1| bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP diphosphatase HisIE

MNNKCNDIYTDEVDEFIRSIKFDDKGLVPVVVQEVVSKDVLMLAYMNKEAIKKTLKDKVACYFSRSRQELWVKGETSGNTQKVVKMSYDCD
VDTILLFVEQTGVACHTGNYSCFYRDLFDDTAKMELEVQTNILKELYDLINERKNNPVEGSYTNYLFEKGIDKILKKVGEESSEVIIASKNTDKSELI
YEISDLVYHTLVLMIEKGVEIDEIKKELLKRRK

>CORE_REP|Org81_Gene2772#(WP_021387784.1| response regulator transcription factor

MNKIKVLIVDDEKLIRKGLKIILSSYNDLEIVGDASNGYEALEFCKTNDVDIVLMDIRMKVCDGVLGTRLIKEYNNSITLLILTTFNDDEYIKDAMKF
GASGYLLKDSSDKVLHEGIRSSFFGNIVLDKSVAEKIMTSEKTIKQEYLYDMYNLTEKEISIIRLIANGLNNKEISQELFLSEGTIKNNITNILAKLELR
DRTQLAIFAFKNKIVIE

>CORE_REP|Org75_Gene481#(WP_003436678.1|imidazole glycerol phosphate synthase subunit HisH

MNIIVDYGLGNIDSVSRGFRKAGIETKISSDIDEIKQADSLILPGVGAFRDSISALDKLGLIPIIKEHVSKGKFMIGICLGMQLLYEKSYEYGEYEGLG
LIKGSIDKLDISLKVPHMGWNNLKFNKANDDILKYINEDDYVYFVHSYYANSSNEELIAFSEYEKKIPAIVRKGNVYGIQFHPEKSGEVGLNILRAY
GEMIK

>CORE_REP|Org2_Gene2029# (|WP_236879159.1| serine O-acetyltransferase)

MFKKINKDIEYIMKNDPAARSKIEVFLLYPSVHAMIMHRMAHALYKKKKLFTARLISQISRFMTGIEIHPGAKMGEGILIDHGMGVVIGETAEV
GNRVTIYQGATLGATGKDTGKRHPTVGDDVLIGAGTKILGPLNIGSNSKIGANSVVVKDVPNGATVVGIPAKIVKIRNLEPVKKNKKEVSYEYDE
LDNVYYI

>CORE_REP|Org86_Gene2134#(WP_003430598.1| ribosome recycling factor

MKLEIHKQLEEKMNGTIDALKFEFGTIRAGRANAQMLDKIRVDYYGTPTPINQIGAISVPEPRILMISPWDKSAMHEIEKAIANSDLGLNPSND
GEVIRLSVPALTEERRKELAKKASKAAEEFKVRIRNERRDANEKIKKMEKGGELTEDELKKAQDEVQKMTDKFIKEIDTLLSKKEKDIMEV

>CORE_REP|Org20_Gene2996# (WP_003425127.1| signal peptidase

MGEAVKKEVVEWIKVIVIALVLAFAITRFIVPTIVKGESMYPTLVERDYLIVNRIAYKVGEPKYKDIIVFKTDLTEENGKKKDLVKRVIGVPGDHVKI
QDSKVYVNDKLLDETSYIHNNRTDGDIDIVVPEGKLFAMGDNREKSLDSRYDEVGLVDEHTILGKVLVRLYPFSKIGTID

>CORE_REP|Org79_Gene704# (WP_003422909.1| gamma carbonic anhydrase family protein)

MIRDYLEDKPLIDESVFVAKSADVIGNVKIGKDSSIWYNAVVRGDEGPITIGENTNIQDCSIVHGDTETIIGNNVTVGHRSIVHGCKISDNVLIGM
GSIILDNAEIGEYTLIGAGTLITSNKKFPPGVLIMGSPGKVVRELTEEDKRYIDESYEWYLEAAQNQKY

>CORE_REP|Org59_Gene2574#(WP_003416314.1|pantetheine-phosphate adenylyltransferase)

MENKPRKAIFAGSFDPITNGHLDIICRASKLFDELQIGVLNNPNKKGLFSFDERVKLIEKSTSHLNNIKVVTFDGLLINYCQENGIGALVRGVRSG
ADVDYELQMAHMNRELNPDIETIILPSCTKYSFISSSLIKEVLLFDADIKNLVPKIVLEELKKKTSGGN

>CORE_REP|Org41_Gene1716#(WP_003419467.1| ribosome maturation factor RimP)

MKKNLEATIEEIVTKITDEHGFEMVDVEYVKEAGEYYLRVYIDKEEGISLNECELVSRELSPILDEKDPIKENYFLEVSSPGLDRALKKDRDFVRYQ
GRDVDLKLYKPLNGCKQFEGELVGLTEDNNIKIIVNGKEIEFNRKDVAIVRLAIKF

>CORE_REP|Org89_Gene2491# (WP_003419428.1| transcriptional repressor)

MANTMDLLKDKLKETGFKITPQRRAIVEILLKHDHSHLSSEEIYDLVRVDCPEIGLATVYRTMQLLDEIGLISKLNLDDGCIRYEISLHKEDCHNHH
HLICKNCGKIMEAKEDLLDNIEKEIQSLYKFKILDHDVKFYGLCDECNGVSDSEE

>CORE_REP|Org61_Gene3559#(WP_003425882.1| ribose 5-phosphate isomerase B

MKIGLGCDHGGYNLKKEIISYLEGKGIECVDYGTNNATDSVDYPVYGEIVANSVINKEVDYGILCCGTGIGISLAANKVPGIRCAVVSDVFSAKM
SKAHNDANMLSLGERVLGKGLALEIVEAWINTDFEGDRHARRVNMIKSIEEKHNK

>CORE_REP|Org52_Gene2415# (WP_003419409.1| Rrf2 family transcriptional regulator

MKLSTKGRYGLKAMFELALNQDNGPVSLKFIAKKQKISDQYLEQIFSSLKKSGLVKSVRGAQGGYLLSKNAEDITVGDILVVLEGPVALSDCVLD
EDVCENSNMCVTKIVWEKMKKGIEDVIDSITLKDMINDYNKNKLENDITNIKK

>CORE_REP|Org93_Gene1829# (MBY2231329.1| GatB/YqeY domain-containing protein

MSLKQKLQEDLKSSMKNKDTVRKSVVTLIRASIKQYEVDNRVELDEDGIIDVIAKQLKQRRDALVEFEKAGREDLIKETEGEIEVLKEYLPQQLSE
EELEEIVKSTISEVGATSMKDMGKIMSVIQPKVKGRADGKLINKLVKQNLQ

Sequences found to have appropriate physiochemical parameters provided

>CORE_REP|Org40_Gene2650#(WP_009893719.1|sigma 54-interacting transcriptional regulator)

MKQMELAIVSLKKDAGEIYENQIRQFLGDNLKINLYSFEEGNLKFFKEKLILLSAYLKYDEIVKLSHYDAQIIVPKLTFEKNSIDMISKLEKDKIIYVYN
LSKDMAIETISLIHRLGIDNINILPCYPEIEFTPTDAVILTPGEKILPKFKNCEVVDLKYRIIDLSCIVEIATKTKLKHLIKDDLIKKYVEKIIPTSYSTGELLL
DANKFERQFDLLLSIIDDGIICTNNDGIIQFYNHIARKILSINANEMIDSFVGDCIKDINFQNILTNKTPFFEKLIKINHIDINLEIKHIQLNVFDGFILK
MTKFSQLEKKQAKLRAQLVNSGNISKYTFDDILGSSIQTINTKKIANKMAQSNSSILIIGESGTGKELFAQSIHSASRRKDGPFVAVNCSTFQENLL
QSELFGYDEGAFTGAKKGGKIGLFELANNGTIFLDEIGEMDLNSQSKLLRVIQEKQVRRIGSNNVIDIDVRIIAATNRNLKELVSKNMFRRDLYFR
LNVLPLKIHPLRERAADIFEIFGSLKYDIPCNFILSEEVKEIFKMYRWEGNVRELRNLGEYFCYLGKDIIEICDLPEYILDTIDSNYSRTVCNKVSDNIK
KYQFNIGKDKNIMKYDYNFKRSLDEYIFILDNLKKAYDLKERIGRKSLCKIALEENRFLTEQQIRNMLLELQDFGLVDILVGRGGSIITSKGVEFLKN
INRSNKLNS

>CORE_REP|Org95_Gene1329#(WP_009896470.1| c-di-GMP phosphodiesterase PdcA)

MNKHNFEVILNQLQINIYVTNIHTNEIIFMNKKMKEEYNILDPEGKVCWQVLYPEKNSTCSFCKVLELLKNDKKGVLIKWYEKCNKLNRVFENY
DSLITWQDGTVVHMHQSIDIANSTSLNKPIKINEFHEISNNKEEKGVFNFSRDNFDYNSTLLYDALIRGTDEYIYICNMKTGVFRYSPSQVELFDL
PGEIVKNPLVYWKKIVHPEDWNRFYKSNTEIGKNQMDYHTVEFRAKNRSGEYIWLRCRGQLMRDEFGEPSIFAGIMTQLGKQNKIDSLTQLL
NYHEFMSVFEDKISNPMIEKLCIVLLDIDDFKNVNEMYDRDFGDNIIKTLAQSVQSILPDNAELYKLDGDEMGILVDNVEENEILTLYNQIQNMI
IHLQLWRKYGLNITISAGCVIYPKHGDTVKELYKCASYSLQYAKEHGKNRLVFFSQEILKNKMYSLEMMRDLKASINDDFRGFSLRFQPQVDTES
HKIIGVEVLLRWTNDKCKAISPLEFIPILEENDMINIVGAWVLRMALRTFRKWIDYYPFFKVSVNVSAVQILEDTFIEDIVKIIDDENFPYQNLVLEL
TESHTVQNMSILQFKFKALQDLGIYIAMDDFGTGYSSLEVLKFSPIDIVKIDRVFVKDILKSKFDATFIHFIVAICHDVGIKVCLEGVETQEEYDLVK
QIKPDYIQGYLFGKPQTATEIFDLLKLDN

>CORE_REP|Org49_Gene2710#(WP_003422726.1sigma 54-interacting transcriptional regulator)

MKKHNILFVSTDDKINIDISKQLENIFGEFCSIDNLIYVNRINIELSSYELVVCSDNDIKEYIHNNIDKNIPIVIIHRTINIENINQIISIENDSDVMVIDA
YKESADETAKIIRKLGLIHINLIPYYPGCDKSKCEIGIITGSRNSIPQNIKQIIDIGDKIIDINTVIEIFTKLNISIDKLHIIKEKYDEDTVSGYRYYTTMNKT
MKSFLEIIDEGIASIDKLGKFIYCNKVFSNLIGIDQNEIISNNFMDLFSDKVVKKIFFQEDEVNDEVVNLNNKKLIINKVNVYENNERIKSIISIKDISAI
QVLEDKIQNKFQAKGFVSKYTFESVVGESKIIKEKINIARKIAITDFSVLILGENGTGKEIFAQAIHNESLRKNKPFVAVNLSSLSDTLIESELFGYEEG
SFTGAIKGGKMGIFERAHTGTIFLDEIGDISLDVQQRLLRVLQEKEVMRMGGSKIIPIDVRIIAATNKDLKKKIKEGSFREDLYYRINVLHIEIPRLRE
RKEDISLISKYFLDEINSNKCFTEESMKALKLYEWPGNVRELKNLVYYIDTIVEEDRVDYEHLPEQFRFEKNNTLVNENFDSIILDFKQSNFFEESICI
LTSVETWNNKNILLGRNKLQEILKEKGIVLSVDQIRKRIDKLKSHGLLLSGVKKQGSFITDEGKNFISYIKFKGVI

>CORE_REP|Org82_Gene2537#(MBH7044485.1|sigma 54-interacting transcriptional regulator)

MDKKKLILITYDKLNSDHYKEELTNFFGDEIIIETQNILDGIKENLEGEVVLSLSPLTSNFLIKHFKEDIEIIHGTKALSKLGYEKMMKLPPGTKSLLMT
TNKTSAFEMATYLYKIGINHIDFVPTYPDCDEIYDLDTAITPGQIRFIPKYIKNIVDLGWRKISLDTYMSLLVVLKLKNEKFIEKLYKLSKETLSHDFLN
TSLDNISKLKTILYMTIDEIGDGLIFFNTFNKVTFVNKSLLNMLELDEKLIKSPSLMEYMPKSFLDKITKNLNIDNMIIYIDEIDKKFILSKKPFYLYKNI
EGCLITLKDVNNIEILEQKIRSDSVKRGYVAKYKFNNIIGNSSIIKDCIKRAKKMALTDNPILITGETGTGKEAFTQSIHNHSNRKNKPFVAINCASL
PSELLESELFGYEDGSFTGAKKGGKKGLFELAHTGTIFLDEIGDMPHDLQVKLLRVLQEKEIRKIGGTSIIPIDVRILAATNKDLEKLIIENKFRMDLF
YRISMFTLDLPPLRKRLEDIPLLLESFLKELPYKNIKLDKSLLEALNSYTWMGNIRELRNCVEYMAYMGSNYLTINDLPQNISSKLNNNHMSSNM
SIFNDLNQYDKNICISILKSLHMKPMGRTKLMKFMEYNVTEYEVRNMLEYLTRNGYLISSKGRKGSSITEKGIKIIENNII

>CORE_REP|Org36_Gene176#(WP_009895253.1|sigma 54-interacting transcriptional regulator)

MKKSVALVNDSRKDLIDFLENNLKLVFGDSININRYFINEINDNDIINDDVILVMSVERLDKIINNILDKKKVIVVRRTFREDKIYNLLSLPQGTNVLI
VNDSDETTLETISLFYKIGVTNIRPIPYMNDNNYKNIKIAITPGVPEKVPSFISDIFDLGHRYIDISTFIEIINLLQIDSKEIQSNLVKYSEEIISLDTGIKD
KYKELFLKIEELDTILNLSKDGILFTSKDGEINTYNSKVKDILDINEDIYGKYIEDIFVDSLKVLLSEKEILDKVVVFNKKYINVNKKNIYNRDEKMGTY
YSLQEITYIKKLEQNLTKKLREKGQIAKYTFKDIKTNSPKMFECIDLAKKVSKSDLSILIRGESGTGKELIAQSIHNNSNRKNQPFIAVNCAAVPENL
LESQLFGYDKGTFTGGLKDGKQGLFELANNGTIFLDEIGDMPLELQTKLLRVLQEKQIMPVGSHNVINIDVRIISATNKNLEQMIDNSQFREDLY
YRLNTIPINIPPLRERKEDILIIMEDLINKKLIITPEAKKLIQNYMWKGNIRELQNVTSYLNIMCEDIVLEKDLPPNLRSSDNKNTSLKLKYSKNDILNI
LEILILNKESDVGIGRGLILKALLDKNLQITEGKIKKIFEYLKKEELIICSSGRYGSKITQKGEDFYNKLKYKGL

>CORE_REP|Org14_Gene669# (WP_003416780.1|sigma 54-interacting transcriptional regulator)

MILLQKKIGIIASDIELKERIEELYREDVENGTIIIDILNLDLMENQGRILVEKGAQAIIGRGGGYSLVIDTVNVPVIPMNMKSTDLLRAIEIAKKYSK
KVVLILGDNEVSFDYVGWRNVISTEITEEWFESKYEIRSKVVKYIDQKDEVVIVGGGLACSFARQYGIDSVFATASDESIREAVEYCKKLLDTLGEE
KFNNEVLRNILDGIKDGVIAIDSNGSIILYNESAKNMLKVERKCALNKYILDVFPKMEWMLDCLHEKEAVEDRKIRNINNLIVNTRTTLIKVDNST
YGVLGIIQDITKLQNLERKIRFDLNQKGLYARYTFDDFLFKDKLTKEFIEEAKKIGKSDYTTLLYGESGSGKEIIAHSIHNISKRKDRPFVAINCATIAE
NLLESELFGYEEGAFTGARKGGKRGLFELAHGGTLFLDEINSLSFNIQTKLLRVIEERQIMRIGSDYIIPLDIRIIAATNESLTEKIVMGTFRADLFYRL
SSLEINIPPLRDRREDIIPLFNNFVNEVLKDDGLNGINSIDENFVLTKDEIDKLYNYSWPGNVRELKTIAQKYVVTGKIKLRQDRNFKTKQSLSNSE
VDKFNSETTASAEVQDESINISKINDGKISIDIKEVNKYVEEKIISMLFAQGLSKNEVAQVLGISRTSLWKKYNKNI

>CORE_REP|Org18_Gene1724#(WP_009896876.1|transporter substrate-binding domain-containing protein)

MNKKKIVIIGIIYSFLVVFSLTNMYVNMEYNLNVFEYIKKSLPFTEEEKKWLEKHKNLIYSSDQSSPPLRYKGKEDGQYKGIIVDLINSLSIQIGRDFY
FKPNNWWKESFVNSIDDSIKFFDLIPSKERANKFIFTDPIYTLSANILKDKKSQDINSYMDLKGKTVAIPEGDYSINFLKQKIQDINILLTPDIKTGV
NHLMSGKVDAVVGDEPVLRYYINNYGLSNKYSVLSNPIYTKKAVLAVPKQYEELVSILNKGIFKLQKNGVYKDLKKKWYSTYNEVDDILYERGIV
PSIYLFIGIILISIYVFYSYTYLLKIEIKRKTEQVIENKKTLEATFNSITDIIMLVDENNNIVESNKVLYDFMGEMSYKIADLISMIKGVIENTFSENTNKT
SEIEIHNKILKINTFPVEYKKNNTEYIVVLIKDITNDKIVEAKLLRENKMISIGQLASGVAHEIRNPLGIIRNNCYLLKDNVTMEEVNDCVKSIESNVD
RASNIITNLLNFARISDDNLEHINIRNFIENIVKLQYKMLQLKNVEIKIDCEHNLICYINGESLKHVFINLISNSIDAIHQDGKIIIYCYEKNHCLFIDFK
DNGEGIKEDALKDIFNPFYTTKPIGEGTGLGLYITYNEIKKNNGDISVESKLGVGTCFHIKIPLNKEVTI

>CORE_REP|Org51_Gene2854#(WP_021388183.1|2-aminoethylphosphonate--pyruvate transaminase)

MKKIYGEKIKAVVFDWAGTTVDYGCFAPLNVFIEIFKRRGIDVTMEEARKPMGKLKIDHIREMCEMDRIKNLWSDKFGKVPTEDDVNELYAEF
EPMLFETLEDYTTPIPHVVETIEKLRKNGLKIGSTTGYTREMMNIVEPNAAKKGYSPDFLVTPSEVSQGRPYPWMCYKNAEALGVSPMSSMVK
VGDTISDVKEGVNAGMWSVAVIKGSSELGLTQEEVENMDKEELKAKMSIVSKKFKEAGAHFVIETMAELEDILIKIENETIKSDFVPENDYILLTP
GPLSTTKSVRASMLKDWCTWDVEYNNLVQDVRRRLVSLATQNTDKYTSVLMQGSGTFSVEAIIGSTISKDGKLLVIANGAYGKRMKDICNYLD
IEFVDCTFKDIEAVDLNVVENLLKENKDITHISMVHCETTTGRLNPIQEVGKLAKKYNKIYIVDAMSSFGGIEIDVEDFNIDFLVSSSNKCIQGVPG
FGFIIANKEELSKCKGIAKSLSLDVYAQWETMEKNNGKWRFTSPTHVVRAFYQALLELEEEGSVEKRYARYKENQFTIASRLKSLGFDTLVNDNA
QSPVITTFLYPKNAKFEFMEFYTYLKDNGFVIYPGKLTDIDTFRIGSIGEVYPTDMERLADVIEKFINR

>CORE_REP|Org62_Gene1531#(WP_003420306.1|GGDEF domain-containing phosphodiesterase)

MKRFLRRIILVLFILLIFISFISIKLIHNVGDYGKLINYVGIVRGASQRLTKLEMNHKPNDELIEYIDEILQELITGHGNYGLVLTDCNKYNEDLLLLEKK
WEDLNSEIKKVRMKEPNNQLLSISEEFFSLANDTVFEIENFSKEKSNYLMTLIIIISIIGILACIILILQYSKKMIKLEKLNVDLKNIAYKDELTGVNTIEK
FKLDANQNICMHKDKKFAVFYIDFENFKYINDIFGYDYGDMILKRYANLMMNDIGKYEIFAREIADRFVALRCYIDKEDLVVRQRIVDSELINTT
NEIKNKHSITVVSGICCIEDVNEKLSIDGLINRANFAQKTVKNKPGTNYAFYNDSIRKKMIEENTIKSRIHEAIEKREFIVYLQPKVNLHNQKINCAE
ALVRWLTPDKGIISPAIFIPVLEKNFFIALVDKYVFEEVCKWIRKRLDENKPFVQISVNVSRIQFYNTKFVETYSNIQNKYRIPKNTIEIEFTESVAFE
NQNHLLEIIHDLHENGFTCSLDDFGKGYSSLSVLKDLPFDALKLDSMFFKASLDKDKEKIVIKNIVHMLKELNITTVAEGIEYEEQVEFLRDIGCDL
VQGFVFYKPMPILEFEEILDKEFVYNS

>CORE_REP|Org88_Gene3147#(|EFH15286.1| Sigma-54 interaction domain protein)

MLSKLKEFQQEMIKYTETVASVLDVDIEIVDDRLIRISGTGLYKSKINESVVTEGFIYDNVIQTGQELVVLDICDNQLCIECSHYMKCLNKVIIAVPI
KYNNRTIGVIGAISTDKTKKVEISAKIDNYLKFVNHICDLISMKIEEHEVSKNSSRKMDMMIEIIENVEKGVIILDINSKISYINNIALKKLDIDKNIIEN
IVNIVSVESSSNGHELLEIDIDNKIYNINAKIIPVYPYINQYDKIIIFDKTYINHKGHVKVNSGWGNSDIESIIGNSEAMLKVKERTKKLAKSNSTVLIT
GESGTGKELIARAIHAEGSRWNKPFIAINCAAIPENLLESELFGYIKGAFSGASSGGKVGKFELANEGVIFLDEIGDLSMPLQAKLLRVLQERKFAR
IGSNKLIDLDIRVIAATNKNLLKLVNEGKFRDDLYYRLNVIPINLPPLRERKDDIEAIMMKFASKYSLELGIQLNKIEENVMNMLINYNWPGNIREL
ENAVEYMMNLVGDDGIIYKDMLPLDILNYYNINGNICKNKDINIIFEDDIVGGIVENQERILSIKELELTYINKLLNKYGRDTKTKKKIAKDLGIGLA
TLYRKLEEEQS

>CORE_REP|Org45_Gene290#(WP_003419837.1|sensor domain-containing diguanylate cyclise)

MSILLKKAPKLAKHIITSFYINRDIDEVLKYLCENVTWIGPGEQEFLTSFNEIKNYFYAGQYEIPSCDINNDIFEIVSEYENRCMVLGKYTVRTKENA
QMILEVNQRCTFEIIEDREKLLVKHMHISNPYGEMQLDEYFPTKIGTQSYDYLQRLLKEKTEVIEMITNNINGGLKGSNDDSTYSFFYVNEGLPKI
LGYTYNEFMEMSGGSAVGAVYPPDLPKALEDCEQCFAKGPTYSSEYRIRKKDGTLMWVLDSGMKSLNSDGIVKINSIITDITQLKNIESELKLER
ERYRIALQNITDIMFEYDMENDNFIKYQRVEIDKKIELENFETKNYSKLLESGKIIHLDDIGKLLEVLRGNLHETIEIREINSLTKNEWRWIRVQCSVI
YDSDHNPIKTIGVLKDITEDKSKLESLINQAQRDPLTQLYNQRVSQNLIQEYLCSSDSKNNDALLIIDIDDFKTVNDTFGHLEGNEVLVAVSKILLH
NTYDKDIVARIGGDEFTIFIKSLTKDLIIKITNDILNDASKIKVKDNHKITLSIGIAFTDDSTKLYKDLFSKADKALYLSKADGKNCYSVYE

>CORE_REP|Org72_Gene2695#(WP_065986483.1| DAK2 domain-containing protein)

MIQYIDGKRLREMFISGANNLQNNKELVDKLNVFPVPDGDTGTNMSLTISYALKELAKVENDNISDIGKALSKGSLMGARGNSGVILSQIIRGIA
KSIEGKSKLSTEDLAKAFKNGSDTAYKAVIKPIEGTILTVVRESGEFAIKTAKKEKDVVKFLSMLVKESNSSLERTPDLLKNLKEAGVVDSGGKGLV
LIYEGMLASIKGNNIEIKNADLDTNISTSMDFAKSTTSTDNIKYCYCTEFILESSKVEDTKIRDIMMAYGDSLAVVGDDGVIKVHVHTNDPGNVL
QEALKYGQLLTIKIENMKLQHENTLLDVEEKKENDSEPLEEEKEFGFIATSMGEGLANIFKDFGVDHIIEGGQTMNPSTEDFMNAIKDINAKNIFI
FPNNSNIIMAANQAKELSDKNIIVIPTKNTPQGFAALVTFNGELSEDENKEAMMNALNSVKSGQVTFAVRDTVMNEIDVKEGNIIGIAEGNLL
SAGDYVDEVTSNLIEKLVDEDTAIITLFFGEDVTESQANELRTSLEEKFEDVDVELYYGGQPLYYYLISVE

>CORE_REP|Org18_Gene1870#(WP_011861348.1|bifunctional diguanylate cyclase/ phosphodiesterase)

MLKRVRCSYLKKNRLIAKNISIAFIVLFFFSVFTFFYVGNINRVLEYETNDIITVTIAGWIILSFLFLGIIIYILYSKANSQKTIEKVAYTDFVTGYSNWRK
FELDVTNLLKKTSQNNKYAMVIFDIDKFKAINDIYGHKKGNLILKDIADTLNELTDINETFARVSADNFNILLTYNKKEDIINIIKKIMANNELVNLS
FGIYEIKDKDLSVSVYSDRASLAKSSIKNNSDVNFAFFNDKLREKLLFEDKIEKEMEYALESGQFVMYLQPKYNIKLDKFCGSEALVRWQYTEKEV
IYPGDFIPIFEKNGFIRKIDMYILEQACKEIRSLFDKGISPLPISVNFSRVDFFKKDFIENIVNICDRYKIPYSLIEIEITESSMFGDTDTLFNVSRNLQDI

GFIVAMDDFGSGYSSVNMLKNIPLNVIKLDRGFFVDDKDVDKSQIVIKSIVSLIKQLGIRVVAEGIETRSQIEMLKKANCDIVQGYYFSKPLPIKEF
EKLVYKI

>CORE_REP|Org46_Gene2479#(WP_003419821.1 sigma 54-interacting transcriptional regulator)

MNLNLELDLEFYKKILEASHDEICVSDDKGIIIYCNKAFEENYGLKKEDILGKNVSFLEDSGYSTKSPIPVVLKTKSKFSLEQDTQTGKKLIITATPIFD
ENGNLEFTVENCRDITELNNIKNKLEDTKKQVKKYKSEVETLYRTALRIEDTVIMDGIVMRPIINTVNHVSKTDVSVLLLGESGTGKSSLARYIHH
NSNRANGPFITINCATISPQLLESELFGYTSGAFTGASTKGKVGLVELANGGTLFLDEIGDIPQNLQAKFLQLIQDRTFTPVGSLKNKNVDIRIISAT
NADLVSKVKEKKFREDLYYRLNVIEIKLPPLRERRDNLVEIIKYYFNRYSSDFNLNKTISKEAMETIANYRFPGNIRELQNIIQKILLTCTDNHITIHNL
PNILTKNINITNNGNKTHISQINKVITPDSKSINYKNKNFDTLIKEYEKNIILDAYEKFGSSYKVAKHLEISQSKANRLIRKYTNT

>CORE_REP|Org94_Gene1661#(WP_231305334.1| HAMP domain-containing histidine kinase)

MKWKITRNFIFTIVFVAISVVIINIISILYVISTNSFFKVVDSGNNPEEFARSFEKDLYEKDGEFKLSKIGAEKLEKSNSWIQVLNDLGEEVYGVNVPK
YTPKKYTPFQMVNNYKYIETKYVNFVLEKYLNKKHLNIIVGIPSRDISRIILTYSQNNIKKTLNKVIIITLVIDSVVALGVGYLFSRKLTKPISSVLWSIE
TMANGNYSLYLKDRGIYEEVFKNINMLADTLRVNEVERKENEELREEWLANITHDIKTPLASIQGYAEIINDKDYEFEEDEIQEYTEIIYNKSKYIK
DLVDDLNLSTRLKNDTIVLDKKKINLVSLVRNIIIDILNDNRYKNRNIEFESNEDLIEVYVDSILFRRAITNLIFNSIVHNSEGTLISVEIVKKDNIEIIIKD
NGIGISKSDLKHIFKKYYRGTNTGEMHKGSGLGMAISKEIIEIHKGKIYVSSEIGIGTKIIIEIKQN

>CORE_REP|Org37_Gene2294#(WP_004454646.1| aldehyde dehydrogenase family protein)

MEKAVENFEDLSKEYINGYIERARKAQREFECYTQEQVDKIVKIVGKVVYYNAEYLAKLAVEETGMGVYEDKVAKNKSKAKVIYNNLKDKKSVG
IIDIDRETGITKVAKPVGVVAAITPCTNPIVTPMSNAMFALKGRNAIIITPHHKAIGCSTKTVEMINEELEKIGAPENLIQILDQQSRENTRNLISSA
DVVIATGGMGMVKAAYSSGKPALGVGAGNVQCIIDRDVDIKEAVPKIIAGRIFDNGIICSGEQSVIVAEEMFDKIMDEFKNNKGFIVRDKVQK
EAFRNAMFVNKSMNKDAVGQSVHTIAKIAGVEIPEDTKIIVIEADGPGEEDIIAKEKMCPVISAYKYKSFEEGVAIAKANLNVEGKGHSVSIHSN
TVKNIEYAGENIEVSRFVINQCCATSAGGSFFNGLAPTNTLGCGSWGNNSISENLDYKHLINISRIAYYMPENEVPTDEELWG

>CORE_REP|Org85_Gene2194#(WP_003423198.1|PLP-dependent aminotransferase family protein)

MPINSFENYPMNWKPKRPSKGQILYKALAEQLEQDINNGFLLPGTKLPPQRELADFLDVNVSTISRAFKICEKKGLISGVTGSGTFVSYDTRSNL
FLMSSNNKITFIEMGTMNPDFTLEEMNTLFKHIVKEIDFKTIFQYGQRDGAKWQKEAIAKLIYKAGLETTADSLLPASGGQNAIVAILAGLFQH
GDRIGVDPLTYPGIKTAAKMLGVQLIPIKQEHNEISEEGLLYACKNENIKGLYIIPDYQNPTTHIMSQNGRKMIANIASKYNLIVIEDAIHSLLNET
HLNPVASYLPNQTIYITSLSKIIAPSLRLAYISTPKQYRESLSDALYNINLSQSYFLTEIAYRMITSGEADKLINARRKSARRRNKIINQYLSGYNLLGN
EECIFRWLILPEGIMAEKFEIQALKEGVQVYASERFAVGKEKPISAIRIAVCATESIEELKAGLSILKRLLEEKK

>CORE_REP|Org18_Gene1417#(|ARC14034.1| aminodeoxychorismate synthase component)

MCNMIREINTKLNSFEIFTIFRNEHDSFILDSAMDKEKLGRYSFISSQPFKVLKYKDTDENPLEVLKEELHKYRVVNDTNLPFVGGAVGYLSYDLG
NYIENLPRTAVDDIEMPDMYFGFYNHVIVIDHLVQKTYIATPNIDIELEEKIIDDIEQRILKEEKKGIDSICYEEKEVTSIRLKSNFTKEEFKNAVQSV
REYIRQGDIYQANLTQRFSGETELTSFELYRDLRRFSPAPFGAFLNFEDAHILSNSPERFIRCVNKRIETRPIKGTRPRGKDKEEDLRLQQELRNSE
KDRAELLMIVDLERNDIGRISKTGSVKVPELFVIEPYANVNHLVSTVVGELKDDKDATDVIKATFPGGSITGAPKIRAMEIIDELEPTQRNVYTGSI
GYIGFNGDMDFNIAIRTIIKNDKKVYFQVGGGMTWDSDPDEEYQETLDKAKSIMKALRGYYEE

>CORE_REP|Org83_Gene1650#(WP_003423653.1|sigma-54 dependent transcriptional regulator)

MKILIVDDELEYGVVMKKILQKKGYLVDVTLSGEEAINIIKKDKNYDLVLSDVMMKNMDGVQLLDRIKAINKDIEVILVTGYGSIENAVDAMKK
GALSYFIKSNPIENLLEEVEKVKTSKTSVSLQKNNLEFTLESKNRDFNDVIKIAKKAACKDVNILILGESGVGKDILARYIHSISPRKNEIFVPVNCCSF
SENLLESELFGHEKGSFTGAVDSRKGRFELSNKGTLFLDEIGDIPLNVQVKLLRTLEDKSIERIGSNKSIKVDFRLICAMNKEPKVEISNGNIREDFF
YRISTITITIPPLRKRREDLATLIEFFLNKYQIEHDKKIHSIDKEVKDFLLNYNYPGNIRELKNIINRLVVLSEEGNLSKDNLNLISNNVYIDDKISIKPLR
EIRKEFECEYIEKVLSLCGNNISNTAKKLEISRRQLTNKIAEYNIK

>CORE_REP|Org50_Gene2566#(HBH1461641.1|TPA: D-alanyl-D-alanine carboxypeptidase)

MKRNLSLLLICLLIFTSFLGRSNISFADNEPAIVAKHAVLMDYETGKILYNKDGNSKLYPASTTKVWTACLVLKEVKDLNQVIEIKDLPQIDGSSMY
LKEGESFTVKQLLDALLVHSANDAAFVLARYVGGGNVQKFIDLMNSEAKKIGATNTHFNNPHGLPDPNHYTTAHDMALIAREAMNNDTFRQ
IVKTKSLKFEATKAYPYERYFVNTNKFLTSHDKITYKGQPINIKYDIVDGIKTGYTDAAGKCLLSSAVKDGRRVIVAVFNSTNADLYLDSRILIDYGF
DNFKCATIVDKEKYTDTKKVLFTKQHELIYEPKNSYKIFLEKNESKGNYDTKTELNKIDLPIKKGAKVGTLNVYNNGKLENSIDLIAKNNLDSSLPFL
TENNVLMTFVKIIAGILILLVLFIITSNIKKKKKIKKARGKRNMKK

>CORE_REP|Org85_Gene2013#(WP_003424453.1| HAMP domain-containing histidine kinase)

MRRIFDKWEKLSIKYKLFSITTSLLIALALIIYLILYFLLPSYYHEYKIESLQESLKSLVDSSIHFDTYTLEERLYYMAKDQNLAILLKDNQGKIVYGKNEV
VILRYSKYMINSLEDEYRTSIPIYTKDAKDGPYTLELVMPLQPIDEANEVIRKLMPYIISIAILIAIIGAYIYSIVITKPLINIIESEREQEYRRKDFVATISH
ELKTPITIISGQIEGMIYSVGKYKDRDTYLKKSYECTQELKDLVNEMIEVSKSEILEKDLKLVSINISELLNRLVKRQVFLIEEKHMKTILKIEENLEVKA

DQERITKAINNIINNAIKYSPEESEIIIRLYDKNKRISKKNSNQRVVLEIENTGVTIEKRYLEEIFNPFYRIEKSRSRKTGGSGLGLYIVSQIFKSHGFDYSIKNKENSVIFTVEFKN

>CORE_REP|Org14_Gene3214#(WP_003419909.1|	HAMP domain-containing histidine kinase)

MKIVFLYNPEVKKFLSKYVTLIFVIIIISIGFSVINVSLTKDMIVRNNQAIIGTLSSKYPNLESEIVDIITQGKSMENTDYGKKILSKYNYDKSIRINSEPIISKLVLDTIKINIILVCIIFILIFVLVVRYFKSIYNDLSDMTKYVYYSSEGKSFDMKNKNQEGQIGLLKTELLKMTTILNEKVELLKTEKIFLNNTISDISHQLKTPMTSLIMLNDLLYNDIPYEVKIDFLNKIKNQLNRMDWLIKSMLKLSKVEAKVINFKKDKVKFSELIHRAMQSMKIPMEIKNQKLTIEGSDNISYIGDIDWSVEALVNIIKNCVEHTPEFGNITITYKENPLFSELIIKDDGEGIHKKDIPHVFKRFYRGRSSSKEDSVGIGLAMSKSIIESQNGDIYVNSEKGKGTEFHIIFHKMYDSD

>CORE_REP|Org10_Gene510#(WP_165476817.1|D-alanyl-D-alanine carboxypeptidase)

MEDEILKGKIKQLTILALIFIFITPVFAFADTPPVPNSSRAALLIDQETKRILFEKNIDEKMPLASLSKMMTFLLAIEAVDKNQVKETDMVKIDKSTASVGGSTCKLKDGDEISLGELMQGLMLVSGNDAAIAIAKHIGKTEKNFVNMMNKKAEEIGMIDTYYFNPNGLPIYTDPEHKEPPIENMSTAHDIVTLGKYMYDHYENQVTRITTMQVYNDTKKDFTHYNTNPLLVSVPGVDGIKTGYTDNAGYCLAFSMMVPKDAKNERNHRLIGVVLGDGNKKNRISSSATLLKYGKDNFHSKKIAHKGDIIETPCVDGIDDFKITVKVDKDLYGVVSDNENINPKVVFKNMNYPIHKGDIVGVAKYYNDSGKFVGSVDVKSESNIGCIPLKDKIKIKVAKINKKLEIKNSVCFKA

>CORE_REP|Org52_Gene1914#(WP_009902721.1|	HAMP domain-containing histidine kinase)

MINKNVFTSTKNHLIKMYIIVVGSFLIIFSIFIYSYFRGLTYSGIDSEINDELEYIVSQFKRTSFLNPIRLKDPKDMVYVYEDGRISYYTQNEYFDELLPDRRLDKKNSFFKYTENGYTFRELNVDVGRYQIQIIRNIDSEMNSLRQLTSVLIIGILISVIITYFVAVYLTRKALIPIETAWKNQAKFIQDASHELRTPITIVSSKLESMLKSPESTVNDEVETIATAMKETRRLKKMITDLLSLTKEDSIVKVNLEEIDLEKLLEEISEDYIDIAEFQEKRFVFNSKLKNKVIITDKNKLRQLILIFIDNAFKYTKLGDEISLELKEDIEDEVTLLISDTGIGIKKEEIPLIFDRFFRSENVRNKDLEGSGIGLSIARMISLNLSIDINVTSDVDIGTTFELSIPKKLK

>CORE_REP|Org18_Gene2684#(WP_074033631.1|	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase)

MMKVLLSGGGTGGHVYPAIAIANKIRDEHPDAEIIFVGTEKGIESEIVPKYGFELKTVTVQGFKRKIDFDNVKRVFKLFKGLEQSRKIVKKFKPDIVIGTGGYVSGPVLFNASMGKIPAIIHEQNSFPGVTNKILSKTVTKVLTSFEDSHKRFPEAAEDKLVFTGNPVRKEILLSRKNIARKNLSISDEKRMVLCYGGSGGSRKINDAMRLVIKNMVNEDIAFIFATGKSYYDEFMGSISDINLKPYQKVVPYLEDMANALAASDLVIGSAGAISLAEITALGKPSIIIPKAYTAENHQEYNAKSIEKQGAGIAILEKNLTPESLNTAVFKLLGDRELLVDMANASKTIGKPEAIDLIYDEIMKVYNSTQKSTSKKTKKEKVIKEVKEIKKETTPSIEGQAKVIGIKKR

>CORE_REP|Org38_Gene748#(|WP_009893396.1|	M20 family metallo-hydrolase)

MLGKKCMDYLQTLGKISSTTNGLTRLILTQEHKKSIDLISSWMEGLNLDIEIDDIGNVIGTYKSSFPNAPTLVVASHQDSVKCGGIFDGMLGIIVPLVGLEEAKHNNRSYPFNIKLIAFAEEEGTRFETSLMGSKVFAGTFKEELLKSVDENGITLEEAVTKFGFNTKNLTNLHPRKDVDAYLEFHIEQGPVLENESLPAGIVSSITGFKSFKISVNGKSGHAGTLPMNMRLDAGCCACECVLAIEKVAKTTADLVATVGKMNFYPSSSNVVPERAEFTLDVRSCSQEILDNSVEKIFNEISHICENRKLNYTSELAFENVPVPCSNKITKIIEKSFIDLNLNPFYIYSGAGHDAQEMDNITDIGMVFIRCAGGVSHNPNESVSVDDLDTAVKIFLKILDNLDLK

>CORE_REP|Org43_Gene1184#(WP_003422743.1|D-alanyl-lipoteichoic acid biosynthesis protein DltD)

MRKLIYFITPFIIGVVFLFGLDKFLDSKTDELLREKNLLPIMDDTLSDIKDKGVTANNHFLREKDIMILGSSELSNSTKQHPKYYFNTNRSKNKVFAIGRAYTQTLQDAAILGSMNPNIDNKKVVLLISMQWFMEKDGVTSHHYQSRFSPIQFYRFLDNPKISKQNKIEYAKKSSKLLWGSDEYKAEALYAKLYEPKTLLEKAEKVLLEPYFQGRKYCIALKEKGILYKRLIKLDKKRATKRKSPINWSHERKKAIEDAKKRVGKNPLNIDNYYYKQHFKDGIDQYKGRDKDVNLLTSKEFESYKLMLNVCTDLGIKPVVVLIPSMDKFYNLTGISEKERNQYYDKAQNIAESKGFEVLNLKDKGSDKYYLRDVMHLGTKGWVDVCERLFKIFKEQ

>CORE_REP|Org18_Gene1426#(WP_011861220.1|RNA polymerase sigma factor RpoD)

MSVENKSNKKELKKVTAKTLIEKGKKQGSLTLAEIMEAFSETELDKDQVENLYETLGNLGIEITETKNYKADIDFSVADDDLSIGHLDEDAEAISHDDSSAIEIETVDLSLPKGISIDDPVRMYLKEIGKIPLLKPHEEVEFARRMHEGDEIAKQRLVEANLRLVVSIAKRYVGRGMLFLDLIQEGNLGLIKAVEKFDYTKGYKFSTYATWWIRQAITRAIADQARTIRIPVHMVETINKLIRVSRQLLQELGRDPKPEEIAKEMEMTEDKVREIMKIAQDPVSLETPIGEEEDSHLGDFIPDDDAPAPAEAAAYSLLKEQIEDVLGSLNDREQKVLKLRFGLEDGRARTLEEVGKEFDVTRERIRQIEAKALRKLRHPSRSKKLRDYLD

>CORE_REP|Org81_Gene2994#(WP_095903575.1|UDP-N-acetylglucosamine 2-epimeras)

MNDIKVMTVFGTRPEAIKVAPLIKELEKRENIKSIVCVTAQHREMLDQVIETFNINVDYDLDIMEKGQSLNDITCKILNKLPLILNKENPNIILVHGDTTTTLATSLTAFYNKTLVGHIEAGLRTYDKYSPFPEELNRQLTGIIADMHFAPTNLAKKNLISEGKPNNNIFVTGNTAIDALKMTIKENYNHPIID

EIGNDRMILLTSHRRENLGKPMKNIFRAIKRIVDDFEDVQIVYPIHLNPKIRTIADEIFGKFPKKIHIIEPLDVADFHNFLNKSYMIMTDSGGIQEEA
PSLGKPVLVLRDKTERTEGIEAKTLKLVGTNEDRIYNSVSDLLINKDNYVQMSKASNPYGDGNASKYIVDIIIKKFNCKYLN

>CORE_REP|Org96_Gene2580#(|WP_021364696.1|aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme)

MSTNHGANLYSLSSKYGFSKEEFMDFSSNINPFGTSSLAKQYIVNNIDMVSMYPDPDYIDLKTSISNYCKCSIDNIVLGSGATELISSFIHTINPKQ
ALLLSPAYSEYEKELSKINCSIEKYFAKEEDNFHINLENLIKTINAKDYDLVVICNPSNPTGFAFTKVEVREILKNTDSFLMIDETYVEFTDTDTYSCT
QLVDDYSNLFVIRGTSKFFSTPGIRLGYGLISNTNVKNEINKNLDLWNINIIASKMGEIMFSDLDFISNTISLMNTERDYLLKELKNIKSLDIYNTKG
NFILCKIKTKELTAKSLREQLLPQKIIIRDCCSFEGLDEYFFRVCILKPNENKLLISSLKAIFILKTY

>CORE_REP|Org51_Gene1144#(WP_003428368.1|endolytic transglycosylase MltG)

MNFKENRLKIAVLIIVILIILAGIFVFIQIGPYDKNNKKDVIIDVPSGASVGKISDILYENKLIKNELLFKLLVKVSNKAPSIKSGTYLLNQSYSNNDIISLL
VSGKIYQDGIKVTIPEGATSKEIIAMLVSKNLGDKATFENLIKKPQEFYDKFPYLKEDGITSLEGFLYPETYYFNSKKQSEEDILSEMLKVFDSKYTDK
FKKKQKELNMTLQEVMEMASIIEKEAVLDKDRPIIASVFYNRLKVGMPLQSDATIQYIFEERKKIVTYDDLKIDSPYNSYKNKGLPPTPISNPGIES
IEAALYPDKTDYLYFVAKIDGGNNYSTNYQDHLKYVKEYKEARDKQSKDTKATNKENTKR

>CORE_REP|Org58_Gene2738#(WP_003426511.1| mannose-1-phosphate guanylyltransferase)

MKVYNVIMAGGGGTRFWPLSRQEVPKQLINLSGEDALINETINRIDSLAKKDDLFIVTNEKQLEALKDIVKDKCLDSNILPEPCARNTAAAIGFA
AFNIMKKYGDGVMCVYPADHYIKDEKEFKSILEKAIYIAENNDKLVTIGITPTFPSTGYGYINFNRENTIEDVAYEVVEFVEKPNYEIAKEYVNSKK
YVWNSGMFVWKVSKILEDFKRYLPKVYEKLEDISKYLGTKEEMEKIKEIYPTIQSISIDYGIMERSNDVIVVPGDFGWNDVGSWDSLGAIYPTDD
EGNIKRGENITIDTKNSIIYSDDKLISTIGISDLIVVSTNDAVMVCRKDKAQDVKKIVEQLKEEDRQEYM

>CORE_REP|Org39_Gene1501#(WP_003433486.1| histidinol-phosphate transaminase)

MREKESIRELRGYEPNHVNCKVKLDANEGSKRLFKYLIKEISDSDIDLNLYPEDSYSNLKESIIDYINISGVNKKNLLVGNGSSEIIDLIIHTFVDKDEV
ILSFSPSFSMYSIYSQINGSKFIGVESDENLVINIDSVIEKVKENNPKIVIVCNPNNPTGTILKREEIIKLLDSTNSLVVLDEAYMDFGEESMLSDVFK
YDNLIVLRTLSKAFGLAGIRTGYMLSNSSLINSVEKVRPPYNLNSLSDFIATRALRNKDVVKAYIKEVKEEREVLYKEMIGMGIKAYKSQANFILFY
SEIENLSQKLIDRGVLIRKFGGKLENYYRVTIGDKEENSMFVGAIRDILKKEK

>CORE_REP|Org82_Gene1721#(WP_003428627.1| 3-deoxy-7-phosphoheptulonate synthase)

MIVVLKMGADKNEVKKLIEAIGREGVEVNPIDGTELTVLGLVGDTSKIDAKRIEANKIVEKVMHVVEPFKKANRKFHPEPSIINVNGMEIGSKKI
AMIAGPCSVETEDQIVSIAKDVKKSGAGFLRGGAFKPRTSPYAFQGLKYDGLDLLKKAKEKTGLPIVTEIMSTQDIDIFEENVDVIQVGARNMQ
NFDLLKELGKTNKTILLKRGLSATIEEWLMSAEYIMAGGNENVVLCERGIRTFETYTRNTLDLSAILAVKKLSHLPVIVDPSHAAGKSWMVDSLS
KAAIAVGADGLIIEVHNDPAHALCDGKQSIKPNEYDELISELKTIASAVGREI

>CORE_REP|Org50_Gene1894#(WP_003430307.1| LacI family DNA-binding transcriptional regulator)

MKKITINDIANLAGVSKSTVSRYLNNKDISDSTKEKIKTIIDEYGYEPNAFAQSLRAKKTYFIGIITPCLDSFVKSKIMMAIDEELKELKYTSLIINTSRK
IRSEIDSISKLASLKVDGIILIGTEITKEHKNVIEKLDIPIVVVGQKVDGINSIVNDDYGAGYKMGQYIANKGYKNIVYLGVDESDISVGLNRKNGVL
NGLKDKGYDAKVFYTDFDQETSIQRSGEMLESENPDIIICATDNIAIATMKEINKRGKNIPRDISVAGFGGYDILSIISPKLTTIKFENKNAGKVAA
NTIVNLIQERKEPLLKEIKFELIEGESTINKN

>CORE_REP|Org73_Gene1768# (WP_077709045.1|siderophore ABC transporter substrate-binding protein)

MNKKAAIVAAVAIIIGLVTVFALGGSKKNESKTSEDSNNTIKITHNLGETDVKLNPKKVVVFDYSALDTMDALGVAENLVGLPKASLPASLEKYK
DEKYADLGGLKEPDLEGIKSANPDLIIINGRQEDFYEQLSKIAPTISTSKDDKKYLESVKNNIDKIAKIFGVEEKANQEFSKIEKKIEILNKKVTDKNL
NALTIMVNEGNLSVFGEESRFSILYNSFGFENKDKNIKESSHGQNITFEYIAKQNPEVMFVIDRGIATGSDVKESSTAKSVLNNDIIKSMDAYKN
DNIIYLDSPTWYVNDGGLTSLNKMIDDASKAVN

>CORE_REP|Org44_Gene1774#(WP_003422877.1| LCP family protein)

MSKLKKFVILLAFLVVIFPISVYGYFYYKLSAIHDSSISSDLLDNNDHKNEDGIINILLMGTDARPNEDSSRSDAMMILTIDNKHNDIKLTSLARDSY
VDIPGHGKQKLTHAYAYGQADLLIQTIEENFNIDIQNYACVNFESFMYIIDAIGGVEVTIEKGEIRELNKFIPETYKWNKSDDKGSIQYIRNAGKQ
TLNGYQALSFARIRHNDTAFARDGRQRQIIQAIIKKTETLPVTKYPGLLDAVLPYVKTNMKPNAILSLGAQVLKMGDLNIKQFEFPIDDEIHSTG
GIYGKAGWVLRFDPDTLDILHDFIFNDIEFKQ

>CORE_REP|Org4_Gene2815#(|WP_009891198.1| ABC transporter substrate-binding protein)

MKKIKSLAIFISIITTLVLVTACSDKNTEDKDKSETRVVQSVKGEVKIPSNPKKIVDISGSSEELLLAGYKPVATANVDSYETDKLPSYIREELKGVKIV
GHSMMDTMDMEAILEVNPDLIIMSQRQEKIYDQLKEIAPVVMMKDYANDWRSKLTDVSKLFDKEEEAKSWLQKYDEKATKLGKEVIEKNGE

KTYLPVLASSGQFMVFSDGGIGTLINDDMKLARPKNMPKQDGITLPMVSMEGLTDIDADHIVVIATEADKKDLENSAIWSQIRAVKDGNVTIL
DAAPFFSQSYNPIGKELLLESVKNELTK

>CORE_REP|Org85_Gene1827#(WP_003424113.1| HAMP domain-containing histidine kinase)

MFILAFIICTVVIFIVSTKINQKRYDELSLMLNQILEGKEVTYPDTKDTRASKISHQVKKIKDMIEIEVEQSKLEKEAIKGLISNMSHQLKTPLSNITIY
CELLENINISTLQKKEFLQKMKNETFKIDWLLQSLFKMTKLEDGVIEFEVEELLIKDTLIQSISTIFNKAEAKNIRVNLEPFSDIKLVHNKKWIIEAIVN
VLENAIKYSPSDSTITISVIKMELYTKITIKDEGIGIDSRELNDIFKRFYRSKNVANQNGTGIGLYLTRLILEKENGNIIVESKLGSGCCFSIFLQNCKSL
N

>CORE_REP|Org33_Gene1037#(WP_003438004.1|selenium metabolism-associated LysR family transcriptional regulator

MDFKQLEVFVAVAKHQSFSKAARELFLTQPTVSAHIQNLERELETVLINRSNKVITLTKSGEILYEHAIYILNNCKRAIYDIKEYSGKIEGIIDIACSSI
PETYILPDFMKSFSMSYPDVKFSISHYDSQYAISEILNERISFGLVGSKINNPQIEYLDLLDDELVLITPSDFKIDNKNNCIDIGELAYLNFIMRKEGS
GTRNLILNTLSKNNFPVSKLNVIAHVESNEAIKEMVRLGLGVSFISYISAIDYLNAGKIKCYKIKDVDFTRKFFFIYSKKKTFSPLEDKFLNRLCEYFEII
I

>CORE_REP|Org63_Gene2774#(WP_003426478.1| N-acetylmuramoyl-L-alanine amidase)

MKKKLLDGKITLIICKSVKIYTKKGEEMSKGNNNNNSRNKSKKTSHLNRKKRKLNKKKLAVLICFTVLFLFIAFKATQGVVALVKSMDKSNKTSQ
QQNVNSEQFDFGNEEENKKKKYTVFIDPGHGGNDKGTESKTSNRYEKDLNLQIAKKLANKLSKQKDIQVVVSRTDDTYISLKDRAILANNSSAD
VLVSIHLNAEKNGNTATGIETWYRNKATDGSKELAQAVQSTIVSYVKVRDRGIVENNFEVLRESNMPAILIECGFLTTPSEEQKIINEKYQDQLA
EGIVQGVLSYLDSKGNK

>CORE_REP|Org53_Gene987#(WP_021362441.1| glycyl-radical enzyme activating protein)

MSKKGRVVKVQHFSVNDGDGIRTTIFLEGCKLKCKWCSNPDSWSNIVKLGVMKDKCVSCNRCIDVCPQNISSLFDRAQINNKCDLCGECIKVC
LKDAICIMTEEMSVEEIVEEVEKDFIFFFESNGGITFSGGEPTLQIDFLRELVDIFYDKGINIAIETCGYFDWNKVNDVFEKIDHIFVDIKSMDDNIH
KEYTGVSNKIILDNICRLSKLNKSMVIRVPIIYGVNDSEENIRNTALFVKQNVPGGKMELLPYHKFGIDKYKALGLEDYIYEFDEICNNHMLKLKEI
VELTGVKIIEYK

>CORE_REP|Org89_Gene2365#(WP_003419800.1|D-alanine--D-alanine ligase)

MKIAVIMGGISSEREVSLNSGKEIYNNLDKNKYEVVKVIIDDKKDIFTKIPEDIDFAILALHGKFGEDGCIQSILETMDIPYSGCGPLCSGMCMDK
NITKKMLRDSNLPTAPWVLVKSVDEIDYDEIDNIGYPVFIKPNSGGSSVATFFIHSKDEVGEAVRKGLEVDEFVMIEKYIPGGEYTSFILNGEVFP
TISIKSDSGFFDYEAKYSVEKGAKEEVVYLDEELQKRVNEISETCWKIFNCKAYVRVDMIISEGIPYVLELNTLPGMTQTSLIPRSAAARGIKYSELL
DKLIEYSLN

>CORE_REP|Org18_Gene1469#(WP_011861237.1|sigma-70 family RNA polymerase sigma factor)

MIMDTKKENNYENYICVGSSNVSNAMKMYLKEIEEYKMLSAGEEVELAKEIINSSSVAKEKFINSNYRLVVSIAKRYKRDSIDMLDLIQAGNIGLI
KAVEKYDYKKGYKFSTYATWWIKQSITRYIDDCENTIRIPIHLHQRINFVKKKKQELLNVLLREPTIDEIADACGLEVDKVLELLRRDKNVVSLDTP
LKEDEDSSLVEFIPSDADFKDVVIHEVEQHNLKEKIEELLTGLGEQEQQVLRMRFGIDDDDPKTLEQIGKVFGVTRERIRQIEAKAIRKLRHPSKLK
QLKHFY

>CORE_REP|Org72_Gene2726#(WP_003416240.1| YicC family protein)

MAISMTGFGRGEYKDDNYYFLVECKTINHKYSDINIRLPRKISFLEDKVRNLVKNYVKRGRVDLYIKFDLLGKEDVNLNFDEGLASQYIDILKEIKN
KFDIIDDISVMNVAKFPDIVKIEEKEEDEDLLWSMLNQAVEDALIKLREMRSEEGKKLAEDIAMRCDLLKNHIEEIEKYSSSVVEDYREKLNLRISE
LLDDPSIIDENRLAQEVAIYADKSSITEEIVRFKSHIGQLKNTIFKDDSIGRKIDFLIQEMNRETNTIGSKSSDINITNLVVEVKSELEKIREQIQNIE

>CORE_REP|Org66_Gene2694#(WP_009890955.1| LysR family transcriptional regulator

MNLYHLRYFVTLAHLEHYTKAAENLSITQPSLSHAISLLENELGVALFEKEGRNIVLTKYGKIFLKDVEKSLEILDSSVKSLKITGTGEGQIDLAFLRTL
GTDFIPDIVHKFLKSNPAKSIDFKFHTGVTTDIIQGLKERKYDIAFCSKLEKEKGIEFIPVAKQDLVLIVPYSHPLAAKDTIDLKETIPYPQIVFNQRSG
LRYIIDDMFKKINQQPNIVYEVEEDQVIAGLVAKNFGIAVVPNMNMLSFTKVKVIQIIHPSWERNFYLAFIKDRYLPPAIKNFKNFVIKNAQL

>CORE_REP|Org10_Gene2425#(WP_009893591.1| LysR family transcriptional regulator

MNINYLYYFQTVCKYKNMTKAAESIHISQPSITLAIKELEKELGFELFYRIGNKIELTPEGKIFLDKSKHFIKQFEDFQCDALDLGKKRKASLKIGIPTV
LGTFLLSKILPRFNVIYPDIELKIFEVPTFVGAKMIEESTLDFCIGIIDSDIYDDIDSKTIYKTELYLVTNPKNELAKHPIISNYMLKNVPFVILSEGSYHY
KIITKRLEKAKPNIILHSNQLSTIRYLLENDLASTILYKEIFQNTENLCSIPLERAITANIGVLWRRNQYISHSMKLFIEYMASIHIN

>CORE_REP|Org56_Gene2657#(WP_236875716.1| LysR family transcriptional regulator)

MDLLHLKYFQTVARMEHITKASHKLNIAQPALSKTISSLEKELGVQLFDRKGRYIVLNEYGRLFLKRVDSILDLVESSKKELQDTSLENSGEVKILSP
AAANVLPSLLSNFRKLYPNITFNVSHTLPSSYKKSDFDLYISSSFTKLNSENSITLTCEEILLGVSINHPLSLKDEVYLSEVSDENFIVITKGENYREVIDI
LCESANFKPKIAFESDSPYTIYALIKSLQGVGFICGKSWGLSQDPEIKLLHIKDIEFKRYLNLSWFSENYESKAVLLFKNFLINYFKNI

>CORE_REP|Org59_Gene1409#(WP_118822203.1| pantoate--beta-alanine ligase)

MLVKEIKLLRNIIKDWRKHGYSIGLVTTMGFLHEGHQSLIKKAVKENDKVVVSVFVNPTQFGPNEDFNSYPRDIDKDFKYCMDSGATVVFNPS
PEEMYLKGNCTTINVSGLTDFLCGAKRPVHFGGVCLVVSKFLNIVTPDKAYFGEKDAQQLAVIKRMVKDLNIDTEIIGCPIIRENDGLAKSSRNTY
LSEEERKSALILNKSLSLAKEKLVKGNLNPENIKELITAKINSEHLAKIDYVEIVDSETLQPVKQIEHSILVAIAVFIGKTRLIDNFTFKLNI

>CORE_REP|Org11_Gene1255#(|WP_045136015.1| sporulation transcription factor Spo0A)

MGGFLVEKIKIVLADDNKDFCQVLKEYLSNEDDIDILGIAKDGIEALDLVKKTQPDLLILDVIMPHLDGLGVIEKLNTMDIPKMPKIIVLSAVGQD
KITQSAINLGADYYIVKPFDFVVFINRIRELVSNRVTQVEPKPRPVQETQMTRSDFVKNVGNIENVGNIETEITNIIHEIGVPAHIKGYLYLREAIK
MVIDNVELLGAVTKELYPSIAKKFNTTPSRVERAIRHAIEVAWSRGKVDTINQLFGYTVHNTKGKPTNSEFIAMIADKLRLEHSMVK

>CORE_REP|Org12_Gene2351#(WP_003433818.1| MoxR family ATPase)

MIKKEISNFRGSSDYVVSPELMASVNVAIALEKPLLIKGEPGTGKTMLAQAISNELKKDLVIWNIKSTTKAQEGLYVYDTVQRLYDSQFGGEGVD
DISKYIKYGKLGEAFSSNQQVILLIDEIDKADLEFPNDLLWELDKMEFYINETKETVRAKQRPIVIITSNAEKELPDAFLRRCIFHYIEFPDRDMMEE
IVKVHFDKVEEHLLEQVMTTFYWIRSLKDIQKKPSTSELIDWIQALTLSGMPIEKIEKEVPFAGILLKNNEDIESMQRHL

>CORE_REP|Org83_Gene1695#(WP_003423767.1| ATP-dependent sacrificial sulfur transferase LarE)

MEVNFVKEKEKLDKLKKMLLELGSVVVAYSGGVDSNFLLKVAKDTLGENVVAVTIHAMMHSSREIEEAKQYTQNFGVKHIILNIENFDLKEFKE
NGIDRCYHCKKYIFSKIKEVAKEHNIKYIVDGTNIDDLGDYRPGLKALSELGVISPLKDSGLKKEEIRSLSKILGLKTFNKPSFACLASRIPYGVEITDE
NLRIIEKSEEYLSNLGFSQFRVRMHGDIARIEVGQEELGKFFENNNFNKVDTKLKIFGFKYVTLDMSGYKMGSMNLNV

>CORE_REP|Org69_Gene1655#(|WP_003423750.1| amino acid ABC transporter substrate-binding protein)

MKNILKKVGIFTIMLGLLGGVVGCSKPDNEKDKDASKESKKEVVVGFDNTFVPMGFLDEKGNTVGFDVDLAKETFKRLGMEVKFQPIDWSM
KETELNDSKTVDVLWNGYSITDERKKIVSYTEPYLQNKQIIVTLSDSKINSKADLKDKEVGTQQGSTALDAVEKDKDFMNSLKGGAPVLYDTYD
KALRDLEIGRTSAVVGDEVLIRYYMGQKGEDKYKVLKDDFGLEDYVVATSKENPELCEKINETLKEMKKDGTFDKIYDKWFK

>CORE_REP|Org13_Gene1645#(HBF8615296.1| TPA: methionine-binding protein)

MKFKKLLCLLLCLVLTLAVVGCSKAKDDKKIVVGATLVPGGELLEELKPLIKEKGYTLEVKNFDDYILPNEALNNGEIDANLFQHEPYLKEAVKAKG
YKIMAGKKLYVCPAILYSYKIKSVDEFKKGDTIAISNNPSSCSKNLRYLESIGLLTLPKGDGLVSPKDIIENPKGIQFKELDIAQIPSSLPDVTAAFIDTT
YAVPAGLDAKKNGIYTAPINDEYANLLAFRTEDKDSEKIKVLQDVLTSDKARSLIEEKYKGIVIPTF

>CORE_REP|Org83_Gene1388#(WP_003419958.1|MetQ/NlpA family ABC transporter substrate-binding protein

MKLKKLLSVALVSAIAISAVGCSNKEDKKILVGASSNPHAKILEVAKPLLKEKGYDLEVKIFDDYVLPNTALDEGSLDANFFQHIPFLEETVKEKGY
KLTYTSKVHIEPMGFYSEKVKALDEIKDGAVIAVPNDATNGARALKLLAKNKLIEVKDGELITKKDITKNPKNIQIKEMNAEQLPTVLKDVDGAVI
NSNYALTANLNPTKDAIVIESSDSPYVNIIACRENNKDSDKIKALSEAMNSKEVKKFIQDEYKGSIVPAF

>CORE_REP|Org22_Gene2952#(WP_003426481.1| Cof-type HAD-IIB family hydrolase

MIKLIATDLDGTLLDEKSEINPEFYKVFKKLRERGIMFSAASGRQYQNLIKKFEDIKDDMMFISENGTLVVYKGKEILSNPLNKELVNEIIETTRSIK
GKKIVMSGKKYAYIESKDEAFIQEVSTYYAKFKVVEDLTKVEGDILKIAVFDFKGAEHNNNIYFEKFSDRAQVCISGVEWLDLTAKGANKGSAIKK
VQKMLDIKYEETMVFGDQLNDVEMMKSAYHSYAMENANEHLKQIARFRAKRNTENGVVDKIKEVIKIG

>CORE_REP|Org64_Gene2604#(WP_003416101.1| RNA polymerase sporulation sigma factor SigG

MQVNKVEICGVNTSELPVLKNKQMKELLLQIKNGDEEARQQFVRGNLRLVLSVIKKFNNRGENIDDLFQIGCIGLIKAIDNFDLSQNVRFSTYA
VPMIIGEIRRYLRDNNPIRVSRSLKDIAYKALQVRERLIRTNSKEPTVSEIAKELELEVESVVMALDAIQDPISLFDPVYQDNGDAIFVMDQVQDK
KDTDENWLQEISLKEAIKKLNSREKLVLDLRFYKGRTQIEVADEIGISQAQVSRIEKNALKNMRKYV

>CORE_REP|Org28_Gene2625#(WP_009897796.1| response regulator transcription factor

MRAIIVEDEFPARKELRYFIENKSGIEVVSEFTNGIEVLDFIQENKIDVIFLDINIPHLDGMLLAKTLNQFKSRPKIVFITAYESYAVDAFSLDVFDYIL
KPYSEERIISMLNKLEKSEMSDIELSNVNSNLYKYKKEAVNQEIEEITHKISLWKGDKLVVIDIDDIYYCEANERQTFIYTEKEKFILKEGISEVENLIN
DKTFFRTHRSYIVNLTKVKEIIPWFNNTYILKLKNSDYEVTVSRSKVKEFRLLMHI

>CORE_REP|Org8_Gene2346#(WP_167653455.1| IclR family transcriptional regulator

MGEIINALDRALDIILLLYHEKREMGITEISKAMGVYKSTVHRTLVTLENKGFVIQNAENGKYWLGINLYAIGMVVGEKMSLTEIVKPYTKKLNQ
EFNEVVNVSILEERAQDSPRSIIIHKEYGSNQLLSVNPSVGSSSECYCSAVGKCLMAFNDSIDFEKYRKTPIHKYTEHTIDNWDDMMLFLAKIKE
QGYAIDDEELEHGLTCIGAPILDKNNKAIAAISLSGPTIRMREGDFEYKIKRVIETAKSISELFR

>CORE_REP|Org18_Gene1530#(WP_003436672.1| imidazole glycerol phosphate synthase subunit HisF)

MLTRRIIPCLDVRNGRVVKGKKFKDIVDVDSPEVLGKFYSDCGADELVFYDITASNEERKTSLEFVTKVAENINIPFCVGGGVNKLEDFTDILRKG
ADKVSINSSAVKNPELIREASLKFGAQCVVLSIDAKKNEEGSWSVYVKGGREKTNLDAIEWAVKGVELGAGEIVVNSMDEDGMKNGYDIELLS
KITSLVNVPVIASGGAGKKEDFYEAVNKSNVDGILAASVFHFGEIKINDLKKYLKDMGVEVRL

>CORE_REP|Org52_Gene1151#(WP_003430913.1|16S rRNA (uracil(1498)-N(3))-methyltransferase)

MDRFFVEKNNINLQDKTCTIEGEDVKHISKVLRCKLGEKLEICDKNNNEYICEIMNIDKSIVNLEILEKVDINRESELKVRLYQGLPKAPKMEMILQ
KLTEVGVEEIILVQTKRSVVKVDDKKEDKKFERWERIIYEAAKQSKRGKIPKLRGVLSFKEALEDMKKNNVNICPYENERTVSIKHALKKCDSNID
SVGIFIGPEGGFSEEEIEQIQKNNCNVVSLGPRILRTETASVVASTIALYELSDLGGEK

>CORE_REP|Org86_Gene2784#(WP_003426498.1| glycosyltransferase)

MNEPLVSIITPVYNSEEFLSETIKSIQNQTYKNWQLLLVDDCSKDNSSEIIKSFRKEDARIKYIKLEKNSGAAVSRNVGIKNAEGRFIAFVDSDDLW
DSRKLEIQIEYMLKENVGFSFTSYRYMRQDGSKTNKVARAPKKIDYEGLLRNTIIGCSTVVIDKEIVGEFSMPLVRRGQDTATWLQLLKKEKYAY
GIQEDLVNYRLVGNSISSNKIKALKRTWNTYRNVENLSLPKSLYVFCFYVFNAIKKRV

>CORE_REP|Org29_Gene2697#(WP_003426502.1| glycosyltransferase)

MKKNLVSIITPMYNSEKFIEATIKSVLNQTYQEWEMLIIDDCSTDNSPNIVKSYMQQDSRIKCIKTETNKGVSNARNLALSKATGQFIAFLDSDD
QWNSSKLEKQVNFMLENDYVISFTSYELMDENDKKLNKVIKVPPNVDYKRLLKGNILGCLTVVIDKSKLDFEIRMSGVRHEDYVLWLSILKKGHI
AHGINEVLALYRKSSNSLSGNKIKAAMWTWNIYRNIEKIPLYKAIYYFINYGINGIKKS

>CORE_REP|Org18_Gene1810#(WP_003430276.1| response regulator transcription factor)

MVNIILNWRFYFMKEKILILEDEIGIRSFVSINLKREGYEIVEAGTGREAIEKMTTEKDITIALLDVMLPDISGIEVCKFIRENFDQVGIIMLTAKAQE
DDKIEGFISGADDYIIKPFSIKELLVRVSALLRRVAKDDSSVKSSEIVSPPFILDIDKRKLFKNGKEIELTPTEFSIVKYLISNAKQSLSRDQILDEVWGT
NYLYDFKIVDVNIRRIRNKIEDDPSKPKYIQTIWGYGYCFRKEE

>CORE_REP|Org74_Gene1718#(WP_021364494.1| response regulator transcription factor)

MENRVLIIDDEVEILKLLETVLKKEGLNNIYTAKTKKEGLELFKSINPDLIVLDIMLPDGEGYDICKEIRKTSNSPIIFLSAKTEELDKLLGLAIGGDDYV
TKPFSPKEVAFRVKAHLRRLSYFSDAQNESKNLNNNEEKIISFGPYILNESRAELIKDGKSIGLFAKELKILSLFAHNQNQIISKEKLWDKVWGEDY
VGFDNTIMVHIRKIREKLEDNPSKPEYILTIKGLGYKLAVKED

>CORE_REP|Org45_Gene2586#(WP_009905981.1| response regulator transcription factor)

MNSYNILVVEDEKEIADAIEIYLLNQGYNVFKGYNGLEGLKVIENQEIHLAIIDIMMPKMDGITLTMKLRENHNFPVIMLSAKSEEVDKIMGLNI
GADDYVTKPFKPLELLARVNSQLRRYTKYLNMVENKEQKVDDDDGVFAIGGLELNENTKEVSVDGKHIKATPIEFKILSLLMRNAGRVFSADEI
YERVWNDNAVNTDTVMVHVRNIREKIEVDPKNPKYLKVVWGVGYKIEKIQR

>CORE_REP|Org58_Gene1491# (WP_003436675.1| 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerise)

MIIFPAIDIKDNKCVRLTQGEFDKVNVYYDNPLEVAYKWKNEGAEYIHIVDLNGARSEFGVNTKIIEDIANNIDIPIQVGGGVRDKEKVKSLINAG
VTRVILGSIAIENLNLVEELVNEYKEKIVVSIDAKDGKVAVRGWEVVSNVDSLTLCKQLEKIGVQTIVYTDISKDGMLQGPNFDIYERIAKETSLNV
IASGGVTSIEDVKRLKAMNLYGAIIGKALYDKKIDFKEAQQLCLLGE

>CORE_REP|Org32_Gene1458#(WP_003438625.1| polysaccharide deacetylase family protein)

MTSWKKKTVYKCLIAVALFCGIVLISNFSKVSALMMDTNGNVLIKHGSREKKLIAITFDDGPHPKETSQVLDVLKKYNVKATFFIAGKHAKWYKE
PLVRASKEGHEIGNHTFNHPDISNLSSSQIEEEIVKCEDILKEVTGKKPTLFRPPFGSYREKDLIEIAKKHDYKVVLWTGVDVKDWKNPGANSIAD
KIINKVQNGDIILLHDYATNDTVEALDMFIPKMIEKGFKFVTVSELIK

>CORE_REP|Org31_Gene2712#(WP_003431770.1| NlpC/P60 family protein)

MMNIKNKKHILKKFIAMVLIAGVVTVEAGAITASAAEPTNSPMSATVDQCDFLNVRSGASANDAVVGKINTGDKVEVLELHSNGWIKIKSVD
NVTGWVNGDYLTIQGGNVDAKVQNVLNLAFKQQGKPYKWGATGPNSFDCSGFTSYVYKNGAGVNLPRVSRSQATVGKKVSRAELKPGDL
VFFGSGGSINHVGLYVGDSKFIHSPQTGDVVKVTSMAPGTNYAKRLITATRVLQ

>CORE_REP|Org77_Gene971#(WP_009905963.1| response regulator transcription factor)

MNNILLLEDDKSLNRGISFKLKKEGYNVFSAFSIEEAKSIFAKEEICLIISDIGLPDGSGFDFCEEVRKKSDVYIIMLTALDEEVDIVTGYDLGADDYIT
KPFSLMVLISKVNALMKRVNTVKNYTLLVCDDLFFYYIENKLIVRADNKEEEIILSKTETKLLKYLMENSMQTLTKEQLLESLWDSSGNFVDDNTI
AVNIRRLRQKVEKNPSAPKYIKTVRGVGYIWGERSIKKC

>CORE_REP|Org7_Gene907# (WP_009888771.1| response regulator transcription factor)

MSKLIYIADDEDNIRNLVKTFLKNEGHDVMDFKTGDELLEQFNIKECDLVILDIMMPGSSGFEVCTKLREKSTVPIIMLTARDTDIDYITGITLGSD
DYFTKPFSPMSLVMRVKSIFRRIEFEKKQNYDKYSNSIDMELKFGDVIINKKNKIVTSKNVNIDLTPNEYNLLTYLFENIDRAVSRDELLNKIWGYD
IEVETRAADDTVKRLRKKILDTNILIETVWGFGFRLKEKS

>CORE_REP|Org55_Gene486# (WP_003439080.1| response regulator transcription factor)

MEIKPLVLIVEDDKPICKFIKVSLETQNYRCVETDNGGTAISLIHSLDPDLIILDLGLPDIDGIEVIGRVRACAKTNKIIVVSAREHERDKVEALDGGA
DDYLTKPFSVTELLARVRVALRNKAQQDNINNDAPKSFEVKNLKIDYENHIVSINGEEIHLTPIEYKIIELMSKYSGRVLTHKFIIDKVWGNYYESE
NQSLRVFMASIRRKIEKNPAQPEYILTEVGVGYRMADE

>CORE_REP|Org18_Gene2759# (WP_009890976.1| polysaccharide deacetylase family protein)

MYVVGLIIVVALIFLVHSIIPTYYNKLLNKEVLKNMAGENEIALTFDDGPDKRYTEKLLDVLKENDIQAMFFVVAKNAEKEPEIIKRMLRENHIVGL
HSLEHRNAWLYSYSYVKKDFIESTNIMKNLGVDVNYYRPPWGHTNIFSNSFVKKYNLKMTLWDVMAEDWEKDSTVDIIINKLMSRTKENSIIC
LHDAGENSGGAVGAPERTIEALKIAIPKLKASGLKFVTPERM

>CORE_REP|Org34_Gene2492#(WP_003416112.1| response regulator transcription factor)

MNTKVLVIDDEMHIVELLKFNLEVSNYEVSYSYDGFDGFIKAKEIKPDLILLDWMLPNISGIEVLRKIRSDKDLKNIPVIMLTAKNMENDKVEGLE
IGADDYITKPFSIKELLARISSVLRRYNLTSLGEENNILTTGNLKLDLSKHEVTKGSEKIELTLKEFELLKLLIQNKGKVLSRNYLLDKIWGYEYYGETR
TVDVHIRYLRKKIEDEDKSEKYIETIRGVGYKID

>CORE_REP|Org53_Gene1818# (WP_003435302.1| response regulator transcription factor)

MEKILVVEDDSILNKTLSYNLIEDGYIITSKFTAKSALKSIFECEFDLIILDINLPDKSGFELCNEIKGNYNIPIIFLTANDMECDMIKGYELGALDYITK
PFNINIFKQKVKAFLNHLTIKTKQDYYRDGYLEINFSELSANINGNQIIFTPLEYRTLKLLTENPKSILTRKVLLEKLWDIDANFVDEHTLTSVISRIRS
KIEKDNLKYIKTVYGMGYMWLGERNEF

>CORE_REP|Org51_Gene2784#(Select seq gb|EFH05628.1| bacterial sugar transferase)

MSGYTNDECEIPKIKSYPGADKEIASEIDYSIVKGTVLFDLYQRIMDLVLSIIGLVIGLPLIAIFGILIKIEDKGPITYKQERLGKCGRRFYIYKLRSMRT
DAEKFGAQWAEKDDPRITKVGKFIRKTRIDEIPQLFNILKGDMGLIGPRPERPNFTVQFNEEIPGFINRLAIKPGLTGWAQVNGGYEITPEEKLK
EDIYYIKNRSILLDFKILFKTVKVVLTGDGAR

>CORE_REP|Org93_Gene2412#(EQE32499.1| transcriptional regulatory family protein

MYRILLVEDDIDLSKEIALALEKWGFKVGLIDDFEVVLDEFIDRKPDVVLLDVNLPLYNGFYWCEKIRAISNVPLIFLSSRDSDMDLIMGINNGAD
DYITKPFSIEILVTKINGIIRRVYNYSDSNSILYCEDLMFDVGKGIIKHKYKDKSIELTKNEIKILTLLLKNKNRVVSRESLMMTLWDNDEFVTDNALT
VNMNRLRSKVKELGFDDFIKTKKGIGYIIQC

>CORE_REP|Org28_Gene2247#(WP_021359412.1| N-acetylmannosamine-6-phosphate 2-epimerase

MLDKVKGRLIVSCQALENEPLHSPFIMGRMAKAAMEGGAVGIRAQGVEDIIEIKKVTGLPVIGIIKRNYEDSDIYITPTKKEVDELLTTGCEMIAL
DATNRVRPNNEDLKELIKYIKENGVLVMADISNYDEAIKAQEYGVDCVSTTLSGYTPYTKTLEGPDFVLMERLVKDLEIPVIAEGKVNTPQDLKK
VFELGVHSSVVGSAITRPQLITEKFVKAIEINL

>CORE_REP|Org27_Gene1678# (|WP_004454472.1| response regulator transcription factor [

MKVLIVEDNKILLESVVEELSKHFETEKCEDGEEALYLINQNIYDLVILDLMLPNINGFDILKKMRINNIDTPVLILTAKETLDDKVEAFTIGANDYLT
KPFYMEELVARVYAILRTNGKIKERNGLEFKSLYLDTLEKRVYIEKEEIKLQNKQFNLLEYFVLNKGSILLKEQIYDRIWGIDSDATIEIVEVYVSNLR
KKLSKYGYDKYIKTKRKVGYIFDDK

>CORE_REP|Org68_Gene1930#(|WP_009897090.1| response regulator transcription factor

MNLLIIEDDINLNEGLFYAFENDGFNVFKAYTKQEGLNIFNSKNIDFIILDCNLPDGDGFDVCQIIREKSDIPIIMLTARDSEIDEVKGLEIGLDDYIT
KPFSLSVLKARVKVAIRKKSNNKVIYSNGIKLDQKLLKVYKNKECLELSSVEYKLLSYLIENKGQILLKEQILHHIWDSEENYVDDNIVSVNIRRLRVK
VEDDPSNPKYIKTAYGMGYLWNEVE

>CORE_REP|Org49_Gene1942#(WP_003424455.1| response regulator transcription factor)

MNSSILVIEDDSNIQELISEFLSAEGYQVDTANDGLEGIQKFKQGSYDLVILDIMMPNLDGYGVCKMIRKSSSVPIIFLTALNDEGDQLKGFDLEC
DDYITKPFSFNLLIKRVEAILRRSNKTINDKFIVFEKLKLDLNTYIAEIDGEPIELTLKEFNILKALIEKYPQVITREGLLDSIWGYDYYGDTRIVDAHIK
NIRKKISLPYIKTVKGIGYTLEKDI

>CORE_REP|Org89_Gene2194#(WP_003420108.1| bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP diphosphatase HisIE

MNNKCNDIYTDEVDEFIRSIKFDDKGLVPVVVQEVVSKDVLMLAYMNKEAIKKTLKDKVACYFSRSRQELWVKGETSGNTQKVVKMSYDCD
VDTILLFVEQTGVACHTGNYSCFYRDLFDDTAKMELEVQTNILKELYDLINERKNNPVEGSYTNYLFEKGIDKILKKVGEESSEVIIASKNTDKSELI
YEISDLVYHTLVLMIEKGVEIDEIKKELLKRRK

>CORE_REP|Org81_Gene2772#(WP_021387784.1| response regulator transcription factor

MNKIKVLIVDDEKLIRKGLKIILSSYNDLEIVGDASNGYEALEFCKTNDVDIVLMDIRMKVCDGVLGTRLIKEYNNSITLLILTTFNDDEYIKDAMKF
GASGYLLKDSSDKVLHEGIRSSFFGNIVLDKSVAEKIMTSEKTIKQEYLYDMYNLTEKEISIIRLIANGLNNKEISQELFLSEGTIKNNITNILAKLELR
DRTQLAIFAFKNKIVIE

>CORE_REP|Org75_Gene481#(WP_003436678.1|imidazole glycerol phosphate synthase subunit HisH

MNIIVDYGLGNIDSVSRGFRKAGIETKISSDIDEIKQADSLILPGVGAFRDSISALDKLGLIPIIKEHVSKGKFMIGICLGMQLLYEKSYEYGEYEGLG
LIKGSIDKLDISLKVPHMGWNNLKFNKANDDILKYINEDDYVYFVHSYYANSSNEELIAFSEYEKKIPAIVRKGNVYGIQFHPEKSGEVGLNILRAY
GEMIK

>CORE_REP|Org2_Gene2029# (|WP_236879159.1| serine O-acetyltransferase)

MFKKINKDIEYIMKNDPAARSKIEVFLLYPSVHAMIMHRMAHALYKKKKLFTARLISQISRFMTGIEIHPGAKMGEGILIDHGMGVVIGETAEV
GNRVTIYQGATLGATGKDTGKRHPTVGDDVLIGAGTKILGPLNIGSNSKIGANSVVVKDVPNGATVVGIPAKIVKIRNLEPVKKNKKEVSYEYDE
LDNVYYI

>CORE_REP|Org86_Gene2134#(WP_003430598.1| ribosome recycling factor

MKLEIHKQLEEKMNGTIDALKFEFGTIRAGRANAQMLDKIRVDYYGTPTPINQIGAISVPEPRILMISPWDKSAMHEIEKAIANSDLGLNPSND
GEVIRLSVPALTEERRKELAKKASKAAEEFKVRIRNERRDANEKIKKMEKGGELTEDELKKAQDEVQKMTDKFIKEIDTLLSKKEKDIMEV

>CORE_REP|Org20_Gene2996# (WP_003425127.1| signal peptidase

MGEAVKKEVVEWIKVIVIALVLAFAITRFIVPTIVKGESMYPTLVERDYLIVNRIAYKVGEPKYKDIIVFKTDLTEENGKKKDLVKRVIGVPGDHVKI
QDSKVYVNDKLLDETSYIHNNRTDGDIDIVVPEGKLFAMGDNREKSLDSRYDEVGLVDEHTILGKVLVRLYPFSKIGTID

>CORE_REP|Org79_Gene704# (WP_003422909.1| gamma carbonic anhydrase family protein)

MIRDYLEDKPLIDESVFVAKSADVIGNVKIGKDSSIWYNAVVRGDEGPITIGENTNIQDCSIVHGDTETIIGNNVTVGHRSIVHGCKISDNVLIGM
GSIILDNAEIGEYTLIGAGTLITSNKKFPPGVLIMGSPGKVVRELTEEDKRYIDESYEWYLEAAQNQKY

>CORE_REP|Org59_Gene2574#(WP_003416314.1|pantetheine-phosphate adenylyltransferase)

MENKPRKAIFAGSFDPITNGHLDIICRASKLFDELQIGVLNNPNKKGLFSFDERVKLIEKSTSHLNNIKVVTFDGLLINYCQENGIGALVRGVRSG
ADVDYELQMAHMNRELNPDIETIILPSCTKYSFISSSLIKEVLLFDADIKNLVPKIVLEELKKKTSGGN

>CORE_REP|Org41_Gene1716#(WP_003419467.1| ribosome maturation factor RimP)

MKKNLEATIEEIVTKITDEHGFEMVDVEYVKEAGEYYLRVYIDKEEGISLNECELVSRELSPILDEKDPIKENYFLEVSSPGLDRALKKDRDFVRYQ
GRDVDLKLYKPLNGCKQFEGELVGLTEDNNIKIIVNGKEIEFNRKDVAIVRLAIKF

>CORE_REP|Org89_Gene2491# (WP_003419428.1| transcriptional repressor)

MANTMDLLKDKLKETGFKITPQRRAIVEILLKHDHSHLSSEEIYDLVRVDCPEIGLATVYRTMQLLDEIGLISKLNLDDGCIRYEISLHKEDCHNHH
HLICKNCGKIMEAKEDLLDNIEKEIQSLYKFKILDHDVKFYGLCDECNGVSDSEE

>CORE_REP|Org61_Gene3559#(WP_003425882.1| ribose 5-phosphate isomerase B

MKIGLGCDHGGYNLKKEIISYLEGKGIECVDYGTNNATDSVDYPVYGEIVANSVINKEVDYGILCCGTGIGISLAANKVPGIRCAVVSDVFSAKM
SKAHNDANMLSLGERVLGKGLALEIVEAWINTDFEGDRHARRVNMIKSIEEKHNK

>CORE_REP|Org52_Gene2415# (WP_003419409.1| Rrf2 family transcriptional regulator

MKLSTKGRYGLKAMFELALNQDNGPVSLKFIAKKQKISDQYLEQIFSSLKKSGLVKSVRGAQGGYLLSKNAEDITVGDILVVLEGPVALSDCVLD
EDVCENSNMCVTKIVWEKMKKGIEDVIDSITLKDMINDYNKNKLENDITNIKK

>CORE_REP|Org93_Gene1829# (MBY2231329.1| GatB/YqeY domain-containing protein

MSLKQKLQEDLKSSMKNKDTVRKSVVTLIRASIKQYEVDNRVELDEDGIIDVIAKQLKQRRDALVEFEKAGREDLIKETEGEIEVLKEYLPQQLSE
EELEEIVKSTISEVGATSMKDMGKIMSVIQPKVKGRADGKLINKLVKQNLQ

Sequences found in choke point analysis

>CORE_REP|Org49_Gene2710#(WP_003422726.1sigma 54-interacting transcriptional regulator)

MKKHNILFVSTDDKINIDISKQLENIFGEFCSIDNLIYVNRINIELSSYELVVCSDNDIKEYIHNNIDKNIPIVIIHRTINIENINQIISIENDSDVMVIDAYKESADETAKIIRKLGLIHINLIPYYPGCDKSKCEIGIITGSRNSIPQNIKQIIDIGDKIIDINTVIEIFTKLNISIDKLHIIKEKYDEDTVSGYRYYTTMNKTMKSFLEIIDEGIASIDKLGKFIYCNKVFSNLIGIDQNEIISNNFMDLFSDKVVKKIFFQEDEVNDEVVNLNNKKLIINKVNVYENNERIKSIISIKDISAIQVLEDKIQNKFQAKGFVSKYTFESVVGESKIIKEKINIARKIAITDFSVLILGENGTGKEIFAQAIHNESLRKNKPFVAVNLSSLSDTLIESELFGYEEGSFTGAIKGGKMGIFERAHTGTIFLDEIGDISLDVQQRLLRVLQEKEVMRMGGSKIIPIDVRIIAATNKDLKKKIKEGSFREDLYYRINVLHIEIPRLRERKEDISLISKYFLDEINSNKCFTEESMKALKLYEWPGNVRELKNLVYYIDTIVEEDRVDYEHLPEQFRFEKNNTLVNENFDSIILDFKQSNFFEESICILTSVETWNNKNILLGRNKLQEILKEKGIVLSVDQIRKRIDKLKSHGLLLSGVKKQGSFITDEGKNFISYIKFKGVI

>CORE_REP|Org95_Gene1329#(WP_009896470.1| c-di-GMP phosphodiesterase PdcA)

MNKHNFEVILNQLQINIYVTNIHTNEIIFMNKKMKEEYNILDPEGKVCWQVLYPEKNSTCSFCKVLELLKNDKKGVLIKWYEKCNKLNRVFENYDSLITWQDGTVVHMHQSIDIANSTSLNKPIKINEFHEISNNKEEKGVFNFSRDNFDYNSTLLYDALIRGTDEYIYICNMKTGVFRYSPSQVELFDLPGEIVKNPLVYWKKIVHPEDWNRFYKSNTEIGKNQMDYHTVEFRAKNRSGEYIWLRCRGQLMRDEFGEPSIFAGIMTQLGKQNKIDSLTQLLNYHEFMSVFEDKISNPMIEKLCIVLLDIDDFKNVNEMYDRDFGDNIIKTLAQSVQSILPDNAELYKLDGDEMGILVDNVEENEILTLYNQIQNMIIHLQLWRKYGLNITISAGCVIYPKHGDTVKELYKCASYSLQYAKEHGKNRLVFFSQEILKNKMYSLEMMRDLKASINDDFRGFSLRFQPQVDTESHKIIGVEVLLRWTNDKCKAISPLEFIPILEENDMINIVGAWVLRMALRTFRKWIDYYPFFKVSVNVSAVQILEDTFIEDIVKIIDDENFPYQNLVLELTESHTVQNMSILQFKFKALQDLGIYIAMDDFGTGYSSLEVLKFSPIDIVKIDRVFVKDILKSKFDATFIHFIVAICHDVGIKVCLEGVETQEEYDLVKQIKPDYIQGYLFGKPQTATEIFDLLKLDN

>CORE_REP|Org18_Gene1724#(WP_009896876.1|transporter substrate-binding domain-containing protein)

MNKKKIVIIGIIYSFLVVFSLTNMYVNMEYNLNVFEYIKKSLPFTEEEKKWLEKHKNLIYSSDQSSPPLRYKGKEDGQYKGIIVDLINSLSIQIGRDFYFKPNNWWKESFVNSIDDSIKFFDLIPSKERANKFIFTDPIYTLSANILKDKKSQDINSYMDLKGKTVAIPEGDYSINFLKQKIQDINILLTPDIKTGVNHLMSGKVDAVVGDEPVLRYYINNYGLSNKYSVLSNPIYTKKAVLAVPKQYEELVSILNKGIFKLQKNGVYKDLKKKWYSTYNEVDDILYERGIVPSIYLFIGIILISIYVFYSYTYLLKIEIKRKTEQVIENKKTLEATFNSITDIIMLVDENNNIVESNKVLYDFMGEMSYKIADLISMIKGVIENTFSENTNKTSEIEIHNKILKINTFPVEYKKNNTEYIVVLIKDITNDKIVEAKLLRENKMISIGQLASGVAHEIRNPLGIIRNNCYLLKDNVTMEEVNDCVKSIESNVDRASNIITNLLNFARISDDNLEHINIRNFIENIVKLQYKMLQLKNVEIKIDCEHNLICYINGESLKHVFINLISNSIDAIHQDGKIIIYCYEKNHCLFIDFKDNGEGIKEDALKDIFNPFYTTKPIGEGTGLGLYITYNEIKKNNGDISVESKLGVGTCFHIKIPLNKEVTI

>CORE_REP|Org51_Gene2854#(WP_021388183.1|2-aminoethylphosphonate--pyruvate transaminase)

MKKIYGEKIKAVVFDWAGTTVDYGCFAPLNVFIEIFKRRGIDVTMEEARKPMGKLKIDHIREMCEMDRIKNLWSDKFGKVPTEDDVNELYAEFEPMLFETLEDYTTPIPHVVETIEKLRKNGLKIGSTTGYTREMMNIVEPNAAKKGYSPDFLVTPSEVSQGRPYPWMCYKNAEALGVSPMSSMVKVGDTISDVKEGVNAGMWSVAVIKGSSELGLTQEEVENMDKEELKAKMSIVSKKFKEAGAHFVIETMAELEDILIKIENETIKSDFVPENDYILLTPGPLSTTKSVRASMLKDWCTWDVEYNNLVQDVRRRLVSLATQNTDKYTSVLMQGSGTFSVEAIIGSTISKDGKLLVIANGAYGKRMKDICNYLDIEFVDCTFKDIEAVDLNVVENLLKENKDITHISMVHCETTTGRLNPIQEVGKLAKKYNKIYIVDAMSSFGGIEIDVEDFNIDFLVSSSNKCIQGVPGFGFIIANKEELSKCKGIAKSLSLDVYAQWETMEKNNGKWRFTSPTHVVRAFYQALLELEEEGSVEKRYARYKENQFTIASRLKSLGFDTLVNDNAQSPVITTFLYPKNAKFEFMEFYTYLKDNGFVIYPGKLTDIDTFRIGSIGEVYPTDMERLADVIEKFINR

>CORE_REP|Org62_Gene1531#(WP_003420306.1|GGDEF domain-containing phosphodiesterase)

MKRFLRRIILVLFILLIFISFISIKLIHNVGDYGKLINYVGIVRGASQRLTKLEMNHKPNDELIEYIDEILQELITGHGNYGLVLTDCNKYNEDLLLLEKKWEDLNSEIKKVRMKEPNNQLLSISEEFFSLANDTVFEIENFSKEKSNYLMTLIIIISIIGILACIILILQYSKKMIKLEKLNVDLKNIAYKDELTGVNTIEKFKLDANQNICMHKDKKFAVFYIDFENFKYINDIFGYDYGDMILKRYANLMMNDIGKYEIFAREIADRFVALRCYIDKEDLVVRQRIVDSELINTTNEIKNKHSITVVSGICCIEDVNEKLSIDGLINRANFAQKTVKNKPGTNYAFYNDSIRKKMIEENTIKSRIHEAIEKREFIVYLQPKVNLHNQKINCAEALVRWLTPDKGIISPAIFIPVLEKNFFIALVDKYVFEEVCKWIRKRLDENKPFVQISVNVSRIQFYNTKFVETYSNIQNKYRIPKNTIEIEFTESVAFENQNHLLEIIHDLHENGFTCSLDDFGKGYSSLSVLKDLPFDALKLDSMFFKASLDKDKEKIVIKNIVHMLKELNITTVAEGIEYEEQVEFLRDIGCDLVQGFVFYKPMPILEFEEILDKEFVYNS

>CORE_REP|Org88_Gene3147#(|EFH15286.1| Sigma-54 interaction domain protein)

MLSKLKEFQQEMIKYTETVASVLDVDIEIVDDRLIRISGTGLYKSKINESVVTEGFIYDNVIQTGQELVVLDICDNQLCIECSHYMKCLNKVIIAVPIKYNNRTIGVIGAISTDKTKKVEISAKIDNYLKFVNHICDLISMKIEEHEVSKNSSRKMDMMIEIIENVEKGVIILDINSKISYINNIALKKLDIDKNIIENIVNIVSVESSSNGHELLEIDIDNKIYNINAKIIPVYPYINQYDKIIIFDKTYINHKGHVKVNSGWGNSDIESIIGNSEAMLKVKERTKKLAKSNSTVLITGESGTGKELIARAIHAEGSRWNKPFIAINCAAIPENLLESELFGYIKGAFSGASSGGKVGKFELANEGVIFLDEIGDLSMPLQAKLLRVLQERKFARIGSNKLIDLDIRVIAATNKNLLKLVNEGKFRDDLYYRLNVIPINLPPLRERKDDIEAIMMKFASKYSLELGIQLNKIEENVMNMLINYNWPGNIRELENAVEYMMNLVGDDGIIYKDMLPLDILNYYNINGNICKNKDINIIFEDDIVGGIVENQERILSIKELELTYINKLLNKYGRDTKTKKKIAKDLGIGLATLYRKLEEEQS

>CORE_REP|Org45_Gene290#(WP_003419837.1|sensor domain-containing diguanylate cyclise)

MSILLKKAPKLAKHIITSFYINRDIDEVLKYLCENVTWIGPGEQEFLTSFNEIKNYFYAGQYEIPSCDINNDIFEIVSEYENRCMVLGKYTVRTKENA
QMILEVNQRCTFEIIEDREKLLVKHMHISNPYGEMQLDEYFPTKIGTQSYDYLQRLLKEKTEVIEMITNNINGGLKGSNDDSTYSFFYVNEGLPKI
LGYTYNEFMEMSGGSAVGAVYPPDLPKALEDCEQCFAKGPTYSSEYRIRKKDGTLMWVLDSGMKSLNSDGIVKINSIITDITQLKNIESELKLER
ERYRIALQNITDIMFEYDMENDNFIKYQRVEIDKKIELENFETKNYSKLLESGKIIHLDDIGKLLEVLRGNLHETIEIREINSLTKNEWRWIRVQCSVI
YDSDHNPIKTIGVLKDITEDKSKLESLINQAQRDPLTQLYNQRVSQNLIQEYLCSSDSKNNDALLIIDIDDFKTVNDTFGHLEGNEVLVAVSKILLH
NTYDKDIVARIGGDEFTIFIKSLTKDLIIKITNDILNDASKIKVKDNHKITLSIGIAFTDDSTKLYKDLFSKADKALYLSKADGKNCYSVYE

>CORE_REP|Org72_Gene2695#(WP_065986483.1| DAK2 domain-containing protein)

MIQYIDGKRLREMFISGANNLQNNKELVDKLNVFPVPDGDTGTNMSLTISYALKELAKVENDNISDIGKALSKGSLMGARGNSGVILSQIIRGIA
KSIEGKSKLSTEDLAKAFKNGSDTAYKAVIKPIEGTILTVVRESGEFAIKTAKKEKDVVKFLSMLVKESNSSLERTPDLLKNLKEAGVVDSGGKGLV
LIYEGMLASIKGNNIEIKNADLDTNISTSMDFAKSTTSTDNIKYCYCTEFILESSKVEDTKIRDIMMAYGDSLAVVGDDGVIKVHVHTNDPGNVL
QEALKYGQLLTIKIENMKLQHENTLLDVEEKKENDSEPLEEEKEFGFIATSMGEGLANIFKDFGVDHIIEGGQTMNPSTEDFMNAIKDINAKNIFI
FPNNSNIIMAANQAKELSDKNIIVIPTKNTPQGFAALVTFNGELSEDENKEAMMNALNSVKSGQVTFAVRDTVMNEIDVKEGNIIGIAEGNLL
SAGDYVDEVTSNLIEKLVDEDTAIITLFFGEDVTESQANELRTSLEEKFEDVDVELYYGGQPLYYYLISVE

>CORE_REP|Org18_Gene1870#(WP_011861348.1|bifunctional diguanylate cyclase/ phosphodiesterase)

MLKRVRCSYLKKNRLIAKNISIAFIVLFFFSVFTFFYVGNINRVLEYETNDIITVTIAGWIILSFLFLGIIIYILYSKANSQKTIEKVAYTDFVTGYSNWRK
FELDVTNLLKKTSQNNKYAMVIFDIDKFKAINDIYGHKKGNLILKDIADTLNELTDINETFARVSADNFNILLTYNKKEDIINIIKKIMANNELVNLS
FGIYEIKDKDLSVSVYSDRASLAKSSIKNNSDVNFAFFNDKLREKLLFEDKIEKEMEYALESGQFVMYLQPKYNIKLDKFCGSEALVRWQYTEKEV
IYPGDFIPIFEKNGFIRKIDMYILEQACKEIRSLFDKGISPLPISVNFSRVDFFKKDFIENIVNICDRYKIPYSLIEIEITESSMFGDTDTLFNVSRNLQDI
GFIVAMDDFGSGYSSVNMLKNIPLNVIKLDRGFFVDDKDVDKSQIVIKSIVSLIKQLGIRVVAEGIETRSQIEMLKKANCDIVQGYYFSKPLPIKEF
EKLVYKI

>CORE_REP|Org46_Gene2479#(WP_003419821.1 sigma 54-interacting transcriptional regulator)

MNLNLELDLEFYKKILEASHDEICVSDDKGIIIYCNKAFEENYGLKKEDILGKNVSFLEDSGYSTKSPIPVVLKTKSKFSLEQDTQTGKKLIITATPIFD
ENGNLEFTVENCRDITELNNIKNKLEDTKKQVKKYKSEVETLYRTALRIEDTVIMDGIVMRPIINTVNHVSKTDVSVLLLGESGTGKSSLARYIHH
NSNRANGPFITINCATISPQLLESELFGYTSGAFTGASTKGKVGLVELANGGTLFLDEIGDIPQNLQAKFLQLIQDRTFTPVGSLKNKNVDIRIISAT
NADLVSKVKEKKFREDLYYRLNVIEIKLPPLRERRDNLVEIIKYYFNRYSSDFNLNKTISKEAMETIANYRFPGNIRELQNIIQKILLTCTDNHITIHNL
PNILTKNINITNNGNKTHISQINKVITPDSKSINYKNKNFDTLIKEYEKNIILDAYEKFGSSYKVAKHLEISQSKANRLIRKYTNT

>CORE_REP|Org94_Gene1661#(WP_231305334.1| HAMP domain-containing histidine kinase)

MKWKITRNFIFTIVFVAISVVIINIISILYVISTNSFFKVVDSGNNPEEFARSFEKDLYEKDGEFKLSKIGAEKLEKSNSWIQVLNDLGEEVYGVNVPK
YTPKKYTPFQMVNNYKYIETKYVNFVLEKYLNKKHLNIIVGIPSRDISRIILTYSQNNIKKTLNKVIIITLVIDSVVALGVGYLFSRKLTKPISSVLWSIE
TMANGNYSLYLKDRGIYEEVFKNINMLADTLRVNEVERKENEELREEWLANITHDIKTPLASIQGYAEIINDKDYEFEEDEIQEYTEIIYNKSKYIK
DLVDDLNLSTRLKNDTIVLDKKKINLVSLVRNIIIDILNDNRYKNRNIEFESNEDLIEVYVDSILFRRAITNLIFNSIVHNSEGTLISVEIVKKDNIEIIIKD
NGIGISKSDLKHIFKKYYRGTNTGEMHKGSGLGMAISKEIIEIHKGKIYVSSEIGIGTKIIIEIKQN

>CORE_REP|Org37_Gene2294#(WP_004454646.1| aldehyde dehydrogenase family protein)

MEKAVENFEDLSKEYINGYIERARKAQREFECYTQEQVDKIVKIVGKVVYYNAEYLAKLAVEETGMGVYEDKVAKNKSKAKVIYNNLKDKKSVG
IIDIDRETGITKVAKPVGVVAAITPCTNPIVTPMSNAMFALKGRNAIIITPHHKAIGCSTKTVEMINEELEKIGAPENLIQILDQQSRENTRNLISSA
DVVIATGGMGMVKAAYSSGKPALGVGAGNVQCIIDRDVDIKEAVPKIIAGRIFDNGIICSGEQSVIVAEEMFDKIMDEFKNNKGFIVRDKVQK
EAFRNAMFVNKSMNKDAVGQSVHTIAKIAGVEIPEDTKIIVIEADGPGEEDIIAKEKMCPVISAYKYKSFEEGVAIAKANLNVEGKGHSVSIHSN
TVKNIEYAGENIEVSRFVINQCCATSAGGSFFNGLAPTNTLGCGSWGNNSISENLDYKHLINISRIAYYMPENEVPTDEELWG

>CORE_REP|Org18_Gene1417#(|ARC14034.1| aminodeoxychorismate synthase component)

MCNMIREINTKLNSFEIFTIFRNEHDSFILDSAMDKEKLGRYSFISSQPFKVLKYKDTDENPLEVLKEELHKYRVVNDTNLPFVGGAVGYLSYDLG
NYIENLPRTAVDDIEMPDMYFGFYNHVIVIDHLVQKTYIATPNIDIELEEKIIDDIEQRILKEEKKGIDSICYEEKEVTSIRLKSNFTKEEFKNAVQSV
REYIRQGDIYQANLTQRFSGETELTSFELYRDLRRFSPAPFGAFLNFEDAHILSNSPERFIRCVNKRIETRPIKGTRPRGKDKEEDLRLQQELRNSE
KDRAELLMIVDLERNDIGRISKTGSVKVPELFVIEPYANVNHLVSTVVGELKDDKDATDVIKATFPGGSITGAPKIRAMEIIDELEPTQRNVYTGSI
GYIGFNGDMDFNIAIRTIIKNDKKVYFQVGGGMTWDSDPDEEYQETLDKAKSIMKALRGYYEE

>CORE_REP|Org83_Gene1650#(WP_003423653.1|sigma-54 dependent transcriptional regulator)

MKILIVDDELEYGVVMKKILQKKGYLVDVTLSGEEAINIIKKDKNYDLVLSDVMMKNMDGVQLLDRIKAINKDIEVILVTGYGSIENAVDAMKK
GALSYFIKSNPIENLLEEVEKVKTSKTSVSLQKNNLEFTLESKNRDFNDVIKIAKKAACKDVNILILGESGVGKDILARYIHSISPRKNEIFVPVNCCSF
SENLLESELFGHEKGSFTGAVDSRKGRFELSNKGTLFLDEIGDIPLNVQVKLLRTLEDKSIERIGSNKSIKVDFRLICAMNKEPKVEISNGNIREDFF
YRISTITITIPPLRKRREDLATLIEFFLNKYQIEHDKKIHSIDKEVKDFLLNYNYPGNIRELKNIINRLVVLSEEGNLSKDNLNLISNNVYIDDKISIKPLR
EIRKEFECEYIEKVLSLCGNNISNTAKKLEISRRQLTNKIAEYNIK

>CORE_REP|Org50_Gene2566#(HBH1461641.1|TPA: D-alanyl-D-alanine carboxypeptidase)

MKRNLSLLLICLLIFTSFLGRSNISFADNEPAIVAKHAVLMDYETGKILYNKDGNSKLYPASTTKVWTACLVLKEVKDLNQVIEIKDLPQIDGSSMY
LKEGESFTVKQLLDALLVHSANDAAFVLARYVGGGNVQKFIDLMNSEAKKIGATNTHFNNPHGLPDPNHYTTAHDMALIAREAMNNDTFRQ
IVKTKSLKFEATKAYPYERYFVNTNKFLTSHDKITYKGQPINIKYDIVDGIKTGYTDAAGKCLLSSAVKDGRRVIVAVFNSTNADLYLDSRILIDYGF
DNFKCATIVDKEKYTDTKKVLFTKQHELIYEPKNSYKIFLEKNESKGNYDTKTELNKIDLPIKKGAKVGTLNVYNNGKLENSIDLIAKNNLDSSLPFL
TENNVLMTFVKIIAGILILLVLFIITSNIKKKKKIKKARGKRNMKK

>CORE_REP|Org85_Gene2013#(WP_003424453.1| HAMP domain-containing histidine kinase)

MRRIFDKWEKLSIKYKLFSITTSLLIALALIIYLILYFLLPSYYHEYKIESLQESLKSLVDSSIHFDTYTLEERLYYMAKDQNLAILLKDNQGKIVYGKNEV
VILRYSKYMINSLEDEYRTSIPIYTKDAKDGPYTLELVMPLQPIDEANEVIRKLMPYIISIAILIAIIGAYIYSIVITKPLINIIESEREQEYRRKDFVATISH
ELKTPITIISGQIEGMIYSVGKYKDRDTYLKKSYECTQELKDLVNEMIEVSKSEILEKDLKLVSINISELLNRLVKRQVFLIEEKHMKTILKIEENLEVKA
DQERITKAINNIINNAIKYSPEESEIIIRLYDKNKRISKKNSNQRVVLEIENTGVTIEKRYLEEIFNPFYRIEKSRSRKTGGSGLGLYIVSQIFKSHGFDY
SIKNKENSVIFTVEFKN

>CORE_REP|Org10_Gene510#(WP_165476817.1|D-alanyl-D-alanine carboxypeptidase)

MEDEILKGKIKQLTILALIFIFITPVFAFADTPPVPNSSRAALLIDQETKRILFEKNIDEKMPLASLSKMMTFLLAIEAVDKNQVKETDMVKIDKSTA
SVGGSTCKLKDGDEISLGELMQGLMLVSGNDAAIAIAKHIGKTEKNFVNMMNKKAEEIGMIDTYYFNPNGLPIYTDPEHKEPPIENMSTAHDI
VTLGKYMYDHYENQVTRITTMQVYNDTKKDFTHYNTNPLLVSVPGVDGIKTGYTDNAGYCLAFSMMVPKDAKNERNHRLIGVVLGDGNKK
NRISSSATLLKYGKDNFHSKKIAHKGDIIETPCVDGIDDFKITVKVDKDLYGVVSDNENINPKVVFKNMNYPIHKGDIVGVAKYYNDSGKFVGSV
DVKSESNIGCIPLKDKIKIKVAKINKKLEIKNSVCFKA

>CORE_REP|Org18_Gene2684#(WP_074033631.1| undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase)

MMKVLLSGGGTGGHVYPAIAIANKIRDEHPDAEIIFVGTEKGIESEIVPKYGFELKTVTVQGFKRKIDFDNVKRVFKLFKGLEQSRKIVKKFKPDIV
IGTGGYVSGPVLFNASMGKIPAIIHEQNSFPGVTNKILSKTVTKVLTSFEDSHKRFPEAAEDKLVFTGNPVRKEILLSRKNIARKNLSISDEKRMVL
CYGGSGGSRKINDAMRLVIKNMVNEDIAFIFATGKSYYDEFMGSISDINLKPYQKVVPYLEDMANALAASDLVIGSAGAISLAEITALGKPSIIIPK
AYTAENHQEYNAKSIEKQGAGIAILEKNLTPESLNTAVFKLLGDRELLVDMANASKTIGKPEAIDLIYDEIMKVYNSTQKSTSKKTKKEKVIKEVKE
IKKETTPSIEGQAKVIGIKKR

>CORE_REP|Org43_Gene1184#(WP_003422743.1|D-alanyl-lipoteichoic acid biosynthesis protein DltD)

MRKLIYFITPFIIGVVFLFGLDKFLDSKTDELLREKNLLPIMDDTLSDIKDKGVTANNHFLREKDIMILGSSELSNSTKQHPKYYFNTNRSKNKVFAI
GRAYTQTLQDAAILGSMNPNIDNKKVVLLISMQWFMEKDGVTSHHYQSRFSPIQFYRFLDNPKISKQNKIEYAKKSSKLLWGSDEYKAEALYA
KLYEPKTLLEKAEKVLLEPYFQGRKYCIALKEKGILYKRLIKLDKKRATKRKSPINWSHERKKAIEDAKKRVGKNPLNIDNYYYKQHFKDGIDQYKG
RDKDVNLLTSKEFESYKLMLNVCTDLGIKPVVVLIPSMDKFYNLTGISEKERNQYYDKAQNIAESKGFEVLNLKDKGSDKYYLRDVMHLGTKGW
VDVCERLFKIFKEQ

>CORE_REP|Org81_Gene2994#(WP_095903575.1|UDP-N-acetylglucosamine 2-epimeras)

MNDIKVMTVFGTRPEAIKVAPLIKELEKRENIKSIVCVTAQHREMLDQVIETFNINVDYDLDIMEKGQSLNDITCKILNKLPLILNKENPNIILVHG
DTTTTLATSLTAFYNKTLVGHIEAGLRTYDKYSPFPEELNRQLTGIIADMHFAPTNLAKKNLISEGKPNNNIFVTGNTAIDALKMTIKENYNHPIID
EIGNDRMILLTSHRRENLGKPMKNIFRAIKRIVDDFEDVQIVYPIHLNPKIRTIADEIFGKFPKKIHIIEPLDVADFHNFLNKSYMIMTDSGGIQEEA
PSLGKPVLVLRDKTERTEGIEAKTLKLVGTNEDRIYNSVSDLLINKDNYVQMSKASNPYGDGNASKYIVDIIIKKFNCKYLN

>CORE_REP|Org58_Gene2738#(WP_003426511.1| mannose-1-phosphate guanylyltransferase)

MKVYNVIMAGGGGTRFWPLSRQEVPKQLINLSGEDALINETINRIDSLAKKDDLFIVTNEKQLEALKDIVKDKCLDSNILPEPCARNTAAAIGFA
AFNIMKKYGDGVMCVYPADHYIKDEKEFKSILEKAIYIAENNDKLVTIGITPTFPSTGYGYINFNRENTIEDVAYEVVEFVEKPNYEIAKEYVNSKK
YVWNSGMFVWKVSKILEDFKRYLPKVYEKLEDISKYLGTKEEMEKIKEIYPTIQSISIDYGIMERSNDVIVVPGDFGWNDVGSWDSLGAIYPTDD
EGNIKRGENITIDTKNSIIYSDDKLISTIGISDLIVVSTNDAVMVCRKDKAQDVKKIVEQLKEEDRQEYM

>CORE_REP|Org39_Gene1501#(WP_003433486.1| histidinol-phosphate transaminase)

MREKESIRELRGYEPNHVNCKVKLDANEGSKRLFKYLIKEISDSDIDLNLYPEDSYSNLKESIIDYINISGVNKKNLLVGNGSSEIIDLIIHTFVDKDEV
ILSFSPSFSMYSIYSQINGSKFIGVESDENLVINIDSVIEKVKENNPKIVIVCNPNNPTGTILKREEIIKLLDSTNSLVVLDEAYMDFGEESMLSDVFK
YDNLIVLRTLSKAFGLAGIRTGYMLSNSSLINSVEKVRPPYNLNSLSDFIATRALRNKDVVKAYIKEVKEEREVLYKEMIGMGIKAYKSQANFILFY
SEIENLSQKLIDRGVLIRKFGGKLENYYRVTIGDKEENSMFVGAIRDILKKEK

>CORE_REP|Org82_Gene1721#(WP_003428627.1| 3-deoxy-7-phosphoheptulonate synthase)

MIVVLKMGADKNEVKKLIEAIGREGVEVNPIDGTELTVLGLVGDTSKIDAKRIEANKIVEKVMHVVEPFKKANRKFHPEPSIINVNGMEIGSKKI
AMIAGPCSVETEDQIVSIAKDVKKSGAGFLRGGAFKPRTSPYAFQGLKYDGLDLLKKAKEKTGLPIVTEIMSTQDIDIFEENVDVIQVGARNMQ
NFDLLKELGKTNKTILLKRGLSATIEEWLMSAEYIMAGGNENVVLCERGIRTFETYTRNTLDLSAILAVKKLSHLPVIVDPSHAAGKSWMVDSLS
KAAIAVGADGLIIEVHNDPAHALCDGKQSIKPNEYDELISELKTIASAVGREI

>CORE_REP|Org73_Gene1768# (WP_077709045.1|siderophore ABC transporter substrate-binding protein)

MNKKAAIVAAVAIIIGLVTVFALGGSKKNESKTSEDSNNTIKITHNLGETDVKLNPKKVVVFDYSALDTMDALGVAENLVGLPKASLPASLEKYK
DEKYADLGGLKEPDLEGIKSANPDLIIINGRQEDFYEQLSKIAPTISTSKDDKKYLESVKNNIDKIAKIFGVEEKANQEFSKIEKKIEILNKKVTDKNL
NALTIMVNEGNLSVFGEESRFSILYNSFGFENKDKNIKESSHGQNITFEYIAKQNPEVMFVIDRGIATGSDVKESSTAKSVLNNDIIKSMDAYKN
DNIIYLDSPTWYVNDGGLTSLNKMIDDASKAVN

>CORE_REP|Org33_Gene1037#(WP_003438004.1|selenium metabolism-associated LysR family transcriptional regulator

MDFKQLEVFVAVAKHQSFSKAARELFLTQPTVSAHIQNLERELETVLINRSNKVITLTKSGEILYEHAIYILNNCKRAIYDIKEYSGKIEGIIDIACSSI
PETYILPDFMKSFSMSYPDVKFSISHYDSQYAISEILNERISFGLVGSKINNPQIEYLDLLDDELVLITPSDFKIDNKNNCIDIGELAYLNFIMRKEGS
GTRNLILNTLSKNNFPVSKLNVIAHVESNEAIKEMVRLGLGVSFISYISAIDYLNAGKIKCYKIKDVDFTRKFFFIYSKKKTFSPLEDKFLNRLCEYFEII
I

>CORE_REP|Org63_Gene2774#(WP_003426478.1| N-acetylmuramoyl-L-alanine amidase)

MKKKLLDGKITLIICKSVKIYTKKGEEMSKGNNNNNSRNKSKKTSHLNRKKRKLNKKKLAVLICFTVLFLFIAFKATQGVVALVKSMDKSNKTSQ
QQNVNSEQFDFGNEEENKKKKYTVFIDPGHGGNDKGTESKTSNRYEKDLNLQIAKKLANKLSKQKDIQVVVSRTDDTYISLKDRAILANNSSAD
VLVSIHLNAEKNGNTATGIETWYRNKATDGSKELAQAVQSTIVSYVKVRDRGIVENNFEVLRESNMPAILIECGFLTTPSEEQKIINEKYQDQLA
EGIVQGVLSYLDSKGNK

>CORE_REP|Org53_Gene987#(WP_021362441.1| glycyl-radical enzyme activating protein)

MSKKGRVVKVQHFSVNDGDGIRTTIFLEGCKLKCKWCSNPDSWSNIVKLGVMKDKCVSCNRCIDVCPQNISSLFDRAQINNKCDLCGECIKVC
LKDAICIMTEEMSVEEIVEEVEKDFIFFFESNGGITFSGGEPTLQIDFLRELVDIFYDKGINIAIETCGYFDWNKVNDVFEKIDHIFVDIKSMDDNIH
KEYTGVSNKIILDNICRLSKLNKSMVIRVPIIYGVNDSEENIRNTALFVKQNVPGGKMELLPYHKFGIDKYKALGLEDYIYEFDEICNNHMLKLKEI
VELTGVKIIEYK

>CORE_REP|Org89_Gene2365#(WP_003419800.1|D-alanine--D-alanine ligase)

MKIAVIMGGISSEREVSLNSGKEIYNNLDKNKYEVVKVIIDDKKDIFTKIPEDIDFAILALHGKFGEDGCIQSILETMDIPYSGCGPLCSGMCMDK
NITKKMLRDSNLPTAPWVLVKSVDEIDYDEIDNIGYPVFIKPNSGGSSVATFFIHSKDEVGEAVRKGLEVDEFVMIEKYIPGGEYTSFILNGEVFP
TISIKSDSGFFDYEAKYSVEKGAKEEVVYLDEELQKRVNEISETCWKIFNCKAYVRVDMIISEGIPYVLELNTLPGMTQTSLIPRSAAARGIKYSELL
DKLIEYSLN

>CORE_REP|Org72_Gene2726#(WP_003416240.1| YicC family protein)

MAISMTGFGRGEYKDDNYYFLVECKTINHKYSDINIRLPRKISFLEDKVRNLVKNYVKRGRVDLYIKFDLLGKEDVNLNFDEGLASQYIDILKEIKN
KFDIIDDISVMNVAKFPDIVKIEEKEEDEDLLWSMLNQAVEDALIKLREMRSEEGKKLAEDIAMRCDLLKNHIEEIEKYSSSVVEDYREKLNLRISE
LLDDPSIIDENRLAQEVAIYADKSSITEEIVRFKSHIGQLKNTIFKDDSIGRKIDFLIQEMNRETNTIGSKSSDINITNLVVEVKSELEKIREQIQNIE

>CORE_REP|Org11_Gene1255#(|WP_045136015.1| sporulation transcription factor Spo0A)

MGGFLVEKIKIVLADDNKDFCQVLKEYLSNEDDIDILGIAKDGIEALDLVKKTQPDLLILDVIMPHLDGLGVIEKLNTMDIPKMPKIIVLSAVGQD
KITQSAINLGADYYIVKPFDFVVFINRIRELVSNRVTQVEPKPRPVQETQMTRSDFVKNVGNIENVGNIETEITNIIHEIGVPAHIKGYLYLREAIK
MVIDNVELLGAVTKELYPSIAKKFNTTPSRVERAIRHAIEVAWSRGKVDTINQLFGYTVHNTKGKPTNSEFIAMIADKLRLEHSMVK

>CORE_REP|Org12_Gene2351#(WP_003433818.1| MoxR family ATPase)

MIKKEISNFRGSSDYVVSPELMASVNVAIALEKPLLIKGEPGTGKTMLAQAISNELKKDLVIWNIKSTTKAQEGLYVYDTVQRLYDSQFGGEGVD
DISKYIKYGKLGEAFSSNQQVILLIDEIDKADLEFPNDLLWELDKMEFYINETKETVRAKQRPIVIITSNAEKELPDAFLRRCIFHYIEFPDRDMMEE
IVKVHFDKVEEHLLEQVMTTFYWIRSLKDIQKKPSTSELIDWIQALTLSGMPIEKIEKEVPFAGILLKNNEDIESMQRHL

>CORE_REP|Org83_Gene1695#(WP_003423767.1| ATP-dependent sacrificial sulfur transferase LarE)

MEVNFVKEKEKLDKLKKMLLELGSVVVAYSGGVDSNFLLKVAKDTLGENVVAVTIHAMMHSSREIEEAKQYTQNFGVKHIILNIENFDLKEFKE
NGIDRCYHCKKYIFSKIKEVAKEHNIKYIVDGTNIDDLGDYRPGLKALSELGVISPLKDSGLKKEEIRSLSKILGLKTFNKPSFACLASRIPYGVEITDE
NLRIIEKSEEYLSNLGFSQFRVRMHGDIARIEVGQEELGKFFENNNFNKVDTKLKIFGFKYVTLDMSGYKMGSMNLNV

>CORE_REP|Org64_Gene2604#(WP_003416101.1| RNA polymerase sporulation sigma factor SigG

MQVNKVEICGVNTSELPVLKNKQMKELLLQIKNGDEEARQQFVRGNLRLVLSVIKKFNNRGENIDDLFQIGCIGLIKAIDNFDLSQNVRFSTYA
VPMIIGEIRRYLRDNNPIRVSRSLKDIAYKALQVRERLIRTNSKEPTVSEIAKELELEVESVVMALDAIQDPISLFDPVYQDNGDAIFVMDQVQDK
KDTDENWLQEISLKEAIKKLNSREKLVLDLRFYKGRTQIEVADEIGISQAQVSRIEKNALKNMRKYV

>CORE_REP|Org28_Gene2625#(WP_009897796.1| response regulator transcription factor

MRAIIVEDEFPARKELRYFIENKSGIEVVSEFTNGIEVLDFIQENKIDVIFLDINIPHLDGMLLAKTLNQFKSRPKIVFITAYESYAVDAFSLDVFDYIL
KPYSEERIISMLNKLEKSEMSDIELSNVNSNLYKYKKEAVNQEIEEITHKISLWKGDKLVVIDIDDIYYCEANERQTFIYTEKEKFILKEGISEVENLIN
DKTFFRTHRSYIVNLTKVKEIIPWFNNTYILKLKNSDYEVTVSRSKVKEFRLLMHI

>CORE_REP|Org18_Gene1530#(WP_003436672.1| imidazole glycerol phosphate synthase subunit HisF)

MLTRRIIPCLDVRNGRVVKGKKFKDIVDVDSPEVLGKFYSDCGADELVFYDITASNEERKTSLEFVTKVAENINIPFCVGGGVNKLEDFTDILRKG
ADKVSINSSAVKNPELIREASLKFGAQCVVLSIDAKKNEEGSWSVYVKGGREKTNLDAIEWAVKGVELGAGEIVVNSMDEDGMKNGYDIELLS
KITSLVNVPVIASGGAGKKEDFYEAVNKSNVDGILAASVFHFGEIKINDLKKYLKDMGVEVRL

>CORE_REP|Org75_Gene481#(WP_003436678.1|imidazole glycerol phosphate synthase subunit HisH

MNIIVDYGLGNIDSVSRGFRKAGIETKISSDIDEIKQADSLILPGVGAFRDSISALDKLGLIPIIKEHVSKGKFMIGICLGMQLLYEKSYEYGEYEGLG
LIKGSIDKLDISLKVPHMGWNNLKFNKANDDILKYINEDDYVYFVHSYYANSSNEELIAFSEYEKKIPAIVRKGNVYGIQFHPEKSGEVGLNILRAY
GEMIK

>CORE_REP|Org2_Gene2029# (|WP_236879159.1| serine O-acetyltransferase)

MFKKINKDIEYIMKNDPAARSKIEVFLLYPSVHAMIMHRMAHALYKKKKLFTARLISQISRFMTGIEIHPGAKMGEGILIDHGMGVVIGETAEV
GNRVTIYQGATLGATGKDTGKRHPTVGDDVLIGAGTKILGPLNIGSNSKIGANSVVVKDVPNGATVVGIPAKIVKIRNLEPVKKNKKEVSYEYDE
LDNVYYI

>CORE_REP|Org86_Gene2134#(WP_003430598.1| ribosome recycling factor

MKLEIHKQLEEKMNGTIDALKFEFGTIRAGRANAQMLDKIRVDYYGTPTPINQIGAISVPEPRILMISPWDKSAMHEIEKAIANSDLGLNPSND
GEVIRLSVPALTEERRKELAKKASKAAEEFKVRIRNERRDANEKIKKMEKGGELTEDELKKAQDEVQKMTDKFIKEIDTLLSKKEKDIMEV

>CORE_REP|Org20_Gene2996# (WP_003425127.1| signal peptidase

MGEAVKKEVVEWIKVIVIALVLAFAITRFIVPTIVKGESMYPTLVERDYLIVNRIAYKVGEPKYKDIIVFKTDLTEENGKKKDLVKRVIGVPGDHVKI
QDSKVYVNDKLLDETSYIHNNRTDGDIDIVVPEGKLFAMGDNREKSLDSRYDEVGLVDEHTILGKVLVRLYPFSKIGTID