>Dmel\_GPDH-1B

MADKVNVCIVGSGNWGSAIAKIVGANAAALPEFEERVTMFVYEELIDGKKLTEIINETHE

NVKYLKGHKLPPNVVAVPDLVEAAKNADILIFVVPHQFIPNFCKQLLGKIKPNAIAISLI

KGFDKAEGGGIDLISHIITRHLKIPCAVLMGANLANEVAEGNFCETTIGCTDKKYGKVLR

DLFQANHFRVVVVDDADAVEVCGALKNIVACGAGFVDGLKLGDNTKAAVIRLGLMEMIRF

VDVFYPGSKLSTFFESCGVADLITTCYGGRNRRVSEAFVTSGKTIEELEKEMLNGQKLQG

PPTAEEVNYMLKNKGLEDKFPLFTAIHKICTNQLKPNDLIDCIRNHPEHMQNL

>Dvir\_XP\_002051368

MAEKVNVCIVGSGNWGSAIAKIVGANAAALPEFEERVTMFVYEEMIDGKKLTEIINETHENVKYLKGHKL

PTNVVAVPDLVEAAKNADILIFVVPHQFIPNFCKQLLGKIKPNAIAISLIKGFDKAEGGGIDLISHIITR

HLKIPCAVLMGANLANEVAEGNFCETTIGCTDKKYGKVLRDLFQANHFRVVVVEDADAVEVCGALKNIVA

CGAGFVDGLKLGDNTKAAVIRLGLMEMIRFVDVFYPGSKLSTFFESCGVADLITTCYGGRNRRVSEAFVT

SGKTIEDLEKEMLNGQKLQGPPTAEEVNYMLKNKGLEDKFPLFTAIHKICTNQLKPKDLIDCIRNHPEHM

QTL

>Dmel\_GPDH-2

MDKIMICIIGSGNWATTIARNVGRNVLNSQTLDEKVPMYVYEEIVEGRKLTEIINTTHIN

SKYMPNFELPPNIVAVDDIVTTARDADIIIFAIPPTFVSSCCKTLLGKVKPTAHAVSLIK

GFERGDDGQFVLISQIIMRQLKIPCSVLVGCNLAHELAHDHFAEGTVGCRDQKYYRVLHD

IFKSPTFRVVVTEDADCVEICSTLRNIIAFAAGCSDGMELNENTKGGIIRRGFLEMLQFV

DVFYPGCRMGTFFESCGISDLVTSCYANRNRKLAEAFVKTGKPLSELEHILIPGHEPLGP

VTAELVHHMLKKKGLEDKFPLFTTVYRICTGDYPLQRLVETLIKAREDIFHPLHTFQL

>Dvir\_XP\_002049040

MTDRLNVCIIGSGNWATTIARNVGLNVANSQLMEPKVNMYVYEEYIDGRKLTEIINTTHINVKYMPNFVL

PPNVFALDDVVTTARDADILIFAIPPTFVSSCCKTLLGKVKPLAHAVSLIKGFERGDDGQILLISHLIMR

QLKIPCSVLVGCNLAHEISNGNFAEGTIGCRDQKYMRILQDIFKSATFRVVVTDDADCVEICNSLRNVIA

FGAGCADGMELNENTKAGIIRRGFLEILQFVDVFYPGSRLATFFESCGLSDLVTSCYANRNRKLAEAFVK

TGQPLSELEHILVPGHEPLGPITSELIHIMLKKKGLEDKFPLFTTIYRICTGVYPLSRLVETLRFAREDI

YHPNHIFQL

>Dmel\_GPDH-3

MAGKLKICIIGAEGWGSAIAAVVSNNVLEGDFDSRVHLYVYDEMIRDTALSEIINTRHEN

VKYLPGIKLPNNLIAVNDLLEAAQNADILVFSTPLEFVQSYCNILSGNVKESAFAVSMTK

GLLSENGEGIELVSHAISESLGIPCYSMMSAHSAMEMAQGKLCEVTIGCSDNSHSKLLIS

AMQTNNCRVISVNDVDGVELCGTLTDVVALGAGFIDGLRLGENARLAAIHLGVKEIMRFI

KTFFPSSKMSTFYESCGVTNAVASSFVDKNVTFAKSLVTSGQTIEEIEANLHSGRKLLGP

MVASNVNAFLENGLMQHEFPLFTAIHLICQSEAPPELMIEALRNHPDLSSSSISHL

>Dvir\_002054373

MPKHPKVCIIGAEGWGSAIATSVCKNVVDVGEFDSRVHIYVYDELVRSNYLSEVMNEQHENIKYLPGIRL

PSNLIAINDLIAAARNADILIFATPHSFVKSYCNILAGNIKSTAYAISLTKGLEHRDGEIELYSHAITHL

LGIPCYSMMNANSAMEMAQGKLCEITIGCNNDAHANQLNYLLQTENCMVFTIDDVDGVELCNTLKDLVAL

SAGFIDGLHLGENARIACLHLGLKEMMRFITNCNPTTNVTTFLESCSLANSVASAYGDKNVTFAKNFVTS

QKTTQEIEASLLNGRKLLGPIIAGEIFAYLDNEDLHDIYPLFSIIHRICEKEVPPQAIVDTLRNHPDLSP

KKKLSHGKFTPNTEMEVENAILDDVIPKTIDKKLNDKTKFINYKPRRDRDDGSDKKKRGRNNETKKDRRD

ENRNSLDEDQRTLALEATENREDIAFMEKLESDVEKAILEEQVPAAVESKIGEEEATQNLDLIHNKSDEN

TNFTALDQDHTQLKYLKAEQEETLLLEAESADVKRSNQEPIGMSESLDGDSERETKAIQMEDKAQQFLAS

KIHNEKVPKPSSEWDWLLDNDKFDSALEEFKQNKDDAAKKPKPLDLSDFKKKLQTYRLERSQEPEPGRMQ

ELKIDSDLLWPNREQDSNEPTRIEALVKSEEATKNETPEQLVEPRAEWSKDEDTVKYTFPEPTPLMEAQT

NVEKAKDLASPDTDVPEAEDTQLKKEWPKENVSYNIEIEPSAEEKISSIEEPEELKDPRKRRKQKSQEMY

DIARQQFWQAQDEHENKTKRDDLQVSEITKQLTKIMTKGQPAPPQPKERPVDYQGDDPYIKENKKVARHS

YGNMLEGDSKQRSRVVVKPFHPPLNPRVRIPRPPFDVRDHEYHTVNFRPPPDLLRTVNLPKKRTTVTCQA

GQTGTRSVSMLPRPVLKLPPFMMRSSVLAIELGFVAAILSRYKSGRK

>Dant\_CL1818

MAQKTNVCIVGSGNWGSAIAKIVGANCANLPEFEERVTMFVYEEMIDGKKLTEIINTTHE

NVKYLPGHKLPPNVVAVPDLAEAAKDADVLIFVVPHQFIPNFCKTLLGKIKPNAQAISLI

KGFDKAEGGGIDLISHIITRHLKIPCSVLMGANLANEVAEGQFCETTIGCKDPKYAKILR

DLFQANMFRVVVVEDSDAVEICGALKNVVAMGAGFVDGLGLGDNTKAAVIRLGLMEMIRF

VEIQYPGSKLSTFFESCGVADLITTCYGGRNRKVGEAFVKSGKTIQQLETEMLNGQKLQG

PLTAEEVNYMLKNKNLEAKFPLFTAVHKICSGASKPQDLIESIRIHPEHMQNL

>Ccap\_XP\_004529383

MSEKISVCIVGSGNWGSAIAKIVGNNCATLPQFEKCVTMYVYEEMIEGKKLTEIINTTHE

NVKYLPGHKLPENVVAVPDLIEACKNADILIFVVPHQFIPNFCKTLLGKIKPNAVAISLI

KGFDKAEGGGIDLISHIITRHLKIPCSVLMGANLANEVALGNFCETTIGCRDIKYAKPLR

DLFQAPYFRVVVVEDSDAVEVCGALKNIVATGAGFVDGLGLGDNTKAAVIRLGLMEMVRF

VDVFYPGSKLSTFFESCGVADLITTCYGGRNRRVAEAFVKTGKSIEELEKEMLNGQKLQG

PPTAEEVNYMLKNKGLEDKFPLFTAIHKICTNQLKVQDLIDCIRNHPEHMQNL

>Mdom\_ALHF\_11471

MAQKTSVCIVGSGNWGSAIAKIVGANCANLPEFEERVTMYVYEEMIDGKKLTEIINTTHE

NVKYLPGHKLPPNVVAVPDLVEAAKDADVLIFVVPHQFIPNFCKQLLGKLKPNAIAISLI

KGFDKAEGGGIDLISHIITRHLKVPCAVLMGANLANEVAEGQFCETTIGCRDPKYGKILR

DLFQANHFRVVVVDDSDSVEICGALKNIVAMGAGFVDGLGLGDNTKAAVIRLGLMEMIRF

VEIMYPGGKLSTFFESCGVADLITTCYGGRNRKVGEAFVKSGKTIQQLETELLNGQKLQG

PLTAEEVNYMLKNKNLEEKFPLFTAIHKICSGVLKPQDLIECIRCHPEHMQKL

>Mdom\_XP\_005190609

MEKIHVCIIGSGNLGTALGKILAENAAALSDFEERVNMFVYDELFDGIRLSDLINSHHIN

EKYLPQIQLPDNLVACTDLVETAKYADIIVFVMPKQFIEDFCKTLLGKIKPNAMAISVIK

GFVLNEGDDNGGEVASGSGIQLISQTIMKYLKIPCAVLMGVNLASELTLNRYCEATLGCR

DMKHSKLLKDLFSTPNFRVIVIDDADAVEVCGYLKHLIAFASGILDGLQTNENTKSACLR

FALIEMLRFIDVFYPGCKLSTLFESCGIADVLTVCAGSRNRRLGEAFAKSDRSIEQLETS

LMGGEQVLGPLTANAVYLMLQQKGLQERFPLFTIIHRICKREVKPEELLHCIATMPNIIY

HPTQIFPL

>Gmor\_GMOY009911

EKVSICMVGSGNWGTAVAKVVAENAIRLEDVENRVNLFVYDEIFEGKRLSETINQHHINSKYLPYVKLPENLVAFTDLVESAKYADIIVFAIPSKHIIDFCKTLLGKVKPNALAVSLIKGFLPSEGG-IELISHTITKYLKVPCAVLVGVNLASEIVANKFCEATLGCRDTKQTRILKEIFKGPSLRIVVVDDADCVEVCGLLKHILAFGTGLLDGLDCNENIRSALIRFGLLEMMHFIDIFFPGSKLGSFFESSGISDLITVCYGSRNRRIAEAYIRTDYTIEQLEGELLKGQKLLGPMVAKEVNHMLNNKGVEAK

>Gmor\_\_GMOY008210

MSEKTNVCIVGSGNWGSAIAKIVGANCAALPEFEDRVTXXXMYVYEEMIDGKKLTEIINTSHENVKYLPGHKLPENVVAVPDLVEAAKNADILIFVVPHQF

IPSQCQMLLGKIKTNALAISLIKGFDKAEGGGIDLISHIITRHLKIPCAVLMGANLANEV

AEGHFCETTIGCREPKYAKTLRDLFQSENFRVVVVQDSDAVEICGALKNVVAMGAGFVDG

LGLGDNTKAAVIRLGLMEMIRFVEIMYPGGKLTTFFESCGVADLITTCYGGRNRRCAEAF

VKTGKTLVEVEAELLNGQKLQGPLTAEEVNHMLKNKKLEEKFPLFTAVHEICTGQIKPQC

LIERIRAHPEHAQASTPAPKL

>Tdal\_Td\_comp159056

MEKLSVCIVGSGNWGSAIAKIVGANCANMDEFDNRVNMYVYEEVVNGRKLTEIINDTHEN

VKYLPGHKLPENVVAVPDLVEAAKNSDILIFVVPHQFIPSFCKTLLGKIKPNAFAISLIK

GFDKAPGGGIDLISHIINRNLKVPCSVLMGANLANEVAEGNFCETTIGCRDAKHAKIFHQ

LFQSQNFRVVVVDDADAVEICGALKNIVACGAGFVDGLGLGDNTKAAIIRLGLMEMIRFV

DVFYPGSKLSTFFESCGVADLITTCYGGRNRKVSEAFVKTGLTIAQLETELLNGQKLQGP

ATAEEVNYMLKNKGLEDKFPLFTAIHKICTNQLKVEELIECIRSHPEHM

>Aaeg\_XP\_001653595

MADKVKVCIVGSGNWGSAIAKIVGVNAKRLPNFEDRVTMYVFEEMIDGKKLTEIINTTHE

NVKYLPGHKLPENVVAVPDVVEAAKDADILIFVVPHQFIRGLGAQLLGKIKTSAVGLSLI

KGFDVAEGGGMELISHIITKHLKIPCSVLMGANLAGEVAEEKFCETTIGCRDMKIAQTLR

DLFQTPNFRVVVVDDVDAVEICGALKNIVACGAGFVDGMGLGDNTKAAVIRLGLMEMIKF

VDVFYPGSKLSTFFESCGVADLITTCYGGRNRKVSEAFVKTGKSIKQLEDEMLNGQKLQG

PITAEEVNFMLKNKGMEDKFPLFTAIHRICTAQIKPQGFLDCLRNHPEHM---KQRAKL

>Agam\_XP\_001687881

MSDKVRVCIVGSGNWGSAIAKIVGANAKRLATFEDRVTMYVYEEMIDGKKLTEIINTTHE

NVKYLPGHKLPENVVAVPDVVEAAKDADILIFVVPHQFIRGLGTQLLGKIKPTAVGLSLI

KGFDVAEGGGMELISHLITKHLKIPCSVLMGANLAGEVAEEKFCETTIGCRDMKIAQTLR

DLFLTPNFRVVVVDDVDAVEICGALKNIVACGAGFVDGMGLGDNTKAAVIRLGLMEMIKF

VDVFYPGSKLSTFFESCGVADLITTCYGGRNRKVSEAFVKTGKTIVELENEMLNGQKLQG

PITAEEVNFMLKSKGMEDKFPLFTAIHKICTGTVKPQGFLDCLRNHPEHM---QKFS--

>Cqui\_\_XP\_001841997

MADKVKVCIVGSGNWGSAIAKIVGVNAKRLPTFEDRVTMYVFEEQVDGKKLTEIINSTHE

NVKYLPGHKLPENIVAVPDVVEAAKDADILIFVVPHQFIRGLGQQLLGKIKKTAVGLSLI

KGFDVAEGGGMELISHLITKHLNIPCNVLMGANLANEVAEEKFCETTIGCRDMKVAQTFR

DLFQTPNFRVVVVDDVDAVEICGALKNIVACGAGFVDGMGGGDNTKAAVIRLGLMEMIKF

VDVFYPGSKLSTFFESCGVADLITTCYGGRNRKVSEAFVKTGKSIKQLEDEMLNGQKLQG

PITAEEVNFMLKSKSMEDKFPLFTAIHKICTGQIKPAGFLDCLRNHPEHM---QTFS--

>Llon\_LLOTMP002548

ADNIKVCVVGSGNWGSAIAKIVGHNAAKLPNFCDRVTMYVYEEMIDGKKLTEIINEQHENVKYLPGHKLPPNVVAVPDVVEASKDADILIFVIPHQFIRGLAAQMLGKIKTTAVGLSLIKGFDVAEGGGIALISHIVTKHLNIPCAVLMGANLANEVADEKFCETTIGCKDMKIAPVLRDIIQTEYFRVVVVDDEDAVEICGALKNIVACGAGFVDGLKLGDNTKAAIIRLGLMEMIKFVEVFYPGAKLSTFFESCGVADLITTCYGGRNRKVSEAFVTSGKSIKQLEDEMLNGQKLQGPITAEEVNFMLKNKGMEDKFPLFTAIHRICTGALKPKDVIDAIRTHPEHMQTF

>Ppap\_JP550838

ADNIKVCVVGSGNWGSAIAKIVGHNAAKLPNFCDRVTMYVYEEMIDGKKLTEIINEQHENVKYLPGHKLPPNVVAVPDVVEASKDADILIFVIPHQFIRGLAGQMLGKIKPTAVGLSLIKGFDVAEGGGIALISHIVTRHLNIPCAVLMGANLANEVAEEKFCETTIGCKDMKIAPVLRDIIQTEYFRVVVVDDEDAVEICGALKNIVACGAGFVDGLKLGDNTKAAIIRLGLMEMIKFVEVFYPGAKLSTFFESCGGADLITTCYGGRNRKVFEAFVTSGKSIKQLEGEMLNGQKLQGPLTGGEVNFMLKNKSMEGKFPLFSALHRICTGVLKPKDIIDGIRTHPEHMQTF

>Tcas\_XP\_008201416

MIGFLSFYQSLIGRIRIDVGRRFWAVSTLSARFKPQQSRQSLTSKRSSCHSTNLFESSARMSQKLKKVCI

VGSGNWGSAIAKIVGSNAKKLPHFDDKVTMYVYEEMINGKKLTEIINETHENVKYLPGHKLPPNVVAVPD

VVEAAKEADILIFVVPHQFIRTLCSTLLGKIKPTAIALSLIKGFDRAEGGGIDLISHIITRHLRIPCSVL

MGANLAGEVADENFCETTIGCRDTKQGPLLRDIIQTDYFRVVVVDDEDTVEICGALKNIVACGAGFVDGL

GLGDNTKAAVIRLGLMEMIKFVDVFYPGGKLSTFFESCGVADLITTCYGGRNRKVSEAFVKTGKSIKVLE

DEMLNGQKLQGPFTAEEVNYMLKNKGMEEKFPLFTAIHKICTGQKPVAEFIDCIRHHPEHMDNSYDRPKC

KL

>Amel\_NP\_001014994

MAEKLRICIVGSGNWGSTIAKIIGINAANFSNFEDRVTMYVYEEIINGKKLTEIINETHENVKYLPGHKL

PPNIIAIPDVVEAAKDADILTFVVPHQFIKRICSALFGKIKPTAIGLSLIKGFDKKQGGGIELISHIISK

QLHIPVSVLMGANLASEVANEMFCETTIGCKDKNMAPILKDLMETSYFKVVVVEDVDSVECCGALKNIVA

CGAGFIDGLGLGDNTKAAVMRLGLMEIIKFVNIFFPGGKKTTFFESCGVADLIATCYGGRNRKICEAFVK

TGKKISELEKEMLNGQKLQGPFTAEEVNYMLKAKNMENRFPLFTTVHRICIGETMPMELIENLRNHPEYI

DETRNYQECKCSI

>Amel\_XP\_006558427

MATDAKKRVCIVGSGNWGSAIAKIIGANVVKFNNKFETRVTMYVYEEIVNSQKLSDIINQLHENVKYLPG

HRLPENIVAVPDVIEAAKDADILIFVIPHQFITTLCATLLDKIKPTAVGVSLIKGFDRGDGVNIELISKV

IEKNLRIQCYVLMGANLANEVAEEKFCETTIGCRDKRLAPLLKDLIQTSNFRVSIVEDCEAVEVCGALKN

IVACAAGFVDGIGLGDNTKAAVIRLGLIEMVRFVDTFYTGSKLATFFESCGVADLITTCYGGRNRRVCEQ

YVKTGKTIRQLEEELLAGQKLQGPATADEVHGMLKARNLTDKFPLFTTIHRICTEQIRPADLINEIRAHP

ELPTIGDTQDA

>Pcoq\_MNCL01000020

NRGSAIAKIVGANTTRLSQFEDRVNMYVYEEMIEGRRLTEIINETHENVKYLPGHKLPPNIVSVXVAVPDLVEAASGADILIFVVPHQFIRNFCATLLGKIKPTAVGISLIKGFDKATGGGIDLISHIITRHLKVXIPCSVLMGANIATEVADGKFCETTIGCRDLSLSSVFRDLFQAEHFRVVVVDDVDAVEVCGALKNIVACGAGFVDGLGFGDNTKAAVIRLGLMEMIRFVDLFYPGSKLATFFESCGVADLITTCYGXGGRNRKVSEAFVKTGKTIKELEEEMLNGQKLQGPYTAEEVNYMLKNKQMEDKRFPLFTAIHQICKGALPPSEMFNCIRNHPEHM

>Cnas\_XP\_031633500

MASDKVNVCIVGSGNWGSAIARIVGANAANSAQFNERVTMYVFEEMIEGKKLTEIINETHENVKYLPGKK

LPSNVVAVPDLVEAAKDADILIFVVPHQFIPGQCKQLLGKIKKTAVGLSLIKGFDVAEGGGIKLISSIIT

ENLNIPCYVLMGANLANEVADENFCETTIGCQDKKWAPILRDMMQASYFRVVVVDDVNTVEVCGALKNIV

ACGAGFVDGLKLGDNTKAAVIRLGLMEMIKFVEVFYPGSQLATFFESCGVADLITTCYGGRNRKVSEAFV

TSGKTIEQLEAEMLNGQKLQGPPTAKEVNYMLANKKMEEKFPLFTAIHNICIGKLKPDQLIDCIRNHPEH

ICKHITAKL

>Cmos\_VUAH01006225

MASNKINVCIVGSGNWXGSAIAKIVGANAARLENFNDRVTMYVFEEDINGKKLTEIINETHENVKYLPGHKLPPNVVXVAVPDLVEAAKDADILIFVVPHQFIPGQCKQLLGKIKKTAVGLSLIKGFDVAPGGGIELISHIITRHLEIPCYVLMGANLANEVANENFCETTIGCNDKKWAPILRDTMQASYFRVVVVDDINTVEVCGALKXNIVACGAGFVDGLKLGDNTKAAVIRLGLMEMIKFVEVFYPGSKLATFFESCGVADLITTCYGGRNRKVSEAYVTSGKTIEELEQEMLNGQKLQGPPTAKEVNFMLSNKKMEEKITTLHSTLSVSLKSNVFFSCXRFPLFTAIHNICIGKLKPNQLIDCIREHPEHM

>Mdes\_AEGA01000508

MASDKVNVCIVGSGNWXGSAIAKIVGANAARLANFNDRVTMYVFEEMINGKKLTEIINETHENVKYLPGHKLPENVVSVXVAVPDLVEAAKDADILIFVVPHQFVPGQCKQLLGKIKKTAVALSLIKGFDIAEGGGIELISHIITRHLQIPCYVLMGANLANEVAEEKFCETTIGCNDKKVAPILRDMMQAHYFRVVVVDDVDAVEVCGALKIKNIVACGAGFVDGLKLGDNTKAAVIRLGLMEMIKFVDVFYPGSKLSTFFESCGVADLITTCYGGRNRKVSEAFVTSGKTIEELEKEMLNGQKLQGPPTAKEVNFMLKAKKMEDKYVFLHIKSNCRTLWFGQVLIHFIKYSRFPLFTAIHDICIGSKKPNQLIDCIRNHPEHM