

A

GH16-1 M--ILILFAFSAILFNGVHS---VCLKNSITTASGLHAPKNKSLCSGQLIFEDNFNFDLTSK-WHHEQTLGGG-GNNEFEWYTD DRRNSYTSNGQLHIKP
GH16-2 M----NLMKFMALIFHNLRG-----CEKSVTTVSGTHAPL--LPCKGDLIKFDEFNNLDLKK-WQHEVSLSGN-GNWEFQWYTNNSNSYVENGVLHIRP
GH16-3 M---IVICLIVALLVQNIHG-----CGIPLTTVSGSHAPK--AVCSGDLIKFDDNFNLDLTK-WQHEQTLGGG-GNWEFQWYTNNSNSYVENGVLHIRP
GH16-4 MDRRVLVVLTVIVLLQNVHT-----CKKSITTVSGNYAPK--EVCSGKIIIFEDNFDELNLK-WNHEQTLGGG-GNWEFQWYTNDRNSYVKDGLHIRP
GH16-5 MFKLIVITVLISIFYPTVYSQSRICQKPSITTASGTAAPTG-TICPGDLIFEENFNGPPTFKRWEHERTLGGGASNNQFQLYHNNRNSNSFVRDGNLHICP
GH16-6 MFKLILHTILISIFYPTVYQGLGTCQRPSVTTASGIAAPTG-TIFPGDLIFEDNFDPGPTFTKWWTHESLSSGGANNQFQWYQNNRNSNSFVRDGNLHIRP
GH16-7 -----
GH16-8 -----GNNEFEWYTNNSNSYTSNGILHIKP
GH16-9 -----TLTGG-GNFEFEWYTD DRRNSYAENGLHIKP

GH16-1 TFVADEY-GEKFLYSGTIDL-----GAKCTGSDNEGCRRTGSANAI VNP IKSARMRLDSFSFKYGRVEVSAKVPSPGDWLWPAIWMLPSKWV-YGSWPAS
GH16-2 TLVADDY-GNEFLYSGTIDVNGGSPADECTNPQFYGCSRTGSATNIVNPIKSARIRSLNSFSFKYKVEVRAKVPAGDWLWPAIWLLPRYNQ-YSTWPAS
GH16-3 TLVADDY-GNEFLYSGTIDVNGGSPADECTNPQFYGCSRTGSATNIVNPIKSARIRSLNSFSFKYKVEVRAKVPAGDWLWPAIWLLPRYNQ-YSTWPAS
GH16-4 TLLADQY-GNDFLYSGTIDL-----GKECTNSEWFGCRRVGTKTQILNPIKSARLRTANSFSFKYKVEIRAKIPAGDWLWPAIWLLPTYWK-YGWPTS
GH16-5 TLLADDN-GEAFLYNGTISLNGPYPIEHCTISGYDGLCRTGNSIIILNPIKSARIHTAFSFSFKYGRVEARVKVPLGDWLWPAIWLMPKPRNNE-YSSWPSS
GH16-6 TLLANDT-GEAFLYNGTIDLNGAFPIGYCSIPVYDGLCRTGNSIIILNPIKSARIHSAYSFSFKYGRVVARVKVPLGDWLWPAIWLMEPRDNE-YSSWPSS
GH16-7 -----
GH16-8 TFVADEL-GEQFLQSATVDL-----GNKCTNPHNSGCKRTGSPGEILNPVKSARLRTLDTSFIFYGKVEVRAKVPAGDWLWPAIWLLPNKWIENGDWISS
GH16-9 TFVADEHGGDGLYSGTIDL-----GKKCTNNDNEGCKRTGSANAIILNPVKSARIRLNSFSFKYKVEISAKNPSPGDWLWPAIWLLPSKWV-YGWPRS

GH16-1 GEIDIMESRGNRQYY-DPSGQNVGTQLEASTLHWGPNPKFNKFMKTHWEKKNWNGGDWNAHYHQVEWTPPEHIKFSRDDQELGTITPPSGGFQYGDG
GH16-2 GEIDIMESRGNRQLT-NPSGVNIGVQIGSTLHWGPNPNYQYARTHFE-ENLETGYDKAFHNYQVEWTPDYIKFAIDDEEIGRVTPPGGGFELGELSS
GH16-3 GEIDIMESRGNRQLT-NPSGVNIGVQIGSTLHWGPNPNYQYARTHFE-ENLETGYDKAFHNYQVEWTPDYIKFAIDDEEIGRVTPPGGGFELGELSS
GH16-4 GEIDIMESRGNRQLI-SQSGRKGIVQTIQYTLNWGPNPDNLFYKTHFD-SFLDVGYNQEFHFKYQLEWTPDYIKFSLDDKEVGTI VPPSGGFQDLADLTS
GH16-5 GEIDILESMGNKGYI-K-NGVNIGVEVGSSTLHWGPNPYSALNRYPLTHYT-LNNADGWNADPHIYEMIWNTTSITFLIDHVVLGVSVPDGGFELGNF-S
GH16-6 GEIDILETRGNKNYI-K-NGLNIGVQVGSSTLHWGPI-----
GH16-7 -----KELI-KPNGQNIPTLLNNTLHWGANAQTNRYAQTHYE-TTIEGFDQAYHKYQLEWTPDYIKFSLDDREIGKVT PPSGGFELGNLEK
GH16-8 GEIDIMETRGNKELI-KPNGQNIPTLLSTLHWGANAQTNRYAQTHYE-TTIEGFDQAYHKYQVEWTPDYIKFSLDDREIGRVTPPSGGFELGNFEH
GH16-9 GEIDIMESRGNRELIAGSGQNIADLVA STLHWGPDAKNNKFMKTHWE-KTVTGGYDKAYHKYQVEWTPDHLKFSIDDEIGVT PPSGGFELGNFEH

GH16-1 SGLPNPWSRGRMAPFDQEFHLLINLAVGG-AYFNDEFNNAKYPKPTSTEPYRQGMKTFWQANQKWKPTWNLNSDDSHLKVYDVRVWAL
GH16-2 SGLDNPWKRNSKMAPFDQEFYIVINLAVGGVNYFPDNANNSPRGKPSNTSPN--AATNFWEGREQLWPTWNI GTE DSHLQVDYVVKVWAI
GH16-3 SGLDNPWKRNSKMAPFDQEFYIVINLAVGGVNYFPDNANNSPRGKPSNTSPN--AATNFWEGREQLWPTWNI GTE DSHLQVDYVVKVWAI
GH16-4 TGLQNPWKNGTKMAPFDQEFHLLINLAVGGVSYFPDNANVTGKPKPTWNTSPY--APATFNARNEWLPWKMETDESHLKI DYVVKVWAL
GH16-5 TNTANPWAAGTKMAPFDQEFYIINLAVGTSWFSYGVNDGYPKPWKNSDG-RASMTKFWKAKDLWLP TWMNTTDDSHFQIDYIRVYAL
GH16-6 -----
GH16-7 TRLPNPWRGSSKMAPFDAEFYLINLAVGG-YFFPDQADNRSGKPKWSRTSPYRIGMTDFWRN-----
GH16-8 TGLPNPWRGSKMAPFDAEFHLLINLAVGG-NFFPDEADNRSGRKPWSHNVPYRIGMTDFWRNRQOWIPTWNLGTD DSHLKVYDVRVWAI
GH16-9 SQQQNLWKDGSKMAPFDAEFHLLINLAVGG-NFFPDVDNKSGKPKPTSTEPYRQGM-----

B

Dvir GNBP-1	KLPGDWIYPEIYLTP-ANEK--YGL-KSQSGQIRIAFTPGNSDL-----NHLVHGLTIGRWSA
Dvir GNBP-2	KLPGDWLYPILTINP-VKDE--YGP-GYDSGQITIAFCPGNAVL-----SHNVYGGIVISGSPV
Dvir GNBP-3	KLPGDWLYPILYLN- SAET--YGK-YYASGQRIAYTEGNTG-----ANHLKGGVILGDBEP
Dpon AEE61901.1	KLPGDWLYPELYLNS-ESEE--YGS-GYESGQIRIAFAAGNEGE-----SRKLEGGVILGSIPA
Dpon ENN74344.1	KLPGDVIYYPEIYLQD-VANP-----ESLILIAFTRGNENY-----EKNGIDIGGQLYGGPYNISIKD
Dpon ENN74953.1	KLPGDWLYPELYLNS-ESEE--YGS-GYESGQIRIAFAAGNEGE-----NRKLEGGVILGSIPA
Tcas XP_972063.1	KLPGDWIYPQLFLNP-VSEE--YGS-DYASGQIRVAFPLPNQAM-----AQQLYGGCVLGPPTTA
Tcas NP_001164284.1	KLPGDWIYPIYLEK-VSDP-----KDKIWIYSYARGNNQLLKK-----NKQDLGGNLLFGGLVIDPEEP
Tmol Q76DI2.1	KLPGDWIYPELYLNP-VNEE--YGP-GYASGQIRIAFSGGNEDL-----CDRLRGGCILGSRPA
Slit ACI32819.1	KLPYGSWLVEINLEP-LEHT--YGL-NYESGLMRVAFVRGNSYF-----AKKLYGGPVLGHSEP
Pxyl AFK24449.1	RMPRGDWLIPDILLEP-KENL--YGVNRNYSGLLSIASVRGNTAY-----SKTLKGGPILCDKEP
Amel NP_001157186.1	KLPRGDWLFPLITLES-TDMC--TKN-SSIYCDIIVHSNGNSVLSMQ-----DGNDLSGSHLGGAHATDINS
Dmel GNBP1	KLPGDWIYVPLLLEP-LTEW--YQSGYESGQLRVALARGNSVLRMP-----RGKLV DGRSLYGGPVLSTDAH
Dmel GNBP2	KLPGDWLFPYLMQP--VST--YAE-THYAKQLRIAYARGNANLRTK-----QGDDISGNHLYGGGVVWHHGN
Dmel GNBP3	KMPRAQWVTPQIWLQP-RRPI--YGVDDYRSGQLRIAYTRPNGG-----NLDLYGAAVLFADEP
Spur XP_001176934.2	KLPTGDWLWPAIWLLP-KHNG--YGE-WPASGEIDLVE SRGNAD-IKD-ADG--LSAGVDQMGSTMHGPFWPLNGY
Cint XP_002126690.1	KMPDGDWIWPAWMLP-KTNS--YGS-WPASGEIDICE SRGNTD-LKD-DQG--VSHGNDAMGSTLHWGPYWPVNAY
Cgig BAG82629.1	KMPKGDWIWPAIWLLP-HRNA--YGG-WPASGEIDVVS SRGNTD-YHD-ENG--RSQGVDSFGSTLHFGPVYGYDPY
Dvir GH16-1	KVPSGDWLWPAIWMLP-SKWV--YGS-WPASGEIDIMESRGNRQ-YYD-PSG--QNVGTQLEASTLHWGPNPKFNK
Dvir GH16-2	KVPAGDWLWPAIWLLP-RYNQ--YST-WPASGEIDIMESRGNRQ-LTN-PSG--VNIGVQIGSTLHWGPNPNYQY
Dvir GH16-3	KVPAGDWLWPAIWLLP-RYNQ--YST-WPASGEIDIMESRGNRQ-LTN-PSG--VNIGVQIGSTLHWGPNPNYQY
Dvir GH16-4	KIPAGDWLWPAIWLLP-TYWK--YGG-WPTSSEIDIMESRGNRQ-LIS-QSG--RKIGVQTIQYTLNWGPNPDNLF
Dvir GH16-5	KVPLGDWLWPAIWLMP-RNNE--YSS-WPSSGEIDILESMGNKGYI-K-NG--VNIGVQEVGSTLHWGPNYSALNRY
Dvir GH16-6	KVPLGDWLWPAIWLMP-RNNE--YSS-WPSSGEIDILETRGNKN-YIK--NG--LNIGVQVGSSTLHWGPNYSALNRY
Dvir GH16-8	KVPTGDWLWPAIWLLPNKWI--NGD-WISSGEIDIMETRGNKE-LIK-PNG--QNIGTPLLSTLHWGANAQTNQY
Dvir GH16-9	KNPSGDWLWPAIWLLP-SKWV--YGG-WPRSSEIDIMESRGNRQ-LIAGSG--QNIGADLVA STLHWGPDAKNNK
Dpon ENN72429.1	KVPLGDWLFPALWMLP-KDSK--YGS-WPLSSEIDVME SRGNRN-LTD-SSG--NIVGVQSVSNTLHWGPKSKALDTP
Dpon ENN78830.1	KVPAGDWLWPAIWLLP-SDYR--YGG-WPVAGEVDLVE SRGNRN-LTD-STG--LNIGTQLAFSTLEWGPSLEQNY

Dpon ENN78831.1 KLPGGDWLWPAIWLLP-TDWK--YGS-WPVSSEIDLVE SRGNRE-LTD-GSG--FNFQGTQLAFSTLHWGSPSPENQY
Dpon ENN83076.1 KMPAGDWLWPAIWLLP-RYNA--YGT-WPSSSEIDLLE SRGNKD-YVN-PNG--MNVGTQVVGHTLHWAPSVGANQW
Dpon ENN83093.1 KMPSGDWLWPAIWMLP-RFNS--YGR-WPASSEIDIVE SRGNKN-LFN-PQS--VNIGTQEAASTLHWGPFNQVQW
Tmol ACS36221.1 KLPTGDWLWPAIWMLP-RWNQ--YSG-WPISSEIDIME SRGNAD-LVN-ASG--ANIGSKLVSSTLHWGPAINNMY
Tcas XP_970010.1 KLPAGDWLWPAIWFLP-RWNL--YSG-WPVSSEIDLME SRGNRN-LVN-GSG--VNIGTQMVGSTLHWGPASNMY
Aaeg XP_001652521.1 KLPQGDWLWPAIWLLP-KGDT--YGY-WPKSGEVDLME SRGNRN-LVQ--NN--EKIGIQKVVSSCLHFGDNPVNRSS
Aaeg XP_001664288.1 KLPAGDMMWPAVTFELP-KYNQ--YGG-WPASSEIDLLE SKGNRD-LIK--NG--INVGIEQVTSKLFQFNGEYVAG
Aalb AAV90645.1 KLPRGDWLWPAIWLLP-KGDT--YGS-WPKSGEIDLLE SRGNRN-LML--NN--GNIGVGKVVSSCLHFGENPNLRSS
Cqui XP_001845811.1 KLPAGDWLWPAIWMLP-QQDS--YGV-WPKSGEIDLVE SRGNRE-LYQ--DG--KHIGVKLSSCLHFGESWNQKSE
Cqui XP_001845967.1 KLPTGDMMWPAIWMLP-RTNQ--YGT-WPASSEIDLME ARCNVD-YRD-EEG--THLGEVQVLSLHFGPNAWTNAY
Adar EFR28384.1 KIPTGEWLWPAIWMLP-KLNQ--YGT-WPASSEIDLME SRGNLD-YTA--GG--QQIGVEHVGTMMHFGPPALNGY
Acar ACI32832.1 KMPAGDWLWPAIWMLP-AFNS--YGT-WPASSEIDIVE SRGNRN-MLS--NG--VNIGTQEAGSTLHYGPPPLNGW
Sfru ABR28478.2 KLPAGDWLWPAIWMLP-AYNT--YGT-WPASSEIDLVE SRGNRN-MF--NG--VHIGTQEAGSTLHYGPPPLNGW
Onub ACI32836.1 KMPAGDWLWPAIWMLP-AFNV--YGT-WPASSEIDLVE SRGNRN-MLF--NG--VHIGTQETGSTLHYGPPDLNGW
Bmor NP_001159614.1 KMPSGDWLWPAIWMLP-AYNK--YGT-WPASSEIDLVE SRGNKN-MFL--NG--LHIGTQEAGSTLHYGPPPLSGW
Mdar AAZ08492.1 KMPAGDWLWPAIWLLP-RYNE--YGP-WPASSEIDLSE SRGNRN-LTI--DG--LNIGTEICSSSTLHFGPFPDFGW
Mdar AAZ08505.1 KLPAGDWLWPAIWLLP-RYNE--YGS-WPASSEIDLVE SRGNRN-LIK--NG--INIGSELSSSTLHFGFPPLNGY
Cpun AFR46664.1 KLPAGDWTWPAIWLLP-RYNQ--YGS-WPASSEIDLVE SRGNKN-LIN--NG--QNIGSELSSSTLHFGFPPLNGY
Ncor AEK64800.1 KMPAGDWLWPAIWLLP-RYNE--YGP-WPASSEIDLSE SRGNAN-LTS--KG--LNIGKELSLSTLHFGPYWPLNGY
Rvir AEK64797.1 KLPAGDWLWPAIWLLP-RYNE--YGP-WPASSEIDLSE SRGNAN-LTS--KG--LNIGKELSLSTLHFGPYWPLNGY
Rvir ADJ19024.1 KLPAGDWLWPAIWLLP-RFNF--YGS-WPSSSEIDLLE SRGNRQ-LIK--NG--QNIGSELSSSTLHFGFPPLNGY
Pame AFR46666.1 KLPAGDWLWPAIWLLP-RYNQ--YGG-WPASSEIDLSE SRGNLN-YIS-PSG--QNIGSELSSSTLHFGFPPLNGY
Cfor AGA16572.1 KLPAGDWLWPAIWLLP-RFNF--YGS-WPSSSEIDLLE SRGNRQ-LIK--NG--QNIGSELSSSTLHFGFPPLNGY
Cpun AFR46663.1 KLPAGDWLWPAIWMLP-RYNE--YGS-WPASSEIDLSE SRGNRN-LTL--NG--LNIGSELSSSTLHFGFPPLNGW
Lmig AFD54026.1 KLPAGDWLWPAIWMLP-RNNK--YGG-WPASSEIDLVE SRGNLG-LTQ--GG--VNIGAERVASTLHFGFPVVDAY
Bgla ABO40828.1 RISKGDWIWPAIWMLP-RDNV--YGG-WPRSSEIDIME SRGNE-----VGIGISQVSSSTLHWGSPSPENNRW
Calb AAZ04385.1 KIPKGDWLWPAIWMLP-RDRS--YGG-WPRSSEIDIME SRGNK--AVLWG--QNSGVNYVASTLHWGPDFNNRNF
Hdis BAH84971.1 KIPKGDWIWPAIWMLP-PGWPKYGA-WPASSEIDIME SRGNVH-LSE-ANG--ATQGVDRVLSIHYGASPSQHRQ
Pame ABR28480.1 KLPRGDWIWPAIWMLP-KNWX--YGD-WPRSSEIDIME SRGNND-YYD-SNG--VSQDDRMKSTLHWGPDANHNRY
Dpul EFX72300.1 KMPRGDWLWPAIWMLP-TDSA--YGT-WPRSSEIDIVE IRGNAD-LTC--NDGQKIGNSKMFSTLHWGPFDSQNM
Dpul EFX72306.1 KMPRGDWLWPAIWMLP-TDSA--YGT-WPRSSEIDIVE IRGNAD-LTC--NDGQKIGNSKMFSTLHWGPFDSQNM
Dpul EFX65834.1 KMPRGDWLWPEISLMP-ANNV--YGE-WPRSGYIGLVSRGNNA-FTC--NG--QSAGNNVMESSELEWGLNNDHKS
Dpul EFX69035.1 KMPKGDWIWPAIWMLP-TDSV--YGE-WPRSSEIDIVE IRGNAD-FSC--NG--YPIGRQLAGCTLHWGPDQNRNY
Hmag XP_002158311.2 KLPAGDWLWPAIWMLP-KYSV--YGG-WPASSEIDLVE SRGNEN-LTV-SKDLTQIGNRKVSQSLHWGPFPPQNGH
Aque XP_003388466.1 KLPAGDWLWPAIWMLP-RHNQ--YGV-WPSSSEIDIME SRGNAIGYSE-----GGYDSFGSTLHWGIDYMYNFF
Mcir EPB91375.1 RLPTGDWLWPAIWMLP-KYSA--YGS-WPASSEIDILE SKGNPK-YAH-----GNTSTIMSTLHWGPNTYQNKY
Bbas EJP68643.1 RLPKGDWLWPAIWMLP-EGDV--YGA-WPRSSEIDIME SRGNPEYSE-----GGRNWWYGTLHWGPTPRSDAY
Cmil EGX89530.1 KLPAGDWLWPAIWMLP-ESDA--YGT-WPRSSEIDIME SRGNPDYAE-----GGRNWWYGTLHWGPTPKTDY
Clus XP_002618376.1 KLPKGDWLWPAIWLLP-KNNT--YGP-WPASSEIDIAE SRGNVHYPM-----GGHDVSSSLHWGPDVAQDQY
Fmed EJD07749.1 KMPRGDWLWPAIWMLP-KDEK--YGA-WPRSSEIDIVE ARGNSASYPR-----QGNFVFRGSLNWGLDVTV--
Gtra EPQ53062.1 KNPVGDWLWPAVWMLP-VNNT--YGP-WPMSSEIDIME SRGNLSYTA-----QGSNYVHGSLSNWGLPTLWNEV
Cant ACD93221.1 RLPKGDWLWPAFWMMLP-QNSE--YGT-WPRSSEIDITE YRQRP-----QQILGLTHFGAAPPDNKGD
Amac YP_008173608.1 KMPEGQGSWPAFWMLP-TDEV--YGG-WPRSSEIDIVE AVNLKAADAE-----G-NPESHIYGLTHYGEWPNND
Pfla WP_010607480.1 KLPAGQGSWPAFWMLP-TDEV--YGG-WPKSGEIDIME AVNLKVADE-----G-SVESNVHGTLHYGRDWPNNVH
Gjoo WP_017446697.1 KLPAGQGSWPAFWMLP-TDNV--YGG-WPHSGEIDILE AVNLKVPLEG-----SDDLESSVHGTLHYGKSWPNAS
Mmar YP_755478.1 QLPEQGSWPAIWMLP-TDEV--YGG-WAASGEIDILE AVNLGEPRE-----CRGDVENRVTLHYGGEWPEPNTY
Rmai WP_008695923.1 KLPVAGIWSAIWMLP-TNDA--YGG-WAASGEIDIME MKG-----QEPDEVLTGLHYGDVWPRNAY

C

Dvir GNBP-1 YEVPDAVVEVYEPKGFVTSIPDEEGIK-LFAFHGKINDEF-DG-LEAGT-----FARDILKPRNGSWT
Dvir GNBP-2 YEVPAAATVEVYHPKGFVSIPDEEDGK-LFSFHGNINQEM-DG-REAGT-----FSRDLILRPVNGMWT
Dvir GNBP-3 YNGQRTNGKFGNPNVTFPGDFRQAQGLFNQFKNSVSEY-QQ-KNGNGEIKVLNPSNIADLANIFTKNLQKQNPNN
Dpon AEE61901.1 FEVPDATVEAFTPRGLRVSIPDQDGK-LFALHAKINEEM-NG-REAGT-----FSRDLITKAKDGRWT
Dpon ENN74344.1 YQVPTPTFEAFKPKGFRVSIIPDDEKVE-LFAFHGKINKPI-IQ-IEPGD-----FSQDVLKAVNGRFS
Dpon ENN74953.1 FEVPDATVEAFTPRGLRVSIPDQDGK-LFALHAKINEEM-NG-REAGT-----FSRDLITKAKDGRWT
Dpon ENN76697.1 YAVPEPKIDIFDTKGRVSIIPDGFLE-LFAFHGKINEEM-NG-LEAGQ-----FSKDLITKACGDLWV
Tcas EFA01356 FEVPDALVEVFPQGLRVSIPDQEGIK-LFAFHAKVNEEM-NG-REGGT-----FSRDLITKAKHGRWT
Tcas NP_001164284.1 FVIPDVTLEAYAPKGFRAIPALPGIQ-MFAFHMNVNKKI-SQ-VDPGD-----YRQDYTSPDGNVWS
Tmol BAC99308 FEVPDALVEVFRPRGLRVSIPDQEGIK-LFAFHGKINEEM-NG-REGGT-----FSRDLITKAKHGRWT
Bmx BAA92243.1 YEAPPATLEAIHPKGLRVSVPD-BGFS-LFAFHGKLNEM-EG-LEAGH-----WSRDLITKPKNGRWT
Pxy1 AFK24449.1 YEVPKLEAIYPAGLRVSIIPD-DGFS-LFAFHGKLNEM-EG-LEAGH-----WSRDLITRPNKNNRWV
Pint AAM95970.1 YVVPKLEAIYPKGLRVSIPD-DGFS-LFAFHGKLNEM-EG-LEAGH-----WARDITKPKRGRWT
Slit ACI32819.1 FPATPTVEAFQPKGFRVILK-DGYS-FVGFGRNINVDNFNG-LNEGQ-----IHKDITHAQKGYWI
dmel AAF49244.1 YKIPTPTVELLE-TGFSVSIIPDEEGVK-VVAFVNNRNRNF-TSFINEGQ-----YVRLTEPQNGRWT
dmel AAF49246.3 -----EGFEVSIIPDEEGIQ-VVVFYNIIDTC-PA-L-----MDYITEAVNGSWV
dmel AAF50349.1 YEVPKAKIDVFPYKGFVSIIPDEEGIT-LFAFHGKLNEM-EG-LEAGT-----WARDIVKAKNGRWT
dmel CG30148 YEAPAEQVRVFPYPRGFEVSIIPDDEGIS-LFAFHGKLNEM-EG-LEAGQ-----WSRDLIPKAKNGRWT
Ame1 NP_001157186.1 YVPPTPSVEPLYPVGLRMSIADEAGIS-LVAYHVKFNDDF-YS-LEAGT-----IARDIHKPRNGYVW
Spur XP_001176934.2 YDMKNPEISLLTTGGIRFAYPDEPGIT-LFAFHYSINTPL-SG-VNVGQ-----YNYDVTTKTGAYFV
Cint XP_002126690.1 YSVQQPIISLMEPTGLMFYPPDDGNIN-LVSYHYSINTPL-PD-VQAGT-----YNDVSESTNGYFT
Cgig BAG82629.1 LSIQPAIWEQYNGHGKFTIPDDGNYD-FVAVHYSINQPI-AG-VGAGQ-----WAFDVTHTKQSSFV

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Dvir GNB-1 FRD--RETRLKKGD-----I IYYWLYVDYNGRNTLGYRKTDDQYEVRE--FSN
Dvir GNB-2 FSD--RSTKLRVGD-----K IYYWTYVEYGDEYEKRGYPKDDQVFTVTN--LIK
Dvir GNB-3 FL---PIVKVRYEDGPEGPENIYQIIPNKRNSADLSKTLVDLWNNITEPNNTNFTSPTPPSESTGYDE--ST
Dpon AEE61901.1 FYD--SQAKLAVGD-----TLYFVTFVDYFDGERKLG FVRDDQFFTITE--LLP
Dpon ENN74344.1 YTD--PNIKLEKEND-----VINYWIFVQ---HDQLGFRIDEQSWTVDE--LRP
Dpon ENN74953.1 FYD--SQAKLAVGD-----TLYFVTFVDYFDGERKLG FVRDDQFFTITE--LLP
Dpon ENN76697.1 FED--NTEKLVVGN-----TLYYWL FVI---RNRLGHR YDNGK FVVRD--ITS
Tcas EFA01356 FYD--PYAKLKIGD-----T IYYWTYVDYFDGKNKLG YTKDDQEFVVRQ--LLD
Tcas NP_001164284.1 YFN--SDLSLNIGD-----TVNYWIFVQ---HEKLG YR KDNVEWTVTE--LLQ
Tmol BAC99308 FYD--ANARLKEGD-----I LYYWTYVDYFDGKNKLG YPNDDQEFVVKQ--LLD
Bmox BAA92243.1 FRD--RNAALKIGD-----K IYFVTFVI---KDGLG YR QDNGEWTVEG--FVD
Pxy1 AFK24449.1 FSD--KQARLKIGD-----K VYFVTFVI---KNGLG YR QDDGQVWTVEG--FVD
Pint AAM95970.1 FRD--RNVKLLKGD-----K IYFVTFVI---KDGLG YR QDNGEWTVEG--FVN
Slit ACI32819.1 YRN--REVKLNIGD-----TLYYWL FVQ---KNGKGF LTELAYTVTQ--FVN
dmel AAF49244.1 TNF--SSVPLRSQD-----VLYLW TSVQ---HQKAVYQDLAQLPVCN--LGG
dmel AAF49246.3 SK---QKMSLQNN-----K LQISMLVQ---FNEEI FEKSETRVIINTRLLTT
dmel AAF50349.1 FRD--RITALKPGD-----TLYYWT YVI---YNGLG YR EDDGSFVVNG--YSG
dmel CG30148 FRD--HKTKLNHGD-----TLYFVTF YVI---YNGLG YR QDEGAHVVT--Y--
Ame1 NP_001157186.1 YED--RSTRKLLGD-----I IYYWIHVV---YNGLG YNLLDQKHVVNE--FYN
Spur XP_001176934.2 HEN--TEVDVKKGD-----V VNYWVYVN---Y YGPGYQLLEQSWTASE--APA
Cint XP_002126690.1 LQN--FNVAVVPGD-----E VNYWVNV I---TSTGG YLLTDQTWVAQG--PT
Cgig BAG82629.1 HTNDLPAIQVHKGD-----T VYYW LHAQ---KGGTPSEL LQSAVIGD--LTT

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Figure S3. Multiple alignments of *D. v. virgifera* GH16 family protein sequences. A. GH16 family proteins identified from the *D. v. virgifera* transcriptome. B. The active site region sequences. GNB-1 sequences are boxed. The catalytic nucleophile and proton donor residues are highlighted with magenta and green, respectively (based on Viladot *et al.* 1998, *Biochemistry* **34**: 11332). C. The N-terminal conserved domain sequences of GNBPs. Residue shown to be within hydrogen-binding distances and involved in hydrophilic interaction with lamitrihexaoses on *Plodia interpunctella* and *Bombyx mori* proteins are highlighted with yellow, and Arg's involved in binding of triplex β -glucan are highlighted in light blue (based on Kanagawa *et al.*, 2011, *J Biol Chem* **286**: 19158).