Contents

[Peptidoglycan recognition proteins (subset) 2](#_Toc511093565)

[Gram-negative binding proteins 19](#_Toc511093566)

[Absence group PGRP amidase domain nucleotides sequences 29](#_Toc511093567)

[Nucleotide sequences from NCBI 29](#_Toc511093568)

[Protein sequences (Translated from nucleotide sequences in EMBOSS Transeq) 32](#_Toc511093569)

[Toll-like receptor sequences 34](#_Toc511093570)

[a) Full Toll-like receptor sequences 34](#_Toc511093571)

[b) Toll-interleukin receptor domain sequences 70](#_Toc511093572)

# Peptidoglycan recognition proteins (subset)

**Acromyrmex echinatior (NCBI and i5k)**

>XP\_011052663.1

>AECH18862-RA Aech\_09175

>AECH17637-RA Aech\_07904

>XP\_011050201.1 PREDICTED: peptidoglycan recognition protein [Acromyrmex echinatior]

>AECH10739-RA Aech\_00705

>XP\_011056059.1

>AECH17636-RA

**Tumida (NCBI)**

>XP\_019877814.1

>XP\_019877658.1

>XP\_019878098.1

>XP\_019876965.1

>XP\_019877660.1

>XP\_019876017.1

>XP\_019871642.1

**Agrilus\_planipennis (NCBI)**

>XP\_018332570.1

>XP\_018318747.1

>XP\_018318746.1

>XP\_018318744.1

>XP\_018318743.1

>XP\_018318742.1

>XP\_018318741.1

>XP\_018318740.1

>XP\_018331133.1

>XP\_018318745.1

>XP\_018336902.1

>XP\_018336886.1

>XP\_018336893.1

>XP\_018329558.1

**Apis Mellifera (NCBI)**

 >XP\_006565566.1

>XP\_001121036.2

>XP\_006565568.1

>XP\_006565567.1

>XP\_392452.2

>XP\_006565569.1

>XP\_006565570.1

**Atta cephalotes (NCBI)**

>XP\_012056262.1

>XP\_012059667.1

>XP\_012057776.1

>XP\_012059701.1

**Bemisia Tabaci (NCBI)**

>XP\_018900438.1

>XP\_018900438.1

>AJQ31845.1

**Blattela germanica (i5k)**

>BGER015516-PA

>BGER011423-PA

>BGER017966-PA

>BGER013416-PA

>BGER013414-PA

>BGER015094-PA

>BGER013415-PA

>BGER017969-PA

>BGER022191-PA

>BGER013413-PA

**Cimex lectularius (i5k)**

>XP\_014247859.1

>XP\_014247857.1

>XP\_014247856.1

>XP\_014247858.1

**Drosophila melanogaster (includes isoforms) (Flybase)**

>FBpp0081872

>FBpp0081873

>FBpp0081874

>FBpp0297234

>FBpp0297235

>FBpp0297236

>FBpp0099636

>FBpp0099635

>FBpp0099637

>FBpp0113069

>FBpp0422538

>FBpp0422539

>FBpp0088491

>FBpp0088998

>FBpp0088492

>FBpp0289518

>FBpp0289519

>FBpp0290987

>FBpp0300668

>FBpp0312389

>FBpp0073968

>FBpp0300347

>FBpp0076161

**Homalodisca vitrepennis (i5k)**

>HVIT007323-PA

>HVIT027965-PA

>HVIT025475-PA

>HVIT000476-PA

>HVIT000477-PA

>HVIT008922-PA

**Ladona fulva (Includes isoforms) (i5k)**

>LFUL015023-PA

>LFUL009705-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL012351-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL008797-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL019530-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL012356-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL014142-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL002714-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL009033-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL012355-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL008796-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL012357-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL008795-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL014141-PA

>gnl|Ladona\_fulva\_protein\_v0.5.3|LFUL012353-PA

**Oncopeltus fasciatus**

>gnl|Oncopeltus\_fasciatus\_OGSv1.2\_protein|OFAS001578-PA >gnl|Oncopeltus\_fasciatus\_OGSv1.2\_protein|OFAS000511-PA

**Pediculus humanus**

>PHUM581030-PA

**Heliconius erato (Uniprot and Lepbase)**

>heliconius\_erato\_demophoon\_v1\_core\_32\_85\_1\_\_protein\_\_evm.model.Herato0211.36 Peptidoglycan-recognition protein LB OS=Drosophila melanogaster GN=PGRP-LB PE=1 SV=1 [Source:UniProtKB/TrEMBL;Acc:Q8INK6]

MGITPLLLLLSVVVSVLSLPPPRIVGNRDNDLKLVSREQWGALPPKGHSVLRTPVPYVVI

HHTYIPRACQNKIECIAAMRSIQNTHQNSNGWSDIGYNFAVGSDGVAYEGRGWEYVGAHA

YGFNSNSIGIVLIGDWVSAVPPAVQLETTKKLIARGVDLGYISPEYKLVGHRQVTATECP

GSALFNEISTWDRFTKEV

>heliconius\_erato\_demophoon\_v1\_core\_32\_85\_1\_\_protein\_\_evm.model.Herato0211.37 Peptidoglycan-recognition protein LB OS=Drosophila melanogaster GN=PGRP-LB PE=1 SV=1 [Source:UniProtKB/TrEMBL;Acc:Q8INK6]

MYASSIYTCIAIFILNIFLIVHGHPVNEKHKSYTLYTREDWGAAPPTDVEPIKTPVPYVI

IHHTYIPGACNTTAQCKATMKSMQNYHISLDWGDIGYHFCVGSEGGVYEGRGWHTVGIHA

GPANRVSIGICLIGDWRVEEPPHKMLHATKALIADGVRKGVLSSDYKLKGHSQIMATECP

GTALLNIISKWDHFSEGQGLTKA

>heliconius\_erato\_demophoon\_v1\_core\_32\_85\_1\_\_protein\_\_evm.model.Herato0211.38

MLFLMTGAVLVQAMAAVVGAPKLTCQELAGNEVPSYNFPYVRRPQWHARLPKYKEPLSVP

VPYIVIHHSYSPPACYDTISCQQAMRSMQNFHMDEREWADIGYNFGVGGDGIAYEGRGWD

VLGAHSLHFNNFSIGICLIGDWINTVPPLQQLKTTQALIAAGVDMGYIRKDYKLVGHRQV

RNTECPGDALYEFTPNGGNTRAKLRAPTSILYSKI

>heliconius\_erato\_demophoon\_v1\_core\_32\_85\_1\_\_protein\_\_evm.model.Herato0606.4 Peptidoglycan-recognition protein SC1a/b OS=Drosophila simulans GN=PGRP-SC1a PE=3 SV=1 [Source:UniProtKB/TrEMBL;Acc:Q70PU2]

MIKLISIVFFVYLSCADAVCPGVVTKKEWDGLSPLQVQYLPRPVSLVIIQHTVTPACDSD

ASCVDIVQSIQNTHMETLNYWDIGISFLVGGNGKVYEGSGWLHVGAHTYGYNRKSIGISF

IGNFNSDQPTQAALDAAQELIKCGVEQGHLSPDYKLVGHKQISATESPGRKLYNEIRRWP

HFLNDVSSIKN

>heliconius\_erato\_demophoon\_v1\_core\_32\_85\_1\_\_protein\_\_evm.model.Herato0606.5

MNLKKCIDLIVITSICNVVVATSDCDVVPIEKWGDSPSVRKIYLEKPVKMAVVQHTVTPE

CASDEECEKILNNIRKFQTQISQFDDIAQSFLVGGNGKIYEGAGWRVGAHTLGFNDKSIS

ISFLGDFREKLPVPQALQAAKNFLSCSTENNNLDKDYRLIGHMQLSATLSPGAVLQSEIE

TWPHWYNINKN

>heliconius\_erato\_demophoon\_v1\_core\_32\_85\_1\_\_protein\_\_evm.model.Herato2101.399

MWPGKDGGPETNSAYCNNACSDVAVIDDRAVATAVPPAPVVSTLNVTKSSKVHIGTKIVS

VTQNVHNVEVVKELPFLTYLWNLIRNSSRTERLSCVAVLIVLITCITLIVYFSVKRVDDG

DPEDRPSNLWNISSEMWLAQPYDDNPIAKNFLPLMLVIVQHTVSGECTKFAQCAAELRTM

QGWFIRDKGYNIPYNFIVGNDGRVYEGRGWNKEGAHTFGYNRCSLGIAFIGDYRESRPHH

SRVTDLQLNRTRMLLDEGVRRGYMRPDYLIVGAKDVQSTQSPGSNLHNALQQWSNFDHHG

RFQNMNCVVNTTLLSVIPTQETNEALHPPILCLIMKKDESYITFRNLVSLIRR

**Triboleum castaneum (NCBI)**

>EFA01279.2 Peptidoglycan-recognition protein SC2-like Protein [Tribolium castaneum]

MPNSEVVLKSENEDSAVTELEDLCCSSDASFTPTAINVENSKDVIIGPVTQFHGPVTIYQNVTQSSASRGTIGNGSANTT

DLNGKLVKSESTCSDSPHAEKPKNSFLYSKHVKYLGISLVVIVILVTTTCVLILPRKTEKSPETPDTNTATPRLPLGPGA

IIEKKIWGGRATLNFSKPLPHPTHFVIVSHTVTPTCSDFPACSQRVQSMQDYHVGNLKSPDIGYNFVIGGDGNAYVGRGW

DIRNFHMDDSIGISFIGNFLHDHLTTEMISVAKKLLDEGVKSGKLARDYKLVAHNQTFRTESPGPNVYKEIKNWPHFDAG

IYYSR

>XP\_008192537.1 PREDICTED: peptidoglycan-recognition protein LA isoform X1 [Tribolium castaneum]

MTLISASDNSAFHVFPLGMPNSEVVLKSENEDSAVTELEDLCCSSDASFTPTAINVENSKDVIIGPVTQFHGPVTIYQNV

TQSSASRGTIGNGSANTTDLNGKLVKSESTCSDSPHAEKPKNSFLYSKHVKYLGISLVVIVILVTTTCVLILPRKTEKSP

ETPDTNTATPRLPLGPGAIIEKKIWGGRATLNFSKPLPHPTHFVIVSHTVTPTCSDFPACSQRVQSMQDYHVGNLKSPDI

GYNFVIGGDGNAYVGRGWDIRNFHMDDSIGISFIGNFLHDHLTTEMISVAKKLLDEGVKSGKLARDYKLVAHNQTFRTES

PGPNVYKEIKNWPHFDAGIYYSR

>XP\_008192547.1 PREDICTED: peptidoglycan-recognition protein LE [Tribolium castaneum]

MQPEGTLANPLTSDGEDTVSTSSEDDNECDGAVVLHEDDRPEVPSFGNISVMNSNDIHFGNKTFYQGPVTIKQFLYANGK

TTSDKSDSEVVLDATTLADSGLENPTFVNDNNTASEKTNAASKPAVQENSSGIVKGFRRLQKFFQENVVILVSLLAVLIV

SLAILMVVLLLRHSPNPIEDDQITREKLDEQEKNTPVDSPIDPQANLTLPPKLKLVSRLEWLAQPPVQPANPLAVPVPYV

IILHTATENCSSQAQCIFHVRFIQTFHIESRSWWDIGYNFLVGGDGEAYEGRGWKSEGAHTYGYNAKSIGIAFIGTFNSF

KPPERQITACKQLIAKGVELGFIRKDYKLLAHRQLETTQSPGAALYEEMKTWEHWAKTP

>EFA01280.1 Peptidoglycan-recognition protein LE-like Protein [Tribolium castaneum]

MQPEGTLANPLTSDGEDTVSTSSEDDNECDGAVVLHEDDRPEVPSFGNISVMNSNDIHFGNKTFYQGPVTIKQFLYANGK

TTSDKSDSEVVLDATTLADSGLENPTFVNDNNTASEKTNAASKPAVQENSSGIVKGFRRLQKFFQENVVILVSLLAVLIV

SLAILMVVLLLRHSPNPIEDDQITREKLDEQEKNTPVDSPIDPQANLTLPPKLKLVSRLEWLAQPPVQPANPLAVPVPYV

IILHTATENCSSQAQCIFHVRFIQTFHIESRSWWDIGYNFLVGGDGEAYEGRGWKSEGAHTYGYNAKSIGIAFIGTFNSF

KPPERQITACKQLIAKGVELGFIRKDYKLLAHRQLETTQSPGAALYEEMKTWEHWAKTP

>XP\_008192927.1 PREDICTED: peptidoglycan-recognition protein 2 [Tribolium castaneum]

MGRKFVIIFSILHQILARTESNLPAVCPEIVSRTRWGARTALEVDYALIPVENVVVHHTVTNTCSTEEECAAILRNIQNF

HMENLDFHDIGYNFLVGGDGQIYEGAGWHKVGAHTRGYNSRSLGLGFIGNYTTQLPNKKQIQAAKDFLQCGVELGELGKS

FKLFGARQVSATESPGLKLYRELQNWPHFTRSPPK

>EFA12467.1 Peptidoglycan-recognition protein SA-like Protein [Tribolium castaneum]

MGRKFVIIFSILHQILARTESNLPAVCPEIVSRTRWGARTALEVDYALIPVENVVVHHTVTNTCSTEEECAAILRNIQNF

HMENLDFHDIGYNFLVGGDGQIYEGAGWHKVGAHTRGYNSRSLGLGFIGNYTTQLPNKKQIQAAKDFLQCGVELGELGKS

FKLFGARQVSATESPGLKLYRELQNWPHFTRSPPK

>XP\_008193407.1 PREDICTED: peptidoglycan-recognition protein SC2 [Tribolium castaneum]

MFRLVLLLAAWPHLAHSACPTVISRSEWGARAPKSSQPLAQKPAPFVVVHHSDGSNCLSLQACKSRVKGIQNYHIDHNGW

QDIGYNFLIGGDGNVYEGRGWGIWGAHVPRYNSKSIGICVIGNFQSTAPTQTQLDALKQLISCAQEGNYVQSDYRLIGHR

QGSRTSCPGNQLFNEIGGWTHFDATARP

>EFA11602.1 Peptidoglycan-recognition protein SC2-like Protein [Tribolium castaneum]

MFRLVLLLAAWPHLAHSACPTVISRSEWGARAPKSSQPLAQKPAPFVVVHHSDGSNCLSLQACKSRVKGIQNYHIDHNGW

QDIGYNFLIGGDGNVYEGRGWGIWGAHVPRYNSKSIGICVIGNFQSTAPTQTQLDALKQLISCAQEGNYVQSDYRLIGHR

QGSRTSCPGNQLFNEIGGWTHFDATARP

>XP\_968926.1 PREDICTED: peptidoglycan-recognition protein LE [Tribolium castaneum]

MATQSEDEKKNKVCQNYMKDENFNDSSFNKCGEILEKCNLSDSSSDYLSTLEENNEGNVLNIKSENVCFTNKMIATNNQL

QQDFLTIDNILSKGPNQYNNIQIYKSQNVHIGDVTHINGPVYINHLTPTINQNIVINTNTNNDEDYPIVARRTWLAQPPL

DPDDVKFFKKPPKFVIICHSASEEAYTQTDNNLLVRLIQQFHVESRKWNDISYNFLVGAEGSVYEGRGWKTVGAHTQGYN

SVSIGICFIGCYIQNLPPSVALRKAKELIRYGVKIGAISEDYTLLGHCQCRSTESPGRRLFEEIKSWERWDGKISLENPS

PLIE

>EFA01375.1 Peptidoglycan-recognition protein LE-like Protein [Tribolium castaneum]

MATQSEDEKKNKVCQNYMKDENFNDSSFNKCGEILEKCNLSDSSSDYLSTLEENNEGNVLNIKSENVCFTNKMIATNNQL

QQDFLTIDNILSKGPNQYNNIQIYKSQNVHIGDVTHINGPVYINHLTPTINQNIVINTNTNNDEDYPIVARRTWLAQPPL

DPDDVKFFKKPPKFVIICHSASEEAYTQTDNNLLVRLIQQFHVESRKWNDISYNFLVGAEGSVYEGRGWKTVGAHTQGYN

SVSIGICFIGCYIQNLPPSVALRKAKELIRYGVKIGAISEDYTLLGHCQCRSTESPGRRLFEEIKSWERWDGKISLENPS

PLIE

>KYB28764.1 Peptidoglycan-recognition protein SC2-like Protein [Tribolium castaneum]

MCPLMKLIRVNSSRYRQKSDVVSRSQSGKLVKSESTCSDSPHAEKPKNSFLYSKHVKYLGISLVVIVILVTTTCVLILPR

KTEKSPETPDTNTATPRLPLGPGAIIEKKIWGGRATLNFSKPLPHPTHFVIVSHTVTPTCSDFPACSQRVQSMQDYHVGN

LKSPDIGYNFVIGGDGNAYVGRGWDIRNFHMDDSIGISFIGNFLHDHLTTEMISVAKKLLDEGVKSGKLARDYKLVAHNQ

TFRTESPGPNVYKEIKNWPHFDAGIYYSR

>XP\_015833415.1 PREDICTED: peptidoglycan-recognition protein SC2 isoform X2 [Tribolium castaneum]

MLNGRPRSFSVTKPKNGSVALISASKSKFASMSMTVMCPLMKLIRVNSSRYRQKSDVVSRSQSGKLVKSESTCSDSPHAE

KPKNSFLYSKHVKYLGISLVVIVILVTTTCVLILPRKTEKSPETPDTNTATPRLPLGPGAIIEKKIWGGRATLNFSKPLP

HPTHFVIVSHTVTPTCSDFPACSQRVQSMQDYHVGNLKSPDIGYNFVIGGDGNAYVGRGWDIRNFHMDDSIGISFIGNFL

HDHLTTEMISVAKKLLDEGVKSGKLARDYKLVAHNQTFRTESPGPNVYKEIKNWPHFDAGIYYSR

>XP\_008194895.1 PREDICTED: peptidoglycan-recognition protein LB isoform X2 [Tribolium castaneum]

MSELVVVPREGWHARPPTATEPMANPVPFVITHHSYIPPACHTPEACVQSMQTMQDMHQLQNGWNDIGYSFGVGGDGNAY

EGRGWSKVGAHAPKYNNISIGICVIGDWTKELPPENQLNTVHKLIAFGVEKGYIREDYKLLGHRQVRDTECPGDRLFEEI

STWEHFGVKGERRQENNGVEDNKLFFFKHKS

>XP\_969556.1 PREDICTED: peptidoglycan-recognition protein LB isoform X1 [Tribolium castaneum]

MYTFLFCFAAFLATGQMSELVVVPREGWHARPPTATEPMANPVPFVITHHSYIPPACHTPEACVQSMQTMQDMHQLQNGW

NDIGYSFGVGGDGNAYEGRGWSKVGAHAPKYNNISIGICVIGDWTKELPPENQLNTVHKLIAFGVEKGYIREDYKLLGHR

QVRDTECPGDRLFEEISTWEHFGVKGERRQENNGVEDNKLFFFKHKS

>EFA05744.1 Peptidoglycan-recognition protein LB-like Protein [Tribolium castaneum]

MYTFLFCFAAFLATGQMSELVVVPREGWHARPPTATEPMANPVPFVITHHSYIPPACHTPEACVQSMQTMQDMHQLQNGW

NDIGYSFGVGGDGNAYEGRGWSKVGAHAPKYNNISIGICVIGDWTKELPPENQLNTVHKLIAFGVEKGYIREDYKLLGHR

QVRDTECPGDRLFEEISTWEHFGVKGERRQENNGVEDNKLFFFKHKS

>XP\_008192540.1 PREDICTED: peptidoglycan-recognition protein SC1a/b-like [Tribolium castaneum]

MVFIATNPELKQNKQKSLVILDLKECVAFFLVVFLAMLAIIFALSAIGIHFSVTKDDPLILPYDKWTIPQKFFNREQWGA

KPPLNQTRLQHPVDLVIIGHTVTDFCWNFEQCSHIVAAIQNYHLELKMSDIAYNFLIGGDGNIYEGRGWDVANSQRNHSI

SVSFIGNFILDELNLNMIDAFQQLMIDGVNGEKLSKKYKIMCHNQTKATLSPGKNVYKIVKTWPHFRSGVLKN

>XP\_970847.1 PREDICTED: peptidoglycan-recognition protein 2 [Tribolium castaneum]

MSGSDPLTNTQQSDQDYYHPLCYSIQVDDENEQSALLPAFHQRKSLRVQDKIFIVFLFSILITGLAIGLYLLATEGHEWK

AAGVYNITVREQWQAHVPSSTMPKLELPVRRVLFLPANTTSCGSKSHCAKVLQELQLQHMLQWKEPDISYNFIMTADGRI

FEGRGWDFETSVQNCTVNDTVTVAFLDELDAKAPTFRQAEAAKMFLEVAVTEGKLERCFNTAVWGGNKFFIDLARNVQDV

LSECEGIT

**Zootermopsis nevadensis (NCBI)**

>XP\_021940814.1 peptidoglycan-recognition protein SB1-like [Zootermopsis nevadensis] >KDR07310.1 Peptidoglycan-recognition protein LB [Zootermopsis nevadensis]

MGQRAVVVELCSVIAIILLMSEGAIVRRDASCLNIVTRAEWSAKPAKQRDNITSLPVPFVILHHTYIPKDCNSSEECKEA

MRSMQHMHQDLRGWFDIGYNFCVGETGEVYEGRGWDIQGAHAPRYNNRSTGICFIGDFMNSLPTPEMMEAAKDLIKCGVN

RGSIAEDYKLLGHRQVRNTLCPGDTFYENITTWPHWDPLQDVVPVPKQ

>XP\_021940816.1 peptidoglycan-recognition protein LB-like [Zootermopsis nevadensis] >KDR07311.1 Peptidoglycan-recognition protein LB [Zootermopsis nevadensis]

MLRRIIKNTLCVLFITHLAMTACPEIVPRADWGAVAAVSIVVLTSLPVPYVVIHHTFLPGFCNTSQTCEAAMRSMQNYHQ

NTNQWHDIGYHFCIGGTGKVYEGRGWDVVGTHTPKYNSNSTGICFIGDFRTELPTPEMLSAAKSLIECGVERGSISPEYK

LLGHSQTRNTECPGAALFNEIKTWPHWDPLNNTSST

>XP\_021940116.1 peptidoglycan-recognition protein SC2-like [Zootermopsis nevadensis]

MQSSWASLFLIGNFFAFGYAALPLQILTWGKTPPPFHITIWATLVQNPVQSICSCPLPDTKRLSYPTACPRIVSKDEWGG

RPPKGPTEKMNVPVPFTVVHHGGSKDYCTTEERCAAIVRSYQTSHMDSNGWNDIGYNFVVGEDGNVFEGRGWEAVGAHAP

TYNTKSIGICIIGDFTDRLPNEAALKAVQSLIECGVEQNKIQRQYQLIGHRQNTASSTVCPGTKLFEEIMTWPQWTPDPK

NVKGFQTNWD

>KDR07939.1 Peptidoglycan-recognition protein SC2, partial [Zootermopsis nevadensis]

TACPRIVSKDEWGGRPPKGPTEKMNVPVPFTVVHHGGSKDYCTTEERCAAIVRSYQTSHMDSNGWNDIGYNFVVGEDGNV

FEGRGWEAVGAHAPTYNTKSIGICIIGDFTDRLPNEAALKAVQSLIECGVEQNKIQRQYQLIGHRQNTASSTVCPGTKLF

EEIMTWPQWTPDPKNVKGFQTNWD

>KDR18042.1 Peptidoglycan-recognition protein 1, partial [Zootermopsis nevadensis]

IPVSTGEDDCPRIISRSGWGARPSKHVEYMKIPVEYAIIHHTVTPKCNSMAECVEKVSSIHSFHVNTNGWDDIGFSFLVG

GDGNVYEGRGWHQVGAHTYGFNKKSVGIALIGEFSDSLPPRVQLDALKRLLKCGVKEGELAEHYKLLGGRQISATKSPGL

ALYQEIQTWPDWVENP

>XP\_021922592.1 peptidoglycan-recognition protein 2-like [Zootermopsis nevadensis]

MELFNTALLVALMTAIRPTEGEDDCPRIISRSGWGARPSKHVEYMKIPVEYAIIHHTVTPKCNSMAECVEKVSSIHSFHV

NTNGWDDIGFSFLVGGDGNVYEGRGWHQVGAHTYGFNKKSVGIALIGEFSDSLPPRVQLDALKRLLKCGVKEGELAEHYK

LLGGRQISATKSPGLALYQEIQTWPDWVENP

>KDR12888.1 Peptidoglycan-recognition protein LE, partial [Zootermopsis nevadensis]

SFGNIVVSSSSDVHFGNKTFYNGPVTIKQFVCTTKNGTIDAHHSENGYRNCDDSKVDVDEVLDPMSNQEVEPMVGWKNRM

LQWGRKMKCTRTRLTMLAIICVCVMVVLVAVLFSLPRLEEETATNNAVSGTLRIINRRTWLAQPAVRPSNPLQHPVPYVV

ILHTATDNCSTQAECVFIVRHIQTFHIESNGWNDIGYSFLVGGDGNVYEGRGWDTEGAFAYGYNSRAIGIAFIGTFTVDV

PEPKQILAGKQLMELGVTMGKISPHYKLLAHRQVSPTESPGLAFYEFLKTWPHWAEHP

>XP\_021932121.1 peptidoglycan-recognition protein LC-like isoform X3 [Zootermopsis nevadensis]

MSLSKKHVLLPLRHRASPCGPVQRVGSAAPSVGYVRRSGMVESRRDVERAADSDSVPGPKEDDDSEGDLHHLEREGRQGV

DQWSDQVVLDDSEEEEDAESTSDIYRDDGDDDDSDLKIDSACSSNALALEAKKISESRPSFGNIVVSSSSDVHFGNKTFY

NGPVTIKQFVCTTKNGTIDAHHSENGYRNCDDSKVDVDEVLDPMSSGLPNGKVQCPTPSSPNVIISVPSALAVTSEPSPG

VNGSLLQIWQPSGTTNNAVSGTLRIINRRTWLAQPAVRPSNPLQHPVPYVVILHTATDNCSTQAECVFIVRHIQTFHIES

NGWNDIGYSFLVGGDGNVYEGRGWDTEGAFAYGYNSRAIGIAFIGTFTVDVPEPKQILAGKQLMELGVTMGKISPHYKLL

AHRQVSPTESPGLAFYEFLKTWPHWAEHP

>XP\_021932119.1 uncharacterized protein LOC110835818 isoform X2 [Zootermopsis nevadensis]

MSLSKKHVLLPLRHRASPCGPVQRVGSAAPSVGYVRRSGMVESRRDVERAADSDSVPGPKEDDDSEGDLHHLEREGRQGV

DQWSDQVVLDDSEEEEDAESTSDIYRDDGDDDDSDLKIDSACSSNALALEAKKISESRPSFGNIVVSSSSDVHFGNKTFY

NGPVTIKQFVCTTKNGTIDAHHSENGYRNCDDSKVDVDEVLDPMSSGLPNGKVQCPTPSSPNVIISVPSALAVTSEPSPG

VNGSLLQIWQPSGNQEVEPMVGWKNRMLQWGRKMKCTRTRLTMLAIICVCVMVVLVAVLFSLPRLEEETATNNAVSGTLR

IINRRTWLAQPAVRPSNPLQHPVPYVVILHTATDNCSTQAECVFIVRHIQTFHIESNGWNDIGYSFLVGGDGNVYEGRGW

DTEGAFAYGYNSRAIGIAFIGTFTVDVPEPKQILAGKQLMELGVTMGKISPHYKLLAHRQVSPTESPGLAFYEFLKTWPH

WAEHP

>XP\_021932118.1 peptidoglycan-recognition protein LC-like isoform X1 [Zootermopsis nevadensis]

MSLSKKHVLLPLRHRASPCGPVQRVGSAAPSVGYVRRSGMVESRRDVERAADSDSVPGPKEDDDSEGDLHHLEREGRQGV

DQWSDQVVLDDSEEEEDAESTSDIYRDDGDDDDSDLKIDSACSSNALALEAKKISESRPSFGNIVVSSSSDVHFGNKTFY

NGPVTIKQFVCTTKNGTIDAHHSENGYRNCDDSKVDVDEVLDPMSSGLPNGKVQCPTPSSPNVIISVPSALAVTSEPSPG

VNGSLLQIWQPSGNQEVEPMVGWKNRMLQWGRKMKCTRTRLTMLAIICVCVMVVLVAVLFSLPRLEEETGTSVRLPEDGI

ISATFSYRATNNAVSGTLRIINRRTWLAQPAVRPSNPLQHPVPYVVILHTATDNCSTQAECVFIVRHIQTFHIESNGWND

IGYSFLVGGDGNVYEGRGWDTEGAFAYGYNSRAIGIAFIGTFTVDVPEPKQILAGKQLMELGVTMGKISPHYKLLAHRQV

SPTESPGLAFYEFLKTWPHWAEHP

>XP\_021921579.1 peptidoglycan recognition protein-like isoform X3 [Zootermopsis nevadensis]

MATLIGSIQNPHGESHHHTAAAAKYNKMACLCLHWRIFLPTLAVIVLLVIILTAIIIHFSSSSRDDLPKQTFYPAPEDPE

PNPNTTLPGDHVIYSKEDWYGVAPKFERQLKHPTPFVVISHTATPACYSPVVCAARMRNFQDVHMGDSHNFPDIGYSFVV

GGDGNVYVGRGWDATNMHSGFVKRCNIGISFIGNFVHDTPTNGQIQAVQELIKLGVSLGKIDKNYKLVAMNETFTTLSPG

VVLYGIIAKWPHFWKPSHDDIGMCPYTV

>XP\_021921578.1 peptidoglycan recognition protein-like isoform X2 [Zootermopsis nevadensis]

MPVDNNINDTTINMTASIPSRKADMQKKDVLATDDGSCTHSNGSSTSEDEEDPDYEGVSTHEVSEVSTGALCLSGSPSNF

HMENNSDVQIGPRLHYNAPVTINQFVHVLGSNEVSPDGILQEAVRAPIHGLDAEESNISQDPEPNPNTTLPGDHVIYSKE

DWYGVAPKFERQLKHPTPFVVISHTATPACYSPVVCAARMRNFQDVHMGDSHNFPDIGYSFVVGGDGNVYVGRGWDATNM

HSGFVKRCNIGISFIGNFVHDTPTNGQIQAVQELIKLGVSLGKIDKNYKLVAMNETFTTLSPGVVLYGIIAKWPHFWKPS

HDDIGMCPYTV

>KDR18605.1 Peptidoglycan recognition protein I-alpha, partial [Zootermopsis nevadensis]

IYSKQDLGAIKELCSEQLVHPTPVVVISHTTTRQCTSFDTCSEAARLIQLNIIGKRGSQNSANAADIGYNFLIGGDGNVY

EGKGWDEMSSHRTPEGILGISFIGNYHKDRLTYGQIEAAQELLALGVKLEKLSPSYILVAHYQTASTDNPEPNPNTTLPG

DHVIYSKEDWYGVAPKFERQLKHPTPFVVISHTATPACYSPVVCAARMRNFQDVHMGDSHNFPDIGYSFVVGGDGNVYVG

RGWDATNMHSGFVKRCNIGISFIGNFVHDTPTNGQIQAVQELIKLGVSLGKIDKNYKLVAMNETFTTLSPGVVLYGIIAK

WPHF

>XP\_021921577.1 peptidoglycan-recognition protein LA-like isoform X1 [Zootermopsis nevadensis]

MPVDNNINDTTINMTASIPSRKADMQKKDVLATDDGSCTHSNGSSTSEDEEDPDYEGVSTHEVSEVSTGALCLSGSPSNF

HMENNSDVQIGPRLHYNAPVTINQFVHVLGSNEVSPDGILQEAVRAPIHGLDAEESNISQATLIGSIQNPHGESHHHTAA

AAKYNKMACLCLHWRIFLPTLAVIVLLVIILTAIIIHFSSSSRDDLPKQTFYPAPEDPEPNPNTTLPGDHVIYSKEDWYG

VAPKFERQLKHPTPFVVISHTATPACYSPVVCAARMRNFQDVHMGDSHNFPDIGYSFVVGGDGNVYVGRGWDATNMHSGF

VKRCNIGISFIGNFVHDTPTNGQIQAVQELIKLGVSLGKIDKNYKLVAMNETFTTLSPGVVLYGIIAKWPHFWKPSHDDI

GMCPYTV

>XP\_021921586.1 peptidoglycan-recognition protein SC2-like isoform X2 [Zootermopsis nevadensis]

MKLLRGSTRHRGNAFFQSPLITGSGPSVPPLRIPRTRPRENQFNNEVGTNPNAALRDHAGANLHRQTTTTPKKSVIVRLL

WVFIVIISFTTVCLITAFAIQNSQYEELVSVGMKSSSHFNASVSVGFDPMMKTPSSEPFRLPGGHYIYSKQDLGAIKELC

SEQLVHPTPVVVISHTTTRQCTSFDTCSEAARLIQLNIIGKRGSQNSANAADIGYNFLIGGDGNVYEGKGWDEMSSHRTP

EGILGISFIGNYHKDRLTYGQIEAAQELLALGVKLEKLSPSYILVAHYQTASTDSPGKNIVKVIEKWPHWSPSYRIT

 >XP\_021921582.1 peptidoglycan-recognition protein LA-like isoform X1 [Zootermopsis nevadensis]

MKMAGGSRDTTEVTLTDDDDDEESDSDEEPHRITLQALQQVPAQSVVVDDSSDVHVGPRLTYNGPVIVNQILQLTGEGRG

LSDISQQGLLRQAITAPGNTADPLSNNTKENQFNNEVGTNPNAALRDHAGANLHRQTTTTPKKSVIVRLLWVFIVIISFT

TVCLITAFAIQNSQYEELVSVGMKSSSHFNASVSVGFDPMMKTPSSEPFRLPGGHYIYSKQDLGAIKELCSEQLVHPTPV

VVISHTTTRQCTSFDTCSEAARLIQLNIIGKRGSQNSANAADIGYNFLIGGDGNVYEGKGWDEMSSHRTPEGILGISFIG

NYHKDRLTYGQIEAAQELLALGVKLEKLSPSYILVAHYQTASTDSPGKNIVKVIEKWPHWSPSYRIT

**Ephemera danica (i5k)**

>gnl|Ephemera\_danica\_protein\_v0.5.3|EDAN001633-PA

LCLIIKKRRVEDKVMLFTSFTMLNVSVLTVALVLSVTEACPSIKSRSSWGSKPSVTPAANQKNPSTLAIIHHSDTPPCTTTQQCEARVRQIQSFHVNNRGWGDIGYNFLIGGDGTIYEGRGWGKVGAHAKGYNSISTGICFIGNYKTSPPPRHLLQLAKDLIACGVTKKFINPNYGLRGHRQVGQTECPGNALYKEIMGWPPLLLTITAELVLTACPNIKARSTWGAKNPKKPLSPLTQNPAPYVIIHHSDSPPCTTSQQCQARVLSIQADHQTSARGFDDIGYTFLIGGDGNVYEGRGWGKSGAHAPNYNSKSVGICVIGDFMATNPPNNMLQLVKDLIACGVDSGKIRSNYKLLGHRQVRATSCPGDKLFNEIKTWPKWSSQP

>gnl|Ephemera\_danica\_protein\_v0.5.3|EDAN016974-PA

LTPVTMAKDSNNLNSNRLYVECSDSDESDSDSDTVAVDNIDTTVPPSYFGNIDVKNSSNIIFGNTVSYNGPVTVQQFVNSGENAVDNNINSVDLLANTNGVKPITAVAEKSLPVSFNHKPQHPSHLSQQFSIVLAKDESEESSSKWKPRRWFIVAVGSCILVVVTLIVVLAIVLSGPANPTSKKDDTDWENYYNKSQTLLNGTEGIAPFYSRADWLAQPVGPGDKLKTQHAPLVIISHSATAPCFNNSQCIFQVRKIQTFHMESQGWRDIGYNFLAGGDGGVYEGRGWDLIGAHAYGYNNVSIGICTLGTFTKEAPPQKQIRAVKLLIEEGVRQGKISPRYKLLAHSQVSATESPGAAYYKVIQTWPHWVPRPNATLPEPDEKLKT

>gnl|Ephemera\_danica\_protein\_v0.5.3|EDAN015174-PA

MKTAIVFLACVTYVAAQAGCPNIVSRAEWGARPPTATSPMSNPVPYVVIHHSEGASCTTQTSCESVVRGIQDYHMDSNGWNDIGYSFLVGEDGNAYEGRGWSNVGAHAPGYNSNSIGICFLGSFMTRVPNNAALNAGKQLIQCGVSNGYIRSAYSLYGHRQVTATDCPGDALYAEIQTWTNYDPTP

>gnl|Ephemera\_danica\_protein\_v0.5.3|EDAN013912-PA

MQSRKLAGLVGAVALLIMAHSVQSWPVSSAEVVTPSGSTNAALLIRPRSAWRALEPREVQPLKFSPAPFVVLHHTYIPAFCPSAAECEVSMREMQRMHQQDRGWFDIGYTFVVGGDGAVYEGRGWGRDGAHAPRYNDKSVGIAFVGDFRTSVPSSEMMLAAQNLISVGVREGHIRADYALLGHRQTRDTECPGDALFAEISSWPHFRAEPPADPQDFEAFLAANTTLTPLQ

>gnl|Ephemera\_danica\_protein\_v0.5.3|EDAN008911-PA

MKTAIVLLACFAYALAQPGCPNIVSRSEWGARPPKSTTPMYNPVQYVVIHHTAGSTCTTQTSCSAEVRAIQNQHMDVNGWNDIGYSFLVGEDGNAYEGRGWSNVGAHAPGYNDVNRIPNNAAINTCKQLIQCGMDARYVQYAHSLLGHRQAVATECPGDALYAEIQTWDNYDPTP

>gnl|Ephemera\_danica\_protein\_v0.5.3|EDAN005909-PA

MFMYARKFLSYIYDNFSQQVVVALCWPQVRYLQRCHIKQRRLGDISFNFLVGGDGNVYEGRGWTTACGDDTTGLPLICTFHDFQVENLCRRQQRALQGLLQMAVARRTLAKNYQLLVLHPILDTIMRHWSKPEDMEVVNREKWGTIDPEHTYFLTDQLTYVIISHSVFQFCSSSKQENIEYIRYIQNVHAHEMGWGDIGYNFLIGGDGRVYEGRGWHAKSAHTYAYNHLALGVCFVGDFRVEAPSEVQLQACQKLLRIAVARGQLAPHYKLVGHCQVRNTASPGQALMEVIKTWPHWSSQL

>gnl|Ephemera\_danica\_protein\_v0.5.3|EDAN011265-PA

MMVRKQSTHSMQLVPLALVLTAAAAPSHLVIAASIVTEAPTELRIVSRDEWYAREYRTTTPQRVPVPFVVIHHGGIPEYCINITTCSEQVRKYQMLHMDDRGWDDIGYSFLVGEDGNVYEGRGWRRVGAHAPQYNNQSIGICIIGDFSKQLPNKLALDAVHALIKHGVQEGLILPQYTLLGHRQVRETQCPGEALYQEIMTWTHFDLSPFPRKYCTPCNPITATCNFTTILPTCNTATSRKNIGLLLFLAIPMIVLRYITLT

>gnl|Ephemera\_danica\_protein\_v0.5.3|EDAN015175-PA

MKTAFVLLACVAYAAAQAVDQGRYIKMKTAFVLLACVAYAAAQAGCPNIVSRSEWNARPPTSTSPMSNPVPFVVIHHSAGASCTTQSSCTSQVQGIQNYHMDTNGWNDIGYSFLVGRVPNNAALDAGKQLIQCGVSNGYIRSAYSLYGHRQVTATECPGDALYAEIQTWTNYDPTP

Frankliniella occidentalis (i5k)

>gnl|Frankliniella\_occidentalis\_protein\_v0.5.3|FOCC016414-PA

MESRLPHLTYCVTLLPAAPAPCRHWLAALVGLVLGVGITALLAGVIILAIQRSGADEQPQTPPTAGDPFSERSNCLPFSEGWGWQNKSGESRHGIPHASQTRKIQEFHMGKENNWSDIGYNFLVGGDGLVYSGRGWDIVGAHTKTWNNKSIGVGVIGSFSEVAAFPWQLSAMKGLLAWGVSKGKLTADYGVMGASQVQDTDSPGQRLMQDLRAWKHWRNYTYTTSTLHTAHGGT

>gnl|Frankliniella\_occidentalis\_protein\_v0.5.3|FOCC016412-PA

MTGLSAPALAPVLPWPPPRRRSSDVPSLGSRDGCWLVDSTPSSGVACVLWDCPCPAPDLWGGRRVSARNSMLICTPSSDSNGENDSGDSGSSCSGGSCSGDSCSGSPSSSSFRGGSSCSDNVLVTPMDAKKVAHLAVTQSCARMAVGSVSMTNASAQIGNISNFNGPVTVVVGSAGGELDRAEDARPEPPQLPDRLHDKCPTVESAPALSQPDSQTSTARGKFKSVRELQREHMDVRAPALDDIEFNFLVGGDGAVYEGRGWDAVGRPLGGWHHESLSVAMIGTFHQRQPTAAQADAALRFVEWAMSDLERIRTDYRAAGACQFEDTDSPGARVMDMLVVWPHWWNHSTVDAPCIPMRKAQSALS

>gnl|Frankliniella\_occidentalis\_protein\_v0.5.3|FOCC001419-PA

ARCGTRLDIGTRSPHLAFPPAAPYQESASASLPAMRSATRTAAAAADARILGPLLIILSLTLQAPGARGACPDIIPRRRWGAASSERVDYIPFPVRDVIVGHTVGGSCASEEACAQEAVSIQKQHKALGWGDIGYGFLIGGDGLIFEGQGWHKEGAHTYGYNKKSIGVAFMGDFSERRASTAQLKALRALLRCGVELGELSEDVRLYGQRQVQQTESPGRELYKQIKELPEWVAAP

>gnl|Frankliniella\_occidentalis\_protein\_v0.5.3|FOCC003455-PA

MAEKVGVTYTGLGAGRRIAASSAEPLITLPVNCMCVKAANMGPRDVCGLPSPPPPAYTTKSSGTVTPDGMVVLVDVASVPPPPVPSPTATRVHATLADGSCYCSATDDGDSSNSSGTGSVWTNFSDGCRGCRSSIGNITLANSTAQIGSVMNYITVLVPDEAAATKTGGDRDLAGVALQAATLAAKEKLSCLHPNEDKELPSSLTASQTLAMRRHLRWPCVAVPIALLAAILVVYFMVLIQHQSEDAVPGPVTLPNGVTLAGREVWHAQPPRKRMPRLFTPVKYVVVHHTATDHCFHLEHCANMVRAFQQYHQDALGRDWDDIGYNYLVGGDGVVYEGRGWDWVGAHFELTEWGNKTMNIALIGNFVNAVPPAFQRDQLRKFIAWGVEMGKIRRDYQLMGACQIKDTQSPGLRFMDDLRTWTHWWNFAATALVLVAVVVVLGILVLTRPGPSDSASQTALDTNKATTTTAAATTTTTTMTTFTVPSTTDSTPLVGSTSKRPFEAEVLVSRGEWRARGARNPGSVLMTPVMDVIVQHTAGYQCATRAECSAEVRCSLPLLLLRTLRRGREKRNEHTSLCPQVLRIQDSQMDWRHRPQPFSDIGYNFLVGGDGHAYWGRGWDTVGAHTYGWNTKSIGVGIIGTFTNETAPPALQSALRRLLEWGVSLGKLTGNYKIMGACQVQSSDSPGWSFMEDLRTWSHWSNYTSVPWACMT

>gnl|Frankliniella\_occidentalis\_protein\_v0.5.3|FOCC016416-PA

MVANDVCGTVSVGDTTLVQEDAHTQVVATPGNTRAVRDVVVSSRGSLDSGLAIARYDDDENDASSDSASSGGSVAPWSSEGSSGSEMVVADITITDGSANIGIFKNYVNVFMCEGKGEQLTGFPGAEGLPTAALKNAQVKVQAAAPVPAGPCALQDTDKKGREVDQTAKCRGPVDACWNNLNKVLRWPWSIVPSAAVSVAILVVIYFTLLSPPQSNSSDPTDPIILPNGIQYASRKVWKAVPPKRKMPGLTLPSTAVIIHHTATSACYTTKVCIDMVAAMQRYQMDVEGARRDWADIGYNFLVGGDGVVYEGRGWEHAGGHFEKEIWSPQTVGIAVIGDFTETLPPENQLQQLRKFVAWATTVGKVASDYKLYGVCQLKATKSPGLLLMARLRTWPHWDSFVAKPNVASASAAAALSDRMFDDVLHTGDDDGDVDGDGWSSPGSSDCTSLESVWSGAGGTQGADGPGVNVDKLKMVNSTAQIGNINNYKGPVTVVVTNEANNVGCVSMPAVLSPGGGLVLSAGTLEHVVSQEQLLGPTNTGSAPTTPAAETNRALKKFLRWPCVTVPVTMLVAALGLVVTVVLVSLPRADGIIELKNGVKLAKRSFWHARNPKKPADILRTPVDIVIINHSGTEFCFDAQECIDRISMIQSYNMDSVNRSWDDIAYNYMIGGDGVTYEGRGWDAVGAHVQGWNTKSLGVGIIGNFTWQTPTDVQRDQLKKFLAWGVELGKVRRDYKLAGACQLHASDSPGRRFMDELRTWPHWWDYMFKENACSGGSAVGPQTVNPDREVAGRNDHLLSLGELASGGQSGTLSLAQSLSYESVSVEGSRNVQIGNNIHIHGEVTLVLPVDSSGLPSAKIRDELGEKPADADKDRPLHSAQDSSKKQTGKAEFPGLVTRREWNAWDPRYAKVPDELPLPVRTVIVHHTTTRPCDSRADCAKIDLAFDTDNDDIPYNFLVGGDGLVYEGRGWGLIGGAVYGWNSEALVFALVGTFDYVEPTPPQRASLLRLLQWGLDHEKVHAEYRIAGACQLKVNATSTPGLRFMDDLKTWDHWWDFMIRPNRSCTLRLLVVLLVVLVVLLVAGVVVLVLTITTALQAGEDEPDTQHTFKAVDLMTRDDWLGRLSRGTPSRMTMPVDLVIIHHTAYEVCTTKAKCKQQVKRVQNQHMDDPNFRYFDIGYNFLVGADGLVYEGRGWDAVGAHLHGWNQKAVGVAILGTFTNVTAPPALQTALYSLLQWGESLGKLTKDYGIIGACQVRATKSPGRRFMGDLCTWSHWRNQTSVSKACTE

>gnl|Frankliniella\_occidentalis\_protein\_v0.5.3|FOCC006882-PA

MGYIISVGTGEDGRRPEQQRQNCFRAPSSALTCVCPRIVPRDEWGARPPKAVLEMHNPVSTVVIHHTYSPSYCASAAACEEAMRSMQTFAVGGDGRVYKGRGWNRVGAHAPPYNQDSIGITLIGDWTAQAPPKEMLDAVSWLIRCGVDTGRIAPDYQLIGHRQARDTACPGDGLFAVVRTMPRWTATPAPPKHHGLSAAAPAAPALDHLSSDLPIPAAAVPEAPAAATAAAAPVVLEVSATPSPAARAGTYDPSTPVASRDAVEVRQLNKRASLRAGSLWDRLVLIWEHEAARQESEAAAAASQDAVVVS

>gnl|Frankliniella\_occidentalis\_protein\_v0.5.3|FOCC016415-PA

MELDRAGARSGDTAEGVVLDQHGCLAEQNGGVAGALSLAQPLSYESIAVEDSRNMQIGNNIHIYGEVNWLQLKALSNDDDIPYNLLVGGDGLVYEGRGWSVVGATLPDWDSEILSLALIGNFDHASPTEQQRAALASLLQWGVSNGKVDKAYRLAGACQLREYEYFNDTSPGVLFMPELQTWDHWWDFMVRQRQNLALDSMNMSDIDYNFLVGGDGLVYLGRGWGGAGAHTLLHNNESIGVAAIGRFTFVTAPPALQNALLRLLEWGVRLGKLTEDYRVVGHCQLRPASDSPGRRFMQDLRTWSHCSSYTAVPEACTT

**Dendroctonus ponderosae (NCBI)**

>XP\_019768562.1 PREDICTED: peptidoglycan-recognition protein LC-like [Dendroctonus ponderosae]

MSLQLSSSGLNRVDSSCSSSTASSGSDELQVLPLGYQIDHPSPNELIIRNNITEGTTTANIVNSPHATVG

TNLHIVLGDNANLYVGDGSRTLHDQANYAALRLTPGSPRSSSPESGANEAQPPRKAAIRSKIVYVPLILV

FSVSLIIIGVVVWAQTERTEETTTTEETEVPTSTTPVVTTEVPDYDGFYIPREVWGGADPTSPSIKAEPA

MLFVIKHTAGETCTNQKQCSKVVREIQKEHMEVLGFADISYNFLVGGDGKIYNGRGWGVQNEGRNDSLDV

AFMGNFNVDDPTTKMMNAALRIQITGQSAGQVKYGKYRVMNHNQTEPTDSPGKRLFAKTISNLNYYSGAV

CYHNASGQVVIDYDCP

>XP\_019756553.1 PREDICTED: peptidoglycan-recognition protein SB2-like, partial [Dendroctonus ponderosae]

LENYQLSLPFLETDWVFRAFRPLWNLRKIVRKTQQFQPVKCKSPLKHLNSTVVSFLDSAFDNTPIIEHDQ

PHATKQKPSLASIQVLLPLAGFIAVGLVLTGIIVWRVRANYATTNEEAVTELVSTTVDYPLFVPREGWNA

LEPTSPPIPIAPALVFVGKHTGGSSCATPAECVARVQEIQREHMEVKGLADISYNFLIGGDGRIYTGRGW

GVENEGRNDSVDVALIGDFNIEVPTTEMVFLVRRLENRGPREGGLDYANYWAVNHNQTEPTDSPGAHLFA

RLASNGYFHYSSAVCYRNVSGGFEVDYQCPP

>XP\_019769175.1 PREDICTED: peptidoglycan-recognition protein LB-like [Dendroctonus ponderosae]

MKLSLLCFGAVLVVAVCFQERQCAVCSMGPEIVSRDDWGAREPLLRENMTNPVPFVVIHHSYMPDACYTQ

EGCIEAMQWMQDLHMINNSWNDIGYSFAAGGDNRVYVGRGWSSVGAHAPGYNNRSIGICVIGDWSDRLPA

ESQLQAVKQLINMGIRNGFIQENYKLIGHRQARDTECPGDALYSEIQTWSHWIEDPTLDIKSSLAKEGLQ

PDPREIQDTPEEHNAVKRQSKAIKL

>XP\_019768774.1 PREDICTED: peptidoglycan-recognition protein 2-like [Dendroctonus ponderosae]

MKTACFCLLLASLRGAAPAEPPKVECANLTVSRADWGARRPFAVDYSIIPVRNVVVHHTVTPGCSSGSQC

AGTLREIQNFQIDTLEFPDIGYNFMIGGDGRVYEGAGWHKVGAHTRGYNTKSIGVAFIGNFSDERPDAAM

LQALRRLLACGVAMGELHEQYRLFGGRQVTATASPGSRLYAELKTWPHFTLDPLSS

>XP\_019763557.1 PREDICTED: peptidoglycan-recognition protein SC2-like isoform X3 [Dendroctonus ponderosae]

MSPKLPISDVWIARRLQRNNSRGFIWLQNVSKHRSVEIGIFVIVVILFFIVLMVLLVLGRSPAVVSNPSN

DLTTSSQKDTNLRMVSRYEWVAQPPIKKTTTLQTPVPYVIIHHTATEFCTSQAQCVFHVRQIQTFHIESR

GWFDIAYNFLVGGDGAAYEGRGWTGEGAHTLYWNKNSIGIAFVGTFLTTAPPEIQILACQKLIDLGVKLG

YIQQNYTLLGARQLFATESPGLALFEIIKKWDHWHSL

>XP\_019763556.1 PREDICTED: peptidoglycan-recognition protein LF-like isoform X2 [Dendroctonus ponderosae]

MTLVATSDLSCTNQLPSSAPCNCSSDEESESDCSGDDSMCVQQLQSDSKCNEDCLMQSLGYPNSNIFPSY

GEVSIENSNDVHIGNKNFYNGPVKIKQIVYANGNPALVNSSDKAKDNLGFEMDSGHSAAEVKDCCKDPEL

ADQAAAESPQSPIRNGFIWLQNVSKHRSVEIGIFVIVVILFFIVLMVLLVLGRSPAVVSNPSNDLTTSSQ

KDTNLRMVSRYEWVAQPPIKKTTTLQTPVPYVIIHHTATEFCTSQAQCVFHVRQIQTFHIESRGWFDIAY

NFLVGGDGAAYEGRGWTGEGAHTLYWNKNSIGIAFVGTFLTTAPPEIQILACQKLIDLGVKLGYIQQNYT

LLGARQLFATESPGLALFEIIKKWDHWHSL

>XP\_019763555.1 PREDICTED: peptidoglycan-recognition protein LF-like isoform X2 [Dendroctonus ponderosae]

MTLVATSDLSCTNQLPSSAPCNCSSDEESESDCSGDDSMCVQQLQSDSKCNEDCLMQSLGYPNSNIFPSY

GEVSIENSNDVHIGNKNFYNGPVKIKQIVYANGNPALVNSSDKAKDNLGFEMDSGHSAAEVKDCCKDPEL

ADQAAAESPQSPIRNGFIWLQNVSKHRSVEIGIFVIVVILFFIVLMVLLVLGRSPAVVSNPSNDLTTSSQ

KDTNLRMVSRYEWVAQPPIKKTTTLQTPVPYVIIHHTATEFCTSQAQCVFHVRQIQTFHIESRGWFDIAY

NFLVGGDGAAYEGRGWTGEGAHTLYWNKNSIGIAFVGTFLTTAPPEIQILACQKLIDLGVKLGYIQQNYT

LLGARQLFATESPGLALFEIIKKWDHWHSL

>XP\_019763554.1 PREDICTED: peptidoglycan-recognition protein LC-like isoform X1 [Dendroctonus ponderosae]

MTLVATSDLSCTNQLPSSAPCNCSSDEESESDCSGDDSMCVQQLQSDSKCNEDCLMQSLGYPNSNIFPSY

GEVSIENSNDVHIGNKNFYNGPVKIKQIVYANGNPALVNSSDKAKDNLGFEMDSGHSAAEVKDCCKDPEL

ADQAAAESPQSPIRNGFIWLQNVSKHRSVEIGIFVIVVILFFIVLMVLLVLGRSPAVVSNPSNGTSAEPN

IIKPIEYDPDLTTSSQKDTNLRMVSRYEWVAQPPIKKTTTLQTPVPYVIIHHTATEFCTSQAQCVFHVRQ

IQTFHIESRGWFDIAYNFLVGGDGAAYEGRGWTGEGAHTLYWNKNSIGIAFVGTFLTTAPPEIQILACQK

LIDLGVKLGYIQQNYTLLGARQLFATESPGLALFEIIKKWDHWHSL

>XP\_019763552.1 PREDICTED: peptidoglycan-recognition protein LC-like isoform X1 [Dendroctonus ponderosae]

MTLVATSDLSCTNQLPSSAPCNCSSDEESESDCSGDDSMCVQQLQSDSKCNEDCLMQSLGYPNSNIFPSY

GEVSIENSNDVHIGNKNFYNGPVKIKQIVYANGNPALVNSSDKAKDNLGFEMDSGHSAAEVKDCCKDPEL

ADQAAAESPQSPIRNGFIWLQNVSKHRSVEIGIFVIVVILFFIVLMVLLVLGRSPAVVSNPSNGTSAEPN

IIKPIEYDPDLTTSSQKDTNLRMVSRYEWVAQPPIKKTTTLQTPVPYVIIHHTATEFCTSQAQCVFHVRQ

IQTFHIESRGWFDIAYNFLVGGDGAAYEGRGWTGEGAHTLYWNKNSIGIAFVGTFLTTAPPEIQILACQK

LIDLGVKLGYIQQNYTLLGARQLFATESPGLALFEIIKKWDHWHSL

>XP\_019763551.1 PREDICTED: peptidoglycan-recognition protein LC-like isoform X1 [Dendroctonus ponderosae]

MTLVATSDLSCTNQLPSSAPCNCSSDEESESDCSGDDSMCVQQLQSDSKCNEDCLMQSLGYPNSNIFPSY

GEVSIENSNDVHIGNKNFYNGPVKIKQIVYANGNPALVNSSDKAKDNLGFEMDSGHSAAEVKDCCKDPEL

ADQAAAESPQSPIRNGFIWLQNVSKHRSVEIGIFVIVVILFFIVLMVLLVLGRSPAVVSNPSNGTSAEPN

IIKPIEYDPDLTTSSQKDTNLRMVSRYEWVAQPPIKKTTTLQTPVPYVIIHHTATEFCTSQAQCVFHVRQ

IQTFHIESRGWFDIAYNFLVGGDGAAYEGRGWTGEGAHTLYWNKNSIGIAFVGTFLTTAPPEIQILACQK

LIDLGVKLGYIQQNYTLLGARQLFATESPGLALFEIIKKWDHWHSL

>XP\_019754891.1 PREDICTED: peptidoglycan recognition protein 1-like isoform X2 [Dendroctonus ponderosae]

MTCPQTFVFILVSICVFSRNTDGCSEIKKRNSWGAVNANEQTKLVQNPPPLVIVHHSATRSCNSQDDCKK

LVSSIQHYHIFTNGWSDIGYNFLIGSEGTIYEGRGWGLIGAHAVGFNNNSIGICLIDNSPSEVQLSSLKS

LIACGVSTGKIHRNYTLIGHRQVSSTLCPGDKLYNILKNMPRFEPQPL

>XP\_019754890.1 PREDICTED: peptidoglycan recognition protein 1-like isoform X1 [Dendroctonus ponderosae]

MTCPQTFVFILVSICVFSRNTDGCSEIKKRNSWGAVNANEQTKLVQNPPPLVIVHHSATRSCNSQDDCKK

LVSSIQHYHIFTNGWSDIGYNFLIGSEGTIYEGRGWGLIGAHAVGFNNNSIGICLIGNLQDNSPSEVQLS

SLKSLIACGVSTGKIHRNYTLIGHRQVSSTLCPGDKLYNILKNMPRFEPQPL

>XP\_019773772.1 PREDICTED: peptidoglycan-recognition protein LE-like isoform X2 [Dendroctonus ponderosae]

MGTANRVVFEFDKMCTIRELSDANFTEPVKEENKSTKCMGRDQQLEVTDQNPNDHDSDLSDADTTEIDEE

ESRTSESDRQLVLKNQELNYLDGDIDEGLCNAFETKMNTLPRYRSNLMDTAAGIIRDTLNDTSRSRIADL

ISVEGGGPVHIGHIFNITEQVVLNIENNDQNCERPMKVYPKDPFPLLKRISWLAQPSVAEIEYLKEPAKY

VIICHTATEEGFSQAENVLILRLMQTFHIESRGWRDIAYNFCIGSDGNAYEGRGWFQVGSHTSSYNRNSV

GIAFIGCFLNHPPPQGALKKCQQLIAHGVEIGSINPDYQLIAHSQCRPFLSPGASIFEEIKSWKNFNPDF

KPTCAIKNEKM

>XP\_019773771.1 PREDICTED: peptidoglycan-recognition protein LE-like isoform X1 [Dendroctonus ponderosae]

MGTANRVVFEFDKMCTIRELSDANFTEPVKEENKSTKCMGRDQQLEVTDQNPNDHDSDLSDADTTEIDEE

ESRTSESDRQLVLKNQELNYLDGDIDEGLCNAFETKMNTLPRYRSNLMDTAAGIIRDTLNDTSRSRIADL

ISVEGGGPVHIGHIFNITEQVVLNIENNDQNCERPMKVYPKDPFPLLKRISWLAQPSVAEIEYLKEPAKY

VIICHTATEEGFSQAENVLILRLMQTFHIESRGWRDIAYNFCIGSDGNAYEGRGWYKEGRHSVSYNKFSI

AIAFVGCFLKHLPPKKSLIRCQKLINHGIEIGAISPDFQLVAHCQCRPTLSPGPRLFEEVKTWKNFNPII

KNSHLCVLASKD

# Gram-negative binding proteins

Amino-acid sequences

>XP\_018898503.1 PREDICTED: uncharacterized protein LOC109031452 [Bemisia tabaci]

MHHFRCLISIGVYLFLFGVQKEVSASKGDYIGCFQDQEENRLLSETKERSAELTSSWCIEFCSEKGYPFAGTQYSSECYC

GYNRLPLIAKRPDSECSRPCSGDSKTRCGGELRLSVYETGISALGAFPNGFHLGCFKENAEKDNRKLLPDLHQQFDNLTP

KICSEFCFKNGFKLSGVQNGDDCFCTNKKLDNSDHKKILFRTGCDVPCSGDASKKCGGAQELNVYATGLTDIPATGRTYA

CYEDGPDSKGQLVRALPNFRAELRKILTPRICLNMCYQMGFNWAGVEAGYECFCGVWLPSIEKTAKDTECSVPCEGGPGE

TCGGLWRIQVYRTPLPEPQRESDTKEYLGCYQDQKGHRLLGEVREWSAELTPSSCIDLCSKGGYAFAGLYHSSDCFCGHN

RPPLLAKRPDAECSAPCSGDSKQKCGGTQNGLSVYKTGLSGIGALPSEFYLGCFSENTAKTAQRLLPEMKQEFNDLTPKM

CAEFCFRKGFKLAGLQGANCFCSSKKLDLTKKVDSKECTTNCEGDSSKKCGGSPLPVLSYLSVYATGLTEAPATGKQIAC

YKDGPNDENDRRLRALPDFRTALRGVSSPGICMNICYQMGFNFAGLQAGYECFCGVWQPAEVKSRPDTECNVICEGAPAE

ECGGHWRLQVYKTPLLGDEPEELVAYLGCYSDQENDRLLGDFREASPTMSPTFCSDLCSKGGYPFAGLHYSTECFCGHNR

PPLAVKRPDQECSLPCSGSNNQKCGDKNKLSIYQTRVPGIGSVPKGFYVGCFAENPFPDLQQSFKELTPQRCSEFCFERG

FKLSGVQGKNCFCTNSKLDLKKKVKDKECSTSCEADSSKKCGAKGRISVYTTGLTDSPATGRLVGCFEDEPTKSGQLQRA

LPNFRSDIRETNSPRTCLNICYQMGFRFAGLQDGYKCFCGKWQPAQEKRKSDAECNTQCSGDPSEKCGGNWRLQVYRTPL

ADEGAVTLGPSTTRGTTHPSTTKKTPSQQQKVTTTPSPTSNCQLSATIVNGKRACKNSVVFYDDFRKFDGTRWSHEVKVA

DKPDYEFTVYNSKAENTYMRNGALHIQPTIFDDNFVESGSIHLERCTGEVINDECTRNTDYFILPPTQSARINTRQKFSF

KYGVVEVQARLPVGDWIVAEMALIPSDNSYGPYYESGKIRIISRGNLNLQYDDGREMGSQTVEGSVMLGYGTSVKAKKAY

FSEKSGWRNVFHNFTMIWTPDDIAFMVDGRRKQNMMVNAHGSRLSDVLGFSNSEIKLWNIGTTIAPFDQSFYLSLGLYVG

GVRDFDEGASSNGYIKPWSNTDPRAMLTFWNRRNEWQRTWEGDSAFVIKSIKVTALLSHQSRHVHSFIICTKFNLTRCSF

GTIYLIRWAHSFLKIYFNGENGTPIKSPKKENRGLLALKTGLDAERTSLALGTVVSLLDPLNVAHKPVLKPSPPNSPPPL

GIGIATYQPSGPISQGTYQPVGPANQATYQPSGPINQGTYQPSGPANQATYQPSGPINQGTYQPSGPINQGTYQPSGPIN

QETYQPSGPINQGTYQPSAPAQGTYQPSGSANQGTYQPSGPVDQGTYQPPSSVNQGYQPPGSVNQETYQPVAPINNNQET

GRPSAQLNQETTGAGSQTNCPVSTTIVNGHRTCKNSVVFYDDFRKFDTDFWSHEVKVANKPDYEFTVYDSKPENTFYRNE

VLHIQPTIFDDSFVENGHIQLERCTGEVVNNECSRNTDYFILPPVQSARISTRQKFSFKYGILEVQARLPIGDWIVSEIA

LLPADHTYGTYYDSGKIRMMSRGNRHLKYDDGREMGSQTVEGSVMLGYGTRVKSKPVYFTDRNGWRNELHNFTIIWTPDD

IAFMVDGRKKQNVMVNAHGSRLSDVVGFPSSEIKLWNAGTSIAPFDQPFYVSLGLYVGGVRDFEEGASSNGYSKPWSNTD

PRAMLSFWNKRNEWQRTWQGDSAFVIQSVKITAL

>XP\_018898564.1 PREDICTED: uncharacterized protein LOC109031490 isoform X1 [Bemisia tabaci]

MCSLNFRQFFAFCLILCYHHIKVVSSSRSGHYVGCYKENSGKDFETLGRYFSDFRHDFDDMTPKRCFQLCFRRGFKYAGV

QFGRECYCTNKELDKHKKTADGACQMPCPGDETKKCGGVMRLSVYATGLMAIESLPHGFHLGCFKENSGKEFETKGRFFS

DFRQDFDTLTPQLCMEVCFRAGFKLSGVQFKRECYCSDKALDLTKQTDEGTCDLPCSGNANQRCGGVLRLDVFATGWTAI

DSLPRGFHLGCFKENSDAISDAMRIFPEYRQDLDNLTPKLCTDVCSRNGFAYAGVQFGKECYCSSMPVDMTKQTDEKTCN

MPCAGDASQRCGGTLRLNVYATGHKQGKAEESPPSGSHLGCFKENSGREFETLGRYFPDFRRDFDDLTPKRCFELCFRRG

FKFAGLQFGVECYCTNKELDEHRKTVDSACQIPCPGDAAEKCGGKLRLNVYATGLTAIDSLPSGFHLGCFKENSGHEFDT

KGRFFPDFRQDSDHLTPKLCLKICFENGYKLSGVQFGRECYCSNKKLDITKQTDEDSCKMGCTGDSKQKCGGVMRLNVYA

TGVSSINSLPNGFHLGCFRETEGHDVQNSERIFPDFREDFDHLTPKLCLRLCAKKQFRLAGVQFGKECYCSNRELDMSRQ

TKPDECKMTCSGDVSEKCGGVWRMNVYATGVSEAGGENHVQDKVDSPTQQTMPTTSSSCVPARTMITNEKGPRRHKPACK

NSVILFDDFEKIDLDRWQYDVKIPSKPDYEFSVYDSKPENIFIKHGALHIQPTLLNESFVENGKLELERCTGDMFNDECT

RGTEFFILPPVQSARITTKQKFSFQYGLIEIQAKFPSGDWIAADIRLIPVTYSYGPFYESGTIRILSRGNSNLKTEDGRE

IGGRTVEASAMLGYGAKVRSKSVYYNDRSEWHQGFHNFTILWTPDDIMFMVDGKQRQNMMSNAPGLKLSDAVGFPSSEIK

LWNTGTSIAPFDRPFHVSLGVSVGGIRDFEDGCDNNGKPKPWSNSDPRAMTSFWNNRQEWQTTWRKEDSAFIVKSIKITA

V

>XP\_018898567.1 PREDICTED: uncharacterized protein LOC109031492 isoform X2 [Bemisia tabaci]

MYSFKLHRFGFSSLFVLCFCQVTIEVSAEYLGCYLDQSENRLLGEIREWSDQLTPSACIDICSKGGYPFAGAQWGSECFC

GYNRPPQIAKRPESECSKPCSGDAKEQCGGNYRMNVYTTAVSGLGALPSGFYQGCFKENAGISTIFNLSERLLSGFRQDF

NGLTPKMCFEFCFKKGFKLSGLQWGKECYCSNKRLDLIMKKKVDDIECSSPCDGDDSKKCGSGWRLSVYATGLTDVPANG

RLIGCYSDSPPKATGEDAQLQHRRVLPDFKIDLTKTNSPRTCMNLCYQMGFSYSGVQYEFECFCARNGPPQHRIKPDDNC

NKKCPGDSAETCGGGWRIQIYKTPLADKSEPKFTDRPVLPVKTTAAPMQSTTQRNNCVLSTTTVKGKRVCKNSVIFSDDF

KKFDPKRWRHEIKIAAKPDYEFAIYDAKPENTYTKDGVLHIQPTVFDDNFVENGRIDLERCTGDAFNDECSRNTDFFILP

PIQSARISTKQTFSFKYGIVEIQAKLPIGDWIVPEIWLVPADNAYGSYYESGKIRFTSRGNSDLKYKDETDMGYQTLEGS

VMMGYGQTIKSRSVYYSNTNGWRDDFHNFTIIWTPDDVSFLVDGRKKQNIMQNAYGSRLSDMIGFSSSEIRVWNAGSPIA

PFDQPFYISLGVSVGGLRDFEDGATSNGHVKPWTNTDPRALLKFWNQRSEWLPTWQKDTSLVVKSIKVTAL

>XP\_018898566.1 PREDICTED: uncharacterized protein LOC109031492 isoform X1 [Bemisia tabaci]

MYSFKLHRFGFSSLFVLCFCQGITIEVSAEYLGCYLDQSENRLLGEIREWSDQLTPSACIDICSKGGYPFAGAQWGSECF

CGYNRPPQIAKRPESECSKPCSGDAKEQCGGNYRMNVYTTAVSGLGALPSGFYQGCFKENAGISTIFNLSERLLSGFRQD

FNGLTPKMCFEFCFKKGFKLSGLQWGKECYCSNKRLDLIMKKKVDDIECSSPCDGDDSKKCGSGWRLSVYATGLTDVPAN

GRLIGCYSDSPPKATGEDAQLQHRRVLPDFKIDLTKTNSPRTCMNLCYQMGFSYSGVQYEFECFCARNGPPQHRIKPDDN

CNKKCPGDSAETCGGGWRIQIYKTPLADKSEPKFTDRPVLPVKTTAAPMQSTTQRNNCVLSTTTVKGKRVCKNSVIFSDD

FKKFDPKRWRHEIKIAAKPDYEFAIYDAKPENTYTKDGVLHIQPTVFDDNFVENGRIDLERCTGDAFNDECSRNTDFFIL

PPIQSARISTKQTFSFKYGIVEIQAKLPIGDWIVPEIWLVPADNAYGSYYESGKIRFTSRGNSDLKYKDETDMGYQTLEG

SVMMGYGQTIKSRSVYYSNTNGWRDDFHNFTIIWTPDDVSFLVDGRKKQNIMQNAYGSRLSDMIGFSSSEIRVWNAGSPI

APFDQPFYISLGVSVGGLRDFEDGATSNGHVKPWTNTDPRALLKFWNQRSEWLPTWQKDTSLVVKSIKVTAL

>XP\_018898565.1 PREDICTED: uncharacterized protein LOC109031490 isoform X2 [Bemisia tabaci]

MCSLNFRQFFAFCLILCYHHIKVVSSSRSGHYVGCYKENSGKDFETLGRYFSDFRHDFDDMTPKRCFQLCFRRGFKYAGV

QFGRECYCTNKELDKHKKTADGACQMPCPGDETKKCGGVMRLSVYATGLMAIESLPHGFHLGCFKENSGKEFETKGRFFS

DFRQDFDTLTPQLCMEVCFRAGFKLSGVQFKRECYCSDKALDLTKQTDEGTCDLPCSGNANQRCGGVLRLDVFATGWTAI

DSLPRGFHLGCFKENSDAISDAMRIFPEYRQDLDNLTPKLCTDVCSRNGFAYAGVQFGKECYCSSMPVDMTKQTDEKTCN

MPCAGDASQRCGGTLRLNVYATGHKQGKAEESPPSGSHLGCFKENSGREFETLGRYFPDFRRDFDDLTPKRCFELCFRRG

FKFAGLQFGVECYCTNKELDEHRKTVDSACQIPCPGDAAEKCGGKLRLNVYATGLTAIDSLPSGFHLGCFKENSGHEFDT

KGRFFPDFRQDSDHLTPKLCLKICFENGYKLSGVQFGRECYCSNKKLDITKQTDEDSCKMGCTGDSKQKCGGVMRLNVYA

TGVSSINSLPNGFHLGCFRETEGHDVQNSERIFPDFREDFDHLTPKLCLRLCAKKQFRLAGVQFGKECYCSNRELDMSRQ

TKPDECKMTCSGDVSEKCGGVWRMNVYATGVSEAGGENHVQDKVDSPTQQTMPTTSSSCVPARTMITNEKGPRRHKPACK

NSVILFDDFEKIDLDRWQYDVKIPSKPDYEFSVYDSKPENIFIKHGALHIQPTLLNESFVENGKLELERCTGDMFNDECT

RGTEFFILPPVQSARITTKQKFSFQYGLIEIQAKFPSGDWIAADDIMFMVDGKQRQNMMSNAPGLKLSDAVGFPSSEIKL

WNTGTSIAPFDRPFHVSLGVSVGGIRDFEDGCDNNGKPKPWSNSDPRAMTSFWNNRQEWQTTWRKEDSAFIVKSIKITAV

>XP\_022173857.1 uncharacterized protein LOC111036217 [Myzus persicae]

MMFKLLSFSLFATTVLAAQNTDYKFLGCFLEENLLTLGEESRILNPVTPQSCSDFCSEKKYTFFILKHDTCYCSKNYISR

LMRQLDFECSKKCSGDSSASCGGSPNLVSSYITDSSKASNFMGHGGYPIPIYLGCYAETPNDDGNRLLKGPAGPYTYNTP

QKCSEICFKMGYLFFGVTYGSECWCGNQRPAKSAKVEDINCDSPCSGDSKQFCGGGWKMGIYSTGITDYVPKKYIGCFDD

DGKKTKGKYLSFSMDINNSPKRCMNLCNTHRFKYAALKGNICECKNYEPSFNLKRSFSDCNTLCTENPSEYCGGSVTFSV

YKTLYSDPLAKVSVTPIGCFTNLKRHPVLNGWRISHARLTPKHCVYSCHTRRFPYAALISSKECLCTSTKPSYEAKTEDA

MCTIPCSGSSQHTCGGNNAINVYTTGLEWKTDTIGNNYLGCYEESQNNRIFNGYSRSFTVNTPEFCSNLCYKLGYTYSGV

TYKTECFCGSQSPNEPKFPRVEDKQCNTKCSGDANQFCGGGWRMGVFSTGLNDFQVEGRLLGCYVMQENTLNNIKFELIN

TNMPSKCSAICNNGGYQFSGVLGINCYCGNRAPENDQKVFESDCDTPCAGDSSKTCGGEDRIQIYDLMKVISINIPNTNS

SNDLVDEFDTLNLESIWSHDIFIAQEPDYEFVVYNNSEKNTFIKNGELVIKPTILSDNYVKNGCLVLKGCTKYEGSSGCS

MNASSYNIIPPIVSSRLTTKNNMFFLYGQLEVIAKMPTGDWMMPEIALVSKTNEQNKLVLATSFGNNNLKCNGEDESIAV

LKYGLKIDEQYHVKPIMMKSISASRWSEDYHTFGLSWTPENIVFKIDGESHQLDTSTLPLDLIFDSEYYISIGVSVGGMT

NFRDGCLSNNHLKPWKNFDIKAMLNFWKDRNNWVSTWNDEKSSLKVKRVKFTLLDNVKYL

>XP\_001944473.2 PREDICTED: uncharacterized protein LOC100164352 [Acyrthosiphon pisum]

MFKLLSFSLFVTTVLAAQNTDYKFLGCFLEENLLTLGEESRILNPVTPQSCSDFCSEKQYTFFILKHDTCYCSKNYISKL

MRQLDFECSKKCSGDSSASCGGAPNLVSSYITDSSKASNFMGHGGYPIPIYLGCYAETPNDDGNRLLKGPAGPYTYNTPQ

KCSEICFKMGYLFFGVTYGTECWCGNQRPAKSAKVEDINCDSPCSGDSKQFCGGGWKMGIYSTGITDYVPKKYIGCFDDD

GKKTKGKYLSFSMDINNSPKRCMNLCNTHRFKYAAVKGNICECKNYEPSYNLKRSFSDCNTLCTENPSEYCGGSATFSVY

KTLYSDPLAKVSVNPIGCFTNLKRHPVLNGWRISYARLTPKHCVYSCHTRRFPYAALVSSKECLCTSTKPSYEAKTEDAM

CTIPCSGSSQHTCGGTNAINVYSTGLEWKTDTIGNNYLGCYEESQNNRIFNGYSRSFTVNTPEFCSNLCYKFGYTYSGVT

YKSECFCGSQSPSEPKFPRVEDKQCNTKCSGDANQFCGGGWRMGVFSTGLNDFQVEGRLLGCFVMQENTLNNIKFELINT

NMPSKCSAICNNGGYQFSGVLGIHCYCGNRAPENDQKVLESDCDTPCAGDSSKTCGGEDRIQIYDLMKVISINIPNTNSS

NDLVDEFDTLNLESIWSHDIYIAQEPDYEFVVYNNSEKNTFIKNRELVIKPTILSDNYVKNGCLVLKGCTKYEGSTGCSI

NASSYNIIPPIVSSRLTTKNNMAFLYGQLEVTAKFPTGDWIVPEIALVSKTNEQNKFVLGTSFGNNDLKCNGEDESISVL

KYGLKIDEQYHLKPVMMKSTLTSRWSEDYHTFVLSWSPENIVFKIDGESHHLDTSNLPLDLIFDSEYFISIGVSVGGMTN

FRDGCLSNSHLKPWKNFDIKAMLNFWKDRNHWASTWNDEKSSLKVKRVKFTLLDNFKF

>XP\_022166764.1 uncharacterized protein LOC111031217 [Myzus persicae]

MTFYFVSLVLFSFSLCVTAASQRSNYKFLGCFLEDNLLTLGEESRVLTPISPQSCSEFCFGKKYLFFILKNENCYCSKNY

ISRLMKQFDNECTIKCTGDDTASCGGKPNLVSSYTTDSSISHNYIERGSFPIPIYLGCYSETPNDDENRLLKGPAGPYNN

NTPQRCLEICFRMGYLYFGNTYGSECWCGNQKPSKSSKVEDINCDSPCSGNSNQFCGGGWKMGIYSTGITDYVSKNYVGC

YDADDDENISKEKHLIFQMGTNNSPKRCMNLCNTQRFKYAAVKGNACECMNYEPNFSLKRSYSDCNTLCTENPSEYCGGR

NTFSIYKTLYLDPQGKVSVNKIGCFKNFKRHPLINGWGIISSNLTPKNCVYSCYARGFPYAALVSSKECLCSFTKPSNEG

MTEDNMCMTLCSGSSKDTCGGLNTINVYNTGLEWRTSTIGNYYLGCFEESQNNRILNGYSRSFSVNTPEFCSNLCYKFGY

VYSGVTYKSECFCGSQSPNEPKFAKLEDKQCNTKCSGDANQFCGGGWRMGVFATGLYDFPIEDRYIGCFVQEENSLSVTK

FELINTNVPSKCSAICHNAKYQFAGVMGINCLCSNIAPENNQKVDDANCDTTCVGDSSKTCGGEDRIQIYDLMRQINETE

SISIPDPMNYDDPFEYLNLNSAWSHDVFIAQEPDYEFVVYNSSEKNSFVKNRELVIRPTIQSDSFIRSGHLSLNGCTKQK

GSVGCEMVASSYIIIPPIVSARLTTKNYLSLLYGQVEVIAKLPIGDWIVSEIALVSKSNEKNRLVLAKSSGNTDLKCNGD

DESTTVLKYGLEIDELYHVKSKMMKLTSQNTWHNGYHSFKLSWSPENIVFKIDEEINHLDITNLPLDFIFDSEYFMSIGV

SVGGMNHFRDGCLSHGHLKPWRNFDTKAMLNFWKDKNHWSSTWNENKSALRVKRVKFTSLDS

>XP\_008182377.1 PREDICTED: uncharacterized protein LOC100165182 [Acyrthosiphon pisum]

MTVYFFSLILLSFSLCVTAAPQRSNYKFLGCFLEENLLTLGEESRVLIPISPKSCSEFCFEKKYLFFILKNENCYCSKNY

ISRLMKQFDNECTIKCTGDESASCGGKPNLVSSYTTDSSISNNYIERGSFPIPIYLGCYSETPNDDENRLLKGPAGPYNN

NTPQRCLEICFRMGYLYFGNTYGSECWCGNQKPSKSLKVEDINCDSPCSGNTNQFCGGGWKMGIYSTGITDPQGKVSVNN

IGCFRNFKRHPILNGWGIISSKLTPKNCVYSCYARRFPYAALVSSKECLCSFTKPSIEGMIEDSMCTTVCSGSSKDTCGG

LNAINVYNTGLEWRTSTIGNYYLGCFEESQNNRILNGYSRSFSVNTPEFCSNLCYKFGYIYSGVTYKSECFCGSQSPNEP

KFAKLEDKQCNTKCSGDANQFCGGGWRMGVFATGLYDYPIDDRYIGCFVQEENSLSNAKFELINTNVPSKCSAICHNAKY

QYAGVMGINCLCSNHAPENNQKVDDANCDTTCVGDSSKTCGGEDRIQIYDLLRQINETESIQISDQINYDDTFEYLNLKS

AWSHDVFVAQEPDYEFVVYNSSEKNSFVKNRELVIIPTIQTDSFIRTGQLSLNGCTKHEGSVGCEMVASSYNIIPPVVSA

RLTTKNNFLFLYGQVEVIAKLPIGDWIVSEIALVSKSNEKNRLVLAKSFGNNDLKCNGDDESATVLKYGLEIDELYHSKS

KMMKLTSQDTWHNGYHSFKLSWSPENIVFKIDEETNHLDTMNLPLDFIFDSEYFMSIGVSVGGMNNFRDGCLSNGHLKPW

RNFETKAMLNFWKDKNYWSSTWNENKSALRVKKVKFTSSDS

>XP\_015374238.1 PREDICTED: uncharacterized protein LOC107169111, partial [Diuraphis noxia]

MMFKCLSFSLFVTAVLAAQNTDYKFLGCFLEENLLTLGEESRILNPVTPQSCSDFCSEKQYTFFILKYDTCYCSKNYISR

LMRQLDFECSKKCSGDSSASCGGAPNLVSSYITDSSTKTEDAMCTIPCSGSSQHTCGGNNAINVYTTGLEWKTDIIGNYY

LGCYEESQNNRIFNGFSRSFKVNTPEFCSNFCYKFGYTYSGVTYKSECFCGSQSPNEPKFPRVEDKQCNTKCSGDANQFC

GGGWRMGVFSTGLNDFLVEGRLLGCFVMQENTLNNIKFELINTNTPSKCSAICNNGGYQFSGVLSINCYCGNRAPENDHK

VFESDCDTPCAGDSSKTCGGEDKIQIYDLMKVISINISNTNSSNDLVDEFDTLNLESIWSHDIFIAQDPDYEFVVYNNSE

KNTLIKNGELVIKPTILSDNYVKNGCLVLKGCTKYEGSNGCSMNASSYNIIPPIVSSRLTTKNNMLFLYGQLEVTAKMPS

GDWMIPEIALVSKTNEQNKFILGTLFGNQDLKCNGEDESNSVLKYGLKIDEQYHLKSIMMKSTLASXWSEDYHNFVLSWS

PENIVFKIDGESHQLDVSNLPLDLIFDSEYYISIGVSVGGMTNFHDGCLSNGHLKPWKNFDIKAMLNFWKDRNH

>XP\_001948384.2 PREDICTED: uncharacterized protein LOC100159492 isoform X2 [Acyrthosiphon pisum]

MSFKHESPRLWNHVIVYLLYTCNFSILASSPEYLGCFLNEDLNISNGLNISLASLTPQECSDECYANNYTYAAINNEPFC

RCTNNYMSKLTKELDDDCNGSCNAARNGSNDRCQMHFKMFKTYNTSIIGEEKYPQAIYLGCFGERMGDDKNRLLKFPHER

YDDNSPQKCSEECFKIGFLYSGTTNGEKQGAACWCGNQYPSEKFKISDAKCNAICSGDSSKNCGGLWRLSVYSTGIVDYP

LRNLVGCYNLDGFSRYDKKVYILKETIDPHRCFYICNERGYKYVAVNEDHCECSDETPSADERKKLEECRKCAGDESEYC

GGPERISIYENDWFGIVTGNLSSTHFGCFENSWMYPVMDGWNISFPSELTTQKCASSCFTRGFPFVALVSSTKCLCSFDS

PPVEAKVKAGGLHCNVTCSGGTESVCGDRTHYNVFTTGLKTSRVAGDHYLGCYEETDVYRAFKKNQSVEFPYVNTPKICS

RHCDSVGYEYFQLSNRESCFCGNSHPADDGAVRVDDNNCSAQCSGDANKYCGGVFKIAAFRIGMVADIQYNCSTDCECYF

LPKRNVSKIDCSKSNLIDPSKIIPDLKTTSSSIDLILRDNLIEILPNLTSFHLNLLDISNNSIATLDTNLLPKSLKVLFA

DNNKLTTLNGNVLRLMQSLDVIMLSKNPWPCECDLLNTFLKYKSKIGDMNKITCTSSTVPLVHMNEYELCKKWKINYFYL

FIALGFVSFVCLLSVYFKLHRSVWLYILRNIQCDSCDVMSVQHTNNNGKDSEETFMQRIQYDELVLATDNWNQNRVLGEG

GFGVVYKGNWRHTDVAIKRLKAEGVAEKVVNMHTLGDGLLQNPSKEIMYLNAVKHDNVLSMYGFCFHSTGSCLIYQFMAN

GSLEDRLQCKSGTNPLSWKMRGNIATGIARGLQFLHNVETPLIHGDIKSANILLDSNLEPRIGDFGLARTGPLREQLINK

SVGFDVSHVCGTKPYLPEDFCRSRKLSTKVDTYSFGVVMFEIATGLRAFNRYKSYKYLKELVNKHDKPSIANIADKMAGH

DSFHIFEILITLGKACVADIAESRPEMVVVYMNLKNVLSSDTNVINVETSGEKHNNMANVHLKETKNPDIIKLNEIKASL

LAPLNEIPSISNLYSSPVHEADPRKIITTEVKSVSNEISDEGFFTTDF

>XP\_016663430.1 PREDICTED: uncharacterized protein LOC100159492 isoform X1 [Acyrthosiphon pisum]

MSFKHESPRLWNHVIVYLLYTCNFSILASSPEYLGCFLNEDLNISNGLNISLASLTPQECSDECYANNYT

YAAINNEPFCRCTNNYMSKLTKELDDDCNGSCNAARNGSNDRCQMHFKMFKTYNTSIIGEEKYPQAIYLG

CFGERMGDDKNRLLKFPHERYDDNSPQKCSEECFKIGFLYSGTTNGEKQGAACWCGNQYPSEKFKISDAK

CNAICSGDSSKNCGGLWRLSVYSTGIVDYPLRNLVGCYNLDGFSRYDKKVYILKETIDPHRCFYICNERG

YKYVAVNEDHCECSDETPSADERKKLEECRKCAGDESEYCGGPERISIYENDWFGIVTGNLSSTHFGCFE

NSWMYPVMDGWNISFPSELTTQKCASSCFTRGFPFVALVSSTKCLCSFDSPPVEAKVKAGGLHCNVTCSG

GTESVCGDRTHYNVFTTGLKTSRVAGDHYLGCYEETDVYRAFKKNQSVEFPYVNTPKICSRHCDSVGYEY

FQLSNRESCFCGNSHPADDGAVRVDDNNCSAQCSGDANKYCGGVFKIAAFRIGMVADIQYNCSTDCECYF

LPKRNVSKIDCSKSNLIDPSKIIPDLKTTSSSIDLILRDNLIEILPNLTSFHLNLLDISNNSIATLDTNL

LPKSLKVLFADNNKLTTLNGNVLRLMQSLDVIMLSKNPWPCECDLLNTFLKYKSKIGDMNKITCTSSTVP

LVHMNEYELCKKWKINYFYLFIALGFVSFVCLLSVYFKLHRSVWLYILRNIQCDSCDVMSVQHTNNNGKD

SEETFMQRIQYDELVLATDNWNQNRVLGEGGFGVVYKGNWRHTDVAIKRLKAEGVAEKVVNMHTLGDGLL

QNPSKEIMYLNAVKHDNVLSMYGFCFHSTGSCLIYQFMANGSLEDRLQCKSGTNPLSWKMRGNIATGIAR

GLQFLHNVETPLIHGDIKSANILLDSNLEPRIGDFGLARTGPLREQLINKSVGFDVSHVCGTKPYLPEDF

CRSRKLSTKVDTYSFGVVMFEIATGLRAFNRYKSYKYLKELVNKHDKPSIANIADKMAGHDSFHIFEILI

TLGKACVADIAESRPEMVVVYMNLKNVLSSDTNVINVETSGEKHNNMANVHLKETKNPDIIKLNEIKASL

LAPLNEIPSISNLYSSPVHEADPRKIITTEVKSVSNEISVCLNGFKYRNIK

>XP\_016663431.1 PREDICTED: uncharacterized protein LOC100159492 isoform X1 [Acyrthosiphon pisum]

MSFKHESPRLWNHVIVYLLYTCNFSILASSPEYLGCFLNEDLNISNGLNISLASLTPQECSDECYANNYTYAAINNEPFC

RCTNNYMSKLTKELDDDCNGSCNAARNGSNDRCQMHFKMFKTYNTSIIGEEKYPQAIYLGCFGERMGDDKNRLLKFPHER

YDDNSPQKCSEECFKIGFLYSGTTNGEKQGAACWCGNQYPSEKFKISDAKCNAICSGDSSKNCGGLWRLSVYSTGIVDYP

LRNLVGCYNLDGFSRYDKKVYILKETIDPHRCFYICNERGYKYVAVNEDHCECSDETPSADERKKLEECRKCAGDESEYC

GGPERISIYENDWFGIVTGNLSSTHFGCFENSWMYPVMDGWNISFPSELTTQKCASSCFTRGFPFVALVSSTKCLCSFDS

PPVEAKVKAGGLHCNVTCSGGTESVCGDRTHYNVFTTGLKTSRVAGDHYLGCYEETDVYRAFKKNQSVEFPYVNTPKICS

RHCDSVGYEYFQLSNRESCFCGNSHPADDGAVRVDDNNCSAQCSGDANKYCGGVFKIAAFRIGMVADIQYNCSTDCECYF

LPKRNVSKIDCSKSNLIDPSKIIPDLKTTSSSIDLILRDNLIEILPNLTSFHLNLLDISNNSIATLDTNLLPKSLKVLFA

DNNKLTTLNGNVLRLMQSLDVIMLSKNPWPCECDLLNTFLKYKSKIGDMNKITCTSSTVPLVHMNEYELCKKWKINYFYL

FIALGFVSFVCLLSVYFKLHRSVWLYILRNIQCDSCDVMSVQHTNNNGKDSEETFMQRIQYDELVLATDNWNQNRVLGEG

GFGVVYKGNWRHTDVAIKRLKAEGVAEKVVNMHTLGDGLLQNPSKEIMYLNAVKHDNVLSMYGFCFHSTGSCLIYQFMAN

GSLEDRLQCKSGTNPLSWKMRGNIATGIARGLQFLHNVETPLIHGDIKSANILLDSNLEPRIGDFGLARTGPLREQLINK

SVGFDVSHVCGTKPYLPEDFCRSRKLSTKVDTYSFGVVMFEIATGLRAFNRYKSYKYLKELVNKHDKPSIANIADKMAGH

DSFHIFEILITLGKACVADIAESRPEMVVVYMNLKNVLSSDTNVINVETSGEKHNNMANVHLKETKNPDIIKLNEIKASL

LAPLNEIPSISNLYSSPVHEADPRKIITTEVKSVSNEISVCLNGFKYRNIK

>XP\_022165610.1 LOW QUALITY PROTEIN: uncharacterized protein LOC111030435 [Myzus persicae]

MSFKHVTKLPLWIHITVYLLYTCNFSVLASSPEYLGCFSNNDLNISNGLIIPLASLTPQECSDECHANNYSYAAINNEPL

CRCTNNYMSKLTKEMDDYCNVSCSAAGNASNERCQTRFKMFKTDNTSIIGEEKYPQAIYLGCYGERMGDDKNRLLKFPHE

RYDDNTPQKCSEECFKIGFLYSGTTNGEKQGAACWCGNQYPSEKFKISDAKCNAICSGDSSKNCGGLWRLSVYSTGIVDY

PLRNFVGCYNLEGFARYDKKIYILKETIDSHRCFYICNERGYKYASVNEDHCXCSDEVSGADERKNPEECIKCAGDESEY

CGGPDRLSIYENDWFGMDTGNLSNTHFGCFENSWMYPVMDGWNISFPNELTSQKCVSSCFTRGFPFVALVSSTKCMCSFD

SPPIDAKVKAGGPHCNVPCSGGTESVCGDRSHYIVFATGLKTSRVAGDHYLGCYEETDVYSAFKKNQSVEFPYVNTPRIC

SKHCDRAGYEYFQLSNRESCFCGNNHPVDDGAVRVDDNKCSAQCSGDANKYCGGVFKIAAFRIGMVADIKYSCSTDCECY

FFPKHNESKIDCSKSNLIDPSTIIPDLKTTSSSINLILKDNLIEILPNLTSFRIALLDISNNSITTLDANLLPTSLKVLF

ADNNKLTTLNGNALRLMQNLDVIMLSKNPWLCECDLLNTLLKYKSKIGDMKKITCTSSTVPVILMNEYELCKKRKIDYFY

LFIALGFVSFVCLLSVYFNLHRTVWLYIRNIQCDFCDLMSMQHTNNDGKDSEETFMQRIQYDELVLATDNWNQNRVLGEG

GFGVVYKGNWRHTDVAIKRLKAEGVAEKVVNMHTLGDGLLQNPSKEIMYLNAVKHDNVLSMYGFCFHSTGSCLIYQFMAN

GSLEDRLQCKNGTNPLSWKTRGNIATGIARGLQFLHNVETPLIHGDIKSANILLDSNLEPRIGDFGLARTGPLQEQTDKS

VGFDVSHVCGTKPYLPEDFYRNKKLSTKVDTYSFGVVMFEIATGLRAFNRYKNYKYLKELVNKHDKRSIVNIADKMAGHD

SFHVFEILITLGKACVEDIAEKRPEMVVVYMNLQNVLSSKTNVNNVEASGENYNMTKVHLKETKNPDIIKLDGIKAALLA

PLHEIPSISKLYSSPVHEADPRKIITTEVKSVSNEISVCLNGFKYRKI

>XP\_015370807.1 PREDICTED: beta-1,3-glucan-binding protein-like, partial [Diuraphis noxia]

STGMTDYLAKNYIGCYDDANNVDENKTKEKHLIFQMGTNNSPRRCMNLCNTQRFKYAAVKGNVCECMBYEPNSSLKSSYS

NCNTLCTENPSEYCGGRSTFSIYKTLYLEPQGKVAVNKIGCFKNLKRHPLISGWGIISSNLTPKHCVYSCYARRFPYAAL

VSSLCFQIDNVLKINFKNVLRDYEFVVYNSSEKNSFVKNRELVIRPTIQSDSFIRNGHLSLNGCTKHKGSVGCEMVASSY

IIIPPIVSARLTTKNNLLFLYGQVEVIAKLALGDWIVSEIALVSKLNEKNKLVLAKSFGNTDLKCNGSDESAIVLKYGLE

IDELYHVKSKMKKLTSQDTWHNGYHSFKLSWSPENIIFKIDEEINHLDTTNLPLDFIFDSEYFLSIGVS

>XP\_015365978.1 PREDICTED: WSC domain-containing protein ARB\_07867-like [Diuraphis noxia]

MTFYFFSLMLLSFSLCVTAASQRTNYKFLGCFLEENLLTLGEESRVLTPISPQSCSEFCSGKKYLFFILKNDNCYCSKNY

ISRLMKQFDNACTIKCSGDDSASCGGKPNLVSSYTTDSSSKKECLCSFTEPSNEGMTEDSMCMTLCSGSSKETCGGLNAI

NVYNTGLEWQTSTIGNYYLGCFEESQNNRILNGYSRSFSVNTPEFCSNLCYKFGYTYSGVTYKSECFCGNQSPNEPKFAK

LEDKQCNTKCSGDANQFCGGGWRMGVFXTGLYDYQXEDRYIGCFVQEENSLSVTKFELINTNVPSKCSAICHNAKYQFAG

VMGINCLCSNHAPENSQKVDDANCDTTCVGDSSKTCGGEDRIQIYDLMRKINENESTSTPDSTYYDDQFEYLNLKSAWSH

DVFIAQEPLDSCILFSLMADHHSLISDY

# Absence group PGRP amidase domain nucleotides sequences

### Nucleotide sequences from NCBI

>XM\_015512754.1 PREDICTED: Diuraphis noxia N-acetylmuramoyl-L-alanine amidase AmiD-like (LOC107164800), mRNA

ATGATTTGGATTTCAAGTCATGTTGGAATCCTCGAAAATGTCGTACCAGAAACTTTCGTATCGTTTCACTCTGGAAGATC

CTCATGGGGCAACTACTCCCAAATCAATCCCATATCAATAGGTATCGAAATCGTTAATTTTGGACATAATGAAATTGATG

ATTCGTGGGACCCGTTTTTTCAAGAACAAATTCGCATTGTTGGTTTAACGGTGACTCGAATGGTCAACCAGTATAAAGTG

TTACCACACAATATAGTTGGACACTCGGATATTGCCCCGAATAGAAAAACTGATCCTGGTGTAATGTTTCCTTGGGGCCA

ATTGTACAAGGACTATGGCATAGGTGCTTGGTTGGACAGCGATGAAATGAACGAGACAGTCATTATCGCCAAGTACCGTC

CCTCAACACCRTGTCCGCGTATACCAGATCAGAAGCTGTTTGTCAATTATTTGGGTATTTACGGATACAATATAACCGAT

GAGGTTCAAGCCATTAAGGCTTTTAAAGCACACTTTACAGCCAATCAAAAACCAGAATTATATAATCAAAATGTAACACA

TCTTGAAATGTACTGGATTTGGGCTTTGGTAGCTAAGTATTTACATTAACGAAAGTCTAAATTGTAATTCACTATAGATA

TAGAATATTATAGAATTAATATATCACATAATAAAAATTCAATTTTATCATGG

>XM\_022324430.1 PREDICTED: Myzus persicae N-acetylmuramoyl-L-alanine amidase AmiD-like (LOC111040498), mRNA

 TATAAAATATATATTTATTTGTAATAAGTTTAATATTTAAACTCGTAATAATGATAAAATATATATATATTGTTACATTT

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TAAATGTTTTCGTGTGACAGAACACAATGAAATCATGGTGTATAAAAAATACCTCAATCCAATACATGGTTATGCAATCA

GTCCATTTAAAAGTCCAAATGAAAGTAGAAATCATTTCCATAACAGAAATGTGAATGATAAGATAATGGTTATAGTACTA

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ATCACGCCGGAATATCTTTATGGGGCAACTACTCGTCAATCAATTCCATATCAATAGGTATCGAAATCGTTAATTTTGGG

TATAATGAACCAAATGATTCGTGGGACCCGTTTTTTCATGATCAAATACGTATTGTCGGTTTAACGGTGGCTCGAATGGC

CAACCAGTATAAAGTGTTACCGCACAATGTAGTGGGACACTCAGATGTAGCTCCAAACAGAAAAATTGATCCTGGCGTAA

TGTTTCCGTGGGGAGAATTGTATAAGACCTATAGCATAGGTGCTTGGTTGGATGACGATGAAATGGACGAGACAGTCGTA

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GCGTATTTCTACATTTTTCAGTGCCAGAAATCTAGAACCCTGTTAATGACCTGCGCAAAACATAGGTATAATTTCTTAGA

AACTTAATTTCATCCAAAGACCAGAGCCTTAACTTGGCTTACTTTATAGGAAACTAAGTTCGAACACCTAATATATTATA

TGATCCTTATTTTTGTATGTTCCGTAATATTTTATTATAAACTATTTAAATGTAATGATAATAAACAATGTATAATAATT

TATA

>XM\_008181682.2 PREDICTED: Acyrthosiphon pisum N-acetylmuramoyl-L-alanine amidase AmiD-like (LOC103308396), mRNA

TTAATTCTCATGAAATGTATCACTCATAATATAACTGATTCATAAAATCACAAATATAGTGCAATAGTTTTTTTTTAATA

CATTTGTAAAATAGGAAATATTAATTTTTCTTAAAAGTTTAAACATTAATAATAAATAATAATGAAAAGCTATATATTTA

TTGTTACATTACATTTGATTTTTCTGCCATTTTTTGAATGTACAAATACAACATATGATCAAGTACTACAACCTATTGAA

ATTATTTATCCTAAATGTTTTCGTGCGACAGAACGAACAGAAATCATGGTGCATAAAGAATACTTCAATCCAGTGCATGG

TTATGCAATTAGTCCATTTAAAAGTCCAAATGAAAATAGGAATCATTTCTATCACAAAAATGTGAATAATAAGATAAAGA

TTATAGTACTGCATTTTACTGGTATAGATTTTGGAGCTACTGTAAAAGAATTTACTTCTAAAAGAAGTAATACTTCTAGA

AATGTCAGCTCTCATTATGTAATCGCGAGACCTACCGAAGCTGGAACACACAATCAACTACTGCAGGTCGTGCCAGAAAA

TTACGTTTCGTATCACGCCGGAATATCTTTATGGGGCAACTACTCGTCAATCAATTCCATATCAATAGGTATCGAAATCG

TTAATTATGGATATAATGCTACTAATGATTCATGGGACCCGTTTTATCAAGATCAAATTAGCATTGTCGGTTTAATGGTG

GCTCGAATGGTCAACCAGTATAAAGTACTACCACACAATGTAGTCGGACACTCGGATATAGCTCCGAACAGAAAAATTGA

TCCAGGCGTAATGTTTCCGTGGAGCCAATTGTATAAGAACTATGGCATAGGGGCTTGGTTGGATGACGATGAAATGAACG

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GGTGTTTACGGTTACAATATAAGTGATGAGATTAAAGCCATTAAGGCATTTAAGGCACACTTTACGGCCAATCAAAAACC

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GAAACCTAGTATGTTAAA

>XM\_008471213.2 PREDICTED: Diaphorina citri N-acetylmuramoyl-L-alanine amidase AmiD-like (LOC103506806), mRNA

AAACAATAATATTGTTTGTCTAAATGTTTATGTACTTACGTGTGTATATTTTGGCAAATGAGGTGAAAAATATTCATGGA

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TTGTTAATCCTGTTCATCAATTGAGTTAGTATTTATTTTTCACTAACGCGACTAACTTGGTGAAATCATGTAGTGATCAA

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GAATCTATGTGATGCCTTCTTCTATCCATGGTATGCCAGGTTACGTGATAGATCCATTCCCGGAGTGGGAGAAAAATCGC

AATCATTACGACAGTCGCGATGGAATGTCCGTAAAATATCTCATTCTACACTACACTGTGTACAATTTTGCTCACATAAT

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CCGGGGGCAAAGTTATACAGATTGTACCTGACAACATGAGAGCCTGGCATGCAGGCATCGGCAAGTGGAGGAGGGACAGA

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GTAGTGTCATAAGAGCGTTCAAAACACATTTTTCAGCCAATCAGAATCCAGAGCGAATTTATGCTGACATCACAACTGAA

GACATGTTTTGGGCTTGGGCACTTGTAGCGAAATACGGCTCAATGTGAACCCTGGTTCAATAAAGAGATGGTGATTCGTC

CTCGAAAAGTTTTATTAGTTATACCAATTAATAAGAATGTATGTATTATTGCAAATCGATATCTTGA

### Protein sequences (Translated from nucleotide sequences in EMBOSS Transeq)

>WP\_019231199.1 N-acetylmuramoyl-L-alanine amidase [Occidentia massiliensis]

MKHIDDGVTNICNILINKGDKMLQNENISAKQHIPIEDVIAAFKGKNTGIYLSLDNIHNISGYTMDPFPEAEKNRNHWDS

RGEGSVIKYLIMHYTVSNLCRTMELFTENKPDNRVSAHYVISQKEQEVSGGIPIRVVPDSERAWHAGVSFWGGKKNLNAT

SIGIEHVNQGFVDEEGIRKWFPFDENQIRISGIMSQDIVKEYGILPTHVLGHADIAPGRKQDPGILFPWGEIYYDYGVGA

WLNEDEKKPEVIVEKYDPKIPCPTEVDLSLFLQLLGKYGYEIPSDVNIAKINVNQSESDFLKVTPLLEAFKAHFSANGQP

ERYDSQITNEDMFWAWAITAKYSDDLVGENYPLTGEEFM

>XP\_008179904.1 PREDICTED: N-acetylmuramoyl-L-alanine amidase AmiD-like [Acyrthosiphon pisum]

MKSYIFIVTLHLIFLPFFECTNTTYDQVLQPIEIIYPKCFRATERTEIMVHKEYFNPVHGYAISPFKSPNENRNHFYHKN

VNNKIKIIVLHFTGIDFGATVKEFTSKRSNTSRNVSSHYVIARPTEAGTHNQLLQVVPENYVSYHAGISLWGNYSSINSI

SIGIEIVNYGYNATNDSWDPFYQDQISIVGLMVARMVNQYKVLPHNVVGHSDIAPNRKIDPGVMFPWSQLYKNYGIGAWL

DDDEMNETVIISKYSPSTPCPCTPDQKLFVNYLGVYGYNISDEIKAIKAFKAHFTANQKPKLYNSLITRLEMYWIWALVA

KYSY

>XP\_022180122.1 uncharacterized protein LOC111040498 [Myzus persicae]

MIKYIYIVTFHLILVPLFSSTNITYDQVLQPIEIIYPKCFRVTEHNEIMVYKKYLNPIHGYAISPFKSPNESRNHFHNRN

VNDKIMVIVLHFTDVDFGTTVKIFTSNRSNTSSNVSSHYVIAKPTEAGTHNQLLQIVPENCVSHHAGISLWGNYSSINSI

SIGIEIVNFGYNEPNDSWDPFFHDQIRIVGLTVARMANQYKVLPHNVVGHSDVAPNRKIDPGVMFPWGELYKTYSIGAWL

DDDEMDETVVIAKYRPSTPCPRIPDQKLFVNYLGVYGYNTTDEVQAIKTFKAHFTANQKPKLYNQNITQLEMYWVWALVA

KYSH

>XP\_015368240.1 PREDICTED: N-acetylmuramoyl-L-alanine amidase AmiD-like [Diuraphis noxia]

MIWISSHVGILENVVPETFVSFHSGRSSWGNYSQINPISIGIEIVNFGHNEIDDSWDPFFQEQIRIVGLTVTRMVNQYKV

LPHNIVGHSDIAPNRKTDPGVMFPWGQLYKDYGIGAWLDSDEMNETVIIAKYRPSTPCPRIPDQKLFVNYLGIYGYNITD

EVQAIKAFKAHFTANQKPELYNQNVTHLEMYWIWALVAKYLH

>XP\_008469435.1 PREDICTED: N-acetylmuramoyl-L-alanine amidase AmiD-like [Diaphorina citri]

MQISCSKTIFIFFVVVLFLIICYFNFPREPGYPILQVFPRVFKRGSGIYVMPSSIHGMPGYVIDPFPEWEKNRNHYDSRD

GMSVKYLILHYTVYNFAHIITAFTSNRAHNLHSSHYVISEKEGKYLPGGKVIQIVPDNMRAWHAGIGKWRRDRNLNSMSI

GIHLVNGGVVGEKFRSTNYYPFDENQIHTLGLLGKDIVSQFKIKPQYVLGHTDIAPGSKMDPGPLFPWGKLYLDYGIGAW

LSPDEMTVEAIVRKFKPARPYPRKLDRGIFLELLKAYGYNVTITNKRSVIRAFKTHFSANQNPERIYADITTEDMFWAWA

LVAKYGSM

# Toll-like receptor sequences

### Full Toll-like receptor sequences

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MCSMWLTSALLALSALPVWSASLSATTGTRYQAPDECRWNNEDEESGVTLLCRLRTINSE

LENTNFSAIQPHLTVRLRLECSDALFFQSSLAPGSFRQLIELRELTIEYCKIGNLSDGAF

TGLRELRNLTIRTHNTDWSTMSLEVTPTAFSRDVQNLERLDLSENNMLSFPEGALCSLRN

LGYLNMTGNRMRDVTHFQFSSAHRHPTEKCGDNLLILDLSRNLIDTIPPGLLSGLRRLQK

LYLQGNGLNSVADRALEGLISLTTVRFSDNQLTSLPPELFSDTKELKEIYFNNNTITVLA

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QILKMQDNYIEHIPENVFSTLGNLHTLILSNNRLTNIESFAFMGLPGLSVLSIDSNLITK

IHPHALRNCTSLQDLHLNGNRLDEVPIALREIPQLKSLDLGENLLVNIENASFMAMQQMY

GLRLTENNIGNISKGVFDKMKSLKILNLSRNKIHKIEAGAFDGNINLQAIRLDGNYLADI

DGLFAKLPNLVWLNISDNRLKLFDYAMIPTGLQWLDIHANRIAELGNYFEIESQLSLSTF

DASSNRLTEITGSAIPNSVEMLYLNDNLISKVQSYTFFKKPNLTRVDLYGNKITSLDPNS

LRISAVPQDKSVPEFFIGGNPLECDCTMEWLQKINTGNRARTQPKLMDLDSIYCKLLYNR

GNAYVPLVEAASHQFLCKYEFHCFALCHCCDFDACDCKMTCPNNCTCYHDQSWSANVVEC

SNAGYVNTLPERIPMEATQLYLDGNDIKMLPSHAFIGRKRLKILYLNASNIETIHNRTFN

GLKELEVLHLDHNNLITIEGQEFNGLDNLRELYVNNNKIKTIGKEMFNHMPRLKILHLDH

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TDVAIYNESMFEDSRYGFKIIEENGTICTGLPSINNSINGNLTSTKTVINDEETNYVFVI

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QIEFRQALQRALHKNPHKLILVAVGQVARDPDLKSYFKTGLEITWKEKRFWERLRYAMPS

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>HeliconiusTLR\_CHMEL006338

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>HMEL016235-RATLR-H

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>BmToll3-1

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>BmToll3-2

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>BmToll3-3

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>BmToll6

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>BmToll7-1

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>BmToll7-2

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>BmToll7-3

MFQFLTLLFVTFGVNAAYARGVDNCSRQSKGDNSTLCRVRTLDADGSSLASAPTETTKRLDIECNQLLLFESYLEANYFQRFHELTELTIRNCKLLRIPGNAFEGLRELKKLSIRSKNYDWSSNKNLELSLGTFNGLRELQALDLGQNNLKTIPSEVFCPLDNLQTLNVTGNKLKSVDRLGFGKNCGSGLRRLDLSRNEIKSLPEESEIIGLKRLQELKLQHNNITDISGETFNGLISLRILNVSYNNIQFIPEGTFASTKELREVYLNNNLLFELARGVFHRLEQLLVLDLSYNQLSSAHIDGGTFVGLIRLVILNLSNNALTRIDSKTFKDLFFLQILDLRNNSIGYIEENTFLPLYNLHTLNLAENRLHMIDEYLFNGLFVLSKLNLNNNLLINIDINAFKNCSDLKELDLSSNQLLDVPNAIWELSQLKTLDLGENQIKDIKNGSFKSLDQLTGLRLIDNQIGNLSVGMFSELPSLQVLNLAKNKILAVELGSFQNNKQLEAIRLDGNFISDINGVFSRLMSLLWLNLSENHLVWFDYAFIPSNLKWLDVHGNFIEHLGNYYKLQDEIRIKTLDVSHNRIVDISPLAIPNSVELLFINNNHINNIQVNTFMEKHNLTRVDIYANEISHLDINSLRLSPVPLNKSLPEFYIGGNPFDCDCSMEWLPLINNMTTMRQHPRIMDLENVLCKMTHTRGVTHIPLSNLKSTDFLCTYETHCFTLCRCCDYVACDCQMTCPYNCSCYHDPTWNKNVVDCSSQSAIEIPEKIPMDATEVYLDGNDFKILQNYAFIGRKNMRSLYVNSSQVESVHNKTFAGLSSLITLHLGNNKLKHLNGYEFEHLTQLNELYLQDNFISHIANLTFSTLYSLRILRLDGNRLIDFSIWSLNANKQLSSLSIGNNMWSCKCRYLQKFTAFISDNVPKIVDVTDISCWNVDTKTTQKKELNLNGTICSDYYAGDSVIDNILVSNYMPMMVTTLSGFMLIMLVILVIFIFRDTVRIWLFTSCGIRLFPFNGAYDDTDKLYDAYVCYSPKDDDFVIQTLAAELENGNPSYHLCLHYRDIPQHNVAYMQCTLPLPECAEASKRIILVLTRNFIETEWSRFEFRQALHEIVKSRIYTLVIIEEGSILPEAECDPDLRPYLKTSSRIRWGQNKFWEKLRYAMPDKRYKSKTSAYRNNINSYSMRSATQNGTMRSFSFTEKMRGSADGVSTSPEFVDPASQHVPVASYGPDGRPPSDHIYSSIDSDYSSLELGANNPNRRREFRHWPPPPPLIDTQSSGQAYLV

>BmToll8

MYSTWFANALLVLSTAFTARSASLSATTNTRYQAPDECGWMTDYDGAGVALQCRLRTINSELENTNFSAIQPHPTVRLRIECSDALFFQSSLAPGSFRQLIELRELTIEYCKIGNLSDSAFTGLRDLRNLTIRTHNTDWSTMSLEITPSAFSRDVQNLERLDLSENNMLVFPDGALCSLRNLEYLNMTGNRMRDISHFQFSTAHRHPTEKCGDNLLILDLSRNVIDTLPPNLLNGLRRLQKFYVQGNGLTSVADRSLEGLISLTTIRFSDNQLASLPPELFSDTKELKEIYLNNNTITVLAPGLFSDLVQLLVLDLSYNELTSDWINTSTFSGLKRLVYLDFSHNRVTKLEIALFRDLHNLQILKMQDNFIEHIPENVFGSLSNLHTLTLSNNRLTNIESHAFTGLQALSVLSVDSNRISRINPQALRNCSNLQDLHINGNRLDEVPEALKEIPQLKTLDLGENLIVSIENASFMTMEQMYGLRLTENNIGNISKGVFDRMTSLKILNLSRNKIHKIEAGSFDGNINLQAIRLDGNYLTDIGGLFAKLPNLVWLNISDNRLEWFDYAMIPTGLQWLDIHANRIAELGNYFEIESQLSLSTFDASSNKLTEITGSAIPNSVQMLYLNDNLISKVQSYTFFKKPNLTRVDLYGNKITSLDPNSLRISAVPQDKSVPEFFIGGNPLECDCTMEWLQKINTGNRARTQPKLMDLDSIHCKLLYSRGNAFVPLIEAAPHQFLCKYESHCHALCHCCDFDACDCEMTCPNNCTCYHDPSWSANVVECSNAGYTNDLPEKIPMEATELYLDGNSIKELPSHAFIGRKKLKILFLNASHIEIVHNRTFNGLKELEVLHLDHNSVTSIEGQEFNGLDNLRELYLNNNKIKNIGKEMFNHMSRLRILHLHRNYLISLSVWQINPAITEITLSYNPWSCDCEYTEMFREWTKRVSSVTDLSNIQCVYTQGNTSNILVLNDTVFDDPSSGFKIAYENGTLCTGLPSINNSINGNLTATRTIITNEDVQDYIPLLIATLGGFLLVLILSVMLFIYRQEMRVWCHSRFGVRLFYRASDLEDSEKMYDAFVCYSSKDEAWVTEELASSLERGDPSYKLCLHYRDVGGYVTDKIRQAVESSRRTIMILSENFLRSEWVRYELKSAMTHVLRDRRKRLIVVLLGQVSQKDLDQDLRLYIKTNKCLNANDRLFWEKLKFALPDVRYNQRCRGMPSPNSGGGMPMHRHHHPRNHLGMLPPPPVHGAHPVLPPHPSHASHQLPPRASPRTMSVHV

>BmToll9-1

MILKIIKLLKFFLLFIASAETRKTQKCLTGYMTDVQTWVNEDGVLTKTIDQSTAIDLSSHFDPVPFLHQIMSEFKTDNGQRVRYLSLAKCRLTRVPPVFHLSDSMGRWLSQTVEYMTFYGNKFVDRSVAGEQYNMIINATGAVETEPVFSLQYQGTTVWSTSIEYVSFPSLKELDLRRCSIQVLRSNMFRGMPSLEALYIGENEIYQVESNTFAGLNKLLHLDFSRNEAFDSTGSPKNLITPQTPLFDGLTSLVSLDLSFTKMSKRNVAVLTGLGPNLRRLSICDTGLQDLRSDIFSKTNLTYLDLSENNGILNTPNILRGLEDTLVVLYANTIGTGRVDMLKNFHRLEILQLLNNEITSLPQEVAATWRSLQILDLNKNRIITWFEPIFSLIPNLKFLALKHNNINVIREDMIVDFRNISYLALAGNFFMCNCNSRDFLETAARNERNRQNGYIKSVYESKNLFLYHRGFEDFNTLIAQRKPVVFENSISEWDNEEESVYLLTDFYGRNYICASFASDEGEAIFMGDVPTCYARRDMQYDEKMIKNQYKLIALILLPCVLLPLLMLFVFRRTIFYFLIMMRNSAALTMINKDKTGVDGTIFNYDVFVSYCNEDRVWVLDHLLPQLESNCNISVCLHERDFQIGLSILENIVACMDRSRAIMLIISKRFLMSQWCQFEMHLAQHRLLETRRNDLILVLLEEIPRRIRPTTLHYLMLTKTYIIWPKVAHERNIFWRRLRKGLVTQKLKHTENVSLA

>BmToll9-2

MLLVHCLWLLLYNVYISRGDLIEVYKELSHTILYPQEKSDDLPVELGQDGYSGCICRASKQNGVVVCFGNYECRMFPKIKVKCEFLRVRTTVITNIRKGHLDSLYFLKVLEIEANHQLRHIEAGVFKNLTSLQQLSISYNTHLHSIDEHTFIGLVNLRNLTLVNNGFTNILAITPAFKPSILPALRGLDISENAFEIIPEDAFVPMKGTTLMKLDLNLCRLDFIHPKSFLPLKNLRELHIGENDLNSTLIGDFLLKMKDERIYLMYLDLSGMGFRKNPPRDLMEIIAETSVRRLILSHNQFEFIDDDSFPKMENIELMDLRKVLAMQIGSNAFNPHKFPNLKVLLLSGNNLPGLHKAPFSDQLLFLDLSDNKGSPTNPMYYEIDRNTFVQSKELKILNLAFNRIRAIFEYTFRGLENLQILSMENGTLYHIGDKSFKPLKRLEMLNLANNPLEQNENLTSSMFDGLNDLKILILENCGIKRFYDDDNIFEMMPNLTHLVLRNNQLYYISAETLKPLKLLKVLDLSENLFVSWWQPLFLASGVKPITLNLKNNKLSHFSMSMIQDISYLLENNGNSRIEIELMDNIFICDCSSMYKMYSWLQANGSEVLRKFIQSSKFQCSSPDIWEDKRVADYLSSIKTLRCLMTEKMTNIMYLVWTAPSLVAVALILFIIVFIFKFKTYIRYWMFLAKLALGRNFRRKSGKHVETKDYKYDAFISYCSEDRDFVVHMINNLELEPPFLKLCVYERDFDIGSFISEAVLKSVNESKYVILVISNGFAKSQWCRWETQLAEYHRIFLEDGTSYDPLVLVRIGDVQNKYLTTTLKYLLKTKIYHTWDENNQDEFWKKLRNVLTRKI

>BmToll10-1

MSLCVLFYCHAVDRSVAAETPHECAYRSSEAETSGSTVLFCKIRTISSLDHLLQNISKTHYDDVISLHVQCSEILFFESTLTTSAQKPTGKHTSLGKLRDLVIDRCKLRQIPARAFESFKDLKRLHVTTHNSEWSAMTMELNEEAFAGLNELVELNLSNNNIWSTKTETFCSLYSLKVLNLTNNHLQNIKTIGFSDSLREQNLSLRTCNLVIETLDMSYNDLIVVNDNSLSKLRSLSKLLLQNNALSNLEGGAFEGLLSLEVLNLSSNFMNTLPPDLFSETKSLKEINLSNNTINNLPPGLFDNLDQLQVLDLSLNELTSQWINKNTFVGLLRLVILNLSYNKLSRIDRYMLQDLYSLQKLNLEHNDISTIDKHAFSELRNLHSLTLSNNQLVHIETHLFTDLHVLHELFIDNNKIKHIEDNAFDNMTAIEDLSLNDNFLSSVPASIRKLRSLRSLDIGNNNITHLTRENFRGLSELFGLRLVDNKVTNLNEDTFEHLPQLQVLNLASNKIRHVASGCFRKNINLKLLRMDGNEITKFDGIFSTLNSLVWLNMSANKLSYFDFRSFPESLEWLDLHKNSISTYKNDDTHSNVNIKLLDLSYNNITEITVTSIPNSVEKLYLNDNNIQNIQVGSFSKLQRLSTVTLNNNKLVHLDMNAFRLDQIDEDSDLPEFFISGNTFICDCSMEWIQRINHLSHSRQYPRVLDLDKALCSLVHSRAKRKKLIIDMSPSDFLCPYESHCFALCQCCDFVACDCEMICPNDCRCYHDIPWNANVVDCSNAGYTEVPKHIPMDATEIYLDGNHISHLGNHVFIGKKKLQGTSFGKHKLVELKGDEFLHLNSLNELYLDHNAITHVANNTFSSLKSLSVLRIDDNKLVNFFPWKLLASSSESLAHVSIEGNQYSCDCKSIAELDSWLRRDPGDPEKMLCTDSEGKPTKITIASVLSHCKEYMGSISDPTMSRDEVISKSVFLPDNYFAVICGIIIIVVVICLIFAIFYAFRYEVSDWVYTKYGVPLFKEQSCPNVDHVMEGNPNHMYDYYVICNTKDTGFIYHNIMSEIEFRKMCSKSFSLNEATLNILTLDSFSKSPKLSKRLLIVLTNNFICNDLSDIQFKNIFFGYLKSLNRSESNKVIFINIVDNIQLSDELCFALDKFKNISWNDPRFWDRFMVLLNSTDTIITVKGSEASVFKKSLRNTPSLRYTTMPVPNDSCSKQNFTNSLQFCKRYDGETSLNESSPSSDNNTYGEGNTSNNSYMSIENRSCPRFNYDLRLSPSSGHVYSRVDDISPTTPRTATVSSKGRTYFV

>BmToll10-2

MIINFRGMDSLKVWICFVVVATARAHTAPPAPTGCQWDYSDPKLSESNFLTCNIKTIGSVDFLFKNITTAQAYNVNKLKLTCTDLLFFESSLHMNTGSFLGQLRKLEDLHIEYCKIRYVPATVLSPLRDLTSLTLRSFNNDWPAMTMEFHAESFRGLMELRTLDLGDNNIYMLPSEVFCPLFSLEILNLTNNRIQDISEIGFSDWGKGPIAPGKSCNTGLKTLDLSRNNILRLPDNGLSSLRSLEVLNIQNNLINEICDRAFVGLNSLKILNLSGNKLVAVPPELFQSSRVIREISLGNNSLSVLAPGLLEGLDQLEKLDLSRNRLTNDWVNRDTFAGLIRLVILNLSYNLLARIDPKSFHDLNNLQVLNLDNNAIETISNGAFAELRNLHQLSISDNKLKSLNEYVFSNLFVLSQLYLDNNQISSIHERSFENITYLQDLGLNGNSLSVIPDGIKRLRFLKSLDIGKNNITKVTNTSFEGLEELYGLRLVDNYISSIPKDTFSTLPSLQLLNLASNKIETIEQDAFVSNPTLKAIRLDGNSLTDIRGVFNKLSTLGWLNISENRLIYFDYSYIPDNLEWLDLHSNNITKLENEKNVQRNIRMLDASFNALENVDALSIPDSIENLFLNNNKIHTIHPGTFLQKRDLEKVVVTDNKLRTVELSAFTLPHIPKHKTLPNFFIANNPFVCNCHMIWLQKINLWNHMRQYPRFMDLESVMCEVVNNKYGGKANLVDVPETQFLCSYETHCSSNCFCCEFEACDCKMTCPEGCSCFHDSNWNSNVIDCSNVGYTEIPEKIPMDATELYLDGNDFGALGSHLFIGKKKLHKLYLNNSNIASIDNDTLNGLHSLNILHLENNHLVELSGGEFSQIKHLRELYLNDNLLKSVPNKTFEVLSSLRTVYLQENKIFDLDKKLSHIMHLDNVNVRGNVFTCTCDNIASLQNWLKKIHEDPLEVFCVDENQLISNLTVFDAIDKCHGSNVMDNTVPTENQPYQYDEVSTIKLNFVPLLAVVLISVILILLFGALAFSFRQNVRLWAHSKYGVRLFKSASIQESELDRDRLYDGYAVYSLLDDDFVSKVVAPEMEHSGYTMCFHYRDLQHGPDNYLCEQITNAAESSKRILVFVSFNFLQNEWCKATFKAAIKHVITTIHPSIRRHRVVFILTTDVSALNLDVDFQSYLKTCNVLLWGEKKFWEKIRFVMPDISNLHWNKDTMNYNHGICPNARRHPSRYTASPTAPEHWYKYDAIPPQTPTTANVGINIEDDTSMLTNTTLTSQVQDGENLHHSYISIDTQNYEQPYGGRPRPPNTLRKHPDHHSPSILDEQGYLQPRSSVHDCLPQTHSVLHR

>BmToll10-3

MSMEFHRDTFRGLTDLRSLDLGDNNIWILPSEIFCVLYNLKELNVTQNRLQDISNLGFSDWGNGPTAPGKSCNTVLETLDMSYNEISGLPDNGLSSLRALQKLFLQNNRISNVADRAFVGLSDLQILNLSTNALTALPPEMFQSSRDIKQIYLNNNSLSVLAPGLLEGLDQLQILDLSVNELTSEWINRDTFSGLVRLIVLNLSHNRITKIDALLFQDLNNLQFLSLEYNNVGRIAEGAFSNLKNLHSLSLAHNNIIEVDSGHFSNLYVLNQLFLDGNRITKVDIRSFENITKLHDLGLSGNQLTDVPEAIKTLRFLTSLDLGMNKITKVITSHFDGLDDLYGLRLVGNKIEKISKDTFAALPSLQILNLASNNIDQIDDGAFASNQQLKAIGLDGNKLVDLKGIFTKTQPLVWLNVSNNELLWFDYSHIPSNLEWLDMHENKIDKLDDTYGLKETTMVKMLDVSNNKIKSVDELSFPSSIETVVLNNNNIEKVSPGTFLQKYNLNKVMLYSNKIKTLELGAFAISSVPDDKDLPEFYISENPFVCDCTMEWLQTINQVSDLRQRPRVMDLESVRCSLTHSRRKSETLLLEVKSSEFLCEYESHCFTVCHCCDFDACDCKMTCPDRCSCYHDQTWTTTNVVDCSNAGYDHVPDRIPMDATEIYLDGNSLKELGNHVFIGKKKLQVLYLNNSNIDIIQNRTFNGIDSLRVLHLENNNLEVLRNTQFTRLPHLNELYLSSNKIKFIENDTFNYLPSLEFLDLDNNGYVDYMPWRVISDSDPRMRVSVDGNNWICDCKDVAQLNQWLIKKSKDTENMMCYFAHGQPMNKTIATVAKECKTETTTEETGTETLKRLFIESNDGVENYIPYIAAVLIIAIILLLMCALLFMFREDFKLWMHSRYGIRIFSSSPRDLNDSKNKRFDAFFVYNPRDEDFVTRAVSSELENMGHTLCLQHRDLQLIERRSGDSLVSAAESSKRLIIVLSINFLQQEWYAPESKAAVQSAINSVNVRHRRQKIIFLVTTDLSGINIDPDLKVLLKTCTVIVWGERNCWEKLNFRLPDVDVTLPNRTLHNAYNIIKSGNREGFGRHGNLRYTAPPTSHDPWYKYGMAPPILMMSSPLHSTSASAEVSARSTEDETCSVASSEGRPDDRLPHHHSYVSIDNHQCEERPLRPGQQIPMSSTAHTRKTYFV

>BmToll12

MLRYYLAAVLLQVVAATNISCPTDANCTCGGTLAIELDCNIDGSVVNINLVPEIYINVKCENATALDYSKLPRCTNITDSFQSVSFKDCPLPETSFKDVLDNMGVTKTMALIFQNAKNLSGYLDRKHFAGLQDLTKLLLSINGVIHLPDDAFVDINKLTWLNIRSKTIYLSEELFKPLERLETLEISHNHMTNITSNLFSHLSFLRKLSLWQSNVTWFSQDFFNGVDVLEELDLSSNGLNKLPATIFKPLKKLKKLTLFSNKFSSLPKNLFIGNNELETVVILNNDVKLRVLPERLFGNLPNLKQVYVQRSGIEVVPRDTFKNSPAITNISLAFNDLKRLPEEVFNNQINLLNLDLSHNKIFDLATRTFSTLVRLEILNLCNNQLVFIDGSLFSSLLSLIDLNIENNNLKIITSDLFRNNKQRMSISLANNNLDFEQTVYANNCLSLEPRSPFANTYNLKLLNLSHNAFRISFVDWWINGHETVDVSHNAIKTLVAYNEYSDLYEGVTRKPLKELWVFNNPIQCVCNNYMFVDLLQDVTNRKIMDARLFRCPKWQITFCSIRVLTISAIILGLCVMYAVITMAYYIYKCRAYETLKWKLSLLSKKGIRIIEQELIIRYSEKDEEFVMKEILPTLKNEKNLKVYTNAIRCPSDISPDNLKTCVKDAYKYTTLIVFSPNYLTTAYSNVDIKKIHSEMLKAEYTVYVFVDIGPENFLYVFLKSQRDTNTMVVWGEANFWLKFLVTLAQYDITYPDLNKISDKITFAEVEENDKKNCHLCYLGTHRCHSCCYGIILDQSLV

>DPOGS200002-PA

MYHVLLLSLTLALVAAEYDFMSGVIWGGPERGCDSSEGAGQAVVSCTLASGNITLNVDRSASWLKITCEENSSFSCSELLEARPHISRYVTVNGQKDRQISRLDVDSCRLPEESLACLLDLVNASSAVLLRLIHCEGRVTDSSLAGVDTVKFRMNYVDKNTTSVPYPALSELPSLLSFTLKGGSLVLDVQNVTLPKLRTLELADGGLEVIPSNVFTNTPNIQTLMLWGNRISKLEEDAFKGLKELANVSLNSNKISSLPNKIFSHTPLTRRVDLYDNRLVILQKDLFSGLQHLEEVIITSNKANLTLEDTFANLPSLKNLKLETSNIEELPENLFRNSTSLRTLLLGGNKIENLPPTIFSDQKLVVLNLYDNRISELPAVLLKNQSSLERLDLRRNLIKNIPGGLFSDANKLKILSLARNNLTISEGMNTIALTPSDEYYTGDYSRTFQYYSVFKSLKYLKTLNLSKNNVSIICEDWRQLVGLKKLDLSYNSIDFLSDVSMHFDLSDAIIDVRHNRITTIVPPVYTSDSDKPTFILDYNPFACDCYLYELIQRYKSGKNTPILQMDKTKCASPRSLRNTQITQLSPEQLFCDVPCSDCSCKIRPYNRRFVLDCDEMPAAPPEVPEVFEALELSNEIHLKRSTDFIPSYYRYVDMASLNLTAAPSVAGPLELNLTNNNLRSAPLALLVTNCSLYLSNNPFLCGCDDYESVENLIRYKHLIRDFKEIRCEDGGLVSNVNTGQICVARDAAIIGSTIAMFGVILAIFTATAYKYSTEIRILLRKYHLWWGDEFDCEKEYDAFVSYSHQDEGYVVEQLVPNLEGGKPPLRLCVHYRNWVIGDFIPSQIARSVEQSRKTIIVLSKHFVNSIWGHMEFRTAHGKGKVIILMLDDLSADDSLDPELKAYIAMNTYVKSKDPLVFDRIRDAVLSKPPNKSPMGLNVQLKDGKLVNVNKDIDIAIK

>DPOGS205295-PA

MYAVTTVFCVLLHFVWSVPSYGLDKCVRQDSGNSIICRIRTLDSDGSSISTVNSETYALNIECNHLLLFESTLRAHYFSTVGSLTDLTINNCKLLSVPDNTFQDLNKLRRLKIRSKNSEWSPIKNLELTLNSFNGLSEMQSLDLAQNNIKFISSGIFCSLENLNTLNVTRNRIRTVGQIGFGQGCGSGLHTLDLSHNEIKTLSEESELVKLRSLQYIYLQYNNISDISSEAFKGLGSLRVLNISHNRLHTLPEGLFAYARELREIYLNDNSIFELARGIFHRLEQLIVLDLSSNQLTSNHIDDGTFLGLIRLIVLNLSNNALTRIDGKTFKDLFVLQILNLKNNSIGYIEENAFLPLYNLHTLNLAENRLHTVDENLFNGLFVLSKLTLNNNLLVNIDRKAFKNCSDLKELDLSSNQLIEIPDALWELPFLKTLDLGENQISDFKNGSFKNLNQLTGLRLIDNQIGNLSAGMFWDLPSLQVLNIAKNKIQSIERGTFSRNSQLEAIRLDGNFLSDINGVFSTLASLLWLNLSENHLVWFDYAFVPSNLKWLDVHGNFIEHLGNYYKLQDEIRIKTLDVSHNRIVEISPMSIPNSVELLFINNNFLNNIHVNTFFDKKNLTRVDMYANEIVHLELNSLRLANVPMNKSLPEFYIGGNPFKCDCTMEWLPIVNNMTAMRQYPRVMDIENVLCKMTNTRSGTQVPLTNLKKSDFLCAYETHCFAICHCCDYDACDCEMTCPQNCTCYHDPLWNTNVVDCSGQSSMEIPHKIPMDATEVFLDGNNIRELQNHVFIGRQKMRSLYVNNSNVDSIQNRTFAGLNALEILHLGNNKLRELKGYEFHQLSNLKELFLQNNLISHIANISFLSLKSLETLRLDGNRLVDFGVWSFADNSNLKALSLGNNLWSCKCRYLQELTAYLAENAQKIIDITDVWCWNGDAKPPQKKELNLNGTACSDYYADNSVIGNMLVSNYVPMMVSTLTGFMLILLALVVLFLFRDSLRVWLYTNCGIRVFSLSNGYEENEKLYDAYVCYSPKDEELVLQIFANELENGNSSYNLCLHYRDIPHHGAQYMQYAPPVLDFAEASKRIILVLTRNFMQTEWSRFDYRKEFHEVLKGYVYKLVLIEDYSVVQEAMCDEELRPYLKTGSRLRYGQKNFMERLKFMLPDSTQSHHKKRNSSNCRKNINTYTLDSSVPNGGNRTLSYPDKSPVLGNSGQGASAPPEYSTEVRQSPSTIRQMQGVSYGPDGRPISDHIYSSIDSDYSSLEQGMAPGRRRDMRQWPPPPPIVDTGSGGVQAYLV

>DPOGS211472-PA

MEVLRSRSLVSVLVSVLVFVSAETPRCPPTAKSDLCVDKGSALDEYFFVIKGKAWTIKYDLKELSFTCRKDLQLDSEELPRFTTLTIIPVVSLTACAPPSIGFAAALKTLNVTVRGGLVLEEMPATPTLNATHLHGLELRAFDLNAPFAPAPFLEPEDNFLEPLKGLLDLRLVRVTLTLKNTQSFPVGLRRLILHHANLTTLPAEVFARLPDLVDLFVVDETLQELDVSTALALRAVVVAAPLNGITLGSRVDTATLRKIRSAEIRGNCSGLRSLSIEELNVPPPTAWLARCGVRELRLRYLSPGVLGAGELRGTRDLLRLEIHGCGLRILPPDWLADSSRLKILDLSENELETIPSAIISACPRLSEVILPNNLLNSSVVKALVAAPLTKLVLDGNPLGDLCRTGSGLIADAMSTLWNRRELIYLSLRSTGVTRICHDWCRLPKLTQINLRNNSISKLEFEDLQWSSAVVVDLRGNPVKDVSYSQEQYEKVLLAPVTRDSISAMIRLDSHLRCDCNEYWFSLALRARPQHGQASVHAICENEKTFTSVPPTDLLCEVPELCPEGCKCKVDGERSHISCPNAGLIALPTIPPLPPLASLSLPGNDITILDFTNISTSFKLLDLTNNQIKHIDAATVATLFADNRRVLLDGNPLSCECRDVALQRELANRAEAGENGDARRQCRDVAEAACAMALWALPVAILVLSAAVLATCLVRPAARRRLKLFLFERGMCVRWVLGAAPDAVAEAAREYDAFVSFSHHDSEYAAAIAARLERGPRARRLCLHERDWTPGEWIPEQIATSVRRSRRTVALVSESFLVSQWARAELREAYTAALREGRARLLAVLLPGMEPPRAATAPELRAYLAAVTYLRWDDPHFWDKLLLAVPPPPNPSTAAPSPPTLCSPPPPP

>DPOGS203198-PA

MSLEIASESFTAVRQLEKLDLSYNNIWSFPENLFCPLTNLVYLNVSSNRLQDVSDLGFRERAMHQALISEHEGPSPSTSTSPHTSCSLDIEVLDASVNQFVLMPENGFMALRRLKELHIHDNEISMVADKALSGLKQLQIIDLSNNKIVALPQDLFRDCRPVIKEIYLQNNSISVLSPSLFANLDQLLALDLSNNHLTSTWINENTFTGLIRMIDAYALNGLYVLSLLSIDNNHLEELHPEAFRNTSSLQDLNLNGNRLKKVPTALKNMRLLRTLDLGENQIMSLEEPGFVGLHNVYGLRLIGNKIENISKEVFTDLPSLQILNLARNKIKQIDMDAFETLSNLQAVRLDANQLKDIQGLFVNIPSLLWLNVSGNQIEWFDYAVIPVGLQWLDVHSNNIKELRNNYRLDKELRLQTLDASFNLMTKIFTYSIPSSIELLFLNDNQITQVEAQTFVGKTNLTRVDLYANQITSMDLNALRLTPVDPGRPLPEFYIGGNPFQCDCTMEWLQRINKLDHLRQHPRVMDLESIYCKLLYNRERTYIPLIEAESSQFLCTYKTHCFTLCHCCDFDACDCEMTCPSNCTCYHDQPWSANIVDCSGAGYAEIPNTIPMDATELYLDGNNFGGLTSHAFIGRKNLKILYANNSNIDALYNNTFSGLKRLTVLHLEKNNIKELLGFELSPLENLRELHLQDNKIHYIDNRTFMELRHLEVLRLEGNNIYSFAVWQFTMNPYLVEISLSRNPWSCDCQYMHKFRNWFKNNLGKVEASDKITCIFDNVTNAVGPLMSDFNSTICTSHVGGSSSIIENQVINDYLPLLLISLFVFVMSSALICGIFYWRRELRVWVYYHCGFRMCYKSTAFDDEADKDRLFDAYISYSVKDEAFVAQMLAPGLESTDPSFRLCLHYRDFNASAYVADTIIEAVESSKRTIIVLSKNFINNEWCRFEFKTALHEVLKERRRRLIIILLGDLPNRDMDPELRLCLKANTCIEWGDRQFWQKLRFAMPDLRKCQYHRSTVNIYASVSPVGAGRAPAPTPPPPPGKLPPLLADGLADRLGMPTSVHRDHHSHRMPPHAQLWA

>DPOGS205293-PA

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>DPOGS203200-PA

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>DPOGS215274-PA

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PSYVD

>AgToll

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>AgToll-1

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>AgToll-5

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>AgToll-6

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>AgToll-7

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>AgTrex

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>AgToll-9

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>AgToll-10

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>AgToll-11

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>PxToll\_6

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>PxToll\_8

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>PxToll\_9

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>Px004048

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>Px006338

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>PxToll\_10

MTKNFYSMVSLKVWMCLVLVAGARARSAPPAPVGCQWDYSDAKLSESNFLTCNIKTIGSADFLFKNITTAQAYNINKLKLTCTDLLFFESSLHMNTGSFLGQLRKLEDLRIEYCKIRYVPATVLSPLRDLTSLTLRSYNTDWPAMTMEFHAESFRGLMELRSLDLGDNNIYMLPSEVFCPLFSLESLNLTNNRIQDISEIGFSDWGKGPIAPGKSCNTGLKMLDLSHNNVLRLPDNGLSSLRSLEVLKIQNNLINEIGDRAFVGLNSLKILNLSGNKLVAVPPELFQSSRVIKQISLANNSLSVLAPGLLEGLDQLEKLDLSRNRLTNDWVNRDTFAGLIRLVILNLSHNSLIRLDPKSFQDLNNLQVLNLDNNAIETISNGAFAELRNLHQLSISDNRMKALNEHIFSNLFVLSQLYLDNNQISVINERSFENITYLQDLGLNGNSLNMIPDGIKKLRFLKSLDVGKNNITKVSNTSFEGLEELYGLRLVDNHITSIPKDTFSTLPSLQVLNLASNKIENVEQDAFLSNPTLKAIRLDGNKLTDIRGVFNKLNTLGWLNISDNKLIYFDYSYMPESLEWLDIHSNNITKLDNEQNAQQNIRMLDVSYNALENVDERSIPDSIEVLFLNNNKIHTIHPGTFLQKRNLEKVIITDNKLRTVELSAFTLPHIPKHRMLPKFFIGNNPFVCNCHMIWLQKINLWNHMRQYPRFMDLDTVTCEVVNNKYGGKANLMDVPETQFLCSYETHCSSSCSCCDFEACDCKMACPEGCSCFHDSNWNSNVIDCSNVGYTEVPEKIPMDATELYLDGNDFGALNSHLFIGKKKLHKLYLNNSNIISIDNDTLNGLHSLNVLHLESNHLTELTGGEFSQTKHLRELYLNDNLLTSVANKTFESLSSLRIAHLQGNKILDLDKKLAHIVHLENVNVQGNLFTCTCANVMPLQNWFKKNYEDPADMFCASENGVTSNLTVYDVIDNCRDSSVTDNTIPTENQPYQFDEVSTIKLNFVPLLAVVLISVILILLFGALAFSFRQNVRLWAHSKYGVRLFKSASIQESELDRDRLYDGYSVYSLLDDDFVSKVIAPAMEHAGYTMCFHYRDLQLAHESYLSDQVTNAAESSKRILVFVSFNFLQNEWSKVSFKEAMKHVISSIHPSIRRHRVVFILTTDVSALNLDLDFQNYLKTCTVLLWGEKKFWEKIRFVMPDISNLQWNKDSLHYNHDNMCPNARRHPSRYTASPTAPEHWYKYDAIPPQTPTTVNVGINIEDDTSMLTNTTMTSQIQDGDPLHHSYISIDTQNYEQPYGGRPRPPNTLRKHPGHVSPSALDEQGYLQPRSSVHECLPQTHLSTHRL

>Px009819

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>Px009907

E

>Px014888

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>MsToll\_1

MQARRWCAALLLMQMLSWLGVSGHLPRPECAPAADCQLIRDNIIDGYAQFYFNVSVKFEHYIGNDFDVELSCNYIAMDNAMLPRFSTTFSVNVIVVKECALPRSGSIDAAVAALNINVLTELTLDKFLEPAVITRAHLTSLQRLERLELHGNSNTSLAPGALAALSAASALKCLVLHAVRVPAADLARLPSSLQELALLDVGAASMHLDSSVNLTSLFVIDTHYPVVVNVSNAVALRDLHINTPSTVLTEDVLPSSLNSLELEGWNETHPVPKTRCVLLKELNVIGTDNDAYPVTLPDEWLSNCGQLRDLEMISVPISAVLPARMLANAIRLETITIWNCNLTALPSGLLDDTLNLATLDLSNNQLASLPRKLFEHTKLLRSLILSNNQLTSEVVWTLSTVTSLVELKLSNNNRIGDLCSHDSVSAGPSPLSSLTGLNYLHLSNTGVSHVCSDWREKLTYLTNLNLRDNPITLYNLADLQFRRIWVDARVYLGHFKQQFTRTDYELASNNNTEAVVTLSGSLECDCNSYWAAQVFRMKAWQASSSMIYCEKKPVIEVDPDTFTCLEPAKCAALADSCTCRIRDDIQYKQVVVVHCTGLAEFPRLPLTTDKWILHLPHNNISYLAAADVSPNIVELDLRNNSIKNIDVQASAKLAFVPLQLGGNPIECDCEALKMLAPLLKPDSKLLDRKDVKCENDAQITLAMLKLCTKSSNGLVYLLFLLLLLAFVVTGLLARTAIRLRIKMILMRLGWMSRLLEPADDDRPYDAFVSFAHEDEELVMEQLAARLESGSRPYRLCLHYRDWAPGEWIPAQIAASVRASRRTVAVVSAHYLQSGWALAEIREATAASLQEGMPRLIIVLLDDTDRLMLDIDPELRAYVRNNTYVRWHDPWFWEKLKQALPPPREQRSQIAPSLPALALSHDSLTLRTYSPRESDPAPAAKPAHTPHETDEPAPGASPCYK

>MsToll\_2

MRSLWLTLTLALTLTWTRTSALCPKACQCGSGDELEYSCKLAGGKVTITATLRDNFNIDCEGGALTCSDFPSLPIAGNRSLYSLSIRECSLPDPLSCIARKLDATGVNLLLLRNVSTPLEKVHVEGLGIEKLYLYSAEAQSSIPSEAISSLPSLRYFRLCGGDVTLTGQDFRHAPPLTYLELGTDQITTLPADAFQGLAQLKTLNIWGNNISEIHEDALRGLSQLESLFVSAARARSLPARLLARAPALHALALERSRLGALPAELLRGLTQLQQVTISNDAPLTLEPLTFANLPITSLKLDQASLSALPPSLLVNCTSLVNLTLTRNKLQHIPDMFEGLISLERLDLSYNRIRNISSKLFLGLKALKELKMDANLIEELPEELFSGLRHLESLSMNSNRLQYIAPGAFRGASLRHVSLARNELSLAAPRAGYRDLELYSPLNNQLKLRTLILSDNKISTMFYDWRNVLLDLVELDLKRNSFEELTPADVQFLSSQITVDLRYNNISTIILTPGYPQGSHDLDPSGTSASILLAGNPLHCDCRLYMLAKRLRGDRPFTAEPSLILDETICVSPPSLQGLNFNKIPLDEFVCDVECSCQCQIRPFIDALDLICNNGSNIPDPNEYGLSHSILKLRHLPKNLSALPEYVSVLNLTDLGLEKAPEVPKTVELVDLTNNKLQEFPIELLSTNVSLKLSGNMFVCDCSTVREIALLNKHHDQIIDWQTLKCKDGSYLWRLEVEKLCLVQRATILGSVLATVGLVLAILAVIMHRYSVEIRIFLSNRGLCCFVDEYDATKKYDIFVSFAHEDEAFVIDKLLPKLEVNYKVCVHHRDWRVGDLIPTQIARSVEESRRTLIVLSRHFLASTWGMLEFRAAHVQAAKERKVRVVVLLLEDISDIEIESELRAYLTTNTYIKWGDQWFWEKLQYALPRRAKAEDVRSEKRAKIAADNMAKGGLQVTLTPDGKLVNTAMNKIVI

>MsToll\_3

MQARRWCAALLLMQTLSWLGVSGHLLRPECAPFADCQFIRHDSSEFHKLRFYFNVSVKFEHHIGNDFNVELSCNYIAMDNAMLPRFSMIFPVKIVKFRECALPKSVSFASAVVALNMTGFSQLILDKFQEPAVITRAHLTGLQRLETLELHGNSNTSLAPGALAALSAASALKCLVLRTVRVPAADLARLPSSLQELALRDVGAASMHLDSSVNLTSLIVIDTHYPVVVNVSNAVALRDLHINTPSTVLTEDALPSSLNSLLLRGWNETHPVPKTRCVLLKELNVIGTDNDAYPVALPDEWLSNCGQLWYLVMKSVPISGILPARMLANATMLKTIIIQNCNLTALPSGLLDDTLNLARLDLSNNQLASLPRELFEHPKLLRSLILSNNQLTSEVVGTLSTVTSLVELGLSNNNRIGDLCSHDSVSAGPSPLSSLTELNYLYLSNTGVSHVCSDWREKLTYLMALDLIDNPITLYNLADLQFRRMHKLARVYLGHFKQQFTRTDYELASNNNTEAVVTLSGSLECDCNSYWAAQVFRMKAWQASSSMIFCEKKTVIEVDPDTFTCLDPAKCATLADSCTCRILDDIQYKQVVIVHCSGLAEFPRLPPTTDKWILHLPHNKISYIAAADVSPNIVELDLRNNSIKNIDVQASAKLAFVPLQLGGNPIECTCEALKMLVPLLKPDSKLLDRKDVKCENDAQISLAMLKLCTKSSNGLVYLLFLLLLLAFVVTGLLARTAIRLRIKMILMRLGWMSRLLEPADDDRPYDAFVSFAHEDEELVMEQLAARLESGSRPYRLCLHYRDWAPGEWIPAQIAASVRASRRTVAVVSAHYLQSGWALAEIREATAASLQEGMPRLIIVLLDETDRVMLDIDPELRAYVRNNTYVRWHDPWFWEKLKQALPPPREQRSQIAPSLPALALSHDSLTLRTYSPRESDPAPAAKPAHTPHETDEPASGASPCYK

>MsToll\_4

MQARRWCAALLLMQTLSWLGVSKIIPRPECAPVADCQLIRNYITYEYAQFYFNVSGHEVVFIYHDKTYEVELSCNYIAMDNAMLPRFSTTLSVYVMVVNECALPRSGSIDAAVGALNINILSELTLNKFQEPAVITRTHLTGLQRLQKLVLYGNSNTSLAPGALAALSAASALKFLVLHTVRVPAADLARLPSSLQELELWDMGVASMHLDSSVNLTLLLVIDTHYPVVVNVSNAVALRDLHINTPSTVLTEDALPSSLNSLLLRRWNETHPVPKTRCALLQVLNVIGTDNATYPVSLPDEWLSNCGQLWYLKMESVPISGVLPARMLAKTTALKVITIRNCNLTALPSGLLDDTLNLATLDLSNNQLASLPRELFEHTKFLRNLILSNNQLTSEVVEALSTVTSLVKLKLSNNNRIGDLCSHDSVSAGPSPLSSLTRLNDLYLSNTGVSHVCSDWLEKLTYLTDLYLSDNPITLYNLADLQFRRMHKGARVYLGHFKQQFTRTDYELARNNNIEAVVTLSGSLECDCNSYWAAQVFRMKAWRASSSMIFCEKKPVIEVDPDTFTCLDPAKCAKLADSCTCRIRDDIQYKQVVIVHCSGLAEFPRLPQTMDKWILHLPHNNISYIAAADVSPNIVELDLRNNSIKKIDVQASAKLAIVRLQLGGNPIECDCEALKLLAPLFKPDSKLLDRKNVKCENDTQITLTMLKLCTKSSNGLVYLLFLLLLLAFVVTGLLARTAIRLRIKMILMRLGWMSRLLEPADDDRPYDAFVSFAHEDEELVMEQLAARLESGSRPYRLCLHYRDWAPGEWIPAQIAASVRASRRTVAVVSAHYLQSGWALAEIREATAASLQEGVPRLIIVLLDETDRLMLDIDPELRAYVRNNTYVRWHDPWFWEKLKQALPPPREQRSQIAPSLPALARTHDSLTLRTYSPRESDPAPAAKPAHTPHETDEPAPDASPCYMVLVS

>MsToll\_5

MQAWRWWCTTLLLALVPGLAGGSNRPECASNTYCKFAEESFRREFFYNVSGLNVRIVFTDALLFYLSCDNLALDDPNLPRFSSVVRVNKVNFENCTPPRNGSVANAIAALNVTSFSSLSLDKLPPKSVIKHEHLAGLQQLEKFSLYGSNNASLAPGALAALSVAPALHTLHLNWVHTPAADLLRLPQSLQKLKLWDVDAVSGYFQWLPNLTLLDVSEKHPIAVDVSNNTALKTLSVIAPDTVISENALPPTLTTLKLRKWNDTKPKPKTRCAQLEVLMLTGTDNERYPVSLPDEWLSSCIRLRELYIYNVPVRGVLPARLLAKATALKDISIKYCNLSALPQGFLDDTLNLTKLDLSNNKLTSLPSGLFLRTKLLEELNLSHNLLISAVAEALSVVFSLRNLRLNNNNIGDLCLSGSNSTEPADTSMLRNLTNLHSLYLSYTNVSRVCYDWRVKLLNLKTLDLNNSAVTNLTCDDLHYSRVTTATVVLGKYKLLCQRRDYDKSLASYRINAFVTLDGSLVCDCNTYWAARVFQNNVLDVITPQCKNYNYHKSIANMNHDNLTCSASEECAALPASCTCRKRDDYEHGSVVIVRCVGLTEFPRLPRQPDATHKWRLHLANNNISHIDAADILENIVELDLRNNFIRRVDGATATNLTSVLQLQLAGNPLECGCEAYTMLRALLEAKSLVDKKDVRCNGTGQRLVAVTPTACPGQGLMSVLPWVLPLVVLLAVAIFAYGFITRPATRLWIKFFLMRLGWIPRPFEPADEDRPYDAFVSFAHEDEELVVEQLAARLESGPQPYRLCLHYRDWAPGEWIPAQIAASVRASRRTVAIVSTHYLQSDWARAEFREATAASLRDGTPRLVVVLLDDPDRLMLEVDAELSAYVRHKVYVRWGDPWFWEKLKQALPLPRARHLKSVPSFPASAPDIPLVLTHAGRETALAPAPPSQDYDKPMPGATLCST

>MsToll\_6

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>MsToll\_7\_1

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>MsToll\_7\_2

MYAIAAVFCALLQVGWTVMQNGSDKCVRVADRGSEGGVLCRIRTLEGEGGSISSVTSDTSRLTVECNNLLLFESSLRAHYFAPVQGLTDLSINNCKLLGVPDNTFQDLKKLKRLKLRSKNFEWSPTKNLELSLNAFNGLLELQSLDLAQNNIKFVPSGVFCALENLNTLNLTHNRIKTVGQIGFGQGCGSSLHSLDLSHNMIKSLPEDSELLKLRSLQHLYLQHNNITDISSGAFNGLVSMRVLNISHNHLHTLPEGIFANARELREIYLNDNTLYELARGVFHRLEQLIVLDLSSNQLTSNHIDDGTFLGLIRLIVLNLSNNALTRIDGKTFKDLFFLQILNLKNNSIGYIEDNAFLPLYNLHTLNLAENRLHTIDENLFNGLFVLSKLTLNNNLLVNIDRKAFKNCSDLKELDLSSNQLMEVPDALWELSFLKTLDLGENQISDFRNGSFKNLNQLTGLRLIDNQIGNLSVGMFWDLPSLQVLNIAKNKIQSIERETFKRNGQLEAIRLDGNFLSDINGVFSTLASLLWLNLSENHLVWFDYAFVPTKLKWLDIHGNFIEHLGNYYKLQDEIHIKTLDVSHNRITEISAMAIPNSVELLFINNNFLNSIHVNTFFDKKNLTRVDMYANEIVHLELNSLRLSTVSGNRTLPEFYIGGNPFQCDCTMEWLPIINNMTAMRQYPRVMDLENVLCKMTNTRSGTHVPLTNLKTSDFLCKYETHCFAICHCCDYDACDCEMTCPQNCTCYHDPLWNTNVVDCSGQSSVEIPHKIPMDATEVFLDGNNIRELQNHVFIGRQKMRSLYVNNSNVDSIQNRTFAGLNSLQILHLGNNKLKELKGYEFHQLSNLKELFLQNNLISHIANISFLSLRSLETLRLDGNRLVDFEVWSFNSNPNLKALSLGNNLWSCKCRYLQELTAYLAENAQKIIDITDVWCWNGDAKPPQKKELNLNGTACSDYYADNSVIGNMLVSNYVPMMVSTLTGFMLILLALIVLFLFRDTLRLWLYTTCGIRVFSFAGSFEESQKLYDAYVCYSPKDEESIVQSLVNEFENGTQSYNLCLHYRDVAHHGAQYLPCAPPVVETAEASKRIIIVLTRNFMQTEWSRYEIRQRLHEALKGCIYKLVLIEESSVVEDAMCDPDLRPYLKTGSRLRWGEKRFWERLRYMMPELSGHSHKARSHSYRKSINTYTLDSSVPNGANVAPFPDKSPVLGSAVQGVSAPPEYTTEVRQSPSVVRQTQGVMYGPDGRPISDHIYSSIDSDYSSLEHGMAPGRRRDMRQWPTPPPVVDATNAVQGYLV

>MsToll\_7\_3

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>MsToll\_8

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>MsToll\_9\_2

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>MsToll\_10\_1

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>MsToll\_10\_2

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### Toll-interleukin receptor domain sequences

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>BmToll6

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>BmToll8

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IMVVSENFIKSEWCRFEFKSAHQSVLRDRRRRLIVIVLGEVPQKELDPDLRLYLKTNTYL

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>DmToll-6B FBpp0297410 type=protein; loc=3L:15337225..15341769; ID=FBpp0297410; name=Toll-6-PB; parent=FBgn0036494,FBtr0306307; dbxref=REFSEQ:NP\_001246765,GB\_protein:AFH04436,FlyBase:FBpp0297410,FlyBase\_Annotation\_IDs:CG7250-PB,UniProt/Swiss-Prot:Q9VUN0; MD5=6ba90717bb0165f76352123615612eef; length=1514; release=r6.20; species=Dmel;

PNDAYFAYSLQDEHFVNQILAQTLENDIGYRLCLHYRDVNINAYITDALIEAAESAKQFV

LVLSKNFLYNEWSRFEYKSALHELVKRRKRVVFILYGDLPQRDIDMDMRHYLRTSTCIEW

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>DmToll-9 FBpp0077898 type=protein; loc=3L:complement(join(20365624..20365918,20364666..20364896,20364341..20364562,20362507..20364125,20362309..20362436,20362040..20362247)); ID=FBpp0077898; name=Toll-9-PA; parent=FBgn0036978,FBtr0078240; dbxref=FlyBase:FBpp0077898,FlyBase\_Annotation\_IDs:CG5528-PA,FlyMine:FBpp0077898,GB\_protein:AAF51581.1,REFSEQ:NP\_649214,GB\_protein:AAF51581,UniProt/TrEMBL:Q9VPH1,modMine:FBpp0077898; MD5=b6383d5b4c9ecdc6ec1e488d044c973b; length=900; release=r6.20; species=Dmel;

VYDIFISYCQNDRTWVLNELLPNVEETGDVSICLHERDFQIGVTILDNIISCMDRSYSLM

LIISSKFLLSHWCQFEMYLAQHRIFEVSKEHLILVFLEDIPRRKRPKTLQYLMDVKTYIK

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PNDAYFAYSLQDEHFVNQILAQTLENDIGYRLCLHYRDVNINAYITDALIEAAESAKQFV

LVLSKNFLYNEWSRFEYKSALHELVKRRKRVVFILYGDLPQRDIDMDMRHYLRTSTCIEW

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>DmToll-1C FBpp0303187 type=protein; loc=3R:join(26837737..26838956,26839074..26841207); ID=FBpp0303187; name=Tl-PC; parent=FBgn0262473,FBtr0330154; dbxref=FlyBase:FBpp0303187,FlyBase\_Annotation\_IDs:CG5490-PC,REFSEQ:NP\_001262995,GB\_protein:AGB96375,UniProt/TrEMBL:A0A0B4KHY4; MD5=bb73e39dd397e5a472d3532a6a61c0ea; length=1117; release=r6.20; species=Dmel;

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>DmToll-1B FBpp0084431 type=protein; loc=3R:join(26837737..26838956,26839074..26841147); ID=FBpp0084431; name=Tl-PB; parent=FBgn0262473,FBtr0085059; dbxref=FlyBase:FBpp0084431,FlyBase\_Annotation\_IDs:CG5490-PB,FlyMine:FBpp0084431,GB\_protein:AAN14086.1,REFSEQ:NP\_524518,GB\_protein:AAN14086,UniProt/Swiss-Prot:P08953,modMine:FBpp0084431; MD5=d2cdeaa04f3b449545ad80366aae48e1; length=1097; release=r6.20; species=Dmel;

KFDAFISYSHKDQSFIEDYLVPQLEHGPQKFQLCVHERDWLVGGHIPENIMRSVADSRRT

IIVLSQNFIKSEWARLEFRAAHRSALNEGRSRIIVIIYSDIGDVEKLDEELKAYLKMNTY

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TYDAFISYSHKDEELISKLLPKLESGPHPFRLCLHDRDWLVGDCIPEQIVRTVDDSKRVI

IVLSQHFIDSVWARMEFRIAYQATLQDKRKRIIIILYRELEHMNGIDSELRAYLKLNTYL

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>DmToll-5B FBpp0312090 type=protein; loc=2L:join(13435749..13436794,13437923..13439264); ID=FBpp0312090; name=Tehao-PB; parent=FBgn0026760,FBtr0346423; dbxref=FlyBase:FBpp0312090,FlyBase\_Annotation\_IDs:CG7121-PB,GB\_protein:AHN54415,REFSEQ:NP\_001285901,UniProt/TrEMBL:Q9VJX9; MD5=f867e613eccf2bcb0ab81a0221bf3fe3; length=795; release=r6.20; species=Dmel;

TYDAFISYSHKDEELISKLLPKLESGPHPFRLCLHDRDWLVGDCIPEQIVRTVDDSKRVI

IVLSQHFIDSVWARMEFRIAYQATLQDKRKRIIIILYRELEHMNGIDSELRAYLKLNTYL

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>DmToll-9B FBpp0300870 type=protein; loc=3L:complement(join(20365624..20365918,20364666..20364896,20362507..20364125,20362309..20362436,20362040..20362247)); ID=FBpp0300870; name=Toll-9-PB; parent=FBgn0036978,FBtr0308647; dbxref=FlyBase:FBpp0300870,FlyBase\_Annotation\_IDs:CG5528-PB,REFSEQ:NP\_001246845,GB\_protein:AFH04516,UniProt/TrEMBL:M9NDW9; MD5=839c88f144d503bb29dc68960d351335; length=826; release=r6.20; species=Dmel;

VYDIFISYCQNDRTWVLNELLPNVEETGDVSICLHERDFQIGVTILDNIISCMDRSYSLM

LIISSKFLLSHWCQFEMYLAQHRIFEVSKEHLILVFLEDIPRRKRPKTLQYLMDVKTYIK

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LYDAVLLHSAKDSEFVCQHLAAQLETGRPPLRVCLQHRDLAHDATHYQLLEATRVSRRVV

ILLTRNFLQTEWARCELRRSVHDALRGRPQKLVIIEEPEVAFEAESDIELLPYLKTSAVH

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PNDAYFAYSLQDEHFVNQILAQTLENDIGYRLCLHYRDVNINAYITDALIEAAESAKQFV

LVLSKNFLYNEWSRFEYKSALHELVKRRKRVVFILYGDLPQRDIDMDMRHYLRTSTCIEW

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>DmToll-1 FBpp0303188 type=protein; loc=3R:join(26837737..26838956,26839074..26841147); ID=FBpp0303188; name=Tl-PD; parent=FBgn0262473,FBtr0330155; dbxref=FlyBase:FBpp0303188,FlyBase\_Annotation\_IDs:CG5490-PD,REFSEQ:NP\_733166,GB\_protein:AAF56624,UniProt/Swiss-Prot:P08953; MD5=d2cdeaa04f3b449545ad80366aae48e1; length=1097; release=r6.20; species=Dmel;

KFDAFISYSHKDQSFIEDYLVPQLEHGPQKFQLCVHERDWLVGGHIPENIMRSVADSRRT

IIVLSQNFIKSEWARLEFRAAHRSALNEGRSRIIVIIYSDIGDVEKLDEELKAYLKMNTY

LKWGDPWFWDKLRFALPHR

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LYDAIILHSEKDYEFVCRNIAAELEHGRPPFRLCIQQRDLPPQASHLQLVEGARASRKII

LVLTRNLLATEWNRIEFRNAFHESLRGLAQKLVIIEETSVSAEAEDVAELSPYLKSVPSN

RLLTCDRYFWEKLRYAIPIE

>DmToll-3 FBpp0081104 type=protein; loc=3R:complement(join(7368641..7369305,7366303..7368535)); ID=FBpp0081104; name=MstProx-PA; parent=FBgn0015770,FBtr0081585; dbxref=GB\_protein:AAF54021.2,FlyBase\_Annotation\_IDs:CG1149-PA,FlyBase:FBpp0081104,FlyMine:FBpp0081104,GB\_protein:AAF54021.3,REFSEQ:NP\_649719,GB\_protein:AAF54021,UniProt/TrEMBL:Q9VIA4,modMine:FBpp0081104; MD5=f1eea74b4ec67c20c304e8f1ea696079; length=965; release=r6.20; species=Dmel;

RFDAFLAFTHKDEALLEEFVDRLERGRPRFQLCFYLRDWLAGESIPDCIGQSIKDSRRII

VLMTENFMNSTWGRLEFRLALHATSRDRCKRLIVVLYPNVKNFDSLDSELRTYMAFNTYL

ERSHPNFWNKLIYSMPLL

>AgToll

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VRWGDPWFWDKLRFAMPHP

>AgToll-1

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VRWDDPWFWEKLHYAMPHK

>AgToll-5

RYDAFISYSHKDEEFVTGQMLPRLESEELNFKICWHVRDFMPGEMIASQITKAVEDSRRT

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>AgToll-6

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LVLSKSFLYNEWTRFEFKGAIHEVLKRRRKLIIILYGDLPQRDLDADMRLYLRTNTCIEW

DDKKFWQKLRIALPHV

>AgToll-7

LYDAILLYSAKDAELVARSIAGELENGRPPLRLCLQHRDLPEDASHLQLLEASRASRRIV

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TRVRRGDRHFWEKLRYALPVE

>AgTrex

LFDAFISYSSKDEAFVAEELAPMLENEDPSYKLCLHYRDFPVGAYIADNILQAVESSRRT

IMVLSENFIKSEWCRFEFKSAHHQVLRDRRRRLIVILLGEVPQKDLDPDIRLYLKTNTYL

QWGDKLFWEKLRFALPDV

>AgToll-9

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VVSMNFLQTEWSQPQFRVALQSVIESIRPAHRRHKIVLVLTAPVEIVAMDPIMHLLIRTC

TVACWGERKFWDKLRYALPDV

>AgToll-10

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CTVIAWDDRRFWDKLRFAMPDL

>PxToll\_6

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IIVLSKNFINNEWCRFEFKTALHEVLKERRRRLIIILLGELPNRDIDPELRLCLKANTCI

EWGDRQFWQKLRFAMPDL

>PxToll\_8

MYDAFVSYSSKDEAWVAEELAPMLERGVPSYKLCLHYRDFPVGGYVADNIVQAVESSRRT

IMVLSENFIKSEWCRYEFKSAHHQVLTDRRRRLIVVLLGEVSQKDLDPDIRLYLKTNTYL

HWGDKLFWEKLRFALPDV

>PxToll\_9

KYDAFVSYCNEDRDFVLEMIAEMESNPPFLKLCVYERDFEIGSFISESILNSINESRYII

LVISNGFAKSQWCRWETQLAEYHRLFLEDGTSYDPLVLVRIGHIEPKYLSTTLKFLLKTK

IYLSWEEQRQDEFWKKLRNVLTKR

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WPKEKAERRVFWRRLQKCIVLQ

>PxToll\_10

LYDGYSVYSLLDDDFVSKVIAPAMEHAGYTMCFHYRDLQLAHESYLSDQVTNAAESSKRI

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>Px014888

RFDAFFVYNLKDKDFVTRAVSSELENSGRALCLQHRDLQLLERHQSDSLVAAAEYSKRLVIVLSINFLQQEWYSPEIRAAIQSTINSVNIRHRRQKIIFLVTTDLSAINIDPDMKVLLKTCSVIVWGERNCWEKLNFRLPDV

>MsToll\_1

PYDAFVSFAHEDEELVMEQLAARLESGSRPYRLCLHYRDWAPGEWIPAQIAASVRASRRT

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YVRWHDPWFWEKLKQALPPP

>MsToll\_2

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LSRHFLASTWGMLEFRAAHVQAAKERKVRVVVLLLEDISDIEIESELRAYLTTNTYIKWG

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>MsToll\_3

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YVRWHDPWFWEKLKQALPPP

>MsToll\_4

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>MsToll\_5

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>MsToll\_6

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EWGDRQFWQKLRFAMPDL

>MsToll\_7\_1

LYDAYVCYSPKDEEFVVETLARELENGYPSYHLCLHYRDVPQFEATYAQFPDLVVEATEA

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>MsToll\_7\_2

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>MsToll\_8

MYDAFICYSSKDEAWVTEELVPMLERSDPSYKLCLHYRDVGGYVTEKIRQAVESSRRTIM

VLSDNFLRSEWVRYELKTAFHQVLRDRRKRLIVVLLGQVLQKDLDQDIRLYLKTNKCLYA

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>MsToll\_9\_2

HYDVFVSYCNEDRGWVLDHLLPHLESDCSISACLHERDFQVGLSILENIVSCMDRSRSIM

LIISQKFLMSQWCQFEMHLAQHRLLETRREDLTLVLLEEIPRRLRPTTLHYLMLTKTYIV

WPAADAERALFWKRLRKSLVTQ

>MsToll\_10\_1

LYDGYAVYSLLDDDFVSKVVAPEMEHSGYTMCFHYRDLQHAPENYLSEQITNAAESSKRI

IVFVSFNFLQNEWSKATFKAAIKHVITSIHPSIRRHRVIFILTTDVSALNLDLDFQSYLK

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>MsToll\_10\_2

LYDGYAVYSLLDDDFVSKVVAPEMEHSGYTMCFHYRDLQHAPENYLSEQITNAAESSKRI

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>MsToll\_10\_3

RFDAFFVYNPRDEDFVTRAVSSELENMGHTLCLQHRDLQLIERRSGDSLVSASESSKRLVIVLSINFLQQEWYAPESKAAVQSAINSVNIRHRRHKIIFLVSTDLSAINIDPDLKVLLKTCTVIVWGERNCWEKLNFRLPDV