

S5 Table. Protein sequences, identified domains and genomic locations in VectorBase of other immune-related NMRI and BS-90 *Biomphalaria glabrata* plasma proteins eluted from sporocyst membrane-enriched fraction (Mem) affinity columns.

Protein ID	Scaffold No.	Predicted Protein Sequence
<p>PREDICTED: Lipopolysaccharide-binding protein-like [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013070669.1</p> <p><u>Domains:</u> -Bactericidal permeability-increasing protein (BPI) / Lipopolysaccharide-binding protein (LBP): 1-193/ 180-384</p>	<p>LGUN_random_Scaffold1023: 50441-50613; 50252-50331; 49394-49526; 46627-46718; 45543-45623; 43433-43591; 40841-40951; 39401-39593</p>	<p>MLLINLLGHYFNSFRLNVAIPDIDMSFNVPVQRGLTMNLRNLGVDVLLDYRVRYKLLFVPISSSGGVSVN FRGVELTATVIGIDQFEDTSPRLVSRSCSAAGDFNINFSGSMAWLLNLLKGLFRGKIRDITIRSKICKDKVT EAINTQGADKLRQIPLESADIADKFVIDYRLLSPVLFTDSYLETQHKKLYKRGTLGYAAHTHGYLQYVISP DKLPAQSKGFLNTPCPSACAGTLIPLLAEKYPNSFVTLTISSSKAPDFNITSNGLGLTLYGTLDLSTTS ASAVVTANVVISIAGAAAFVRNDRIVGNVAQFRTVLADIDSQRLISLYTFQISSINKALDDGMNMVVIPQL NAVGDGTGIALPVLKDLTFQNPRIVYQDKSVLISTNVQYQGIV</p>
<p>Thioester-containing protein 1.5 (TEP1.5) [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: ADE45333</p> <p><u>Domains:</u> -Signal peptide: 1-21 -Proteinase-binding alpha-macroglobulins: 126-219/ 463-599/ 718-808/ 978-1241 -Thiol ester: 929-958 -Alpha-2-macroglobulin-receptor: 1342-1426</p>	<p>LGUN_random_Scaffold4524: 9507-9566; 9149-9332; 8894-8916; 4705-4867; 1865-1933; 1610-1736; LGUN_random_Scaffold10725: 6705-6750; 4397-4481; 2567-2681; 2042-2159; 1413-1527; LGUN_random_Scaffold9700: 5915-6144; 3125-3226; 2777-2839; 709-909; LGUN_random_Scaffold8482: 12144-12290; 10814-10917; 10616-10675; 10307-10337; LGUN_random_Scaffold2300: 37595-37626; LGUN_random_Scaffold76986: 250-267; LGUN_random_Scaffold8482: 10166-10290; LGUN_random_Scaffold7766: 10058-10180; 9732-9849; LGUN_random_Scaffold45951: 828-903; LGUN_random_Scaffold7766: 277-407; LGUN_random_Scaffold53075: 386-529; LGUN_random_Scaffold6063:</p>	<p>MRMKNLNLILFVYLVFQECQGKGFISAPRNVVPGTAYDISVDILKQDIGNVTVEAILQDYSFSIPEGPK SLLTANGTFSPGVRGTLSPIDFNLHCSYCRILLKGYNPLQFEQDIFIQISSDILSIQTDKAIYKPK RVNFRILAVYYNLQLYGTGFHYEILDOPYDNKINVLGVSFGTGVVEGFFDLSDQPSFGTWKINVRTETVS GAESQFFEVAEYDLPRFQVDVGLPPFALLSDTTLSGSVEAKYTFGQPVYGLVLLQIGENVDTIDKCNVNR KVTEISFEIKGKGNFVPLEDIRRSVHLNEKKKIKITAFVIEASTGIKLNSSVITYYGNRYQIKFLEMT PAVFKPGLQYTAYVQVTTDPDGLPPTESNLSLSVYTSVTYQMTVPDQELYSPPSSFGSYPLPGQNMSLPAN GILSIDIDIPLNATSIDIKVSLNKQTAEKRISKSYSMSNNYLQLSLLSKLVAESDVLIKITSTEAIDS LAYEIRSRSDHVKSGVLELNGQREFNATFKVGPSPWAPIAQLLMYYIRRDSNEIVTDSLAFNVEGMFENKV NVAFKENETDINKNVSELSADSDSQIYVLAVDQSVLLKTGNDLTPNKVKDSFISKFKHKEVPTDSNFA LSYSGSSINEVFSNMGLVIATDLNIFAPFRPIALGRFPSSGFDRQGMGAPMAMFRDDNAMESASFEMD VATSTKPVERVRSFFPESWLWTSVKSINGHATLTTTVPDTITSWIVSAFATNSDTGLGVAPTTSKLRVFR PFFVSLTYPRSVTRNEQFIVQATVFNYLPVDLMVTVSLKENPFLTPITPGPNQASNIQVRANEQGIVYF SLSALTVGSLDTEVSARSNMAADAIVRQILIKHEGAPVVYNNPILINLSNNQSTFEKNIAFTLPDSLVPE SQRIRVKVTGDLIGSTVQSLTLLTPTGCGEQSLVKFTPNIHIGRYLKATNQLSEELNKKIDLLNDGY QRQLTYKRYDNGFSAFGNYSSTWLTALVVTSAFAEQEFIFVDKEIILKASMLLIDRQNIIDGFSNEFG KVLDRNTQGTTAGPALTAFLVLLKAKELADVDCKNNNKCRYLLGNATLNATRNLERLMLADSIDD QFSLAVASYALAEAKSQAQSTFEKLLTFVKQEGGLEYSANSTVNNEELNRFINWRPRLQARPIDILI TSYAILTYSSLGRLEALPSVRWLTQKNAQGGFVSTQDQTVVGLQALSFGSKSFRPDTNITIYVSDMNT HLTMMNVNSENALSLLQIEIQSNQDQSITASGSLALLDIEYSFNVLKELSKPVFDANTVLLDDKLDLDFN IMVCTKFLMKHDTGMVVQELSIPSGFVDPDLSTLQVAVGKRSEKGSIVAIYFDKISGSSLCYSIVMTRE AKVAKSQKSYVRTYDYEPANQATVFYQPRTLRDSTVCDVCLNCCP</p>

	<p>31434-31613; 29915-29997; 25214-25375; 23259-23332; LGUN_random_Scaffold7260: 85338740; 5514-5738; 11544- 11696; 11926-11989; 12187- 12304; 13837-13988; 15855- 15963; 16394-16478</p>	
<p>Thioester-containing protein (TEP) [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: ACL00841.1</p> <p><u>Domains:</u> -Signal peptide: 1-21 -Proteinase-binding alpha- macroglobulins: 126-219/ 463-599/ 718-808/ 978-1241 -Thiol ester: 929-958 -Alpha-2-macroglobulin-receptor: 1342-1426</p>	<p>LGUN_random_Scaffold4524: 9507 9566; 9149-9332; 8894- 8916; 4705-4867; 1865-1933; 1610-1736; LGUN_random_Scaffold10725: 6705-6750; 4397-4481; 2567- 2681; 2042-2159; 1413-1527; LGUN_random_Scaffold9700: 5915-6144; 3125-3226; 2777- 2839; 709-909; LGUN_random_Scaffold8482: 12144-12290; 10814-10917; 10616-10675; 10307-10337; LGUN_random_Scaffold2300: 37595-37626; LGUN_random_Scaffold76986: 250-267; LGUN_random_Scaffold8482: 10166-10290; LGUN_random_Scaffold7766: 10058-10180; 9732-9849; LGUN_random_Scaffold45951: 828-903; LGUN_random_Scaffold7766: 277-407; LGUN_random_Scaffold53075: 386-529; LGUN_random_Scaffold6063: 31434-31613; 29915-29997; 25214-25375; 23259-23332; LGUN_random_Scaffold7260: 85338740; 5514-5738; 11544- 11696; 11926-11989; 12187- 12304; 13837-13988; 15855- 15963; 16394-16478</p>	<p>MRMKLNLILFVFLVFQECQGKGYFISAPRNVVPGTAYDISVDILKQDIGNVTEAILQDYSFSIPEGPK SLLTANGTFSPGVRGTLSPIDFNLHCSYCRILLKGYNPLQFEQDIFIQISSDILSILIQTDKAIYKPK RVNFRILAAAYNLQLYGTGFHYEILDPYDNKINVLGVSQVGFVVEGFFDLSDDQPSFGTGWKINVRTETVS GEESQLFEVAEYDLPRFQVDVGLPPFALLSDTTLSGSVEAKYTFGQPVYGLVLLQIGENVDTIDKCNVNR KVTEISFEIKKENFSVPLEDIRRSVHLNEKKIKITAFVTEASTGIKLNSSVITYYGNRYQIKFLEMT PAVFKPGLQYAYVQVTTDPLPPTSDNLSLVYTSVYQMTVPDQELYSFSSFGSYPLPGQNMSLPAN GILSIDIDIPLNATSIDIKVSLNKQTTAEKRISKSYMSNYYLQLSLLSKLVKAESDVLIKITSTEIDS LAYERSRSDRVKSGVLELNGQREFNATFKVEPSWAPIAQLLMYYIRRDSNEVVTDSLAFNVEGMFKNKV NVAFKENETDINKNVSLELPADSDSQIYVLAVDXSVLLKGTNDXTPXKVKDSFXSFHKGAIPTDSNFA LSYSGSSIXEVFSNMGLVIATDLNIFAPFRPIALGRFPSSGFDRQXMMGAPXAMSFDDXAMXSASFEMD VTTSTKPVERVRSFFPESWLWTSVKSINGHATLTTTVPDTITSWIGSAFATNSDTGLGVAPTTSKLPGFR PFFGSLTYPRSVTRNEQFIVQATVFNYPVLDLMTVSLKENPFLTPVTPGPGNQASNIQVRANEQRTVYF SLSALIVGALDIEVSARSNMAADAIVRQILVRHEGAPVVYNNPILISLNNQSTFEKNIAFTLPDSLVE SHRIRVKVTGDLIGSTVQSLTLLTPTGCGEQSLVKFTPNIHIGRYLKATNQLSKELNKKIIDLLNNGY QRQLTYKRYDNGFSAFGNLDSSSTWLTALVVTSFEEAQEFIFVDKEIILKASMLLIDRQNLDDGSFNEFG KVLDRNTQGTAGPALTAFLVALLKAKELADVQYCKNNKCRYLLGNATLNATRNLERLMLADSIDDQ FSLAVTSYALAEAKSQAQSTFEKLLTFVKQEGGLEYSANSTVNNEELNRFINWRPRLQARPIDILIT SYAILTYSPLGRLDEALPSVRWLTQKNAQGGFVSTQDQTVVGLQALSTYGSKFRPDTNITYVSDMNT LTMNVKSDNALSQIQEIQNSQDFISITASGSLALLDIEYSFNVLKELSKPVFDVNTVLLDDKLDSEFNI MVCTKFLKHDGTGMVVQEVSPSGFVDPDLSTLGQVAGVKRSEKGSIVAIYFDKISGSSLCYSIVMTREA KVAKSQKSYVRTYDYEPANQATVFYQPRTLRDLRSTVCDVCLNCCP</p>

<p>PREDICTED: CD109 antigen-like [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013071291.1</p> <p><u>Domains:</u> -Proteinase-binding alpha-macroglobulins: 47-138/ 348-500/ 649-740/ 918-1168 -Thiol ester: 869-898 -Alpha-2-macroglobulin-receptor: 1271-1355</p>	<p>LGUN_random_Scaffold108: 84237-84416; 83387-83461; 82641-82779; 80795-80861; 78882-79106; 78232-78463; 76389-76589; 76048-76202; 75142-75294; 51880-52111; 41664-41787; 35799-36007; 39854-39999; 39487-39666; 39487-39666; 39487-39666; 38763-38921; 36931-37116; 35799-36007; 34930-35082; 32766-32916; 31828-32071</p>	<p>MESLHFLFYSQLPADLPSSTYTLNVKSGGLTFDKSENLYNNKETS VFIQLNKAIFKPGDVTNFRVFGV YSDLKSYTDPIDISYDANSNKIKQWLKVTPTNGVITQELTSTQPVLDGWKISVDAGRTKEEKVFTVAE YVLPKFEVDVVTSPYALTTDNDVTVTVKSKYTYGKPVNGTADVLVKLHESFNTFDYSRALPVTTLQVPLN GEAKVIIIPMSQVKAIKANLNQHLVIVANVTESLTGNQMSGNGVTLYDKGVKLDFFASNPKTFFKALQY IAYLKVTQPDGLPMTSTAEQVKV SIRVTAELPGTTPPYWYVPPTESRDLPALSLAIPDNGLVAIPVDV PADAKDVHVTANFQGVSKELTLGKSHSPNSYIQLILKSGSVIKFQLSRGGIVKTGTVDANGQLVYQFS IPSDSSMAPNARIVLYVRADGEIVTDSISFDISGAFKNKVSIDLKTDVPEGDDVTVTKADPDSTAYC LAIDQSVLLKGGNDVTDNDVYTELKEYDTITESGSNKIIDCPMCKRRKRMWWPFPTYGGSDAQQIF SNAGVVVLTATVYHYQEPIHLNIPNFFQCGRSLNGQLRKRCAFSPVMNLVSSVSDPITLPVTETE TKTEDLQQPTKTRSNFVETWLVNSLDIGANGSASITATVPDITISWVASAFAINSASGLGVAPTQAHLRV FRPFVSLNLPYSVTRGEHLALQANVFNMTEDMQVRVTLAKSDNFFNIEIDANGAEVLKQVESVQDVMII KAGEAKSVYFPIVPADLGKIDIEVKAQSTKAADAVRRQLLVEAEGVPKIVNPVVLIDLTEGKTSFSKTVD LTLPSNTVKGSELARISAVGDLMGPTIAGLDSLLQMPTGCGEQTMIGLAPDVVYTDYLKSVNQLSGDIQT KALSYMESGYQRELYKHTDGSFSAFGNSDASGSMWLTAFVTRVFKQAKAHYIIDDEVLIKAIQWMVSKQ NANGSFPEPGNVHKNMQGQAGSGVGLTLFVLISLLENKDLLVNTNAAGILVDEARQKALVYAEQEVAKT DDLILNMAAYAFQLANSSQVQTVLSKLEQKATVKDGRKYWHQPEQPKTTNTWDYPNPTKAVDIEMTSYA LLTYAARGNIVAGKSIMQWLTEQRNSNGGFSSTQDVTLALNALSEFAKQTSYNNFNQVITTQLNATTSYT FNIDKTNLLLLQSRETPNVPSQVKIDATGSGMALVQVAVSFNVESEIFETTFDLTVKLIETINNLVET CAKWLGS GPSSAMAVQEIGIPSGFEADIESIPQLDILKRIETQNKKVILYFDQIGTTPVCLNFRAVRTGL VAKSQPAAIRVYDYYEPRNQVTA FYQS QILKDSTVCDVCKECDNCV</p>
<p>PREDICTED: Heat shock protein 70 kDa cognate 4 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013082115.1</p> <p><u>Domains:</u> -Heat shock proteins, Hsp70 chaperones: 6-612</p>	<p>LGUN_random_Scaffold253: 223515:226430: BGLB007783</p>	<p>MSKAPAVGIDLGTYSVGVFQHGKVEIANDQGNRTTSPYAFDNERLIGDAAKNQVAMNPENTVFDA KRLIGRRFDDPTVASDMKHWPFTVINEGGPKIRVEYKGEKTTFFPEEISSMVLTKMKETAAYLGKTVT DAVVTVPAYFNDSQRQATK DAGTISGLNVLRIINEPTAAAIA YGLDKKVGGERNVLIFDLGGGTFDVSIL TIEDGIFEVKSTAGDTHLGGEDFDNRMVNHFIQEFKRKHKKDISENKRAVRRRLTACERAKRTLSSTQA NIEIDSLFEGIDFYTSITRARFEELNADLFRGTLEPVEKSLRDAKLDKAQVHEIVLVGGSTRIPKIQKLL QDFFNGKELNKSINPDEAVAYGA AVQAAILHGDKSEEVQDLLLLDVAPLSLGIETAGGVM TALIKRNTTI PTKQTQTFTTYS DNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDIDANGILNVSA ADKSTGKENKITITNDKGRLSKEEIERMVNDAEYKNEDEKQKTRISAKNALESYAFHMKSTVEDEKLD KISADDKKIIIDKCNEIHWLDANQLADEEEFQHKQKEIEGVNCNPIITKLYQGMGGAGGMPDFSGAAGAG AQHSAGTGGGSGPTIEVD</p>
<p>Heat shock protein 60 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: ACL00842</p> <p><u>Domains:</u> -Cpn60_TCP1 : 45-548</p>	<p>LGUN_random_Scaffold791: 163741:171751: BGLB013300</p>	<p>MLRVASVFRSSATRQLVPM LCRHYAKDIKFGSDARALMLQGVDLLADAVAVTMGPKGRNVILEQSWGSPK ITKDGVTVAKGIDLKDKFQ NIGAKLVQDVANNTNEEAGDGTTSATV LARSIAKEGFERISRGANPVEIRR GVMLAVDAVVEHLKMSRQVTTPEEIAQVATISANGDKSIGELISSAMKKVGRDGVITVKDGKTLKDELE TIEGMKFD RGYISPYFMNTAKGAKCEFDALVLLSEKKISSIQSIIPALELANQARKPLLIVAEDVDGEA LSTLV LNRIKVGLQVCAVKAPGFGDNRKNTLIDMAIATGGVVFGEENLYKLEDIQMQDFGNVGEVTVTK DDTLLMKGKGNKADIEKRIAQKDEIEISTSEYEKEKFGERLAKLSNGVAVLKIGGTSEVEVNEKKDRIN DALNATRAAVEEGIVPGGGTALLRCISVLDSVKTENEDQITGVNIIKALRVPALTIAQ NAGVDAHVVVE KVLNSSGDIGYDALNNEYVN LIEQGIIDPTKVVRTALVDAAGVASLLTTAEAVVVLDLPKEEKEAGMGGMM MGGMGGMGGMM</p>
<p>Biomphalysin [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: AGG38744.1</p>	<p>LGUN_random_Scaffold10: 1097564:1099282: BGLB000137</p>	<p>MFLQIFVAVTLVQVSSQCTYSSWWYSFDTPGQSKCNEINSYINALDRNDVNWADDALSNLEGVQCCRPP APWNNVEQQVYEDWTATLDSYTWAFCRVGYFLQLGLYRSDTGWPRFKGYLFNLESARCTK PANHPLNYG TCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLKKIRCCTPAAKPLEMDEKSKIQTRIMDTTLW NMATLAHYMGYGCYGC HGLAVGEDFTRNGFTWAADTRTFWGWKCEGDKNGERLNLVFGDWGFAVKEIY</p>

<p><u>Domains:</u> -Signal peptide: 1-17 -Aerolysin: 195-531</p>		<p>GKSVIEDLQAESVDSGVLYNRASSPVTESIERSKTIQETITHSTTSTFTNSHGLGVELEFEIASVKGKAS YKTRFEYSTSTTNSKSISETQGFTKQSSITLGPMEGAKYEVIMSKSRTTVPYTAIITTKFSTEMKGFLRW EDGNGNFHQDYRTNSGRPTFNRYRFGDSSVPFYKALKKQSDNNEGVMMWGMLFQKFPDARRVTNRLTDEQ YQFTLAGKLEKVEGTSVNVKWEKMKLNRRDVSNGNDEPGSNITTYIAASGPADKPAVVEYPKVNLLNKEPF KPIEIPVTEVKV</p>
<p>Dermatopontin 2 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: AAZ80786</p> <p><u>Domains:</u> -Dermatopontin: 11-156</p>	<p>LGUN_random_Scaffold8114: 1204:2972: BGLB013420</p>	<p>MASVASAAYVNDWDQPFNFRCPDGQVVSIVSSIHNNRREDRRWEFLCRSTRQTHSCTDSGYVNDQDFGLV YTCPGNKVMGVHSHYHNNRREDRRFGFYCCDVQGSTPRDCYTTNYVNDWDEKLTLVVPEGTAVKAAAYSHH DNRREDRRWQFQICTL</p>
<p>PREDICTED: Millepora cytotoxin-1-like [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013061974.1</p> <p><u>Domains:</u> -Signal peptide: 1-24 -Dermatopontin: 29-174</p>	<p>LGUN_random_Scaffold7789: 3993-4096, 5800-6107, 8666-9418</p>	<p>MPRMERYISIVLCSLLVLTNVHCVTYQTEEQEDWTECAPNHVITDIVSDFFSDDLWNITCAPIRPKI NITECVWSNYHNAPQYDFLFDPCPMNSILAGISSFHRSRDRVFKFYCCTNKDYLHVACQHHTLTINNAKGFI SFRVPEAMYVRGLFSSYDSTAGDRLYRIHLCKLDPADPTVECPTELTQAVTKLVNQETPLLESESED</p>
<p>PREDICTED: uncharacterized protein LOC106068782 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013083706.1</p> <p><u>Domains:</u> -Signal peptide : 1-20 -Zn-dependent metalloprotease, ADAM-like or reprolysin-like subgroup: 31-228</p> <p>PREDICTED: ADAM family mig-17-like isoform X2 [<i>Biomphalaria glabrata</i>] (42%); XP_013069827.1</p>	<p>LGUN_random_Scaffold286: 44298-44384; 42897-42974; 39464-39607; 36011-36117; 34918-35050; 34015-34151; 32322-32458; 31272-31438; 29557-29654; 27862-28646</p>	<p>MVRRIAVLLCLSILVMTSSCQVQNLVAEYVVVEDSTVQSYAQSSPAQTIAEATNSLRNDIDLVTQTN VLLSSLVQYGINIEVRKRKVDILSTNIINTFLETTYIADSSAAKASFQSWLNLQNAAYSTLNYDFAVLWT GFDLFGTSGIFENSITSAAMCKSTGVSVMEFDPTARDIVATAKIIAYLLSSLNDGITSTYIMAIINAPD DANRWFYSNSSAQSIKEFVALPRASCLLSTNSASVKPAVYATYTGSLDPPVICQRSLNDSRSYMCKSL PQIYNNQPPKGNAVCSQIYCRIPKTSICTPAFTSDGMICENQKRCTKGQCSSYPTSPVDPNCLWGDQKTL DYPLIPFSGTCKPFLDTYGAANCYTRPINETCCNTCKTYNSGIPGCEYGDKSSACVLFTQAQVCPYKNT LCCNYCRNYVGRRSVPEGGYPELTPSPQQNVTEVPVVG DYLGKRR</p>
<p>PREDICTED: uncharacterized protein LOC106068784 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID : XP_013069827.1</p> <p><u>Domains:</u> -Signal peptide: 1-21 -Disintegrin and metalloproteinase: 90-333</p>	<p>LGUN_random_Scaffold286: 70002-70112; 67477-67586; 65313-65458; 63714-63819; 62425-62557; 60967-61102; 60466-60602; 58410-58575; 53454-54138</p>	<p>MWSPAVILCFALLVLTKSCQGQTYVLEAYIVADDSAVQNQVREIATTESYSVKYTKAVANLRKDIDYIVT QVNVLLGSLSQNGVTMEMRIRRLDILSGNIITTFMPGTSYVVDSIVARNFQNWLNQAYANINYDFAL LWTGFNLYGTSGLDNSITNVAQMCGAAGITVVEFDPTAREAVATARAIGNLLGASNDGALSTSIMAIIN APGDVNRWSYSTCSASSIKDFIKLPKASCLLTNIASITKPSVTFSSYTGNLFDPIICQALNDSRTYMC KSLPQIYNNLLPKGNAVCGQIFCRIPNTMTCTPVYTS DGLVCDNQKRCSLGQCSSYSTPVVDNTCVFGDQ KKLEFPAPVPFYGTCAQAFISQYGA VNCYSSPINESCCSTCKSYNNGRVGCEYGDRLDCVKYTKASICPTY KNTLCCGYCYNVYVGRSPSDEPVPKLNITLPIKIQEPDIMPFEFNSQP</p>

<p>PREDICTED: ADAM family mig-17-like isoform X2 [Biomphalaria glabrata] (44%) XP_013069827.1</p>		
<p>PREDICTED: ADAM with thrombospondin motifs 9-like [Biomphalaria glabrata] (100%) Sequence ID: XP_013075983.1</p> <p><u>Domains:</u> -Metallopeptidase :36-152</p>	<p>LGUN_random_Scaffold16032: 213-334; 1737-1893; 3892-4003; 5778-5914; 7097-7228; 10218 -10401</p>	<p>MYGVNVEARIKKLDILSSNIIPSSALLPGTENVAPSENAMATFENWLVAQNSYNNIQYDFAIFWTGYDLR DAEDLEGRTHIGTICDSRYAVSMSEFDRTYHTALLTAQQISELLGSQHDGVLSSITNRWFFSSAVAGDIK NKLASLSPNCLLTTSATSTKPFVEVYEDGHILNPDITCQRRNLNYTNSYMCTGWHLYNQATGGDRVCTT IYCNEMDEVNCKRIETPEGMICESGKRCRHGSCVVDIHTPTNIDPSCVFGDQKEVTLGNFTGTCHEYIRM FSARVCYNSFVNQVCCMSCKAHTGT</p>
<p>PREDICTED: Serpin B6-like protein [Biomphalaria glabrata] (100%); Sequence ID: XP_013077880.1</p> <p><u>Domains:</u> -Signal peptide: 1-27 -low complexity: 50-61/ 63-76 Serpin: 92-458</p>	<p>LGUN_random_Scaffold1827: 27197-27439; 31889-32190; 39463-40100; 39670-40571; 39564-40002</p>	<p>MNTRSRLVVLVFLVLLAVIALTKRADAGDEQELSAAKNEISRYRRTLLSRNRGGNRDRDRNRTKQKGGKGN NSKKQKLSPEERIGVANSHVALNVFTSLYPSINSNTIFSPHSLHTALAMTMLGAKKDTKKEFYISLGLKA AKVGKSEVHGIIYKLLQSLSSRPDIILSYANSVYVKSGLLKKKFRGLTTHYHAKVDNFMNMTDPEGPER SINAWVANATRGKISDILKKGVDNINTAMIIINAVYLNASWAIQFQTFNTKPKPFYSLNSGVQTIPTMHI VQFYNYANHHDEVIELNFNGLAMYLPSAKSNLNQLLQNMKASSALANPFDELLTGLERRNLNLSL PTFKIQSDVIDLVPALKNLGLKAFNSSQADFQKQKLFQKAVISVNETGCEAAAATDVIFGL KSSRPTPALEVKKVDRPFLYVIRSKAQKVVLFMGTFVGV</p>
<p>PREDICTED: 14-3-3 protein epsilon-like [Biomphalaria glabrata] (100%); Sequence ID: XP_013082420.1</p> <p><u>Domains:</u> -14-3-3: 4-245</p>	<p>LGUN_random_Scaffold260: 178321:180720: BGLB007883</p>	<p>MADREDNVYQAKLAEQAERYDEMVSMMKVAQQDTELVEERNLLSVAYKNVIGARRASWRIVSSLEQKD EGKVSEKQITREYRKQIESELNSICHDLVSLVIDNLLIPNAATGESKVFYKMKGDYHRYLAEFATGND RKEAAENSLVAYKAASDISMTELAPTHPIRLGLALNFSVFYIEILNSPDRACRLAKAAFDDAIAELDTLS EESYKDSTLIMQLLRDNLTWTSMDMQGENDGGEEQQTVDIEGEDAS</p>
<p>PREDICTED: transforming growth factor-beta-induced protein [Biomphalaria glabrata] (100%); Sequence ID: XP_013079848.1</p> <p><u>Domains:</u> -Signal peptide: 1-17 -FAS1 (fasciclin-like): 59-158/ 195-296/ 376-476/ 513-614</p>	<p>LGUN_random_Scaffold209: 176383-176605; 177276-177462; 179882-180008; 180681-180831; 188684-188904; 189702-189891; 192064-192299</p>	<p>MKYFCLVITVVISLTKGQTVTPFPDVVSALTASGHFETFLDLLKPSGLLERINSSSHFTLFAPTDDAFK LPADTFNALKSDPIQLALVLGYHVVLSSSFKAGTQQDVLKSSNGLPIRINTYSLIHSNAASGVNITLKN IPVVHGYIQGVNTVNLNPPIGNIVQIAMNRTDLKFTTSWVVSNNLVQFFLNDDDVTFLVFNDDAIKLSPT TLDYLNHPSALADVLKYHVMSDYTLFTIGMTHSMTLKSADQHDLMLLEDGNGGLFVNHAKIVERDIA CIEGVLHIIDNVLIPPHVLVAIQDTSVAVGKQKQIMKSIYLLAVLLLKRGSQTTAPPLPDVEDVLAAD SRFTTFYQLLKTDDLLEINETNHFTIFAPTDAFAKLPAGSLDALKADVDKLKETIGYHVVLNSSYHVH GSQQDSILKSSTQLPIRINTYSLAHTVTAEGVNITIRNISVNHGYIQGIDGVMKPPTGNVVDLGTTRSDI STFESLLVKANQTAYFTSDHSTTLFIPTDDAFKLSAETLDYLNHHISDLTDVLRFHVYVKQYSLSLGMK HAFTIQSADHSHDYLMLEDDNGGMRVNQAKIIEKDISSINGVIHIIIDDVLIIPRVLVAIRDQSIVVG</p>
<p>PREDICTED: neo-calmodulin-like protein [Biomphalaria glabrata]</p>	<p>LG27_random_Scaffold161: 16903:18554 :BGLB001498</p>	<p>MAEQLTEETIAEFKEAFSLFDKDGDTITTKELGTVMRSLGQNPTAEALQDMINEVDADGNGTIDPFEFL TMMARKMKDTEELREAFRVFDKDGNGFISAAELRHVMTNLGKLTDEEVDDEMIREADTDGQGQVNYD GECHSASYHMLLHLPRGFHPPQRSS</p>

<p>(100%); Sequence ID: XP_013067017.1</p> <p><u>Domains:</u> - EF-hand, calcium binding motif: 12-40/ 48-76/ 85-113/ 121-150</p>		
<p>PREDICTED: GATA zinc finger domain-containing protein [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013076718.1</p> <p><u>Domains:</u> -Signal peptide: 1-25 -Cu-Zn SOD : 352-497</p> <p>Superoxide dismutase (Cu-Zn) [<i>Megathura crenulata</i>] CAF22060.1 (40%)</p>	<p>LGUN_random_Scaffold1689: 27317 -27807; 36361 -36477; 37754-38211; 52024-52107; 66296-66541; 76688 -76877</p>	<p>MKPMQMFNLRVLFVSVILVILSVHCQKFSKKGKHLNEQYKPNLIKENKFINIGGNVSLNDTIEQNITSE ETQDNKENMNETISLKTVNAKENVTSVETQMTSQIEFLNASNHISDLDIVNITQDETLSNSSESYKKPS TSCDCHVHHLMDKLLKDLSSMRTYVKERHNPIQIHQYKGEKIKSSQMSEPSKDNDKELGKGTQDQSKS YSKQLNKNDDDLQDQHVHVHSGNLRHNHNSKYNHHSLSLNQDLRRNYQNGHSNVKYKPKNTKFHNQITHD HYEPSVSRQRHFQVQETHIHLNIQVSGRNEEDAKEKERHKMSVEQIKKEGLEKDLTAKNEIPIFARCDM KTYNSGHNISGTVFLHQLPGQYLKVEVQLHGFSVQSNHRSTDIKEEKQFLNLSNDISLNKQLHGFHVHE FGDSKKGCHSMGGHFNPEGVHHGYRNNSHGHVGDWGNIDVDMYGDSSNSNFTVQAASLIGPNSILGRGIVV SLHAITHKELLECEKVDG</p>
<p>PREDICTED: uncharacterized protein LOC106059379 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013072448.1</p> <p><u>Domains:</u> -Copper type II, ascorbate-dependent monooxygenase: 1-100</p>	<p>LGUN_random_Scaffold1196: 16772-16869; 15959-16119; 14884-15048; 11587-12745</p>	<p>MSIQLYRNKVLIIYNLTNDELYNLDAPVTHYPKQHVQILPGDEIITRCVYNTTSAATSDPSGQVQGEMCYG YLNVYPQSALRIPDGTCVASTLSYCERSQSIPVDGCDWKTFLSYGDLELIDMYCQLRSSCQLQGSKRV QSSQNNASSPSHDFSSILSIDDTSISMKSNVTDGRVSKGSTDNISATQNNNTDFNSQSIPSDNSIVPN ISLFDVNTQNTTYSSSLIEANTTSVNHSASLADASIVKILSSDSIGNINSQVENYFNETIKHFAGKMSVN QTASNDLDLLETQRQDTSNITSTAHLGGVQLNATLSAKDKVAETRNSSNGLTSTYHNSDTGHISTTHI NNKGQISSTSVDLGHVSTSFIDSNGAICTVYIDSNVSTSYNDGNGRVSTTHIDRKGQISTHLDSDG HISIRIDSKGLVSTIRTDSKGRNSKRDDTSVEVGSYTYGDSIGHVEPKPSVRNETASQSLELFSNPKD IFHNKAISVHKVACYLSFYMCILQIIVTLRL</p>
<p>PREDICTED: uncharacterized protein LOC106079481 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013096101</p> <p><u>Domains:</u> -EF-hand, calcium binding motif : 44-72/ 105-133</p> <p>Calcium binding protein 1 [<i>Biomphalaria glabrata</i>] (37%); Sequence ID: AAV91525.1</p>	<p>LGUN_random_Scaffold6449: 3374-3477; 6563-6717; 7143-7387; 8008-8087</p>	<p>MMFLLALIPALALAQTADLTVTIDGVFDALDYDFDNEIARDELTKFFQTYDANHDNRISRADYTAID ENFPNETHDPIITNAYRNLFVDVLDNNKNGFIEPNLDLDAVFRNADDNNNGVVTRAEFHKYFNEIFFLVLG</p>