

S6 Table. Protein sequences, identified domains and genomic locations in VectorBase of other immune-related NMRI and BS-90 *Biomphalaria glabrata* plasma proteins eluted from larval transformation protein (LTP) 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)/LPS-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>MLLINLLGHYFNSFRLENVAIPDIDMSFNPVQRGLTMNLRNLGVDVLLDYRVRYKLLFVPISNSGGVSVN FRGVELTATVGIQDFEDTSPRLVSRSCSAAGDFNINFGSMAWLLNLLKGLFRGKIRDITIRSKICKDKVT EAINTQGADKLRQIPLESADIADKFVIDYRLLSPVLFTDSYLETQHKKLYKRGTLGYAAHTHGYLQYVISP DKLPAQSKGFLNTPCPSACAGTLIPLLAEKYPNSFVLTISSSKAPDFNITSNGLGLTYGLTDLSTTS ASAVVTANVVISIAGAAFVRNDRIVGNVAQFRTVLADIDSQRLISLYTFQISSINKALDDGMNMVVIPQL 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;</p>	<p>MRMKNLNLILVFYLVFQEQCGGKYFISAPRNVPVPGTAYDISVDILKQDIGNVTEAILQDYSFSIPEGPK SLLTANGTFSPGVRGTLSPIDFNLHCSYCRILLKGYNPLQFEQDIFIQISSDILSIQTDKAIYKPKKE RVNFRILAVYYNLQLYTGTFFHYEILDYDNDKINVLVSGVSGTFFGVVEGFFDLSDQPSFGTWKINVRTETVS GAESQFFEVAEYDLPRFQVDVGLPPFALLSDDTTLVSGSVEAKYTFGQPVYGLVLLQIGENVDTIDKCNVNR KVTEISFEIKGKGNFVPLEDIRRSVHLNEKKIKITAFVIEASTGIKLNSSVITYYGNRYQIKFLEMT PAVFKPGLQYTAYVQVTPDGLPPTESNLSVYTSVYQMTVPDQELYSPPSFGSYPLPGQNMSLPAN GILSIDIDIPLNATSIDIKVSLNKQTTAEKRISKSYMSNNYLQLSLLSKLVKAESDVLIKITSTEIDS LAYEIRSRSDHVKSGVLELNQREFNATFKVGPSWAPIAQLLMYYIRRDSNEIVTDSLAFNVEGMFENKV NVAFKENETDINKNVSELSADSDSQIYVLAVDQSVLLKGTNDLTPNKVKDSFISKFHKGEVPTDSNFA LSYSGSSINEVFSNMGLVIATDLNIFAPFRPIALGRFPSSGFDRQGMGAPMAMSRDDNAMESASFEMD VATSTKPVERVRSFFPESWLWTSVKSINGHATLTTTVPDTITSWIVSAFATNSDTGLGVAPTTSKLRVFR PPFVSLTYPRSVTRNEQFIVQATVFNYLPVDMVTVSLKENPFLTPIPGPNQASNIQVRANEQGIVYF SLSALTVGSLDTEVSARSNMAADAIVRQILIKHEGAPVVYNNPILINLSNNQSTFEKNIAFTLPDSLVE SQRIRVKVTGDLIGSTVQSLTLLPTGCGEQSLVKFTPNIHIGRYLKATNQLSEELNKKIIDLLNDGY QRQLTYKRYDNGFSAFGNYSSTWLTALVVTSFAEAQEFIFVDKEILKASMLLIDRQNIDGSFNEFG KVLDRNTQGTTAGPALTAFLVALLKAKELADVQDCKNNNKCRYLLGNATLNATRNLERLMLADSIDD QFSLAVASYALAEAKSQLAQSTFEKLLTFVKQEGGLEYSANSTVNNEELNRFINWRPRLQARPIDILI TSYAILTYSSLGRLDEALPSVRWLTLLQNAQGGFVSTQDQTVVGLQALSFYGSKSRPDTNITIYVSDMNT HLTMMNVNSENALSQIQEIQNSQDFSITASGSLALLDIEYSFNVLKELSKPVFDANTVLLDDKLDLDFN</p>

	<p>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: 8533-8740; 5514-5738; 11544-11696; 11926-11989; 12187-12304; 13837-13988; 15855-15963; 16394-16478</p>	<p>IMVCTKFLMKHDTGMVVQELSIPSGFVDPDLSTLGQVAGVKRSEKSGSIVAIYFDKISGSSLCYSIVMTRE AKVAKSQKSYVRTYDYYEPANQATVFYQPRTLRDSTVCDVCLNCCP</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:</p>	<p>MRMKNLNLIFVFLVFQECQGKGYFISAPRNVVPGTAYDISVDILKQDIGNVTVEAILQDYSFSIPEGPK SLLTANGTFSPGVRGTLSPIDFNHCSYCRILLKGYNPLQFEQDIFIQISSDILSIQTDKAIYKPK RVNFRILAAAYNLQLYTGTFFHYEILDYDNKINVLGSGTGFVVEGFFDLSDQPSFGTWKINVRTTETVS GEESQLFEVAEYDLPRFQVDVGLPPFALLSDTTLSGSVEAKYTFGQPVYGLVLLQIGENVDTIDKCNVNR KVTEISFEIKGKENSFVPLEDIRRSVHLNEKKIKITAFVTEASTGIKLNQSSVITYYGNRYQIKFLEMT PAVFKPGLQYTAYVQVTPDGLPPTDSNLSLSVYTSVTYQMTVPDQELYSPSSFSGSYPLPGQNMSLPAN GILSIDIDIPLNATSIDIKVSLNKQTTAEKRISKSYSMSNNYLQLSLLSKLVKAESDVLKITSTEIDS LAYEIRSRSDRVKSGVLELNGQREFNATFKVEPSWAPIAQLLMYYIRDSNEVVTDLAFNVEGMFKNKV NVAFKENETDINKNVSLELPADSDSQIYVLAVDXSVLLKGTNDXTPXKVKDSFXSFXHKAIPDTSNFA LSYSGSSIXEVFSNMGLVIATDLNIFAPFRPIALGRFPSSGFDRQXMMGAPXAMSFDDXAMXSASFEMD VTTSTKPVERVRSFFPESWLWTSVKSINGHATLTTPDTITSWIGSAFATNSDTGLGVAPTTSKLPGFR PFFGSLTYPRSVTRNEQFIVQATVFNYPVLDLMVTVSLKENPFLTPTVTPGPGNQASNIQVRANEQRTVYF SLSALIVGALDIEVSARSNMAADAIVRQILVRHEGAPVVYNNPILISLNNQSTFEKNIAFTLPDSLVP SHRIRVKVTGDLIGSTVQSLTLLPTGCGEQSLVKFTPNIHIGRYLKATNQLSKELNKKIIDLNNNGY QRQLTYKRYDNGFSAFGNLDSSSTWLTALVVTSFAEAEQEFIVDKEIILKASMLLIDRQNLDGSFNEFG KVLDRNTQGTAGPALTAFLVALLKAKELADVQYCKNNKCRYLLGNATLNATRNLERLMLADSIDDQ FSLAVTSYALAEAKSQLAQSTFEKLLTFVKQEGGLEYSANSTVNNEELNRFINWRPRLQARPIDILIT SYAILTYSPLGRLDEALPSVRWLTQLKNAQGGFVSTQDQTVVGLQALSTYGSKFRPDTNITYVSDMNT LTMNVKSDNALSLQIQEIQNSQDFSITASGSLALLDIEYSFNVKELSKPVFDVNTVLLDDKLDLDFNI MVCTKFLMKHDTGMVVQELVSIPIPSGFVDPDLSTLGQVAGVKRSEKSGSIVAIYFDKISGSSLCYSIVMTREA KVAKSQKSYVRTYDYYEPANQATVFYQPRTLRDSTVCDVCLNCCP</p>

	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: 8533-8740; 5514-5738; 11544- 11696; 11926-11989; 12187- 12304; 13837-13988; 15855- 15963; 16394-16478	
<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>	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	MESLHFLFYSQLPADLPSSSTYTLNVKGSGLTFDKSENLYNNKETSVFIQLNKAIFKPGDVTNFRVFGV YSDLKSYTDPIDISYDANSNKIKQWLKVTPTNGVITQELTSTQPVLGDWVKISVDAGRTKEEKVFTVAE YVLPKFEVDVVTPSYALTTDNDVTVTVKSKYTYGKPVNGTADVLVKLHESFNTFDYSRALPVTTLQVPLN GEAK VIIIPMSQVKAISANLNQHVLIVIANVTESLTGNQMSGNGTVTLYDKGVKLDFFASNPKTFKPALQY IAYLK VTQPDGLPMTSTAEQVK SIRVTAELPGTTPPYWYVPPTESRDLPALSLAIPDNGLVAIPVDV PADAKDVHVTANFQGVSKELTLGKSHSPNSYIQLILKSGSVIKFQLSRGGIVKTGTVDANGQLVYQFS IPSDSSMAPNARIVLYVRADGEIVTDSISFDISGAFKNKVSIDLKTDVEPGDDVTVTKADPDSTAYC LAIDQSVLLLKGGNDVTDNDVYTELKEYDTITESGSNKGIIDCPMCKRRKRMIWWPFPTYGGSDAQQIF SNAGVVVLTDATVYHYQEPIHLFNIPNFFQCGRSLNQLRKRCFASFSPVMNLVSSVSDPITLPVTETE TKTEDLQPTKTRSNFVETWLNWNSLDIGANGSASITATVPDTITSWVASAFAINSASGLGVAPTQAHLRV FRPFFVSLNLPYSVTRGEHLALQANVFNYMTEDMQVRVTLAKSDNFFNIEIDANGAEVLKQVESVQDVMI KAGEAKSVYFPIVPADLGKIDIEVKAQSTKAADAVRRQLLVEAEGVPKIYNVPLIDLTEGKTSFSKTVD LTLPSNTVKGSELARISAVGDLMGPTIAGLDSLLQMPTGCGEQTMIGLAPDVYVTDYLK SVNQLSGDIQT K ALSVMESGYQRELYKHTDGSFSAFGNSDASGSMWLTAFAVTRVFKQAKAHYIDDEVLIKAIQWMVSKQ NANGSFPEPGNVIHKNMQGQAGSGVGLTLFVLISLLENKDLLVNTNAAGILVDEARQKALVYAEQEVAKT DDLYILNMAAYAFQLANSSQVQTVLSKLEQKATVKDGRKYWHQPEQKTTNTWDYPNPTKAVDIEMTSYA LLTYAARGNIVAGKSIMQWLTEQRNSNGGFSSTQDTVLALNALSEFAKQTYSNFNVQITTLNATTSYT FNIDKTNSLLLQSRTPNVPSQVKIDATGSGMALVQVAVSFNVESEIFETFDLTVKLIETINNLVET CAKWLGSQPSSAMAVQEIGIPSGFEADIESIPQLDILKRIETQNKVILYFDQIGTTPVCLNFRAVRTGL VAKSQPAAIRVYDYEPNQTAFYQSQILKDDSTVCDVCKECDNCV

<p>PREDICTED: complement C4-like (LOC106078805), [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013095289</p> <p><u>Domains:</u> -Alpha-2-macroglobulin-receptor: 12-96</p>	<p>LGUN_random_Scaffold6063: 21546-21671; 19546-19697; 18165-18273; 17575-17738 / LGUN_random_Scaffold7260: 12179-12304; 13837-13988; 15855-15963; 16394-16557</p>	<p>MVCTKFLKHDTGMVVQELSIPSGFVPDSTLGQVAGVKRSERKGSIVAIYFDKISGSSLCYSIVMTREA KVAKSQKSYVRTYDYYEPANQATVFYQPRTLRDSTVCDVCPNCCP</p>
<p>Biomphalysin [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: AGG38744.1</p> <p><u>Domains:</u> -Signal peptide: 1-17 -Aerolysin: 195-531</p>	<p>LGUN_random_Scaffold10:1097564:1099282: BGLB000137</p>	<p>MFLQIFVAVTLVQYVSSQCTYSSWWYFDPGQSKCNEINSYINALDRNDVNWADDALSNLEGVQCCRPP APWNNVEQQVYEDWTATLDSYTWAFCRVGYFLQGLYRSDTGWPRFKGYLFNLESARCTKPANHPLNYG TCQDIDVSSCMGRKGQCSCPGGYFLTGLYRADGDDLYFLKKIRCCTPAAPLEMDEKSKIQTRIMDTTLW NMATLAHYMGYGCYCHGLAVGEDFTRNGFTWAADTRTFWGKWCEGDKNGERLNLVFGDWGFVAVKEIY GKSVIEDLQAESVDSGLVLYNRASSPVTESIERSKTIQETITHSTTSTFTNSHGLGVELEFEIASVKGKAS YKTRFEYSTSTTNSKSISETQGFTKQSSITLGPMEGAKYEVIMSKSRRTVPYTAIITTKFSTEMKGFLRW EDGNGNFHQDYRTNSGRPTFNYRFGDSSVPFYKALKKQSDNNEGVMMWGMFLQKFPDARRVTNRLTDETQ YQFTLAGKLEKVEGTSVNVKWEKMKLNRRDVSGNDEPGSNITTYAASGPADKPAVVEYPKVNLNNKEPF 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>MASVASAAYVNDWDQPFNFRCPDGQVVSYVSSIHNNRREDRRWFLCRSTRQTHSCTDSGYVNDFDGPLV YTCPGNKVMGVHSHNNRREDRRFGFYCCDVQGSTPRDCYTTNYVNDWDEKLTLVVEGTAVKAAYSHH 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>MPRMYERYISIVLCSLLVNTVHCVTYQTEEQEDWTVFCAPNHVITDIVSDFFFSDRLWNITCAPIRPKI NITECVWSNYHNAPQYDFLDCPMNSILAGISSFHRSRDRVFKYCCTNKDYLVHACQHTLTINNAKGFI SFRVPEAMYVRGLFSSYDSTAGDRLYRIHLCKLDPADPTVECPTELTTQAVTKLVNQTETPLESESED</p>
<p>PREDICTED: uncharacterized protein LOC106068782 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013083706.1</p> <p><u>Domains:</u></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>MVRRIAVLLCLSILVMTSSCQVQNLVAEYVVVVEDSTVQSYAQSSPAQTIAEATNSLRNDIDLVITQTN VLLSSLVQYGINIEVRKRKVDILSTNIINTFLLETTYIADSSAAKASFQSWLNLQNAYSTLNYDFAVLWT GFDLFGTSGIFENSITSFAAMCKSTGVSMEFDPTARDIVATAKIIAYLLSSLNDGITSTYIMAIINAPD DANRWFYNSSAQSIKEFVALPRASCLLSTNSASVKPAVTYATYTGSLLDPVICRSLNDSRSYMCKSL PQIYNNQPPKGNAVCSQIYCRIPKTSICTPAFTSDGMICENQKRCTKQCSSYPTSPVDPNCLWGDQKTL DYPLIPFGTCKPFLDTYGAANCYTRPINETCCNTCKTYNSGIPGCEYGDKSSACVLFTQAQVCPIYKNT</p>

<p>-Signal peptide : 1-20 -Zn-dependent metalloprotease, ADAM- or reprolysin-like subgroup: 31-228</p> <p>PREDICTED: ADAM family mig-17-like isoform X2 [<i>Biomphalaria glabrata</i>] (42%); Sequence ID: XP_013069827.1</p>		LCCNYCRNYVGRRSVPEGGYPELTPSPQQNVTEVPVVDYLGKRR
<p>PREDICTED: uncharacterized protein LOC106068784 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013083707.1</p> <p><u>Domains:</u> -Signal peptide: 1-21 -Disintegrin and metalloproteinase: 90-333</p> <p>PREDICTED: ADAM family mig-17-like isoform X2 [<i>Biomphalaria glabrata</i>] (44%); Sequence ID: XP_013069827.1</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 QVNVLLGSLSQNGVTMEMRIRRLDILSGNIITTFMPGTSYVVDSIVARNSFQNLNLQAYANINYDFAL LWTGFNLYGTSGLADNSITNVAQMCGAAGITVVEFDPTAREAVATARAIGNLLGASNDGALSTSIMAIIN APGDVNRWSYSTCSASSIKDFIKLPKASCLLTTNIAS TKPSVTFSSYTG NLFDPDIICQRALNDSRTYMC KSLPQIYNLLPKGNAVCGQIFCRIPNTMTCTPVYTSDGLVCDNQKRCSLQCSSYSTTPVVDTNCVFGDQ KKLEFPVAVPFYGTCCQAFISQYGAVNCYSSPINESCCSTCKSYNNGRVGCEYGDRSLDCVKYTKASICPTY KNTLCCGYCYNVVGKRSPSDEPVPKLNITLPKIIGQEPDIMPFEFNSQP</p>
<p>PREDICTED: Serpin B6-like protein [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013077880.1</p> <p><u>Domains:</u> -Signal peptide: 1-27 -Low complexity: 50-61/ 63-76 Serp: 92-458</p>	<p>LGUN_random_Scaffold1827: 27197-27439; 31889-32190; 39463-40100; 39670-40571; 39564-40002</p>	<p>MNTRSRLVLLVFLVLLAVIALTKRADAGDEQELSAAKNEISRYRRTLLSRNRGGNRDRDNRTKQGKKKGN NSKKQKLSPEERIGVANSHVALNVFTSLYPSINSNTIFSPHSLHTALAMTMLGAKKDTKKEFYISLGLKA AKVGKSEVHGIYKLLQSLSSRPDIILSYANSVYVKSGLELKKKFRGLTTHYHAKVDNFMNDPEGPER SINAWVANATRKGKISDILKKGVDNINTAMIIINAVYLNASWAIQFQTFNTKPKPFYSLNSGVQTIPTMHI VQFYNYANHHDETEIENLNFNGSQLAMYILLPSAKSNLNQLLQNMKASSALANPFDELLTGLERRNLNLSL PTFKIQSDVIDLVPALKNLGLKAFNSSQADFKGIAKQKFLDKVVIQKAVISVNETGCEAAAATDVIFGL KSSRPTPALEVKVDRPFLYVIRSKAQKVVLFMGTFFGV</p>

<p>PREDICTED: neo-calmodulin-like protein [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013067017.1</p> <p><u>Domains:</u> - EF-hand, calcium binding motifs: 12-40, 48-76/ 85-113/ 121-150</p>	<p>LG27_random_Scaffold161: 16903:18554 :BGLB001498</p>	<p>MAEQLTEETIAEFKEAFSLFDKGDGDTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFL TMMARKMKDTEEELREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDEEVDDEMIREADTDGGQVNYD GECHSASYHMLLHLPRGFHPPQRSS</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>] (40%); Sequence ID: CAF22060.1</p>	<p>LGUN_random_Scaffold1689: 27317 -27807; 36361 -36477; 37754-38211; 52024-52107; 66296-66541; 76688 -76877</p>	<p>MKPMQMFNLRVLFVSVILVILSVHCQKFSKKGKHLNEQYKPNLIKIKENKFINIGGNVSLNDTIEQNITSE ETQDNKENMNETISLKTVNAKENVTSVETQTMTSQIEFLNASNHISDLDIVNITQDETLNSSESYKKPS TSCDCHVHLLMDKLLKDLSSMRTYVKERHNPIQIHIYKGEKIKSSQMSEPSKDNDKELGKGTQDQSKS YSKQLNKNDLQDQHVHVHSGNLRHNHNSKYNHIHSLNNQDLRRNYQNGHSNVKYPKNTKFHNQITHD HYEPSVSRQRHFVKQETHIHLNIQVSGRNEEDAKEKERHKMSVEQIKKEGLLEKDLTAKNEIPIFARCDM KTYNSGHNISGTVFLHQLPGQYLKVEVQLHGFVQSNHRSTDIKEEKQFLNLSNDISLNKQLHGFHVHE FGDSSKGCCHSMGGHFNPEGVHHGYRNNSHGHVGDWGNIDVDMYGDSNSNFTVQAASLIGPNSILGRGIVV SLHAITHKELLECEKVDVDFG</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>MSIQLYRNKVLINLTNDELYNLDAPVTHYPKQHVQILPGDEIITRCVYNTTSAATSDPSGQVQGEMCYG YLNVPQASALRIPDGTCAVSTSLYCERSQSIPVDGCDWKTFLSYGDLELIDMYCQLRSSCQLQGSKRV QSSQNNASSPSHDFSSILSIDDTSISMKSNVTDGRVSKGSTDNISATQNNNTDFNSQSIPSDNSIVPN ISLFDVNTQNTTYSSSLIEANTTSVNHASLADASIVKILSSDSIGNINSQVENYFNETIKHFAGKMSVN QTASNDLDLLETQRDQTTSNITSTAHLGGVQLNATLSAKDKVAETRNSSNGLTSTYHNSDTGHISTTHI NNKGQISSTVLDLGHVSTSFIDSNGAICTVYIDSNVSTSYNDGNGRVSTTHIDRKGQISTHLDSDG HISISRIDSKGLVSTIRTDKGRNSKRDDTSVEVGSYTYGDSIGHVEPKPSVRDNETASQSLELSFNPKD IFHNKAISVHKVACYLSFYMCILQVIIVTLRL</p>