

S3 Table. Protein sequences, identified domains and genomic locations in VectorBase of NMRI and BS-90 *Biomphalaria glabrata* VlgL domain-containing plasma proteins eluted from sporocyst membrane-enriched (Mem) affinity columns.

| Protein ID | Scaffold No. | Predicted Protein Sequence |
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| <p>FREP 2.28 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: ADK11410</p> <p><u>Domains:</u> -Signal peptide: 1-20 -lg: 38-148 -FBG: 181-382</p> | <p>500-1158: LGUN_random_Scaffold563550: 640-1300; rev. frame; 1994bp LGUN_random_Scaffold9301: 368-1028; 12407bp 199-502: LGUN_random_Scaffold534902: 1310-1613; 1684bp</p> | <p>MASLPLRLVLLVSMVTLIRSSSWLNFTGNSETIRELIQPLKLTCTFQISKNDSENDSQVLFMSIYHETKRVIASISKYQPVAT SLYPSVTKVQGGQIYHSNESKDSYLQVTWTHPKLSESGKYFCLAHAWNSTSQNSVFDADITVNVIKSSTDDLAVALSIIQD RLDKDGVDSIQISRASPTLPESCRDVISSDRVVVTLASGLKVMCDTKTDGGGWIIIFQRINGYVDFYRGWKEYRDGFG DYDIGEFYLGNEINIFKLTSSKKYDLRIDLEFNNTKYFAFYTRFEILGEQDYKQIGGYSNAGDALTNIHNDKFFSTYDKD NDLGTSGSCAVTHKGAWWYRDCYDSSLNGKWGSDRINWSKLTGITKSVTFTEMKIREIELN</p> |
| <p>FREP 3-2 precursor [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: AAK28656</p> <p><u>Domains:</u> -Signal peptide: 1-18 -lg: 28-134 / 183-301 -Coiled coil: 314-382 -FBG: 451-655</p> | <p>LG3_random_Scaffold2841: 18324:26062; BGLB000204; 253aa/ 655aa; 65764bp</p> | <p>MARLFLFILCVFVSLAGSELVIDVQPNVISPEITPQLVINCSITNNEVQTLDLIKSLTSLRYNETIREFDELIALDSLTLNLKQ FVRFKYSQISFGNRYITLILHNPTQFDARIYKCNATGTNSEGANISLFAKKAVEYETNSTALIEIRRIKKDENYCSFKKDDLS DSKQRSRVYFSGSSDIKERIEPLTKCTFQVLKTDQNETSRLQSLYLHESKGVIAVYVNDQPVVTSLQGSNIQDVEGEIYD NAIKDSYLQVTSNLSKHSSESGKYFCEAHNKYSEGRIDKSSNMLTITVERPTFDDLVEAMHKLFTQVDGAKESLKAINQNI KNINKDLDFEQNITSIKQEVIRNQNNIQLSEDLNIKEQNLTSIKADLSTKQQTFLNIKEDVILNQIIHKIKQDLNNTYRHN MSNIEEHLEVILTNLSTASIKVKNQTDGSGKMSYPPRKRCDVNSTDERVVVTLTSLGLKVMCDTKTDGGGWIIIFQRIN GNVDYFYGWKEYRDGFGDYNIGEFYLGNEINIMLTSTGQYNLRIDLKYNKAFFAQYSGFKILSEKEYKLNIGAYSGNS GDNFSSHNAFFTTFRDNDDEYSNCAVDYTGAWWYHSSCLNCLNGKWGSSDFAKGVNWDLSRFSSVSFTEM KIREI</p> |
| <p>PREDICTED: Ficolin-2-like [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013071685</p> <p><u>Domains:</u> -lg: none -Coiled coil: 12-53 -FBG: 71-280</p> | <p>LGUN_random_Scaffold11134: 377-790; 2673-3506</p> | <p>MLIVTVATATFDDLKVIQKLMKQADEDEKEIQENKQKIKNIQEDFDTRQQNLSPFKDILVNGKKDYKEMNTSDSILPD RPCNVNSTKRRLLVLNLASGLKVMCDTMTDGGGWIIIQRRIKGMVDFNRDWQEYRDGFGDYNIGEFYLGNEINIKLTS GNYELRVDLEINYSFYALYSKFQIMNESNKYKLIKISGYLGNATDSLAWHDNLFSTYKDNKNNIPNCLFKYPGGWW FGAGHGSLNGLVWRSRFRNQGINWYGLTGYKKSAYFSEMIREKY</p> |

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| <p>PREDICTED: Fibrinogen C domain-containing protein [<i>Biomphalaria glabrata</i>] (50%); XP_013072469.1</p> | | |
| <p>PREDICTED: Angiopoietin-4-like [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013069966</p> <p><u>Domains:</u> -lg: none -Coiled coil: 97-192 -Internal repeat: 202-286/ 286-363 -FBG: 403-563</p> <p>PREDICTED: Fibrinogen C domain-containing protein [<i>Biomphalaria glabrata</i>] (47%); XP_013093995.1</p> | <p>LG3_random_Scaffold99: 2047-3202; 5313-5785</p> | <p>MYIFHETNGVIATINKGQTVVTAIQEVGSNNVKGELSDEKLHESYLQVTWRNLRSSDSGKYFCGAHVIGSDGRAERLNE MVTIQVKLPTFEDLVNVIQKLLIQANDDREILQDNKQNIKSQNELRNNQDNVIKMYKDLNHEQNFIRIKKDLDSNQQ NIKIINQDLDNQKQNIIRINTDLSKEQQFTRFNKDLDSKQQDIIRIDKDLNATEHNITRINKDIDSKQQDIIRIDKDLNATE HNITRINKDIDSKQQDIIRIDKDLNATKHNITRINKDIDSKQQDIIRIDKDLNATKHNITRINKDLDSKQQNIIRIDKDLNATK HNITRINKNLDKQQDIISIKQDLESSKDFNEHRQNISIFKDILDVTIYNLSSSLTDVKQELTKELSDGKICISGHIHAASCRN VRSSDITYVFLPSGLKVMCDTKTDGGGWIIFQRRINGKVNFYRGWEEYRGGFGDFDIGEYFLGNENIFKLTSTGQYDLRIDLEFKNTKYFAQYEDFKVLSETEKYKLIQGDYSGYAGDDLSPHNNMFFSTFDRDNDGQKISTVHKVIKNQENLISD SK</p> |
| <p>PREDICTED: Fibrinogen C domain-containing protein [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013072469</p> <p><u>Domains:</u> -Signal peptide: 1-19 -lg: 27-141 -Coiled coil: 383-450 -FBG: 452-627</p> | <p>LGUN_random_Scaffold1199: 57142-57604;61307-61835; 65995-66891</p> | <p>MAHMHVHLTLCVVLVLSSELIIDVDPDIISLEITPQLVINCSITNNKQVHLDVMNSLTLRSYDKTIRDFIALITLDSSTLNLK QLTKFNSQVSFGNLYLALTLHYPTQFDKAVYRCSVNGNANGTDVLSAKKGVETNSTALIEEIRRLKDEDTYKCSF KKTDRPGSRVHFFASSEIIEKRIEPLTLNCSFQVSYLFIHFHNVFNNMSTPEAYETVEHILYEYRMLRNTIEDTTSFETERTG AWLGLTLYGDKRTLQNTGRDLVETNGVIATINKGQPVLTIIHGHSNSRNAKGEIFDNELKDSYLQVTLNQLQFSSESGKY FCEAHVKRSQGGVERLNKMLAISVLSPTFEDLVKIEKVLKRSDEDNIRIRENGQTLRNIQEDSDTKEKNIKSIEEDLNTKQ QNIISLKEDFNAFQRTMNTFREKLEVISANVSKIERERTEDKEIASCREVKTREERVVVTLASGLKVMCDTKTDGGGWIIFQRRTYGIIVDFYRSWQEYRDGFGDVSIGEFYLGNEHIYNTSSAKYDLRIDIKYNRNSYYAQYSDFQILSEKDKYKLGAYS GNAGDLSYHNNMFFSTYDKDNDLYGSNCATNYLSAWWYNSCHNSNLNGQWGSKVNSNGVIWNTLTKGESASFTEI KIREK</p> |
| <p>Galectin-related protein precursor (GREP) [<i>Biomphalaria glabrata</i>] (100%); SequenceID: AKS26835.1</p> <p><u>Domains:</u> Signal peptide: 1-20 lg: 28-133 /208-325 -Gal-binding: 473-610</p> | <p>LGUN_random_Scaffold_18083: 2985-3023; 2124-2167; 2738-2840; 1688-2124; 624-705; 123-183; LGUN_random_Scaffold_47310: 864-1192; LGUN_random_Scaffold_12074 1:407-476; LGUN_random_Scaffold_5606: 17851-18203; 15817-16198</p> | <p>MKRLLPLLLLTSLLQGSLTELIQVNPVTISPGLTPKLTVNCISNESVAELNAIQLSMSRYNETSKTFDVLTYIDKETLSLK QIVELKGAQISFGNLFILLTIPSPSQYDCQTYSCIANGYNKFNGNDSISTKVKVESRTNITEYIKEINRLKKLEANSIMEDNVP LKNIEKLILANMNIQMCSLTTNKTSEDIEKATLHFSVNSKTIKEFLEPMIMKCTFQVSKNNASQNLTVHYMYIRHETNG VLATISRDQQVGISQDTSLSQVQGLSDQDFNISYLQVIWIKPSPSQSGKYYVCGANIVNQEGQLEKLKASLEITIEKTSLED LVPIVIDLLAERTKVRHILEASMKEVIEIKQQVRSVIENVRLINQNSSTSFLVFSNIEFSGCKPNHTSQIKTLAINCLRNVC AALMCAKDLTCTPCDRSAISGLRFPDHGSEMYLKRSLVLSQVEKRLPPVLVLSIAVPSGLRAEDLIYFRVTLLKYDNFYID LYEDNYNINYQFRARCDQCSIKGDCSESDCKSKFVTIGSKTSGFWSRSFVTRDYPFVLNEEFEMYLIIHQSDVDVYIKD KLFANIKTPRKPEDVVRVIQFGGTIVLHELSL</p> |

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| <p>PREDICTED: Uncharacterized protein LOC106063810, partial [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013077728</p> <p><u>Domains:</u> -lg: 1-73 -lectin domain: none (N-term seq only)</p> <p>Galectin-related protein precursor (GREP) [<i>Biomphalaria glabrata</i>] (96%); Sequence ID: AKS26835.1</p> | <p>LGUN_random_Scaffold18083: 1688-2120; 624-705; 75-186;</p> | <p>MSLYNETSKTFDVLYTIDKETLSLKQIVELKGVQISFGNMFILLTIPSPSQYDCQTYSCIANGYNKYGNND SISTKVKVESRT NITEYIKEINRLKKLEANSIMEDNVPLKNIEKLILANMNMQMCSLTNTKTSIEDLIEKATLHFSVNSKTIKELLQPMIMKCTFQ VSKNDASQNFTVHYMYIRHGNKDTTIHWRIQEGGG</p> |
| <p>C-type lectin-related protein 2 precursor, partial (CREP2) [<i>Biomphalaria glabrata</i>] (98.5%); Sequence ID: AKS26832</p> <p><u>Domains:</u> -lg-like: 15-132 -Coiled coil: 142-174 -C-lect: 196-325</p> | <p>LGUN_random_Scaffold35213: 1403 -1468 LGUN_random_Scaffold34937: 746 -1051 (71.9%) LGUN_random_Scaffold205317: 1 -272 (98.2%) LGUN_random_Scaffold46202: 1045-1228 (100%) LGUN_random_Scaffold113935: 1-178 (97.8%)</p> | <p>FRELDLGSRLFTGNSETIKEIFEPLILSCSFQVAKHDVKENGNVILMYIFQETKGVIIATISKGQPFAYSTEPRHTFAQGNIG DEKLNKSYLQVTRKNPNSLESQYFCLAHVRDSAGKDKVFHASIKINIEKSNSDDLVPALGRVLERLDRIERQEATEQKIV DAQEDFNIQIGNLSSVLDQEKPKKEEDNVLCNAGFHKITDQGQISACVWVSNVSMNYIQARDDCKEKGALLTLKTQEK FTLLHKNDPGRYLWIGLTDRLIEDIFKWDDDNSICNPLCRGRLFSTGEPNDSGGEEDCVVYYPTRMKLNDNCCGSTNHY MCEHPI</p> |
| <p>C-type lectin-related protein 3 precursor, partial (CREP3) [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: AKS26833</p> <p><u>Domains:</u> -Signal peptide: 1-19 -lg: 29-145 -Coiled-coil: 226-251 -C-lect: 261-360</p> | <p>LG3_random_Scaffold2051: 76877-77044; 74469-74550; LGUN_random_Scaffold38320: 919-1386; LG3_random_Scaffold2051: 66872-67025; 63650-63835</p> | <p>MKTLHLVLAALCAFIVTVLCSPTVFTANSETVKEQFQPLILSCSVKVSQNEPIQDANVHLLYLHETKRIIARISKDQPVGTS QNPGSIQVQGGQINENKAMHSYLQVTWTPKFTDSGKYFCLAHVRNSTGQDNVLDADITINVGKLTTDDLTMVVSRLL ERVDEGEVKQEENRQNILSVEEDLTDRLVNTTIVVSRLLEEVNNGEEKQDENSRKLLMEEYVYNLIANLSRIQEALNQNI EKATLKMETTITTSRGNCKRGFDKITYGQLFACVWVSSAPLDFFGARDSCALGARLMTLKTTRDKFNLETNNVGNKE FYIGLTDVFTEGIFRWTDDDSISNLSSIQSFFRTGEPNDHAG</p> |

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| <p>PREDICTED: Uncharacterized protein LOC106065543 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013079834</p> <p><u>Domains:</u> -Signal peptide: none -lg: none -Coiled coil: none -C-lect: 144-283</p> <p>PREDICTED: C-type lectin domain family protein [<i>Biomphalaria glabrata</i>] (36%); Sequence ID: XP_013081459.1</p> | <p>LGUN_random_Scaffold20861: 821-2283</p> | <p>MLKINSLVLSRVTSADNDTIEELIILNYESNNTSKTSKNPKGSIGFNGASYVSLTWPNPYSYRDASKYKCEARGVSTSFNKI SAAAYASVETDEPDIRSLVDELLHLRKETYETSNSLKEVKQKYASLNEVLQKSVNKLNAEKQLSKNSFFISSNVFQGKRY MSRKQASNDINKAQATCAFYGGYLVEIDTTDEYTFVNFVFIKSVSANDSTFSCVYNGLMDPENDGIWTHVFTKKDSKFLP WGKGEPQNTADYNMCMLEKSYNWRYNDLPCYYADALRYLCEIPEDEQTVSN</p> |
| <p>PREDICTED: Uncharacterized protein LOC106062883 “CREP-Like” [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013076651</p> <p><u>Domains:</u> -Signal peptide: 1-19 -lg: 26-148 -Coiled coil: 148-176 -C-lect: 199-335</p> <p>PREDICTED: C-type lectin domain family protein [<i>Biomphalaria glabrata</i>] (49%); Sequence ID: XP_013081459.1</p> | <p>LGUN_random_Scaffold16778: 502-660; 1390-2477</p> | <p>MITIPCVFLCVLYVAVSWAATIDIKPNVITVPVTRNLVIVCSLKRVTPELSALFSLTLLHSNAMDEPKFTSLASVNTLDNKI STFSLDESATVAGLINNSGESFLRLTWKNPMSEKSGLYRCSFNGVGVGLGNPLTLTSTGAVVSVTDYDSLTDKMKDFEN SSKELKAKFDILSDYTNLHTNYSNLISRLSRDAAFYSTSSFNRSRYLPRDLVLTQVATCELYGGHLAEIDSNEE FHFVRNFLVSKNLFDVVVTGANDEEKEGTWIYNRNKAPLKVFNWATTEPNSGRIANCQCFWKGGNWYMADARCVY FNNKPNDGYVYSYLCEMPESSTDV</p> |
| <p>PREDICTED: Uncharacterized protein LOC106065054 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013079269; 612 aa</p> | <p>LG4_random_Scaffold311: 172599 -172997; 177150- 177253; 177834-177972; 179067-179206; 182629 182787; 183969 -184116;</p> | <p>MLFLKLVTLVLLYKCNKVLADDDTPAETQSTVNWYCPEGWTFANDGHNITCLWFSNTSLYQVKAQTICKNFGSSLVKL HTEDKIKAFKENFSKLENDIYIGLRKERGYDASYMWDGINGLEIANISILPSTVKDSIHYKLSVYINTQGEWDIDDCEY NFVCEKSVECKPGSFGDKCFNQCHCLGEPCPKSSSEIRCKYGCQTGWMGNACDLEKQDPDVKYKCVNSQEKGKYVNI RIYTKGVHYRSIYGLNVNKRSPWCYSSISEDIDSSLPVTITIPVKEELQEVLES GCAGEHLSNDTYLWTVVIKENEGILLE HDLQVTIKCDFSKSESLIRNSAYSVIGQPTELHKQFLEPQSTEDDVSVMQVVDSSYSGQVISEAAVGSVTLTIKFGLKEGSLI</p> |

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| <p><u>Domains :</u> -Signal peptide: 1-20 -C-lectin: 36-165 -EGF: 170-212 -ZP: 262-474 -Trans-membr: 549-571</p> | <p>185191-185348; 187829-187984; 191164-191717</p> | <p>KGITPYDCYATSPDNKFKKQLIDSQGCPSGSPISAFSERDDNSIQTQWFPLFAFEGEQNVVFQCSFDLCFLKGCQVGC RAFRFHKRSAEDYPETLHEHFTKSTIAVLANKIPISMPESADNNSLSKSSQTPKSSNILAYFNPVTCISIFLVLLVLIIVTYM SFMVALRKSVMGIRREIDYVISRDKLLCYGKIPKDKNCDCNCPYNC</p> |
| <p>PREDICTED: Uncharacterized protein LOC106061984 [<i>Biomphalaria glabrata</i>] (100%); Sequence ID: XP_013075688</p> <p><u>Domains:</u> -low complexity: 25-37/ 58-72 -Ig-like : 88-206 -Coiled coil: 216-276 -lectin domains: none</p> <p>PREDICTED: Fibroleukin-like [<i>Biomphalaria glabrata</i>] (45%); Sequence ID: XP_013070005.1</p> | <p>LGUN_random_Scaffold15796: BGLB005673</p> | <p>MHYRNINCQTANLHFISEFPARLVTTTTSSSTPETTTKILSTKIEWYTSTTAQPKIKTTSTVTMKQPMTTTTVNISSPPESRL QIYGSSEIIQELIEPLTIKCLYKTLIQGERDTSALQSLYLLHETNGVIAIYINKQQPVIATIQGDNFKNVEGEIFDNESKDSYLQ VTWNDLKRSESGKYFCEAYVNHS DGRFDKMNEMLTIIVKSPTFDDLKVIQKLQRAEVDKETVRENQHKIKTIQEDLD TKQQDIISLKEDMNTTKQDIMSIKEDLDTKSQNILSIRENFDTNKHNMIIFQDNLTMTVANLSAALMEVENSQKVFVTFYII SLSLCEAYILN</p> |