

10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180

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aug3.g16532  ....MFFWTIL.....CSYILIASAEEINMEAVMKSMSQSFVVKLEEHGEMSKPELN...FSLNPNENIQDVVRG...YTTAIPGLEE...PFSFFQEA...DDDTTTFSELLK...FGEHED...ILO...NTERSQSF...DMAMSEKFGIDMYVPTDEEPKSK...
aug3.g16533  ....MFFWTIL.....CSYILIASAEEINMEAVMKSMSQSFVVKLEEHGEMSKPELN...FSLNPNENIQDVVRG...YTTAIPGLEE...PFSFFQEA...DDDTTTFSELLK...FGEHED...ILO...NTERSQSF...DMAMSEKFGIDMYVPTDEEPKSK...
aug3.g17763  ....MRNLILII...TLCTFVAADQFN...DAWKKATCQ...KNVEFSKGLAV...YVE...LKDKEVQNAIEE...MSEIFPSSDM...TMADYVTAG...KDD...VLFKMTG...CYRENE...LSKEEEKYEE...SVA...YVNLNFKKYEFKELEDIYKKKHGH...
aug3.g20084  ....MSIVF...VTKSHLILMMOYFI...ITLCFAAAEHHR...EAWRTALC...GNEELKQGDV...YVE...LETSDVODLTRN...VORVLPSSHG...DLKYFTKIA...OTDG...TLFDKADD...CYHEHE...IFKKEVATNKAIV...YVHLFOKHGI...LELENFFKNLENTTW...
aug3.g20082  ....MKYLGLILVL...SIWIYAADEAG...DEWKAALC...NDELLEDIYN...YVE...LEPKAISDP...IKEDFSMSPSSAND...DLKEFTKSV...KDE...ALYEQMDS...CYEYVG...VSAEQETYPE...MTA...YKALFEKHGLVKNARWESKQ...
aug3.g20093  ....MKSLCLILAI...ALLSFAANDHK...EIQNALC...LDEELIDGT...YVE...LEAEIQTAAKE...MTLSPSSD...DIKQFTKEA...GDR...AIFDKLEE...IDQKG...FKDDKENKDEAIT...YVELEFKHGLTEMDLFMRK...
aug3.g16521  ....MFVFWSVLTA...CFLAAFAA...EAP...GGEMDSL...YVE...NVTQSLGNDL...DKAK...LDPPAVK...EALTK...QDTKVLP...YVDT...KAYPFLVAA...KDR...TIFQKISDCMSENAE...SMKDVFDEAS...TK...FEGITKKYGLDIAI...
aug3.g16528  ....MHAYWII...LVF...CSLSIAT...LKAAKICD...KLSVELAAEF...DKND...LDPDNIKSI...IRG...KADVL...LKE...VYYPYLLAG...NDS...SITRKVN...Q...LSEKLA...DVTDEEMAGST...A...YDEVGKKYDIDV...
aug3.g16528  ....MLFSDKMYGVWII...LVF...YVLSVI...ARPEDLCG...KFNKIAAEL...DKND...LAPDYVOKI...ISD...QLRVL...PNEEV...KEFTFLTAG...KDR...SIFSQFREG...LKENEK...VLKPYDLIDTQVSA...FF...
aug3.g16527  ....MYAIWII...LVF...VL...SVT...ALGPEDLCG...TITTEEIA...GEF...DKNK...VDPEYVOKI...VKE...QLKVP...DEEV...KYVPFTTAG...KNN...TIFRTFEN...CMENI...KMTIWDALGS...ACYRNVSIKYDLVWP...
aug3.g16529  ....MNAIWII...FAL...CVLSATAQT...SQP...QSGPEIICD...KITDEI...SAE...FDK...CNK...LDPKHVOKI...VND...Q...LELLP...NEEV...KTKPYFEAG...KDN...SIFRKFEK...CVKDNSK...DMKADFEAGT...K...YVAVADKYNDWP...
aug3.g16530  ....MNAIWII...FAL...CVLSATAQT...SQP...KPGPEIICD...KITDEI...SAE...FDK...CNK...LDPKHVOKI...VND...Q...LELLP...NEEV...KTKPYFEAG...KDN...SIFRKFEK...CVKDNSK...DMKADFEAGT...K...YVAVADKYNDWP...
aug3.g16526  ....MYAYWII...FAL...CVLSATAQT...SQP...VGP...EAV...CE...KLTEELGT...EYDN...YK...LDSEELQI...VLN...HKEVR...PQKTP...SSYSFF...EAA...KNN...DLFNQFYA...GLFRNA...VMOGKNMEKST...H...MQDASKSHGIGWP...
aug3.g16520  ....MYAIWII...LVF...CALSVSA...GPDVICP...KVTIEELGAD...PDK...DE...KDPERVVKV...IRAKH...EVLP...DKEP...NKYNYFVAA...KDP...TLWKT...FNKG...FTRDL...PVDG...PDSFANSA...ACYEELNKKYDIK...
aug3.g16523  ....MHLFWII...LVF...CAASVSA...FEKKKVC...KLTEEI...GA...EFDK...CNT...LIP...EQLK...ING...CKKAAV...PDL...PENVK...TYPY...LV...EAKDR...QKFKTFAD...CMGGHI...ENGKIT...EEHMAENE...RYGEVEEKYDVP...GPKTKKSVLDLVIP...
aug3.g16524  ....MQSVWII...LVF...CVASISA...FGMKKT...CE...KLTEEI...GA...EFDK...CNT...LIP...EQLK...ING...CKKAAV...PDL...PENVK...TYPY...LV...EAKDR...QKFKTFAD...CMGGHI...ENGKIT...EEHMAENE...RYGEVEEKYDVP...GPKTKKSVLDLVIP...
aug3.g16534  ....MNMKQWII...SF...CIVT...SILFYAEGGEINKEGLSLWRRTM...IALEKGDSD...FLNKID...S...FN...LEEKKF...FV...AWKE...LDEI...VPSTGG...S...FELPHNIA...GRDH...SVYDKID...E...MTKEAGRM...L...DEKEPAGM...YK...L...FKNSDYP...ELLVYFRHEG...
aug3.g20095  ....MAIKGLIFAW...C...IFSVVIA...D...QDEKDSF...R...T...IN...KNSD...EL...F...D...LE...D...F...Q...YETK...V...SHEI...TAK...NTK...I...Y...P...SEG...SSPIMVKOA...CKEW...TLWKF...D...D...G...FEYK...HLWDMKEVGE...G...D...YQAVFVKEI...NV...
aug3.g16535  ....MMKIGI...IIF...ISVLT...LVISEKDGKGYGNINLWRKTL...CE...KHGTNLD...RD...L...Q...MA...YDEPFFNANWRN...CFRKIOPKAMG...S...SFOTYQEMA...KDP...SIYHKVDD...CTKKHKPARS...VMNKPALN...CFEVLK...KYHLNELLKKYF...SHVN...
aug3.g16538  ....MMKIGI...IIF...ISVLT...LVISEKDGKGYGNINLWRKTL...CE...KHGTNLD...RD...L...Q...MA...YDEPFFNANWRN...CFRKIOPKAMG...S...SFOTYQEMA...KDP...SIYHKVDD...CTKKHKPARS...VMNKPALN...CFEVLK...KYHLNELLKKYF...SHVN...
aug3.g17764  ....MNLWII...TLLM...CAVVEIYAAEDADHGEYGNNNLWRKTL...CE...KNDES...L...FSEI...DK...VD...LOTKT...I...HEALT...S...M...KKVHP...S...SEG...KYS...LYL...KEA...NNV...PLFLKID...D...MEQHK...SLYKEVGI...GEKALA...LEETMKKHNLRELLEYIDT...EST...EK...
aug3.g16578  ....MMLKWII...FLIFGTISCSALHNLITDVG...EYGNINWRKTL...CE...KHSDVLYS...DMEK...G...LO...LEPKALL...GAL...DE...FT...V...P...AKT...VIAAYVTAA...CKK...ELFLK...VDS...MEEY...E...AV...L...KK...Q...MEM...G...KEAD...YVFAAKKHNLPELFYF...ESAPKS...
aug3.g18376  MHSTKIKSASEEIFOLYRKQNPQSKMLLIQAFFMFGALIFTWSSDSTDHGEYGNONEFRKSI...YVE...SESEGLSHDMEI...YK...LETKAVR...E...GLME...L...K...KASPD...ED...NITAYVKAA...ENK...EIFHTLDAD...YEGMKNOA...SKKKMEVTK...EAGE...YMEAAKKHGLDLVITYFDEY...SK...

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- Silk biased (> 10-fold)
- Venom biased (> 10-fold)

Additional File 7. Aligned translations of members of a putative novel gene family that contribute a significant proportion of expression in the house spider venom gland. The six conserved cysteine residues in members of this family are highlighted in yellow. The pattern of expression bias is indicated by colored ovals to the left of the sequence label: green=venom gland biased ($\Rightarrow 10$ fold), yellow=silk gland biased ($\Rightarrow 10$ fold).