IrAM

EU835901.1| Ixodes ricinus alpha-2-macroglobulin splicing variant 1 precursor, mRNA, complete cds, alternatively spliced

AGTCGAGCTCGGAGACTTGGTGCCCTTCTGTGTGTGTTTGGCTGCTCCCTGGAAAGGAAGAGTGCTGGGT
GTTTTTGTCATCCTCCCGGCGCTTCACGCCTGAGCTTCGCCGCCACGCCATTTGCTTCCGGTGATTTGGT
CAGCCATTGAAGCACGTGATTGAAAGGTAGCCACCAAGCAAGCACAGGCCAGCCATGTTCCTTGCAAGTG
TTCTTTTAATTTCTGCCGCTGTAGCAGCCAGCTACGTCGAAGGAGGGTTCATCTTCACAGCGCCCAAAAT
CCTCCGAAGCGAAACGGAGGCGCTGTTCCGGCTGACCCTCACCGACGTTAAGGACGACGGCAAGGTTTCT
GTACGGCTCCTAAAGTACAACAACGATAGCATCGTGCTCGCTGAACAAGAATACGACATCAAAAACGGGG
AAAGCACCTTTCTTCCATTCAAGGTACCAAAGCACATAGACAGCCAGGCGAAGATTGAAGTAAATGGAAC
CTTTGGGTCCTATGTCTTTGGTGACAAAAAAGAAATAGACTTCCAGAAGTCGAAAACCAATGTGCTCGTT
CAGACCGACAAGGCATTGTACAAACCAGGACAAAAAGTTCAGTTTCGTGTCCTGCCAATAAACAATGAAC
TAAAGCCTGTCACAGATGTTCAGGCCACTATTTACGTCACAAGCCCGGGTGACGTCAGGATAGCCCAGTG
GAACAACGTTACGTTCGAGAAAGGAATTGTTCAAAGAGACTTCAAGCTGTCGGAGGAACCTGAACTTGGG
CTGTGGCAAATTGTTGTTGAGCTTCCGTCTCAGACCGTTAGACAGCACTTTGAAGTCAACGAATATGTGC
TTCCAAAATTTGAGGTAACCATCAAACCACCGTCCTATGTTCTTGCGGATGCCAAGGAAATAACATGGAA
AATTTGCGCGCACTATACATTCGGTCAGCCAGTCGATGGAACACTCAAGGTGAATGTCACCTACGAAAGA
TACTCGTGGGAAAAGGACGACTACCCCCGCGTCTCTCACGAAGGACCGATCAACGGCTGCTTCGACATGA
CCGTCAACACGACAGCCCTGAGGTTTAACGAAAACTACGAGATCTACAAGAGGCTTCTTCTTATTGCCTC
TGTAAATGAGACGGGAACGGGAATCACCATGAACAAGACAAGCTATGTCAGCCGCAGTTTTAACCCACTG
GAGCTGACATTCCTTGAGGGAGAACATGGAAAGAACTATTTCAAGCCAGCAATGCCATTCTATGGATCAC
TCCTGGTGAAGAAGCCAGACGGCGTTCCGGTTGGCGGAGAGCGCATCCAGTTGTGCCTGCTTTCGCAGTC
CGAGATTATCAAACCTTTATGGTGGCGCACCGACAGACGACTCAGTTGCAAAAACTACACCTCAGATGAA
AACGGTTTGGTCAAATTCACCATTCCACCAATGAAGACGACGGTGGTGACAATCAGCGTCGAGGCCGTGG
CCGTGAACTACGACACCGTCAAGTACGACACGTACGGTGTGAAGATCAACCAGCCCAAGAGCACCCTCTA
CCTACAAGCCTGGTACTCGTCAAGCAACAACTTCATCCAGGTCGAGCCGTCCAAGGTCCCCGTGTCCTGC
ACCAGCAGGCATCCGATTCGCGTTCGGTACACCGCCGAAGCCGACAAGGAAATTCAGTTCCACTTTCAGG
TGATGTCCCGTGGCAAAATCCTCAAGGACGCAGTTGTGCCGGTGACCTTCAAGGCCGACCAGGCCGTCGT
GACTGAGGTGGACGAAACGTACCTGGCTGAAGAGGAGCGAAACGAGACATTGCCGAGCAACGTGGCCGAG
GAGCAAGCCGCCACCGGAAGCCTGGAGTACGAACTGACACCAGATTTCAACTACGCGCCTCAGGTCAAAG
TACTCGTCTTCTACGTCCGACCAGACGGGGAGGTCATCGCTGACGCCGAGCAGTTCGAAGTCGAGAAGTG
CCTTCAGAACAACGTGACCATGACTTTTGGTTCAGACACGGTTCAACCAGCCACATCGGCCGCCATTCAC
CTTAACGGATCACCTCACTCCTACTGCGGCGTGGGCGTTGTTGACAAAAGCGTGCATCTTCTCAAGCAAG
ACAATCAGCTTACGAAAGAAAAGATCTACGACATACTTAAACGCCTTGACATCAGTCGGTACACATGGCC
AAAGCAGGCGTCCTATGATTACTGCAGGAAACAACTGGCCAAGAAGCCTCAGCAATACAAGCGCACCATT
TGGAACGGACCACGAACGTCAAACGTTGAGTATGTGGACTCCATCACTGCCTTCGATGAATCTGGAATGG
TTGTGATGTCCGATCTGACTTTGGAAACGAGGCCCTGCAGGAAAGCCATCTACGACAGACCCCCGTACGC
TCTGGCTGCTCCAGCAATGCGCGTCTCGTACTCTTCCACGACGTACACTGGTGGTGCCCCGGGCGTGGCA
ACCCTGGATTCGTTGCCGGAGGCCATTGCCGTCAACCGAGAGATCCCGGCAAAGTCGGCCGTCGAGGTGC
GAAACTACTTCCCGGAGACGTGGCTGTGGGACCTCAAGGAACTCGACGAGAACGGTCAATTGTCCTTCAA
GGAGAAGATTCCCCACACGATCACTGAGTGGGTCGGAAGCACCGTGTGCATCAACTCTCAGGACGGCGTT
GGCGTCTCGGACCCGGCGAAAATCAAGGCGTTCCAGCCATTTTTCGCCTCTTTCTCGCTGCCGTACTCCG
TGGTACGTGGCGAACTCGTGCCCGTCAAGGTCTCCGTCTTCAATTACCTCGAAAAGTGCCTCCCCATCGG
TCTCGCACTCGCCGAAAGCGAAGACTACACGATTCAGGACAGCGCATCCACTACACTCTGCGTGTGCGGC
AGCAAGAGTCTCACTCACAAGTTCCTCGTGCGCCCGACAACAATCGGAGAAGTGAACTTCACGGTGTCGG
CTGCCGGATCAACCAGTGACACTGTCTGCGGTGACCAGAAGGTGGAAAAGGTGGTCGCGAGGGACGCAGT
CACCCGCCCGCTTATTATTGAGGCTGAAGGGTTCCCCAAAGAGGAAACTAAGAGCGTGTTTGTTTGTCCC
AAAGATGTCACCGAGGGCGATGGCAAGAACGAGTTTGACTTGGTTCTTCCCGATGATCTGGTCGAAGGTT
CGGCGAGAGCATACGTTTCGGTCACAGGCGACATTATGGGGCCGGCCGTTCAAAACCTGGATTCCCTGGT
TCGTGTTCCGACGGGTTGCGGCGAGCAGAATATGATCAAGTTCACGCCAAACGTTTACGTCCTGGACTAC
CTGAAGGCGACCGGAAAGCACGAAGAGGACATCGAGAAGAAGGCTGTCGAGAACCTCAAGACTGGCTACC
AGCGTCAGATGAAGTACAGGCACCCAGACGGATCTTACAGCGCGTTCGGAACGAGCGACTCAACCGGCAG
CATGTTCCTCACGTCCTTCGTTGTCAAGTCCTTTAAGCAGGCCGAGAAATACGTCCCCATTGATGCCGCC
AACCTGAAAGAAAGCATCAAGTGGGTCACCACAAAACAGAAGACTAACGGATGCTTCCAGAATGTTGGAA
GAGTGCTCAGCTCTGGGCTTAGGGGCAAGGTGAACGAAACAGCACCTGGCGCGCTCACAGCGTACGTCCT
TGTGGCCCTTCTGGAAGGAGGCCTCGCTGAACCGAAGGTCGTCGAGTCCGCCTTGAATTGCATCGCGGCG
CAGAAGAACCCGAGTCCCCACAACCTGGCGGTTTCCGCGTACGCAGCCGCCCTCGCCGGTCACAGTTCAG
CCAAGGACTACGTGGAGAAGTTGGAAGCGGTTGCCACCCACAAAGGTGGCTTGACATACTGGTCCAACGC
TGCCAGAAAAGGATCGTCTGCGTCCGCTGACATCGAGACTGCTGCCTATGCGGTGCTGACGTACGTGAAG
CTTGGCGACAAGGAGAACCTGGGAAAAGCGCAGCCCATCGTTCGCTGGATGGCTACCCAAAGAAACAGCC

GGGGCGGATTTTCCTCCACGCAGGACACAGTTCTGGGTCTCCAGGCACTTTCTGCGTTTGCTACGCACGT
GAGCAAAGATCCAGTAGACATCTCTGTGAAAGTCGCCGGTACCGATGTGGACGAATCTTACGACCTGAAG
GAGCCCACGAAGCTCGTGATTCAAGAAAAGAAGGTCACCAACCTGCCCAACAAATTGGCAGTAGAGACTA
CTGGATCTGGATGTGCCTTAATCTCGACGACTTTGAAATACAACGTCCACACGCCCCCCAAAAGCGAAGG
ATTTGAGCTGACGGTGACGCCTACACAGGAGCCCAACAAATGCAATACCGCAGATGTGAAGGTTTGCTTG
CGGTTCGATGGTGAACAGCCATCAAATATGGCTGTCGTTGAATTGAAGTTGGTCTCCGGGTTCACAGTGG
ACGAAGATCATGTGTATTCTCTGTACCGCAAAGAAGGAGTGTCGCTCAAAAGGCACGAACTTGAAAAGAA
CCAGCTGAACCTATACTTCGAAGAGATCTCCTCTACAGAAAAATGCTTCGACATTCGTGTCAACCGCGAC
GTTGAAGTTGAGGACGCCAAACCTGCCAATGTCAAAGTTTACGACTACTATGAGCAAGAAAACAGCAAGT
CTGTGAGTTACACCCTCAACACGTCTTGCCAGTGAGCTCCTCACCACGTATAAAAGCTTATGAACGATAT
CGCTTCATCAAAATGAACACAACCATCAAGTCAAGACAGCGCTTCATCCTCGCGTCGCTTCTCGTTTCGG
CGATGGTTTTTAATAACCAAGCATTTTGATACCGGTAACTGTCGTCGCAAGCGCACAGAGTATAACATAA
GAAGGTCACGTGCCCAGTTTGCTGCCAATCGGAAAAGCCGTACCTCTTCTTTTTTTCATTTAAATAACGG
GTAGAGACAGAAATGCACCTACTTTGTTCCTTAAACACCCTTTGCGTTGCAGGTAAAAAAGCGTTATTGT
GCACTTTCTTTTTCTGTGGGTTTAAATAGCTCCGACGTTTAACTGGCTGTTGCAAATTCGATTTGCGAAC
ACATAACCTGACGTGGAGCCACACTTCCTCTGGGCCATGGAAGTCGCCTCTGCAACCCATCTGTCCTGTT
TGCCGATATACGCCTAAATAACTTTAGAATATGTTCATAACATCAATAGGCCACAAAGTGTTTCATCACT
TCCAAAATTTAGACAAAGCAAAAAACTTTAATCGATTGCCACCCGTCTAGATGAGGGTATGAAATAACAA
AAGGCTGTAGTGAAAGTAATTCAGATCACTATATCCTAGTTAGATTGCTCCGTGAACTGTGCGGTTCACA
AGGTTCATATTTTGCTTGGATAAAACTTTAAAGCTTCCTCAGGAGAGGGAACGACGAATCATCCATTTTT
TTTTGGGACACACGAGGTGCACACGTTGCGCGCGGGCATTTATTTTTTTCCTTTTATGTTTCAAGTAGTC
TTGTGGGACAAGAATAGCTTTATAACTTTTGTACTGTCCCCCTGCCGGCACGATACCAAACTTGTACATT
CATCACTTTTCGATCGAGTAATAAAATTGAATCGTTTTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

RT-PCR-primers
RNAi primers

>gi|212549820|gb|ACJ26770.1| alpha-2-macroglobiln splicing variant 1 precursor [Ixodes ricinus]
MFLASVLLISAAVAASYVEGGFIFTAPKILRSETEALFRLTLTDVKDDGKVSVRLLKYNNDSIVLAEQEY
DIKNGESTFLPFKVPKHIDSQAKIEVNGTFGSYVFGDKKEIDFQKSKTNVLVQTDKALYKPGQKVQFRVL
PINNELKPVTDVQATIYVTSPGDVRIAQWNNVTFEKGIVQRDFKLSEEPELGLWQIVVELPSQTVRQHFE
VNEYVLPKFEVTIKPPSYVLADAKEITWKICAHYTFGQPVDGTLKVNVTYERYSWEKDDYPRVSHEGPIN
GCFDMTVNTTALRFNENYEIYKRLLLIASVNETGTGITMNKTSYVSRSFNPLELTFLEGEHGKNYFKPAM
PFYGSLLVKKPDGVPVGGERIQLCLLSQSEIIKPLWWRTDRRLSCKNYTSDENGLVKFTIPPMKTTVVTI
SVEAVAVNYDTVKYDTYGVKINQPKSTLYLQAWYSSSNNFIQVEPSKVPVSCTSRHPIRVRYTAEADKEI
QFHFQVMSRGKILKDAVVPVTFKADQAVVTEVDETYLAEEERNETLPSNVAEEQAATGSLEYELTPDFNY
APQVKVLVFYVRPDGEVIADAEQFEVEKCLQNNVTMTFGSDTVQPATSAAIHLNGSPHSYCGVGVVDKSV
HLLKQDNQLTKEKIYDILKRLDISRYTWPKQASYDYCRKQLAKKPQQY**KR**TIWNGPRTSNVEYVDSITAF
DESGMVVMSDLTLETRPCRKAIYDRPPYALAAPAMRVSYSSTTYTGGAPGVATLDSLPEAIAVNREIPAK
SAVEVRNYFPETWLWDLKELDENGQLSFKEKIPHTITEWVGSTVCINSQDGVGVSDPAKIKAFQPFFASF
SLPYSVVRGELVPVKVSVFNYLEKCLPIGLALAESEDYTIQDSASTTLCVCGSKSLTHKFLVRPTTIGEV
NFTVSAAGSTSDTVCGDQKVEKVVARDAVTRPLIIEAEGFPKEETKSVFVCPKDVTEGDGKNEFDLVLPD
DLVEGSARAYVSVTGDIMGPAVQNLDSLVRVPTG**CGEQ**NMIKFTPNVYVLDYLKATGKHEEDIEKKAVEN
LKTGYQRQMKYRHPDGSYSAFGTSDSTGSMFLTSFVVKSFKQAEKYVPIDAANLKESIKWVTTKQKTNGC
FQNVGRVL**S**SGLRGKVNETAPGALTAYVLVALLEGGLAEPKVVESALNCIAAQKNPSPHNLAVSAYAAAL
AGHSSAKDYVEKLEAVATHKGGLTYWSNAARKGSSASADIETAAYAVLTYVKLGDKENLGKAQPIVRWMA
TQRNSRGGFSSTQDTVLGLQALSAFATHVSKDPVDISVKVAGTDVDESYDLKEPTKLVIQEKKVTNLPNK
LAVETTGSGCALISTTLKYNVHTPPKSEGFELTVTPTQEPNKCNTADVKVCLRFDGEQPSNMAVVELKLV
SGFTVDEDHVYSLYRKEGVSLKRHELEKNQLNLYFEEISSTEKCFDIRVNRDVEVEDAKPANVKVYDYYE
QENSKSVSYTLNTSCQ

used for construction of the phylogenetic tree
KR- putative post-translational cleavage site
S - thioester catalytic site residue

A2M1 (IsAM1)

>VBpre_T005181 cdna:PREDICTED_protein_coding

GGGTTCATCTTCACAGCGCCCAAAATCCTCCGAAGCGAAACGGAGGCGCTGTTCCGGCTG
ACCCTCACCGACGTTAAGGACGACGGCAAGGTTTCTGTACGGCTCCTAAAGTACAACAAC
GACAGCGTAGTGCTCGCTGAACAGGAATACGACATCAAAAACGGTATGCTGCCTGACAAC
CGCCTTTCTGCGTCCGTACCAAAGCACATAGACAGCCAGGCGAAGATTGAAGTAAATGGA
ACTTTTGGGTCCTATGTCTTCGGTGACAAAAAAGAAATAGACTTCCAGAAGTCGAAAACC
AACGTGCTCGTTCAGACCGACAAGGCACTATACAAACCAGGGCAAAAAGTTCAGTTGCGG
GTCCTGCCAATAAACAATGAACTAAAGCCTGTCACAGATGTTCAGGCCACTATTTACGTC
ACAAGCCCGGGTGACGTCAGGATAGCCCAGTGGAACAACGTTACGTTTGAGAAAGGAATT
GTTCAAAGAGACTTCAAGCTGTCGGAGGAACCTGAACTTGGGCTGTGGCAAATTGTTGTT
GAGCTTCCGTCTCTAACCGTTAGACAGCACTTTGAAGTCAACGAATATGTGCTTCCAAAA
TTTGAAGTAACCGTCAAACCACCGTCCTATGTTCTTGCGGATGCCAAGGAAATAACATGG
AAAATTTGCGCGCACTATACGTTCGGTCAGCCAGTCGATGGAACGCTCAAGGTGAATGTC
ACCTACGAAAGATACTCGTGGGAAAAGGACGACTACCCCCGCGTCTCCCACGAAGGACCG
ATCAACGGCTGCTTCGACATGACCGTCAACACGACAGCCCTGAGGTTTAACGAAAACTAC
GAGATCTACAAGAGGCTTCATCTTATTACTTCGGTAAATGAGACGGGCACGGGAATCACC
ATGAACAAGACAAGCTATGTGAGCCGCAGTTTTAACCCACTGGAGCTGACATTCCTTGAG
GGAGAACACGGAAAGAACTATTTCAAGCCAGCAATGCCTTTCTATGGATCACTCCTCGTG
AAGAAGCCAGACGGCGTCCCGGTTGGCGGAGAGCGCATCCAGTTGTGCCTGCTTTCGCAG
TCCGAGATCATCAAACCTTTATGGTGGCGCACCGACAGACGACTAAGTTGCAAAAACTAC
ACCTCGGATGAAAACGGTTTGGTCAAATTCACCATTCCACCAATGAAGACGTCGGTGGTG
ACAATCAGCGTCGAGGCCGTGGCCGTGAACTACGAGACTGTCAAGTACGACACGTACGGT
GTGAAGATCAACCAGCCCAAGAGCACCCTGTACCTACAAGCCTGGTACTCGTCCAGCAAC
AACTTCATCCAGGTCGAGCCGTCCAAGGTCCCCGTGTCCTGCACCAGCAGGCATCCGATT
CGCGTTCGCTACACCGCCGAAGCCGACAAGGAAATTCAGTTCCACTTTCAGGTGATGTCC
CGTGGCAAGATCCTCAAGGACGCTGTGGTGCCGGTGACCTTTAAGGCCGACCAGGCCGTC
GTGACTGAGGTGGACGAAACGTACCTGGTTGAAGAAGAGCGAAACGAAACATTGCCGAGC
AATGTGGCCGAGGAGCAGGCCGCCACCGGAAGCCTGGAATACGAACTGACACCGGACTTT
AACTATGCGCCTCAGGTCAAAGTACTCGTCTTCTACGTCCGGCCAGACGGGGAGGTCATC
GCTGACGCCGAGCAGTTCGAAGTCGAGAAGTGCCTTCAGAACAACGTGACCATGACTTTT
GGTTCAGACACGGTTCAACCAGCCACATCGGCCGCCATTCACCTTAACGGATCACCTCAC
TCCTACTGCGGCGTGGGCGTTGTTGACAAAAGTGTGCATCTTCTCAAGCAAGACAATCAG
CTTACAAAAGAAAAGATCTACGAGATACTTAAACGCCTTGACATCAGTCGGTACACATGG
CCAAAGCAGGCGTCCTATGATTACTGCCGGAAACAGCTGGCCAAGAAGCCACAGCAATAC
AAGCGCACAATTTGGAACGGACCACGAACTTCGAACGTTGAGTATGTGGACTCCATCACC
GCCTTTGATGAATCTGGGATGGTTGTGATGTCCGACCTGACTTTGGAGACAAGGCCCTGC
AGGAAAGCCATCTACGACAGACCCCCGTACGCTCTGGCTGCTCCAGCAAGTACGTCCGTG
AGACCGAGCCCGCCTCCGCCACCCGCATTTGCCAATAGAGTTAGTCTTGTAGGTGGTGCC
CCGGCCGTCGCAACCCTGGATTCGTTGCCGGAGGCCATTGCCGTCAACCGAGAGATCCCG
GCAAAGTCGGCCGTCGAGGTGCGAAACTACTTCCCGGAGACGTGGCTGTGGGATCTCAAG
GAACTCGACGAGAACGGTCAACTGTCCTTCAAGGAGAAGATTCCACACACGATCACTGAG
TGGGTCGGAAGCACCGTGTGCATCAACTCTCAGGACGGCGTTGGTGTCTCGGACCCGGCG
AAGATCAAGGCATTCCAGCCATTTTTCGCTTCTTTCTCACTGCCGTACTCCGTGGTACGT
GGCGAACTCGTGCCCGTCAAGGTCTCCGTCTTCAATTACCTTGAGAAGTGCCTCCCCATC
GGTCTCACACTCGCCGAAAGCGAAGACTACACAATTCAGGACAGCGCATCCACCACGCTC
TGCGTGTGCGGCAGCAAGAGTCTTACTCACAAGTTCCTCGTGCGGCCGAAAACAATCGGA
GAAGTGAACTTCACGGTGTCGGCTGCGGGATCAAACAGTGACACTGTCTGCGGTGACCAG
AAGGTGGAAAAGGTGGTCGCGAGGGACGCAGTTACCCGCCCGCTTATTATTGAGGCTGAA
GGGTTCCCCAAGGAGGAAACCAAGAGCGTGTTTGTTTGTCCCAAAGATGTCACCGAGGGC
GATGGCAAGAACGAGTTTGACTTGGTTCTTCCCGATGATCTGGTCGAAGGTTCTGCGAGA
GCATACGTTTCGGTCACAGGCGACATTATGGGCCCGGCCGTTCAAAACCTGGATTCCCTG
GTTCGTGTTCCGACGGGTTGCGGTGAGCAGAATATGATCAAGTTCACACCGAACGTTTAC
GTCCTGGACTACCTGAAAGCTACCGGAAAGCACGAAGAGGACATCGAGAAGAAGGCTGTC
GAAAACCTCAAGACTGGCTACCAGCGTCAGATGAAGTACAGGCACCCAGACGGATCCTAC
AGCGCGTTCGGAACGAGCGACTCAACCGGCAGCATGTTCCTCACGTCCTTCGTTGTGAAG
TCCTTTAAGCAGGCCGAGAAATACGTCCCCATTGACGCCGCCAACCTGAAGGAAAGCATC
AAGTGGGTCACCACAAAACAAAAGACTAACGGATGCTTCCAGAATGTTGGAAGAGTGCTC
AGCTCTGGCCTTAGGG*TGATAACGATCAATGAGAAAGTGGAAGGCACCCTCATGCATACA*
ATGCGGGACTTTTGTCATGGTCTGGAACGAGGTGTTAGGCGCCCGCACTTTATTACTGAG
CGCCGGTACCGCTACGTAAGCGCTACCAAGAATATCGGACGTCCACACAAGCTAGGACTG

CGCGCTGTAAAGACGGTGCTAGCCAAGAAAACAACACAGCTAGTGCGGCACAATATTAGG
*CAGCTGTTCTATTCTAC*AGGTGGCTTGACATACTGGTCCAACGCTGCCAGAAAAGGATCG
TCTGCGTCCGCTGACATCGAGACTGCTGCCTATGCGGTGCTGACATACGTGAAGCTTGGC
GACAAGGAGAACCTGGGAAAAGCGCAGCCCATCGTTCGCTGGATGGCCACCCAAAGGAAC
AGCCGGGGAGGATTTTCTTCCACGCAGGACACAGTTTTGGGTCTCCAGGCACTTTCCGCG
TTTGCTACCCACGTGAGCAAAGATCCAGTGGACATCTCCGTGAAAGTCGCTGGTGCTGAT
GTGGACGAATCTTACGACCTGAAGGAGCCCACGAAGCTCGTTATTCAAGAAAAGAAGGTC
ACCAACCTGCCCAACAAACTGGCAGTAGAGACAACTGGATCTGGATGTGCCTTAATCTCG
ACGACTTTGAAATACAACGTCCACACGCCTCCCAAAAGCGAAGGATTTGAGCTGACGGTG
ACGCCTACGCAGGAGCCCAACAAGTGCAATACTGCAGATGTGAAGGTTTGCTTGCGGTTC
GACGGTGAACAGCCATCAAACATGGCTGTAGTTGAATTGAAGTTGGTCTCTGGGTTCACG
GTGGACGAGGATCATGTGTATTCTCTGTACCGCAAAGAAGGAGTGTCGCTGAAAAGGCAC
GAACTTGAAAAGAACCAACTGAACCTGTACTTCGAAGAGATTTCCTCTACAGAAAAATGC
TTCGACATTCGTGTTAACCGCGATGTTGAAGTTGAGGACGCCAAACCTGCCAATGTCAAA
GTTTACGACTACTATGAGCAAGGTGAGCATTC

p false exon

IsAM1>VBpre_T005181 peptide:VBpre_P005181 pep:PREDICTED_protein_coding
GFIFTAPKILRSETEALFRLTLTDVKDDGKVSVRLLKYNNDSVVLAEQEYDIKNGMLPDN
RLSASVPKHIDSQAKIEVNGTFGSYVFGDKKEIDFQKSKTNVLVQTDKALYKPGQKVQLR
VLPINNELKPVTDVQATIYVTSPGDVRIAQWNNVTFEKGIVQRDFKLSEEPELGLWQIVV
ELPSLTVRQHFEVNEYVLPKFEVTVKPPSYVLADAKEITWKICAHYTFGQPVDGTLKVNV
TYERYSWEKDDYPRVSHEGPINGCFDMTVNTTALRFNENYEIYKRLHLITSVNETGTGIT
MNKTSYVSRSFNPLELTFLEGEHGKNYFKPAMPFYGSLLVKKPDGVPVGGERIQLCLLSQ
SEIIKPLWWRTDRRLSCKNYTSDENGLVKFTIPPMKTSVVTISVEAVAVNYETVKYDTYG
VKINQPKSTLYLQAWYSSSNNFIQVEPSKVPVSCTSRHPIRVRYTAEADKEIQFHFQVMS
RGKILKDAVVPVTFKADQAVVTEVDETYLVEEERNETLPSNVAEEQAATGSLEYELTPDF
NYAPQVKVLVFYVRPDGEVIADAEQFEVEKCLQNNVTMTFGSDTVQPATSAAIHLNGSPH
SYCGVGVVDKSVHLLKQDNQLTKEKIYEILKRLDISRYTWPKQASYDYCRKQLAKKPQQY
KRTIWNGPRTSNVEYVDSITAFDESGMVVMSDLTLETRPCRKAIYDRPPYALAAPASTSV
RPSPPPPPAFANRVSLVGGAPAVATLDSLPEAIAVNREIPAKSAVEVRNYFPETWLWDLK
ELDENGQLSFKEKIPHTITEWVGSTVCINSQDGVGVSDPAKIKAFQPFFASFSLPYSVVR
GELVPVKVSVFNYLEKCLPIGLTLAESEDYTIQDSASTTLCVCGSKSLTHKFLVRPKTIG
EVNFTVSAAGSNSDTVCGDQKVEKVVARDAVTRPLIIEAEGFPKEETKSVFVCPKDVTEG
DGKNEFDLVLPDDLVEGSARAYVSVTGDIMGPAVQNLDSLVRVPTG**CGEQ**NMIKFTPNVY
VLDYLKATGKHEEDIEKKAVENLKTGYQRQMKYRHPDGSYSAFGTSDSTGSMFLTSFVVK
SFKQAEKYVPIDAANLKESIKWVTTKQKTNGCFQNVGRVLSSGLR*VITINEKVEGTLMHT*
MRDFCHGLERGVRRPHFITERRYRYVSATKNIGRPHKLGLRAVKTVLAKKTTQLVRHNIR
*QLFYSTG*GLTYWSNAARKGSSASADIETAAYAVLTYVKLGDKENLGKAQPIVRWMATQRN
SRGGFSSTQDTVLGLQALSAFATHVSKDPVDISVKVAGADVDESYDLKEPTKLVIQEKKV
TNLPNKLAVETTGSGCALISTTLKYNVHTPPKSEGFELTVTPTQEPNKCNTADVKVCLRF
DGEQPSNMAVVELKLVSGFTVDEDHVYSLYRKEGVSLKRHELEKNQLNLYFEEISSTEKC
FDIRVNRDVEVEDAKPANVKVYDYYE

likely false sequence

used for construction of the phylogenetic tree
KR- putative post-translational cleavage site
S - thioester catalytic site residue

Valenzuela et al. 2002

>gi|22164280|gb|AAM93645.1|AF483723_1 alpha-2-macroglobulin [Ixodes scapularis]
VPIDAANLKESIKWVTTKQKTNGCFQNVGRVLSSGLRGKVNETAPGALTAYVLVALLEGGLAEPKVVESA
LNCIAAQKNPSPHNLAVSAYAAALAGHTSAKDYVDKLEAVATHKGGLTYWSNAARKGSSASADIETAAYA
VLTYVKLGDKENLGKAQPIVRWMATQRNSRGGFSSTQDTVLGLQALSAFATHVSKDPVDISVKVAGTDVD
ESYDLKEPTKLVIQEKKVTNLPNKLAVETTGSGCALISTTLKYNVHTPPKSEGFELTVTPTQEPNKCNTA

DVKVCLRFDGEQSSNMAVVELKLVSGFTVDEDHVYSLYRKEGVSLKRHELEKNQLNLYFEEISSTEKCFD
IRVNRDVEVEDAKPANVKVYDYYEQENSKSVSYTLNTSCQ

A2M2 (IsAM2)

IsAM2 >35256.m000030 cdna:PREDICTED_protein_coding

CTGTACGTCCAGAAGCTTGACGGAACGCCCCAGCCCCAGGAGACCATCCAACTCTGCCTG
TTTGTGGAGTGCGAAGTGTACAAGTGGCGTGCGTGGCAGACAAAACGGATCCTGTCGTGC
CGCAACTACACCTCGGACAATGATGGCGTCGTCCGCTTCAGCCTTCCTCAGTACGGCACC
AGGGTGACCTCCCTCAGCGTGGAGGCACTTGCCGTCAACTTCCCAAGGATCGTTGTCAAG
AATGGCCCAACGCTGGAGAAGCCCTCCGCGCTGCTGACCCTCAAGCCTTTCTATTCGCCC
TCTGGAAACTCGCTTCTTATCGATCGCCGCCAGACCACAGTCCTGGAGTGCAGGGCTACG
TTTTCACCGCAGATACAGATGACTGCCCAGGCCGACAAGGATTACAAACTCTTCTTTACG
CTCACATCGAGTGGCCGCGTCTTGGACTCTCGGAGCACCACCAGACGCTTTGCATCGGGC
GAGCTCATCCAGGAGTCTGCGGACAACACCACGATCCAGAATGAGGGTGCTCCGCCAGAG
GGGAGTGTGGAGCCTACGGCCGGCGAGAACCCGACGCCCCACAGTGTGGCCGTCTTTACC
TACGAAGCAACTCTCCCCGAAGATGCCAGCCCCAAGGTCCAGCTTCTCGTGTACTACGTG
CTCCGGGACGCCCAAGGGAACCCACTGGAAGTGGTCTCGGACTCGGCCGAGTTTGCAGTT
GACAAGTGCCTAGAAAACAAGGTCTCCCTGTCCTTCTCTCCGGACCAAGCCCTTCCGGGC
TCCAAGGTGAGCGTGGAGCTGTCGGCAGAGAGCAAGTCCCTGTGCGGAGTGGGCGCCCTG
GACAGCAGCGTTACCCTCCTGGACGGATACGACCGCATTTCCAGAAACGGGGTCTTGAAC
ACGATCAGCAACCTGAATTACGAGTACTCTCGCACCAACCTCGTCAACCAAAGCTACTGT
TACGAAGACGGCTACAGGTTCAACGAGCCTTACGATACCGAGAGCCCAGCATCTTCTGGA
AGGAGCAAGCGTCAAGTGTTGGCACCTAACGTCGCACCAAGCTACGATTCGCTCACTTCA
TTCGAGAATGCCGGAGTGGTAGTGTTCTCGAACCTGGCGATCCAGACGCGGCCGTGCAAC
AACCGTGCCTTCCCAGGCTACCCCAACAAGCAGGCGCTGCCCTCCCGCTCCTACCAGCCG
TCCTTTGGCGGCGGCGGATTCGGCGGTGCCCTACGTCCGGGCGCCCCAAGACCACCATCG
GGACAGGCAGCCCAGGGCACGCATTCCATTCGCACCCTCTTCCCCGAAACTTGGCTCTGG
CAAATCAAAAGAGTCGGGGAGGACGGCCAGTTGGTGTACGAGGAAACGCTTCCAGACACC
ATCACCCGCTGGGAGGGCAGCGCACTGTGCCTGCACCCAGAGGCCGGCTTTGGCATCTCG
CAGCTGGCCAATGTGACTGGCTTCCAGCCCCTGTTCGTCAGCCTCACACTGCCCCAGTTC
ATGAAGCGTGGCGAAGTGGCCAACGTCATCCTGACTGCGTTCAGCTACGTCGACAAGTGT
GTCGCTGTGCGGGTCCATCTGGAGTCTGTCGGAAACCTGGAGGTTGGGAGCTCCCCCAAC
ACGACGGACGCACTGGTCTGCCCCGGGGGCTCGGCATCCTTCACCTACGGAGTCAGGGCA
ACCAAGCTGGAGACTGCGCGCCTCAGGGCCACGGTTGCCACGCGTCCGGACGCCCAAAGC
GACTATCCGGGCACCGACCTCTACAACGTCAACTCGAGCGACACCGTGCTGCAGACCATC
CAAGTTCGGCCGGAAGGATTCCCTGTCAGGGAAGTGGACACCTATCTGCTTTGTGCTTCT
GATGAAGCCGGAAGCAATGCTCCAAATAGTCTCAAGATCTCTCTCCCAACTCCAAATGCC
CTCGTAGAAGATTCTGAGAAAGTCGTCCTTGTGGCCACAGGAGACATCCTGGCTCTGGAA
GTGAAAGACCTCTCCGTTCCCAAGCTGGTGTTCACCAGTGCTGAAGGAACACTGGCAGTC
CTGGCATCGAGTGCCTACCTGCTCCGCTACCTGGAAGCCACCGGAGCTGACACTCCTGAC
CTCAGGTCCCAGCTGCTGTCGAGGATTCAGCAAGCTTATCAGTCGCAGTACGGTTTCCGT
TCGTCGGACGGCTCGTATGGCCCCTACAGCTCGAGCGAGTACCCTCGTAGCGTGTTTCTG
TCGGCCTTCGCCGTGAAGGCACTCACGGCGGCCAAGCCATACATCGGCAGCGTGGACTCG
GAGATTCAGAGGAGCATCCAGTACGTCCTGCAGCAGAGGGACCGGAACAACGGCTGCTTC
CAGACACTGTCGCCCAGCGGTCCCTTCAATGGAAACTACAAGAATGGAGCGGACCTGAGC
CTGGTGGTAGCCAACTCTCTTCTCGAAGGAGGCTACAATGACAGCACAGTCTACAAGGCG
GTGCTGGAGTGCGTGGATGCCGACAACCTGCCATCCAACCACACCTTGGCCCTTAACGCC
TACTTCTCGGCGCTCATCGGGGAGGACGCCAGGGCCACCAACACTCTGAACAAGCTCCTT
CAGCAGGCCGATAAGAATGGCGGCCTGACTACCTGGGACGACGGAAAGACTGACACTGCT
GGCTATGCCATCTTGACCATGAAGGCCCTTGGTCAAAACCTTGGGGCTGCTCAACCCATA
GTGCGCTGGCTCATGCAGCAGGTCTTTGCACGATACTCCTTCTCCTACTCACAGGCGTAC
AGCGTGGCCGTCCAAGGCCTGACGGAGTACTCCCGGGTGGCCTTTGCCACACCCACCGAC
CTGACTGTGACGGTGGAGGACTCGCAGTCAGGCGCCACTCCTCCTGAGACCTTTGCAGTG
TCCGAACAGAACAAGCTTGTCTACCAGGAGAAGCTGTTGAACAAGCGCCAGTCCTACGAC
CTTGAAGCCACCTTGAACAAAGGCAGCAAGGGTTGTGCAGCTGTTCAGGTGAAATACTAC
TACAACTCGAAGAACAGTCCTGTGCATAAGGGGCTTCAAGTCAATGCTACGTCATCCAGC
GTGGATTGCGGAACACTTGCCTTGGACATTTGTGCTCGTTACACCGAAGGATTCCTGAGT
TCCGCTGCAGTTGTTGAGATTTCGCTGCTTACTGGATTTTCAGCTGATGACCAGTCTTTG
AAGGAG

RT-PCR-primers
RNAi primers

IsAM2>35256.m000030 peptide:35256.m000030 pep:PREDICTED_protein_coding
LYVQKLDGTPQPQETIQLCLFVECEVYKWRAWQTKRILSCRNYTSDNDGVVRFSLPQYGT
RVTSLSVEALAVNFPRIVVKNGPTLEKPSALLTLKPFYSPSGNSLLIDRRQTTVLECRAT
FSPQIQMTAQADKDYKLFFTLTSSGRVLDSRSTTRRFASGELIQESADNTTIQNEGAPPE
GSVEPTAGENPTPHSVAVFTYEATLPEDASPKVQLLVYYVLRDAQGNPLEVVSDSAEFAV
DKCLENKVSLSFSPDQALPGSKVSVELSAESKSLCGVGALDSSVTLLDGYDRISRNGVLN
TISNLNYEYSRTNLVNQSYCYEDGYRFNEPYDTESPASSGRS**KR**QVLAPNVAPSYDSLTS
FENAGVVVFSNLAIQTRPCNNRAFPGYPNKQALPSRSYQPSFGGGGFGGALRPGAPRPPS
GQAAQGTHSIRTLFPETWLWQIKRVGEDGQLVYEETLPDTITRWEGSALCLHPEAGFGIS
QLANVTGFQPLFVSLTLPQFMKRGEVANVILTAFSYVDKCVAVRVHLESVGNLEVGSSPN
TTDALVCPGGSASFTYGVRATKLETARLRATVATRPDAQSDYPGTDLYNVNSSDTVLQTI
QVRPEGFPVREVDTYLLCASDEAGSNAPNSLKISLPTPNALVEDSEKVVLVATGDILALE
VKDLSVPKLVFTSAEGTLAVLASSAYLLRYLEATGADTPDLRSQLLSRIQQAYQSQYGFR
SSDGSYGPYSSSEYPRSVFLSAFAVKALTAAKPYIGSVDSEIQRSIQYVLQQRDRNNGCF
QTLSP**S**GPFNGNYKNGADLSLVVANSLLEGGYNDSTVYKAVLECVDADNLPSNHTLALNA
YFSALIGEDARATNTLNKLLQQADKNGGLTTWDDGKTDTAGYAILTMKALGQNLGAAQPI
VRWLMQQVFARYSFSYSQAYSVAVQGLTEYSRVAFATPTDLTVTVEDSQSGATPPETFAV
SEQNKLVYQEKLLNKRQSYDLEATLNKGSKGCAAVQVKYYYNSKNSPVHKGLQVNATSSS
VDCGTLALDICARYTEGFLSSAAVVEISLLTGFSADDQSLKE

used for construction of the phylogenetic tree

KR- putative post-translational cleavage site

S - thioester catalytic site residue

TEP (IsAM3)

>IsAM3>35419.m000025 cdna:PREDICTED_protein_coding

ATGGTCTCCCTGAGGTTACCGCTTGCTCGAGGAATGGATGCCACGAGGCTACTTCTGCTC
ACGTCGGCATTCCTGCCCCTGGTAGCCCCGCAAAGCAGTGGCATCTACACAATTGTGGCA
CCTCGGAAGCTCCGGCCCAACCTCAAGTATCACGTGAGCACCTCCCTCAGCCAGTCGGCG
TCCTCCCCGCCCGTTGACCTCAGGGTCACGCTCTCCGGCCCGTCGGACAACGGCAGCTCC
AACAGGATCACCAAGCAGGTCCAGCTTCATGACCCGTTTGGGCTTTTGCGTGAGCAGAGA
TGGTCTTCCCAGGTGGGCGACTGGGGCCCTGGCAAGTACAAGCTCTCTGCGTCCGGTTCT
GGTGGTCTGGACTTCTTCAATGAGACCGAACTGACCTACGAGCACAAGAGTTACTCGGTC
TTCGTGCAGACGGACAAGGCAGTCTACAAGCCGGGACAGAAAGTGCTGTTCCGGGTGATA
GTGATGGACCCGTACCTGCTGCCCACTGTCACGGGAGCCATGAATGTCCACGTCACGGAT
GCCAAAGGCAACAGGATTCACCAGTGGGACCGAGTCCTAACTCAGAAGGGCATCTACTCT
TCGGAACTGCAGCTGTCCGACCAACCTGTCTTGGGAGACTGGGCCATCCATGTGGACATC
CTGGGTCAGAAGTACTCGAAGAACTTCACCGTGGCTGAATACGTGCTGCCCACGTTTGAG
GTGAGGGTGAAGCTGCCAGCATACGCCACCTACAACAAGTCGGAGGTGGTTGCCACAGTT
TCTGCCACGTACACGTATGGGAAGCCCGTGAAGGGTACGGTCACGCTGACCGTGGCTCCG
AGGACCCGCTACCACCAGCTGAGGCCCCGCCCTTACGAGCAGTACCAGACCAAGGCAGAG
ATTGACGGGAGCGTGGACATCCCCGTGGCGGTGGTGCGAGACCTGTCCCTCAAGACGGAC
TTTTTCCGGCGGGACATAGAGTTCTTTGCCCTGGTGGAGGAGCGCCTGACCGGGCGCAAG
TACAACTCCACCTCGTACCTCACGCTGCACGATAAGGAGGTCAAGGTCGAGCTGGTCAAG
ACCTCTGAGACCTTCAAGCCGGGCCTCAAGTACACCTGCTTCCTGAAGGTGGCCTACCAG
GACGACACGCCGGTGCACGACGCAGTGAACCAGCTGACGCTGTACCAGGGCTTCAACTTT
AACGAGGACCTCTGGAAGACCAGTCGCCACTGGGTGCCTGCCAACGGGGTGGTGCGCCTC
GAGCTGTTCCCGCCCAACGACAATGCCACCGTCGTGCTGGGCCTGAGGGCGGAGTTCCGG
GGCCAGACGCACTACCTGGAAGGGATCTACCCTGCACGCTCCCCGACCAGGAGCTTCCTC
CAGGCCTGGGTCACGACTGAGGACCCCATGATTGGCGATCTGGTGGAAGTGGAGGTGAAT
TCCACACAGCCGCTGGATCATCTTGTCTACGAGGTGATGGGCCGAGGGGACATCGTGTTT
GCCCAGACCCTCCCTGCTTCCGGGGTGCGCACATACCGCTTCAGCTTCTCGACCAGCTTC
CGCATGGCCCCCCGCGCACGAGTTCTCGTCTACTACGTACGCAAAGATGGGGAGCTGGTG
GCAGATGCAGTCAACTTTGACTTGGGCGGCATCCTCAGGACTCCGGTGCAGGTGCAGAGC
AACCTGGCAGAGACCAAGCCTGGAGGACAGGTGGACATCCTGGTGTCTACCCGACCCAAT
GCCTACGTGGGGCTCCTGGGAGTCGACCAGAGTGTGCTGCTCCTCAAGAAGGGCAATGAC
CTCAGCCAGGAGCAGGTGATTGAGGAGCTGGAGTCGTTCGACAGCGGGAAGCAGGCCAGG
GTCTGGCCACCCTGGTACAGGCGCCGCAGGAGGTCCCTCTGGTGGCCTGGCTCCACAACA
GCCCATGACCTGTTCAAGGATTCCGGCATGGTCGTGCTCACCAATGGCCTCGTGTACGAG
TCGGATGATGGCCTGTTTGCGAGGAAGCAGGTGATTCGTCTCGACACGGATGTCTTGACC
AACCCCGTGCTCCCACCAAGCGACCTCCCCGAGGCCCCGCCTCCGGTGCCGGGTCGCATT
AGGCTTCGCCAGCAGTACCCCGAAACCTGGCTTTGGAGCAATGTCACGGCAAGCCACGAC
GGCCGGGTGGTCATTTCGAGCACCGTGCCAGACACCATCACGTCCTGGGTGATCAGCGCC
TTCGCGCTCGACTCGCTCACGGGACTCGGCATTGCACCATCGCAGGCCAAGGTGACGGTC
TTTCGACCGTTCTTTGTGACGGCCAGTCTGCCGTATTCTATCCTCCGGGGGGAGTCCGTC
GCCATTCAGTGCGTCGTCTTCAACTACAACAACAAGCCTGTTCAGGCGCGGGTGACGCTG
GAGAATGCAAAATCCGAGTTTGTCTTCACGTCTCTGTCCAATGACGTCGGTGGCGAGCAG
AGCAAGGACAGGCGCAGCAAGGAGGTCACGGTGCCGGCTCAGGACGGTGTCGCCGTGTCC
TTCCTTATCACCCCCACCAAGCTTGGCTACATCGACATCCACGTGTCGGCCACGTCCTCC
CTGGCCGGTGACTCCATCCTCAAGAAGCTGCTCGTCAAGCCCGAAGGCTCCAAGCAGCAC
TTCAACCGGGCTGTGCTGGTGGACCGGAGGAACCCTTCTGCTCCGCCCACCAGCACCAAC
ATCTCCATCCCCATCCCCAAGAATGCGGTGCCTGGCTCGGAACGCATCAGCGTCTCGGCA
GTCGGCGACCTGCTGGGCCCCCACGTGAACAACCTGGACCAGCTGCTGGTGATGCCCCAC
GGCTGCGGGGAGCAGAACATGCTGGACTTTGTGCCCAACGTGGTGGTGCTTGACTACCTG
CGCAGGGCCAACCGACTCTCCCCGGCCGTGCGCGGCAAGGCCCTTCGCAACCTCGAGGAT
GGCTACCAGCGCCAACTGACCTACAAGAGGGACGACAACTCGTTCAGTGCCTTCGGGAAC
ACGGACCGCAGCGGCAGCACTTGGCTCACAGCATTCGTCCTCAAGTCGTTTGTCCAGGCG
GTGCCGTACACCAGCGTGGACCCCGCAGTGCTGGAGAATGCCACGCGCTGGCTGGTGGAG
CGCCAGAAACCGGACGGCTCTTTCGAGGAGCCCGGGGAGGTGATCTACAAGCCCATGCAG
AGCGGTGCTGGAAGTGGGGCGGCTTTGACAGCCTATGTCCTGATTGCCCTCCTGGAAAAC
AAGGTGGGCTTTCAGCATGCTCTGCGTTTTGCAGCTAGTGCGGCTGAGGAGTTCCTGCTG
AAGGAGCTGAGGACGCAGAGCGACCCCTACGTGGTGGCAGTGGTGACATATGCCCTGCAC
CTGTCCGGCCACCGGGCAAGGGACGGAGCCTTCCAGAAGCTGCTCTCCCTCGCCACCCGG
GAAGACGACATGGTGTTCTGGAAGGACCCCGGAGTGGCGCCAGTGAACACGACGGACAAG

CAGTCGGACTTCTTCTTCAAGGCCCACTTCAAGGACGTGGAGATGACCGCCTACGCCCTG
CTCACGCTCATGGAGAGGGGAGACGTGAGCGCCGCCATCCCGGTCATGCGCTGGCTCGTC
TCCAAGCAGAACTCCAACGGGGGATATAGCTCCACCCAGGATACGGTGATTGGGATCCAA
GCCCTGGCCCGTCTGGCTGCCAGCGTGGTGTCGCAGACCATAGCGGTGGATGCCTCGGTC
AAGTATGGCGACGGGAGGAAGCGCACCCTCAAGATCCACAGCGGGAATGCCCTGGTGCTC
CAACGCATCGAGCTTCCATCAGACTTGAAGTATGTGGAGATCGAGTCCTCTGGATTTGGA
GTGGCCATTATACAGGTGTCGTGGTCCTTCAACCTGGCCGTATCTTCGGAGGCCCCTGCC
TTCTTCCTCAACCCACTGCTGGATAAGACCTCTACCGAGAGCTACCTACAGCTCAGTGTC
TGCACACACTACCGTGGCGAAGGGGAGGCGAGCAACATGGCGGTGATGGAGGTGGGGCTT
CCTTCGGGCTACCTCTTTGACTTCGACACGCTCAGCAGCATCCACAGGACCAAGGAGGTA
CGCAGGGTTGAGAGCCAGGACTCGGACACCAACGTGGTCATCTACTTCGACAGGATTGGG
AGGGAGGAGCTGTGTGTGACTGTGCCCGCCCACAGAGAGCACAAGGTGGCCAACCAAAAG
CCCGTGCCCGTCAAGGTCTACGACTACTACGACCTCGCCCGCAGTGCCCGGATGTTCTAC
AGCCCGTACAAGACCACCCTGTGCGACGTATGCGACGGGGTCGAGTGCGGCAACGACTGC
AACACCGTCAAGGGCACCAAGGCAGGCACCGACCAGCTGGAACGGGAGACGGAACCCGAC
GCCGCCGCCGACACCAGGGCATCTCTCGCGGCTGTGCTGGCACTGAGCCTCACTGCGGTG
CTCTTTGTCCGCTGGTGGTAG

both RT-PCR and RNAi primers

IsAM3>35419.m000025 peptide:35419.m000025 pep:PREDICTED_protein_coding
MVSLRLPLARGMDATRLLLLTSAFLPLVAPQSSGIYTIVAPRKLRPNLKYHVSTSLSQSA
SSPPVDLRVTLSGPSDNGSSNRITKQVQLHDPFGLLREQRWSSQVGDWGPGKYKLSASGS
GGLDFFNETELTYEHKSYSVFVQTDKAVYKPGQKVLFRVIVMDPYLLPTVTGAMNVHVTD
AKGNRIHQWDRVLTQKGIYSSELQLSDQPVLGDWAIHVDILGQKYSKNFTVAEYVLPTFE
VRVKLPAYATYNKSEVVATVSATYTYGKPVKGTVTLTVAPRTRYHQLRPRPYEQYQTKAE
IDGSVDIPVAVVRDLSLKTDFFRRDIEFFALVEERLTGRKYNSTSYLTLHDKEVKVELVK
TSETFKPGLKYTCFLKVAYQDDTPVHDAVNQLTLYQGFNFNEDLWKTSRHWVPANGVVRL
ELFPPNDNATVVLGLRAEFRGQTHYLEGIYPARSPTRSFLQAWVTTEDPMIGDLVEVEVN
STQPLDHLVYEVMGRGDIVFAQTLPASGVRTYRFSFSTSFRMAPRARVLVYYVRKDGELV
ADAVNFDLGGILRTPVQVQSNLAETKPGGQVDILVSTRPNAYVGLLGVDQSVLLLKKGND
LSQEQVIEELESFDSGKQARVWPPWY**RRRRR**SLWWPGSTTAHDLFKDSGMVVLTNGLVYE
SDDGLFARKQVIRLDTDVLTNPVLPPSDLPEAPPPVPGRIRLRQQYPETWLWSNVTASHD
GRVVISSTVPDTITSWVISAFALDSLTGLGIAPSQAKVTVFRPFFVTASLPYSILRGESV
AIQCVVFNYNNKPVQARVTLENAKSEFVFTSLSNDVGGEQSKDRRSKEVTVPAQDGVAVS
FLITPTKLGYIDIHVSATSSLAGDSILKKLLVKPEGSKQHFNRAVLVDRRNPSAPPTSTN
ISIPIPKNAVPGSERISVSAVGDLLGPHVNNLDQLLVMPHG**CGEQ**NMLDFVPNVVVLDYL
RRANRLSPAVRGKALRNLEDGYQRQLTYKRDDNSFSAFGNTDRSGSTWLTAFVLKSFVQA
VPYTSVDPAVLENATRWLVERQKPDGSFEEPGEVI**Y**KPMQSGAGSGAALTAYVLIALLEN
KVGFQHALRFAASAAEEFLLKELRTQSDPYVVAVVTYALHLSGHRARDGAFQKLLSLATR
EDDMVFWKDPGVAPVNTTDKQSDFFFKAHFKDVEMTAYALLTLMERGDVSAAIPVMRWLV
SKQNSNGGYSSTQDTVIGIQALARLAASVVSQTIAVDASVKYGDGRKRTLKIHSGNALVL
QRIELPSDLKYVEIESSGFGVAIIQVSWSFNLAVSSEAPAFFLNPLLDKTSTESYLQLSV
CTHYRGEGEASNMAVMEVGLPSGYLFDFDTLSSIHRTKEVRRVESQDSDTNVVIYFDRIG
REELCVTVPAHREHKVANQKPVPVKVYDYYDLARSARMFYSPYKTTLCDVCDGVECGNDC
NTVKGTKAGTDQLERETEPDAAADTRASLAAVLALSLTAVLFVRWW

used for construction of the phylogenetic tree
RRRRR- putative post-translational cleavage site
Y - thioester catalytic site residue

A2M3 (IsAM4)

>**IsAM4** tam5VBpre_T004236 cdna:PREDICTED_protein_coding

ATGCAGTCACTTATGGTGCAAGTCAAGTCTACCAACATCATCACATACACTCTGTCCCAT
GGTTCTTGCTGCAGTGCCTTTCTCCTGACGGCACCGCATGCATTAATACCCGGCGCAACC
GAGACACTGGCTCTCAACGTCCTCAATCCCCCTAAGGATGGGCACGCCACAATCCAGTTG
CTAGCGCCCTCTGGCCAGGTTTTGAGCGAGACGAGCATCAAGTCTGCCGGGGGATTTCCT
CAGACCGTGTCCCTCAATGTCCCCAAAGAGCTTCCCGTTGGCAGCTCTCTAGCAGCAATT
GGAAAGTTTGGGCGCTACAGCTTTGACAAGAGGCTCTCGGTGAAGGTGGCTGATGGCAGT
GCTGGTCTCATCATAATCATCCAGACAGACAAGCCAGTCTACCGGGCTGGAGAAGTTGTA
CGGCTCCGAATCCTCAGCATAGACCACCGGAAGCTTCCCTTGGCTAAAGATGCTGTGAGT
AAACGGCCATTGTTGCGCTTTGAAAGTCCTAGACGTTTATCTCTAAACTTTTATTGTTTT
TTTTTTATGTTTTTAGGTGTGATCCAGTTGGAAATGGAATTGTCTAAAGAGCCTCCGCTT
GGACAGTGGAAGATATTTTGCCGTCTCCTTGGCCGAGAAACTCGCAAGCCTTTCCAGGTG
GACGAATATGTGCTGCCGAAGTTTGGAGTAGAGGTGGTGCCTCCACCGTACGTCTTCCCT
GAGGAGACCAACACCACCTGGAAGATATGTGCTCAGTATGTCTATGGCAAGCCAGTGAAA
GGACAGCTCCGGGCCCAGCTCACCTATGGGCGGTTTCACTGGGCATCTGAGGCCACAAAA
GTACTGCCCAGCATTGACCTTGATCTTCCAATAAAAGGTTGTCACGAGTTCACGCTGAAT
GGTCGGGATTTACTGCTGGCTAATGAGGACCTGAACAGGCGTCCGCTGATCCTGACGGCT
GAAGTCACCGAAGAAGCCACCGGTGTGACACAGCATGCGAACGTCACAGTGAGGCTGTCG
TGGTCACGGCTCACTCTGGAATTTCTGAAAGACGGTGCAGTGGCCGACTTCAAGCCAGGG
CTGCCCCACAGAGGAGCGCTGATGGTAACTCAACCTGACGGCACACCAGCGCCCGGCGAG
AGCGTGAACATCTGCTTTCTGGCGGTAAACGTGACGATGCGAGAAGTGTCCAAGGGCTGC
AGGGACTTCAAGAGCGGTCCGGACGGACTCGTTCGGTTTTCAGTGCCTGGACTGCGCAGC
TCTCCCATAATTATGATCTTTAGCTTTATATTTCAAATGTATTTGCAGGCCAAAGCAGAA
GGAGGCAGCTTGAATCCTCCGACCACCACGGTACTTCTGCAGCCATGGAGGTCACTGTCG
CAGCGCTACTTGCGAGTCTTGGCGCCGGGTCAGAAACTAAAGTGTGGCGTGTCAACACCA
GTTCGCTTTCACTACACCAAGCTCAAGAACCACTCTAGTGTGGCCTTCAACTATCAGGTG
GCAGATTCAAGTGCCTGCATTTGCAATTGCCTGCAAAAAGACAACTCGTTATCGTCGGAA
TCGGAAAGCTCTTCGACGGGTGCAACGTCAAGGCCAGATGTGATTTCGGTTTCTCAAGAC
GACACGGACGACAGGATTCCAGTTGAGTCCGGACTCCAGTCCGGGGGCTTCATCACGGCC
GAGCTGAGCCTGGAGCCGAAACCCGAGTGGGGCCTGTCTTCGAAGGCGCGCCTCCTGCTG
TATTACGCCCACCCCAAGGGAGAGCTGATTGGGGACAGTCGCCGGCTGCAGGTTGAACCC
TGCACTTCAAACCCCGTGAGTTTTTTGTGCCCTTGCGGGGATGACAGTGCCTACCCTGGG
ACCACAGTGGGGTTATCGCTGTCTGCAGCATCGGGCTCTCTCTGCGGAGTTTGGGCTCTC
GACCGCGGTCTGTTGCACAAGGACTCCTCTGCGCAGCTCACCGCTGACAAGGTGTGGAAT
CCATGCTTGGATCAGCGAGTCTGGAACAATTGCTGGAGCTTTGGAGCGAAACCAGATCCA
TCCGCGTTTCCAGCAGCCATTGTCGAGACCGCGGGAGAGTTTTTGAAGCGCTTCGCCGTG
ACAGTAAGCCAGAGCTTCAAGGTCTTCTTTGTGACACGACTTCTGGAGGTCTGCTTTTCC
AGAGTTTTCCACAGATGCTGTCTCCCATCATCATGTCCCGTAACTTTCCGTCCAACATTG
TGTCATTTAGGTTTTGACAGGACCGAGTTTGAACCTCGAGCGAACGAACCACGGGTTGTC
CTACCTGAGGAGGACGTTCCTGCAGACCCTCCGAAATCTGCGGTGTCGCTCCGCACACAC
TTCCCAGAAACATGGCTTTGGGAGATGCACAATGTTGACAGGGAGGGTTCTGTTCAGTTT
CAGCGCGAACTCCCGCACTCTGTGACCCAGTGGCAGGCGGGTGCCCTCTGCCTGCACCCC
ACCCGGGGTGTGGGTCTTTCGAATGCGGCCCTGAACGCCCTCCAACCCTTCTTCGCTCAG
CTCACCCTCCCCGCAGTGGCCAAGAGGGGGGAGCTGGTGCCCGTCACCGCTACCCTCTTC
AGCTACCTCCAGGCATGCGTTCCGGTGAAGCTGTCCCTAAATGCGGACAGTGCCTGCATG
AAGCTCCTCGGCGAGCCACAGAAGCGGGATTGCCTGTGTGGCAACGAAAGCATTGTGCTG
CGAGTGCAAGTGCGTCCCCTGTGCCTCGGAGCCATCAACATTACGCTTCATGCCCTTGGG
CTTGCTGAAAACAAAGGACTGTGCGACGAGGGGAAGCCGCTCGAAACGAGGCAGGCCCGA
GACTCTCTCCGGAAAAGCCTCCTCGTCACGGTGAGTCCATCTTGGTCCCATTGGTTGGTT
TTTGCAGGTTCCGGTGAGGGTCCTCAGAAGCACGAATTTCCGCTGGAACTTCCACGCAAC
GTGGTCTCTGGATCTTCAAGGGGTGTTTTTACGCTTTCAGGCAACGTCGGGAGTCCCGTG
TCAGTGGACAGGCTGGACAAGCTGGTTCGTCTGCCAACTGGCTGCGGGGAGCAGAACCTC
GCTTTGCTGGCACCCAACGTCTTTGTGCTCGACTACCTCAACTCTTCCGGAGAGCGTGGG
CATCCCCTGGAGTCAAAGCTGAAAGAGAACATCGCTAAAGGTTACCAGAGGCAACTGAAC
TACCGGCACGCCGAAGGCGGCTACAGCGCGTTCGGCTCGCAAGACCCGGAGCCGAGCCTG
TGGCTGACTGCATTTGCTGTGCGAACGTTTGGGAGGAGCCGTCGCTTTATGCCTATCGAC
GAGGCCGAACTCAGCGGCAGCATTCGGTGGATCCTGTCGAACCAGTACGACAACGGCTGC
TTCCCGTCCGTCGGCAGAGTGCTCAACTCAAGATTAAAGGGAGGATTGGAAGGTCATTCC
CTGGCTCCACTGACAGCATACGTCCTGATCTCGCTGCTCGAAGCCGGGGCAGAGATTCCT

CAGGTTTCGAGAGTGGGTGCCGTGCGATGTCTCCTGCAAGAGCTTCAGCAGCAACAGCAA
GACAGCCACACTATGGCTCTAGCCGCTTATGCATTCTCTCTCTTCGAAGACTCCAAAGCA
TCTGAGCTCCTTGCATCCCTTCGTGACGAGGCTCAGCCTGGAAATGGTGAATCAATTTTT
TTTTTTTTTTTTTTGTCGACGCTCCACTGGCACAAGAACGTCTCGACAGCAGTGGCCGTC
GAGACCGCCAGTTACGTGGTCCTGGCGTCCTTGAAGCTTGGCGGTCGGGCGGCTGCGAAG
TCAGTCTTGCCCGTGGTCCGCTGGGTGCTGGAGCAGAGGAACCACGATGGCGGATTTGTG
TCAACTCAGGCACGTGATACAGTGGTGGCACTTCAGGTGCTGGCAGAGTATGCCAAGGCG
ACCAGCAGTTCTGACACGCGACTGCAGATTCGGGTTTCTTCCGAAGGCCTGGGCTCCACG
TTGACCGTGAATCGAGAGAATGCTCTTCTCAAGCAGGAGCTTTTTCTGCCCGTCGTACCC
ACTGTGCTGCACATAGAAGCCACAGGAACAGGGTGTGCTTTCATTCAGGCAACAGTGAAG
TACAATGTTCCTGCCGCAGAAGAAACAAAAAGTTTTGGATTCTGGGTCACAGCATTGCAT
GCGAATTGTCGGCCACAAGTCAAAGTAAATTTATTTTCCTTTTGCAGCTACCTTGTTTCC
TGGGCCATGTCTGGCATGGTTATCGTTCAAGTCAAAATGCAGTCTGGATACCGTTTTGAA
AAGGTGGGTGCTTCTTCATGGTGCCTCTGTTTAGAGGAGCAGGCTTTGAAGAGACATGAG
GTAGACCAGGACCAAGTGAATCTCTACTTTGAAGAGTTGAGCAATCGCAAATCCTGTGCA
TTGCTGGAGTTGGTTCAAGATTATGTTGTGGAAAATGCAGTCCCAGCCACCGTGACGCTC
CAGGATTACTATGAG

RT-PCR-primers
RNAi primers

IsAM4>VBpre_T004236 peptide:VBpre_P004236 pep:PREDICTED_protein_coding
MQSLMVQVKSTNIITYTLSHGSCCSAFLLTAPHALIPGATETLALNVLNPPKDGHATIQL
LAPSGQVLSETSIKSAGGFPQTVSLNVPKELPVGSSLAAIGKFGRYSFDKRLSVKVADGS
AGLIIIIQTDKPVYRAGEVVRLRILSIDHRKLPLAKDAVSKRPLLRFESPRRLSLNFYCF
FFMFLGVIQLEMELSKEPPLGQWKIFCRLLGRETRKPFQVDEYVLPKFGVEVVPPPYVFP
EETNTTWKICAQYVYGKPVKGQLRAQLTYGRFHWASEATKVLPSIDLDLPIKGCHEFTLN
GRDLLLANEDLNRRPLILTAEVTEEATGVTQHANVTVRLSWSRLTLEFLKDGAVADFKPG
LPHRGALMVTQPDGTPAPGESVNICFLAVNVTMREVSKGCRDFKSGPDGLVRFSVPGLRS
SPIIMIFSFIFQMYLQAKAEGGSLNPPTTTVLLQPWRSLSQRYLRVLAPGQKLKCGVSTP
VRFHYTKLKNHSSVAFNYQVADSSACICNCLQKDNSLSSESESSSTGATSRPDVISVSQD
DTDDRIPVESGLQSGGFITAELSLEPKPEWGLSSKARLLLYYAHPKGELIGDSRRLQVEP
CTSNPVSFLCPCGDDSAYPGTTVGLSLSAASGSLCGVWALDRGLLHKDSSAQLTADKVWN
PCLDQRVWNNCWSFGAKPDPSAFPAAIVETAGEFLKRFAVTVSQSFKVFFVTRLLEVCFS
RVFHRCCLPSSCPVTFRPTLCHLGFDRTEFEPRANEPRVVLPEEDVPADPPKSAVSLRTH
FPETWLWEMHNVDREGSVQFQRELPHSVTQWQAGALCLHPTRGVGLSNAALNALQPFFAQ
LTLPAVAKRGELVPVTATLFSYLQACVPVKLSLNADSACMKLLGEPQKRDCLCGNESIVL
RVQVRPLCLGAINITLHALGLAENKGLCDEGKPLETRQARDSLRKSLLVTVSPSWSHWLV
FAGSGEGPQKHEFPLELPRNVVSGSSRGVFTLSGNVGSPVSVDRLDKLVRLPTG**CGEQ**NL
ALLAPNVFVLDYLNSSGERGHPLESKLKENIAKGYQRQLNYRHAEGGYSAFGSQDPEPSL
WLTAFAVRTFGRSRRFMPIDEAELSGSIRWILSNQYDNGCFPSVGRVL**N**SRLKGGLEGHS
LAPLTAYVLISLLEAGAEIPQVSRVGAVRCLLQELQQQQQDSHTMALAAYAFSLFEDSKA
SELLASLRDEAQPGNGESIFFFFFLSTLHWHKNVSTAVAVETASYVVLASLKLGGRAAAK
SVLPVVRWVLEQRNHDGGFVSTQARDTVVALQVLAEYAKATSSSDTRLQIRVSSEGLGST
LTVNRENALLKQELFLPVVPTVLHIEATGTGCAFIQATVKYNVPAAEETKSFGFWVTALH
ANCRPQVKVNLFSFCSYLVSWAMSGMVIVQVKMQSGYRFEKVGASSWCLCLEEQALKRHE
VDQDQVNLYFEELSNRKSCALLELVQDYVVENAVPATVTLQDYYE

used for construction of the phylogenetic tree

N - thioester catalytic site residue

C3-1 (IsAM 5)

>IsAM5>35417.m000042 cdna:PREDICTED_protein_coding

ATGCGCGACGTGAACGTTGTTGGTCTTTCCAGAGACAACCGGAGAGTGGAAGTTGAGTAC
TCGCTGCCAGACTCGATCACGACGTGGGAAGTGAACGCAGTGAGCACAGCCCCTTTAGGC
GGCATCTGCGCTTCGGAGCCTCTTGAGATCGTCGCCTTCAAGAACGTCTTCGTGGAGATC
AACGTGCCCTACTCGGTGCGAAAGAACGAGCAGGTCGAGATTCCCGCCACCGTTTACAAC
TACGGCCAGAAAGCCATCAAGGCCAGAGTGGCGCTCCGGGGCACCAAGGACATCTGCTCC
GGCACCAGGGAGGGCGAGAGGTCGGCCATTCACAGGATCGACGTTCCGAGCGGCCACGGC
AGGACCGTTATCTTCCCGGTGATTCCGCTCGCCACTGGTGAGCGCTACATCGAAGTGATC
GCCGTGAGCAGCTCGGGCAGTGACTCGGCCAGGGTCAAGCTGAGGATTGAGCACAATGGT
GCCCCCCGAAACGAATCTTTCAACGTACCCCTGAATCCCACCGACGTTAAGAAGCGACAA
CAGCGCAGCATCTTCCACGAACACTACACGGGCGACAAACTCGGTCCGGCGCTAGAGACA
ATGGTCAAAAATCCCGGAAGCATCATGAGTATGCCCACCGGATGCGGAGAGCAAACCATG
ATCAGTCTGGCCCCAACCCTGTACGCTTACCAGTACCTGAGAGCCGTGGGAAGTATCGGC
GGTCCGTACGAAGACCACGCTCTCGGCTTCATTCGTGAAGGCTACAAGAGGATCCTGACT
TACAGAAAACCTGACGGGTCTTTCGCCGTTTGGACCGATCATCCTTCCAGTCTCTGGCTG
ACGGCGTTTGTCCTTCGGAACCTGTGCGAAGCCCGAAAGTCAACCATGATCGACGAGGCG
GTGATAACCAGCGGATTGCGGTATATAATGACGCAACAGCAACAGAACGGAAGCTTCAAA
GACGCCTATCATCTGCACCACAAAGAACTTCTGGGCGGCGTTGACGGACCGGTGCCTTTG
TCGGCCTACGTCCTGCTCACGCTGCAAGAATGCATCAAGGATGGGGTCAGGGGAACCGCC
TACGCCCTGATGGCCTTCCTCTCCGAGAGAGAGAACCGGGACTACGTCGACGGATACGTC
CGCTGGCTCAACGGCAAGATGCAGCCCACGGGAGCCTTGTCGTCCACCCAGGACACTGTG
GTGGCGCTTCAGGCGCTCGCCAAGTACGCCACCGTCAGCAAGGACGACAACATCGACCTC
ACGTGCCAAGTGACCGTGAGCAAACCGAGGGAGTTCAAGGAGGTCGTCCGAATCAAGCGA
GACAACGCCCATCAGCTCACTAGGATTCCGATTCCAAGCGAGGGGGATAAGATCTTCGTC
GACGTGAGAGGCTCGGGCTCTGCTCACATGTATTTCCTCTACAAGTACAACGCTCCCGTT
GAACGCGAAGACATATGCAAGTTCGACATCGCTGTCAACTTTGAGGAGAAGAAACCAGAC
ATTAAACATCTTTTAACACACATTGCAAGAGATGCCAGTAAGCAACGGCGAATGAAGTCC
AAGCTCAGTAGCACGTACAAGATTAAGGTGTGCGCAAGATACCTGGAGCAGAATGCTACG
GGGATGGCCATCCTGGACGTTGGTCTTTTGACAGGTTTCAAGCCTATTGTCGAAGACCTC
AAGAAGCTTGTCACTGACGGAGTAGTTCAATTCTACGAACTGACACGTCGTAGCGTCAAC
TTTTACGTTGAATCTATTCCCACGAATGCTGAGGTGTGCCTGGAATTCGGGCTCGACAAG
GAGTTCGAGGTCGGGCAGATACAGTCCAGCTACGTCAAGGTGTACTCCTATTACGATCCA
GATACGTCCTGCACGGAGTTCTACGCCCCCGACAACTCGAGCCCCCTGCTGAAGCTGCAC
TGCGACGACACCGAAGTCTGCGCGTGTGCCGAAGGGGGCTGTCCACCCGAGAAACCTCTG
GCACCTTTCGTCAAGGAAATCGACGACGTTAACGAGCGTCGAGAGAGTCTGAGAGAGTTT
GTCTGCGATAAGGTGGACTACGTCTGGCTAGGGACGGCGCAAGAGAACTACACGAAGGAC
GGCTTCAAGTTCGTGAAATTCTTGATCAAGGAAGTTCTCAAACCAGGTCGCGAAGCTGAA
GAGGACCTGAAGGGCAAGACTCGGCACATCAAGGCTCGTGAGCGGTGCGCCAGCTTCAAC
CTCGAGCTGAGCAAAGAATACGTCGTCATGGGGCTGGACTCTGAGTACCAGGAGCACGTG
CAGCACGGACTGGTCCAGCCGCTTTACATCATGGACACCGCTGCCGTGGTGTTCCCGAAG
GCCACGCGGGACAAACAGACACGAGACCTCGTGACGTGGTTCATCAGGGAATTCTCAAAC
GAAGAATCTCGCTGTTTTACCTGA

RT-PCR-primers
RNAi primers

IsAM5>35417.m000042 peptide:35417.m000042 pep:PREDICTED_protein_coding
MRDVNVVGLSRDNRRVEVEYSLPDSITTWEVNAVSTAPLGGICASEPLEIVAFKNVFVEI
NVPYSVRKNEQVEIPATVYNYGQKAIKARVALRGTKDICSGTREGERSAIHRIDVPSGHG
RTVIFPVIPLATGERYIEVIAVSSSGSDSARVKLRIEHNGAPRNESFNVPLNPTDVKKRQ
QRSIFHEHYTGDKLGPALETMVKNPGSIMSMPTG**CGEQ**TMISLAPTLYAYQYLRAVGSIG
GPYEDHALGFIREGYKRILTYRKPDGSFAVWTDHPSSLWLTAFVLRNLCEARKSTMIDEA
VITSGLRYIMTQQQQNGSFKDAYHL**H**HKELLGGVDGPVPLSAYVLLTLQECIKDGVRGTA
YALMAFLSERENRDYVDGYVRWLNGKMQPTGALSSTQDTVVALQALAKYATVSKDDNIDL
TCQVTVSKPREFKEVVRIKRDNAHQLTRIPIPSEGDKIFVDVRGSGSAHMYFLYKYNAPV
EREDICKFDIAVNFEEKKPDIKHLLTHIARDASKQRRMKSKLSSTYKIKVCARYLEQNAT
GMAILDVGLLTGFKPIVEDLKKLVTDGVVQFYELTRRSVNFYVESIPTNAEVCLEFGLDK
EFEVGQIQSSYVKVYSYYDPDTSCTEFYAPDNSSPLLKLHCDDTEVCACAEGGCPPEKPL
APFVKEIDDVNERRESLREFVCDKVDYVWLGTAQENYTKDGFKFVKFLIKEVLKPGREAE
EDLKGKTRHIKARERCASFNLELSKEYVVMGLDSEYQEHVQHGLVQPLYIMDTAAVVFPK
ATRDKQTRDLVTWFIREFSNEESRCFT

used for construction of the phylogenetic tree

H - thioester catalytic site residue

ISCW020810
DTYQDPVERECCSRGLKRDKFLRSCSERVDVLREYRDHDESLITEECIAAFATCCEQKEELEASARSGDKDGDSL
DDGEFEYDGTVRHDFRETSLFNQYTIGDNRRVEVEYSLPDSITTWEVNAVSTAPLGGICASEPLEIVAFKNVFVE
INVPYSVRKNEQVEIPATVYNYGQKAIKARVALRGTKDICSGTREGERSAIHRIDVPSGHGRTVIFPVIPLATGE
RYIEVI

anaphylatoxin domain

C3-2 (IsAM6)

>IsAM6>VBpre_T003199 cdna:PREDICTED_protein_coding
ATCGTTACGGCGCCAAACGTCGTTCGTCTGGGAGTCGAAGAGACGCTGGTCGTCTTCAAC
AGAGGCGTCGCCACGAAGGATGTCTCGCTCTTGGTACAAGACTACCCTGGTCGTCTCAAC
ACGCTGTTCAGGCATACTGTCAGCTTGGGCCCCGAGGAATCGCAGGTCATTCGAATGCGG
TTAGACACTGAGAAGATCAACGCAAAAGATGTTACAATGGGCCAACCGAGGTACGTGTCT
CTGATTGCCGAATGCGGAAATACTTACAAGAAAGAAGCCCGCCTGCTGATCAGCGACAAA
GGCGGATACCTCCTTTTGCAGACGGACAAGCCCATCTATACTCCGAAACAGACGGTCAAC
ATTAGAATGGTAGCCGTTGGAGAAAACCTCGTGCCCACCACTGGCCAAGTGAAGTTGAAA
ATCAAGAACCCCCAGGACATCGTCACTTACAAAACCGTTTTGGACACAACTTCCAACTCC
AGCGGGACGGGCATGTTCAGCCATTCCTATCGGTTCCCAGAGTCGCCTATCCTCGGAGAA
TGGAAGGCCGTCGTGACGCACGGAGCTCATCTTACTCAGGAGACGGAAGTCAAGTTCACG
CTGGACGAATACGTACTCCCAACATTTTCTGTGGAGCTGACTTTACCAAGCGTCATTCTA
ACCGACCAGGAATACATCGACGGAGAAGTTCTGGCGAAGTACGTATATGGCAAGCCAGTC
GTTGGATCTGTGGCCTTCAGATTTCGACTGAGAAACGAAGCGAACCAAGACACCGAAGTT
GGGTCGACGAATTTCAAAGAACTCATCGATGGAAAAGGGCGCTTTCGAATCGCGACGCAG
GAGTTTAGAATGATGCGCAGCAAACGGTGGGGTGCCCTGGTGAAAGGAAACAGGTTCGTC
GTCGAAGCCGATGTCCTGGACAAGGCGACTAGCAAGCGAGAATCAACTATAGATGACTCG
GCAATTTTCGCTTCCTCCCCGTACCTCGTGACCTTCAAGAGCACTCCCAAAGACTTCAAG
CCGGGAACCAGCACCATGATCGTGGCGGAGATCAAACATGTGAATGGCAAGCCTGCGATC
GGGATTCCTACCGAACTGACGGCCCTCGACGACCGAGAAGAAGCGGTTTTGGTGGACACA
ACCTCGTCGACGAGCGACAACACGGGAAGGGTAGCTTTCTCTGTCCAGACGTCCAGGTTT
CAGACGGCCCTCAAGATTAAGGTTCAAACAAAAGACCCAAAGTACGCATCTCACCAGCAA
GCGGACGGCAACATTGTGCTGCGTCCATTCACGTCACCGACGAATGCATTTGTATCTCTG
AAAAGGATTGACACCAGGGTTGCGCTTAAGGTTGGCGAACATTTTGACGGTTATGCAAGA
GCGGAGCCCTCTAATATTTCACCGATTTACTACATGGTAATCAGTCGAGGCCAAACAAAG
GCACACGGAAAAGTGAATGAATCAAGCTTCTACAAGACCTTCGGGTTCCAAGTGACTCCA
GAAATGAGTCCAGGGGCCAGGGTGCTGGTGTATGCTTTCCACGAAGGACACCTGCTTGCC
GACTCGATGAATATTGAAGTTGAAGAAGTCTGCACGGGCTCCTCTGATATTGAAATCGAG
CCCGAATTCAGGAGTGAGGAACCTGGATCCTCGGGAGTTCTGAATGTCCGTGGCAGAGAG
GGAACCCGCGTTGGAATTCTGGCCGTCGACAAGGCCGTCTACATTTTGAAAAACAAGGAA
CTTCTGACGAGAGAGAAGCTTTTTACAGTTTTGAAGTCCCACGACCTTGGCTGTGGTCCG
GGAGGTGGCTTGACGTCTGATGTTGTCATCGCAGACACCGGGATCGTGATAATATCTGAG
GAGACTCTAGAAAATGCCATCAGAACAGGTCAGAACTGTGAATCGCGCATTCGAAGACGC
CGTAGTATCCTAAAACGTGCCGCGGATAACTTCCAAGATCCCTTCCTTCGTCAATGCTGC
ATACTTGGTCAGAAAAGGGACCGCCTTGGAAGGACCTGCCAGGCTCGAGCTGACATAGTG
TATGAGCACATGGACGGAAAGGACCAGGCAAAAGAATGTTCCGAGGCCTTTGAGGAGTGC
TGCAAGGAGATTCGGCCACAAGGCCGTCGTGACCCAAATCTCCAAGCTACGGGGGACGAG
CGAGCTCGGCATGGCATCGAGTTTATAACGGAAGACTCGGTGGACGAGGTTGACGGTCCG
TCCACCAGCCCCCTCGTCCGGAGAGACTTCAGGGAGACGTGGCTTTTCGACGAGGGAACA
GTAGGGTCCGACGGCACTGCAAAGTTCAGCGCTAGCCTTCCACACAGCATAACCACTTGG
TCCATCCAAGCTGTGAGTGTGTCGCCGACAGGCGGCGTGTGTGTGCCGCCATCCAAAGAA
GTACGGGCTTTCCAAGACATCTTCCTGCAAGTCAGCATACCCTACAAGGTTGTTCGTAAC
GAGCAGATTGAAGTGCTCGCTACTGTCTACAACTACGGCAGCCGTAGTCTCCTCGGAAAC
GTGTACATCTACGGGGCCGAAGGACTCTGCACCGGGGCACCAGTGGGCCAAAGATCCGAG
CGAAGGCCAATTCAAGTAAACGCCACTTCGGCAACGAGCGTCACGTTTCCGGTGATACCT
CTCAAGGAGGGCGAATTTGTCGTCAAGATTCACGTGAAAAGTACGAGAGGGGAAGATATC
GTTGAAAAAGTACTCAACGTAGTGCCAGAAGGTGTGACCGTGGAGAAAAGCATTTCGATC
CCGATTGATCCAACGAACGAACGGAGAAGGAAAACTCGGAGCATACGTGGTGATCGTTAC
CAAGATTCTTTGGATACGGCGGCTAAAGTGCAAGTCATTGCTGTGAACACACGACTGCCT
CCGGACGCTGTTCCTGACACCAAGCATTGTTCACTATCGGTAATAGGAAACAAGATTGGG
CCTTCTGTTCAAACAACGTTACAGAACATCGAAAATCTGATTGCAATGCCCACGGGGTGC
GGCGAGCAGAACATGATGCTCATGGCCCCTACACTCTACACCCTTGAGTACCTTAAGCAT
AAGGGCGTTTTGAATGCAACGTTAGAAGAGAAAGCGTACAGATACGTCCGGGAAGGTTAC
GAGCAAGAGTTATCATTCCGGAAACCAGACGGTGCTTTTTCGGCTTTTAAGCACAGGGAC
AGCAGTGTCTGGTTGACTGCGTTCGTGATGCGAGTGTTTTGCAAGGCACGGCAGTACGCC
AGCATTGATCCTGAAGTTATCAAGAGCGGAATGCTCTGGTTGGCATCAAGGCAGGAAATT
GACGGAAGTTTCAAGGAGCGCAAACCTATTATGCACAAGGTTATGCTGGGTGGTGTAAAG
GGTTCAGTACCAATGACAGCCTTTGTACTCCTTACCTTTTATGAATGTCAGTCCCCATCT
GACACGGAAGATAAGACGAAGAGCAACGCCGAAGAATACCTTAACCGACACGTGCACGAC

ATACACGAACCCTACGTGGCTGCGTTGGTGGCTTACGCATTAAGCTTAGGAAACAACCCC
GAGAAGCATACCGCCATGGATGTCATGAAAGATGAACTGCTCTACGATCACGCGTTGAAC
ACAAGGAGTACGGGAGAAGAGGCAACACCCTTAGTGGTTGAAGGCACCAGCTACGCCTTG
TTGGCTTTCCTTGAGCATAACGACTTGGAATCAAGTAGCAGCATAGTCAACTGGTTGAAC
ACACACCGTTCAGCCTCAGGATCTTTCGTGTCTACGCAGGACACGGTGGTGGCCCTGCAA
GCACTCACGGAGTTTGCCCTCAAAGCTCGAGAGAGCTATTTGGATCTTATGTGCAACGTG
ACTCTGAGCAACCAACGCAATTTTAAAAAGAGCATCCGGCTAAAGCGAGAAAACGCAGCC
ATTCTTCAGCAACTGGATATTCCTGATGTGAGCGGTAAGATGTTTGTAAGTGCAAGTGGC
ACCGGCAGTGGCTTGCTCTCTGTCAAGATCAAGTACAATGTCTTAGTTCCTCCCGAAGCT
TTGTGTAAGAAATTGCATGTATTTCTTAATTTTAATGCAGTAGCCCTAGTGCATTTTTGC
ATGCTATTCAACGTTTTTCCTTCACTTTTTTTTCAGTTCAATATAACAGTGAAAGCCGAA
GTACATATAGAAAGAAAAAAGAGTGTTAAGAGCCTAGATTTTCCACCAGACCTTCTTGAT
GAACTGCTTGGTCCAGAGCCGAATAGGAGTGAGTATGGTGCCGGTTTTCTATACACTTTT
TTTAAAAGCAAGTTGTTATACGACATTGAAGTTTGCTCACGGTATCTTGGGGGCTCCGAG
TCAAACATGGCAGTCATTGAGGTTGGAATTTTCAGTGGCTTTGTGCCCGTGGAAAAAGAC
CTGAAGGAGGAGACAGCCAGAAACGAATTACTTGCCAAATATGAAATTACTGAGAAAAAC
GTTATCCTCTATTTCGACAAGATCCCCGCAGAGGTGCCGACCTGTGTTAAATTCAGAGCT
GAGCGGGAACATGTTGTGCACAATGTTCAGTCAGCCGTCGTTAAGGTTTACGACTACTAT
AATCCAATGCATTCATGCACCCAGTTCTACGGTCCAGGCTCAACCAGTCCTCTGCTGAAA
CTTATTTGCGAAGACAACCAGTGCCAATGTGCAGAAGCCGAGTGCCCAAACAAGGAGCCT
TTCCACGAGATCACGAAAGCCGGAAGCATTTTCAGACAAAGGAAAAATTTGGGCATAATG
GCTTGCGAGAACCACGACTTTGCTTGGAAAGGTCAAGTATTTTCCAACGAAGTGGAGAAC
GGCTACCGCAACATTCGCTTCAAAGTTGATGTCGCCGTCAAAGAAGGTGCAGAAAACAAA
ACGGCTCTTTTAAGCAACCTCAAGATTCTCAGGGCCAGGGAGCTGTGTCACATGGCCGAC
TTGACAGTCGGAGGAATATACATGATCTTCGGGGAAGACAGCGAGCCTTTCGAAAGAAAC
GGCAATGTCATACGAAGATACGACCTGAACCAAAATGTACGGATATTCAACTTGCACGAC
AGGTCAAGCACTGAAGACTACAGGAAGTTGAGCTCGCTTTTCCAGTGGTTGACTACTGGA
TTCATCAAAAGGGGAGGCTGTGGTCCTCAGTAA

both RT-PCR and RNAi primers
RNAi primers

IsAM6>VBpre_T003199 peptide:VBpre_P003199 pep:PREDICTED_protein_coding
MRLDTEKINAKDVTMGQPRYVSLIAECGNTYKKEARLLISDKGGYLLLQTDKPIYTPKQT
VNIRMVAVGENLVPTTGQVKLKIKNPQDIVTYKTVLDTTSNSSGTGMFSHSYRFPESPIL
GEWKAVVTHGAHLTQETEVKFTLDEYVLPTFSVELTLPSVILTDQEYIDGEVLAKYVYGK
PVVGSVAFRFRLRNEANQDTEVGSTNFKELIDGKGRFRIATQEFRMMRSKRWGALVKGNR
FVVEADVLDKATSKRESTIDDSAIFASSPYLVTFKSTPKDFKPGTSTMIVAEIKHVNGKP
AIGIPTELTALDDREEAVLVDTTSSTSDNTGRVAFSVQTSRFQTALKIKVQTKDPKYASH
QQADGNIVLRPFTSPTNAFVSLKRIDTRVALKVGEHFDGYARAEPSNISPIYYMVISRGQ
TKAHGKVNESSFYKTFGFQVTPEMSPGARVLVYAFHEGHLLADSMNIEVEEVCTGSSDIE
IEPEFRSEEPGSSGVLNVRGREGTRVGILAVDKAVYILKNKELLTREKLFTVLKSHDLGC
GPGGGLTSDVVIADTGIVIISEETLENAIRTGQNCESRI**RRRR**SILKRAADNFQDPFLRQ
CCILGQKRDRLGRTCQARADIVYEHMDGKDQAKECSEAFEECCKEIRPQGRRDPNLQATG
DERARHGIEFITEDSVDEVDGPSTSPLVRRDFRETWLFDEGTVGSDGTAKFSASLPHSIT
TWSIQAVSVSPTGGVCVPPSKEVRAFQDIFLQVSIPYKVVRNEQIEVLATVYNYGSRSLL
GNVYIYGAEGLCTGAPVGQRSERRPIQVNATSATSVTFPVIPLKEGEFVVKIHVKSTRGE
DIVEKVLNVVPEGVTVEKSISIPIDPTNERRRKTRSIRGDRYQDSLDTAAKVQVIAVNTR
LPPDAVPDTKHCSLSVIGNKIGPSVQTTLQNIENLIAMPTG**CGEQ**NMMLMAPTLYTLEYL
KHKGVLNATLEEKAYRYVREGYEQELSFRKPDGAFSAFKHRDSSVWLTAFVMRVFCKARQ
YASIDPEVIKSGMLWLASRQEIDGSFKERKPIM**H**KVMLGGVKGSVPMTAFVLLTFYECQS
PSDTEDKTKSNAEEYLNRHVHDIHEPYVAALVAYALSLGNNPEKHTAMDVMKDELLYDHA
LNTRSTGEEATPLVVEGTSYALLAFLEHNDLESSSSIVNWLNTHRSASGSFVSTQDTVVA
LQALTEFALKARESYLDLMCNVTLSNQRNFKKSIRLKRENAAILQQLDIPDVSGKMFVSA
SGTGSGLLSVKIKYNVLVPPEALCKKLHVFLNFNAVALVHFCMLFNVFPSLFFQFNITVK
AEVHIERKKSVKSLDFPPDLLDELLGPEPNRSEYGAGFLYTFFKSKLLYDIEVCSRYLGG
SESNMAVIEVGIFSGFVPVEKDLKEETARNELLAKYEITEKNVILYFDKIPAEVPTCVKF
RAEREHVVHNVQSAVVKVYDYYNPMHSCTQFYGPGSTSPLLKLICEDNQCQCAEAECPNK
EPFHEITKAGSIFRQRKNLGIMACENHDFAWKGQVFSNEVENGYRNIRFKVDVAVKEGAE
NKTALLSNLKILRARELCHMADLTVGGIYMIFGEDSEPFERNGNVIRRYDLNQNVRIFNL
HDRSSTEDYRKLSSLFQWLTTGFIKRGGCGPQ

used for construction of the phylogenetic tree

RRRR- putative post-translational cleavage site

H - thioester catalytic site residue

C3-3 (IsAM7)

IsAM7>VBpre_T003755 cdna:PREDICTED_protein_coding
ATGGCTACTGATAAGGCTGTCTACATCCTTGACAAGGGACAACTTCTGACTAGGCAAAAG
CTGTTATCATCGTTTCGGTCGCACGATCTCGGATGTGGTCCTGGAGGGGGCATCACGTCC
GAGGAAGTAATTTCTCAAGCTGGAATCGTGATAATATCGGCAGCGATGAAAGAGGACGTG
ATAACAACAGACGGTAGCTGCGAAGCAAAAAGACGGAGACGAAGGAATGCAGTCCGAAAA
TCCATTGAAAGCTACCAGGACCCTCTGCTGAAAGAGTGCTGCTGGCTCGGCATCCAGCCC
GACAAAATGGTCAGACACTGTTCCACCAGGAGCGAGATTGTCAAGAGGTACATGCCGGGT
CCAGAGGGTGCGCGGTGCGCCGACGTTTTCGCAAAGTGTTGCGTCGAGGCGGAGAATTTC
GGACCCACCAGCATTCAAGATGTCATCGACGCAGATTACGACGAAGACCTCTACTCGTTG
TCTTCCATCCGAAAAAATTTCCGGGAGACTTGGATGTTTCGCGAAGAAAATATCGGGAAG
GACGGTATCGCCAAATTCGAAGGAAGCCTCCCGCACAGCATCACTAAGTGGTCCGTACAG
GCGGTGAGCGTATCTCCAAAGGGCGGCATCTGCGTCGCCGAACCGGCCGAAGTCACGGCC
TTCCGCCAGGTCTTCCTCCAGGTCGACCTACCGTACAAGGTGGTCAGGAACGAACAGGTC
GAGGTTCTGGTGACAGTGTACAACTATGGGTCCAAATTGCTTTATGTGACCGTATTTTTG
TACGGAGTTCCGGGTGTGTGTACCGGTGCCCGCCACCAGCTACGCCCAGACCAGAAACCG
GTGGAAGTGAAGGCCCAGTCGGCCGCCAGCGTCACCTTTCCGGTGATACCGACGCTCGAA
GGAAAGCACACGATTCGCATCCTC

GenScan prediction – region DS765537 (2984-3142)

GATACCGTCGTTGCACTCCAAGCTCTCACTGAGTCTGGACTTAAGGTGCGCGACTCCAGC
CCTGACCTCATGTGCAACATCACTGCCAACCGCCCGAAAAATATATTTCACTCTTTCCGC
ATTAATAGAAGAAACGCTTTCATCTTGCAAGAAGTGCAC

GenScan prediction – region DS765537 (10389-10476)

ATATTTGGGAGAGCAAGACTCTAATATGGCTATTTTGGAGGTAGGGATGTTCAGCGGATT
TCACCCTATCGAAAAGGACTTGGCAAAT

IrAM7 cDNA partial sequence

CGAACCGGCCGAAGTCACGGCCTTCCGCaAGGTCTTCCTCCAGGTCGACCTCCCGTACAA
GGTGGTCAGGAACGAACAGGTCGAGGTTCTGGTGACAGTGTACAACTATGGGTCTGCCTT
GCTTTATGGAGCCGTGTTCTTGCACGGAGTTCCGGGGGTGTGTACCGGTGCCCGCCACCA
GCTACGCCCAGACCGGAAACCGGTGGAAGTGAAGGCCCAGTCGGCCGCCAGCGTCACCTT
TCCGGTGATACCGACGCTCGAAGGAAAGCACACGATTCGGATCCTCGTGAACACCTCACA
AGGCATAGACAGCGTCGAGAAAATCCTCAATGTCGTGCCAGAGGGAATCACCGTAGAAAA
GAACATATCGATCGTGCTTGATCCTACAAACCAACAACAGCGAAAAGACTATCGCGTGAA
AGGCGATTTCTTTACAGATTTTCTTGACCCGAAGTCAAAGCGCCAAAACATCAAGATCGA
CACACAACTGCCCCTAGAAGCCGTCCCAAATACAGGGGTCTTATCCTTGGGAGTTATgGG
AAATCAAATGGAATCAACTGCGGAATCAACCATAGCCAACGTCGAGTCCCTCATCTCTTT
GCCAAGGGGCTGCGGTGAGCAGAACATGATGCTCATGGCACCCACcTTGTATGCGTTGGA
ATATCTCAAACACAAAAATTCCCAAAACaCCGCCGTGATGGAGAAAGCCTACCGGTACAT
ACAGCAAGGTTACGAGCAGGAGCTGGCGTTTCGAAATGACGACGGTTCATTCTCGACGTT
CAAACAAAGGAAAGGTAGTCTTTGGTTGACAGCCTTCGTGCTCCGGGTGTTCTGCAAGGC
CACGAAGGTAATCAACATCGACCATCGAGTTCTTCATAGCGGAGTTTCCTGGCTTGCCAA
GCAGCAAAGAGCAGACGGGGACTTCGAGGACGAATCGCCTCTCATGCATGGCCAGATGCT
TGGCGGCGTCAACGGTAGGGTTCCAATGACAGCATTTGTGCTGCTGACACTCTATGAGTG
TGGATCTCGAACAACGGTAGACCAGCAGACGATGTTAAAAGTGACAGCTAGAGCTGAAAA
CTTCCTCAACGAGCGCATTAACGTGACGAAGCAGCCATACGTCGCAGCCCTTGTCGCGTA
CGCACTTAGCCTTGACAAAGGAGAGAAGCAACAAGAGGCATTCCAGGTTCTCAAAGATCA
CCTGCTTTACGATGAAGAGATGAACGAACTAAGTACGGGAAACGATGCGGCGGCCCTGGA
CGTGGAAGGCACCAGTTACGCCCTCCTGGCGTACCTGCGGCACGGTGACGTGGAGGGCGC

TGCCCGCCTCGTCAACTGGCTCAACAGACATCGCTCAGCGTCGGGCTCATTCACCTCTAC
GCAGGATACCGTCGTTGCACTCCAAGCTCTCACTGAGTCTGGGCTAAAGGTGCGCGACTC
CAGCCCTGACCTCATGTGCAACATCACTGCCAACCGCCCGAAAAATACATTTCACTTTTT
CCACATTAATAGAAGAAACGCTTTCGTTTTGCAAGAAGTGCACATAAAAGACATTGGTGG
AAAGCTACTTCTTTCAGTAAGCGGTGAAGGCACAGGTGTCCTTAGAGCGAGACTTCGATA
CAACGTTCTTACACCACCAGAAAACGTTTGCAAGTTTTCGCTGGCAGTTCGTGCCAGCCG
GCCCGAACCCGGGCATACACGCGGAGGACGCTCTCGGATGGTTCCGCCTGAGGTCTGGAA
AGAACTGCTGGGAGACGCCGCTCCGAGGCGCACCCTCGAGCGCATAGGAGGACACAGCAT
GATCCGGAACGACCGCGCTTCGCTGCCTACAGTTGCAGGGCTTAAAAAGGATTCAACGAC
TAGCATTATTAACAAGTGGAAGACCCTGAAAACATACGAGATTGAAGTCTGCATAAGATA
TTTGGGAAAGCAAGACTCTAATATGGCTATTTTGGAGGTAGGGATGTTCAGCGGATTTCA
CCCAAGCGAAAAGGACTTAGGAAATCTGACAGCTACAAATGCCTTACTAGGAAAATATGA
GCTAACAACGAAAGGTGTCGTATTTTATTTTGACAAGGTACCAGCTGACCGCGATACATG
CATCGTGTTCAGAGCCGAGCGTGCGTACAACGTGCTCAACATTCAAACGGCCACTGTGAA
GGTGTACGACTACTATCGGCCTGATCACTCGTGCAGTCAGTTTTATGGTCCCGAGACTTC
GAGCCCGTTGCTGGGGCTCTTCTGTGACGGTCCTCATTGCAAGTGTGCCTCAGCCGAATG
CCCCATCAACGAGACATTTGAGCGACTTTTGAAGTCCAATCCGGACATTACAGACTTCCG
AAACGCCAAGGA

RT-PCR-primers
RNAi primers

IsAM7>VBpre_T003755 peptide:VBpre_P003755 pep:PREDICTED_protein_coding
MATDKAVYILDKGQLLTRQKLLSSFRSHDLGCGPGGGITSEEVISQAGIVIISAAMKEDV
ITTDGSCEAK**RRRRR**NAVRKSIESYQDPLLKECCWLGIQPDKMVRHCSTRSEIVKRYMPG
PEGARCADVFAKCCVEAENFGPTSIQDVIDADYDEDLYSLSSIRKNFRETWMFREENIGK
DGIAKFEGSLPHSITKWSVQAVSVSPKGGICVAEPAEVTAFRQVFLQVDLPYKVVRNEQV
EVLVTVYNYGSKLLYVTVFLYGVPGVCTGARHQLRPDQKPVEVKAQSAASVTFPVIPTLE
GKHTIRIL **missing exons**

IrAM7 peptide
EPAEVTAFRKVFLQVDLPYKVVRNEQVEVLVTVYNYGSALLYGAVFLHGVPGVCTGARHQL
RPDRKPVEVKAQSAASVTFPVIPTLEGKHTIRILVNTSQGIDSVEKILNVVPEGITVEKNI
SIVLDPTNQQQRKDYRVKGDFFTDFLDPKSKRQNIKIDTQLPLEAVPNTGVLSLGVMGNQM
ESTAESTIANVESLISLPRG**CGEQ**NMMLMAPTLYALEYLKHKNSQNTAVMEKAYRYIQQGY
EQELAFRNDDGSFSTFKQRKGSLWLTAFVLRVFCKATKVINIDHRVLHSGVSWLAKQQRAD
GDFEDESPLM**H**GQMLGGVNGRVPMTAFVLLTLYECGSRTTVDQQTMLKVTARAENFLNERI
NVTKQPYVAALVAYALSLDKGEKQQEAFQVLKDHLLYDEEMNELSTGNDAAALDVEGTSYA
LLAYLRHGDVEGAARLVNWLNRHRSASGSFTSTQDTVVALQALTESGLKVRDSSPDLMCNI
TANRPKNTFHFFHINRRNAFVLQEVHIKDIGGKLLLSVSGEGTGVLRARLRYNVLTPPENV
CKFSLAVRASRPEPGHTRGGRSRMVPPEVWKELLGDAAPRRTLERIGGHSMIRNDRASLPT
VAGLKKDSTTSIINKWKTLKTYEIEVCIRYLGKQDSNMAILEVGMFSGFHPSEKDLGNLTA
TNALLGKYELTTKGVVFYFDKVPADRDTCIVFRAERAYNVLNIQTATVKVYDYYRPDHSCS
QFYGPETSSPLLGLFCDGPHCKCASAECPINETFERLLKSNPDITDFRNAK

GENSCAN_predicted_peptide_ region **DS765537** (2984-12943)1|347aa
DTVVALQALTESGLKVRDSSPDLMCNITANRPKNIFHSFRINRRNAFILQEVHIKDIGG
KLLLSVSGEGTGVLTARLRYNVLTPPEKLCKFSLAVRASRPEPGQTRGGRSRMVPQEVW
KELLGDADPARTFERSSDFTTRPGGRSDKWIMTEITEKKDTDYGTHNSNEQLLFAGMGG
HSMIDNGRASLSTGIKKDLTTSIKNKWKALNSYEIEVCIRYLGEQDSNMAILEVGMFSG
FHPIEKDLANLTAINALLGKYELTTKGVVFYFDKVPADRDTCIVFRAERAYNVLNIQTA
TVKVYDYYRPERGMPASGVWLLYSSVFDECSEDKCSFVERKFVCFCTGIAMM

used for construction of the phylogenetic tree
overlapping sequences Ix. scapularis Ix. ricinus
RRRRR- putative post-translational cleavage site
H - thioester catalytic site residue

MCR1 (IsAM 8)

>IsAM8>ISCW003089-RA cdna:NOVEL_protein_coding

ATGCGGCAGGTGCCCCAGAGTGCCAAGCCCGGCAAGTACAAGTTTCGGGTGGAGGGCAAT
GTGAATGGAGTCTTGGGAGGCACAGGCTTCATACAGGAAAGGGATGTGGAATTCCAGCCC
CAGTTCCTCACCATCCTCATCCAGACCAACCAGTTTGTGTATAACTACGACCAGTCCATC
AAGGCCAGGATCGTACTCCTCACCACAGAACTGAAGCCCTACACAGAACCGGTCGATGTA
TGGATGTTATTACTCTTGCAGGACTCTCGAGGCATTGTAATGAAGCGGTGGGTCTCGCAG
TACCCTTATTTAGGCTTTGTCAAGATAAACTTTGAGCTCCCACACGACTTTGCTGTTGGC
TTTTGGACTCTGAAAGTTGTGGCTCTCAGCCAAGTAGAAGAGAAGAAGATCCTTCTAGAG
CGGTGGTACACTGAACGCTATGATGTTTACGTCACGATACCACCTTTCGTCCTGGACAGC
GACGAATACTACGAAGGCGATGTCTCAGCAAACTTCACAACAGTAAATCCTGTATATGGT
AACGCAACTATCAGGCTCTATTTCCAAGCAGGCTACCAGTTCAAGTTCCCAATGTCCGAC
CTAAAGGATCTGGCTGCACCACACTCTCTGGACAAGTGTGAGATTGAAGTAAAGGCTGCA
GTTGGAGAACGCTTCTTGGATATCATTGTTCACGGCTATGCAAGATCCAGAATAATCAAC
TCATCACTCAGCCTCAAAATTTTGGGGGTGAAGCCTCTGGTCTTTAAGCCAGGAATGACT
TTTACCATCTATGTAGCAGTGACCTACCATGACCTTGTGAAACTGCCTGAAGAGAAACTA
AAAGAATCGAACATCACTTTGAGCTTCACTGGTCAAGGAGGTGGTGGAGGACTGAATGAT
ATAGAAACACCACCTAACGAAAAAGGAATGGCCACCGTAGAGATTACACCACCTGAGGGA
ACCGAGAAGATAGTTATACGGGTAAATACCAATCAATACATTGTACCTTCCTACAAAGTT
AAAAATTGTCACAGTTCATGTTGCATTCATTTCATTGCTCTGCAGGCTAAGTACCGAGAC
AAGGAAGATGTTGTCGAGACAGAAGCTCTTGCTGTAGCTCAGCTCTCTCCTGGCAAGAAG
TTCATTCAGATATCAACAAGCACTTCCAATGGTGTTGCTGGAGAGTATGCCATTTTTCAT
GTTCGCACCAACTTCTACATAAAATTCTTCCATTATCTGGTAATTTCAAAGGGGACCGTG
TTACAAGCAGGAGTTCAGAAGGCTTATGGTCTGCTCCAGACCATTACCTCCTTCTCAGTT
CCCCTTTCACCAGAGATGGCTCCAGCAATTAAGGTCATGGTCTACCAAATTTCTGGGAAT
GGTGATCTTACTGCTGATGCAGTCATTGTGCCAGTGAGGGGTATCAACAGAGGCAATTTC
TACCTGTGGAAGAATCTCAAACAAGACCGCTCCAACAATTTAATTGAATTGGTGCCAACC
TACACTACTGAAACCATAGCTGGACTGAACGGTCTAGACAGTGACCTGGTTGCAGTACAA
GGGAAGAATGACCTGACACCGACTTCGGTGATTGAATCTTTCTACCGCATGGAAGATCAC
TGGGGGAGCCATATCAGAGCAATATGGAGAGACCGTGATGGCAAGCCAGATGAAGCAGAG
TATTTTGTGACTCCCAGCTTTGCTCCTGATGTCAACAAAACATTCATTTTTTCAGGATTG
ATTGTGGCCACAAATCTCAACGTCACCACATTGCCAAGTATGTTTCGTTTTTGTACTCCT
GCGTACTGCTTTGAAAGAATGTTCCGTTTTCTTGTCCCTTTCATGCTTTCCCTTGATGAA
CAAACATTTTATGATGGTGAACAAGATGACTTGGAAGACAAGCCTCTGTTTGAGTTTTTC
TTGTACAGAACAAACAGGTTTAACAACTTCTTTGATGCAACTGGTAGTAACTTTGCTTGG
CATCACGTCAAAACAGGCAACCTCAAAGATATCTACACACCGTGCATTGTTCCCAAACCG
CCCACAAATTACATGTTTAATGCCATTGCTGTCAGCAGGAAGTATGGATTCGCGATCATC
GACAAGCCCATATATCACAACAGCATGAGACCATTCTACATGACCTATGAAGCTCCCTCA
ACAGCGGTCATTGGAGAACAAATCGGCATTCGTGTGGTCCTTTTCAACTACCAGAGCTAC
CTAATCCAGGCAGAGCTGCGTGTACTAGGCTCAGATGACTACCGCTTTGTCCAAGTAGGA
CCACTGGGGAGAGTAGGGGCATATAACCCTGTTACCACTAAGGGAGAGATCCAGCACATT
GTCTATATTCAGCCATACCAGCACATTATCATTCATGTCCCTATTGTATCAGTAAAAATT
GGAGACGTGGAGGTGAACCTTGTTGCAACAACTCAAGTAGCAAGGGAGGAAGCTACCATA
TCAATAACTTTCCTGCCTGATGGAGTTCCCCTAAGAATGCACACATCTCTACTGATGGAT
CTGAGAGCACAAGCTTACAATCTCAAGTTTCTCGACCTGAATGTGACTGAAGATCCCATC
ATCCCTTTCGAGAGCCAGTATCGACGCTATCTTTTTGGATCACCTGCAGCCCATGTTTCT
GTCATTGGTGACGTTGTGGGAACTCCCCTTGAAGGAAATGTAGAACCTGAAGACTTTGGC
TTTTCAGCAGCAACAAAGTCAGGAGAACATGCCATGTTTGGTTTTGCCTACAATGTGCTC
AGGCTTACATACTTGCGACTTACTGATCAACTGACACGGGATATTGCCAAGCCTATCTTT
GAAAAACTCAACAAAGCTTATGTTTATCAGAGTTCTTATTTCAAGAATGGAGCTTTCACA
ATGTTCAAAAGGCAACCAAGTGTTTGGCTCACTGCATTCAGCATTCGTATGTACGAGTTG
GCACTTTTTCCGGACTGGGAGAACTTCATTTTCATTGATCCACGGCTCATTAGCCAGGGG
GTCACTTTCCTTCTGAGCCACCAGCAGCCTAATGGAGCATTCTACGAGACAACCAAACAT
CCTTGGAACCGCAGAATGAATGAAAAGGTTCTTGGAAGGGATGGAAGGTATCTCAACAGG
AATGTCACTCTCACAGCACAAGTGGTTTTGGCATTGTCAAAGGTCACACTAACTGGGGAC
ATCAGGCAGCAGGCAACAACTGCAAGGGCAGCAGCCGTGAAATATCTTGAAAGGCAACTG
GCACAGCTCAAGGATGCCTATGCTATTTCAATCACCACTTACGCTCTACTGGAAGCTGGC
TCAAATGAAGCAGAGTACGGCTACAACCTTCTGGAGTCGATAAAGCGAGACGCTGAGGGA
GCTATCTACTGGAGTAGTGTGCCCATTCCACCACCAGTAATTATTTCCCAAAGTCAGCGC

CCCTTCCTAATGCCTCGTTTCCCACACCCGGATGACTCCCTGGCGGTTGAGGCAACGTCG
TATGCTCTCATCATCTACCTCAAGCAAGGAGGCCTCTTCCAGGACCAAATAGTGCGCTGG
CTGAACCGCATGCGCACCACCGACTATGGCTTCATTGGAACACAGGCAAGAGACACCATT
GCGGCTTTGGAAGCTCTTACCCAATACTCATTTCGAACACACGTCCGTGGCATCACCGAA
ATGAAAGTCACTGTGGAGTCCTCATCTAACCCTGGCTTCCCAAGTACTCTTCAAATTTCA
AAAAATGACCTGGCTCGAAGAAAAGTCTTTGATGTGCAGCCAAATGTTTGGGGACATTGT
GATGTCCTCGCAAAGGGCGCAGGTCTTTCTGTGATCCAAATGGATGTTTCCTACAACGTC
GACAGAGACTTCCTGCTTGTACCTCCTGCTTACGAGGCATTTGAGTTGACGCTACAACCT
CACTTCTCAGGAAGAAACAGGTCCCACATCAACATCAAGAGCTGCGTCCGGTGGACCCTA
ACAAACATGAGTGAAGCCAGCGGAGCAGCTGTTCTGGAGCTAGCAATCCCAACCGGATAC
CTGAATTACCGGCCAACACTTGACGCCTATGTCAAGTCTCGCGTCGTACCAAGGTTGCGC
ATGGCCAAAGTCGCACCAAGAACAGCTGTTTTTATGTTTGAATATTTGACCAATGAGTGG
TCCTGTGTGGACTTCCTGATTCAGAGGTGGTACCCAGTTGCCAATTCAACGCGGTATCTT
AAGGCCAAAGTCTACGAGTACAACACCCCAGAAAACTACAAGGAAACAATCTGGGAGAAC
TACGACCTGTTTGTGCTGAGCATATGCGAAGTGTGTGGCTCCTACCAGTGTCCCTACTGC
CCTTACTTCAGCAGTGCCAGCAGCATTAGCTTGAGCTGGGTACTCATGTTCAGCACTGCC
CTCTTGTGCCAAGAACTCTACCGGAAAGTCACCCAATGAGGTGCCAGTTTTAAAGGCACC
TTGTCATCATCACTCATCGTCAAACTTCATGTAGGGTCGTCATAAAAGCAATCCTTGCTA
GCCGGTGGTCGTAACCGCCTTGTCACCTGAACCTGTGAAGCTCCTTCAATATGCTTTGTT
GTTTCCAAGCCAGAGGTGAGCATAGTATTTTTGTTTTGGAAAAAGGGAAGTGCATGAAAA
ACATTGAGAGGAATTTTGGATGAGGCTTGTGAAGTGAAATTGTGCAACTTGCGCAACAAG
TTCAAGACTGCACATAAGGAAGGAGCGTGGCATTCCCGTGAAGCCATAAACAGAAATATA
AATTGAGTTTTAAGTCATTTATTCTTCCGATCACCGGTTGATGAGGGGTGTGATTGTGCT
GTTGTACAGAAGGAGAAAAATAGTGAAACTCTTTGGAAAATACACCATACTATGCTGGTG
TTTAAAGAACCTGTCTTTTGTGTTTGCATTACAGAAGTGTCATACTGGGTGGTTTTACTG
CAGATGTACCGAGTGAAAGCATTGCACATGTGCGAGTGTACAGAAGTGTGAGGGGACCAT
GTTTGATGCGTTCATTACATTTCATCTGATATGTACTCATGAGATTTTAATTTTTCAGCA
GATCATCGGTAGATTGTCACATTTAGATTCCGTACAAAGAACATAGTGTAAAACTAGAAT
GAGCAAAAACTGTATAATTGCTTTCATTAGCTGC

both RT-PCR and RNAi primers
RNAi primers

IsAM8>ISCW003089-RA peptide:ISCW003089-PA pep:KNOWN_protein_coding
MRQVPQSAKPGKYKFRVEGNVNGVLGGTGFIQERDVEFQPQFLTILIQTNQFVYNYDQSI
KARIVLLTTELKPYTEPVDVWMLLLLQDSRGIVMKRWVSQYPYLGFVKINFELPHDFAVG
FWTLKVVALSQVEEKKILLERWYTERYDVYVTIPPFVLDSDEYYEGDVSANFTTVNPVYG
NATIRLYFQAGYQFKFPMSDLKDLAAPHSLDKCEIEVKAAVGERFLDIIVHGYARSRIIN
SSLSLKILGVKPLVFKPGMTFTIYVAVTYHDLVKLPEEKLKESNITLSFTGQGGGGGLND
IETPPNEKGMATVEITPPEGTEKIVIRVNTNQYIVPSYKVKNCHSSCCIHFIALQAKYRD
KEDVVETEALAVAQLSPGKKFIQISTSTSNGVAGEYAIFHVRTNFYIKFFHYLVISKGTV
LQAGVQKAYGLLQTITSFSVPLSPEMAPAIKVMVYQISGNGDLTADAVIVPVRGINRGNF
YLWKNLKQDRSNNLIELVPTYTTETIAGLNGLDSDLVAVQGKNDLTPTSVIESFYRMEDH
WGSHIRAIWRDRDGKPDEAEYFVTPSFAPDVNKTFIFSGLIVATNLNVTTLPSMFRFCTP
AYCFERMFRFLVPFMLSLDEQTFYDGEQDDLEDKPLFEFFLYRTNRFNNFFDATGSNFAW
HHVKTGNLKDIYTPCIVPKPPTNYMFNAIAVSRKYGFAIIDKPIYHNSMRPFYMTYEAPS
TAVIGEQIGIRVVLFNYQSYLIQAELRVLGSDDYRFVQVGPLGRVGAYNPVTTKGEIQHI
VYIQPYQHIIIHVPIVSVKIGDVEVNLVATTQVAREEATISITFLPDGVPLRMHTSLLMD
LRAQAYNLKFLDLNVTEDPIIPFESQYRRYLFGSPAAHVSVIGDVVGTPLEGNVEPEDFG
FSAATKSGEHAMFGFAYNVLRLTYLRLTDQLTRDIAKPIFEKLNKAYVYQSSYFKNGAFT
MFKRQPSVWLTAFSIRMYELALFPDWENFIFIDPRLISQGVTFLLSHQQPNGAFYETTKH
PWNRRMNEKVLGRDGRYLNRNVTLTAQVVLALSKVTLTGDIRQQATTARAAAVKYLERQL
AQLKDAYAISITTYALLEAGSNEAEYGYNLLESIKRDAEGAIYWSSVPIPPPVIISQSQR
PFLMPRFPHPDDSLAVEATSYALIIYLKQGGLFQDQIVRWLNRMRTTDYGFIGTQARDTI
AALEALTQYSFRTHVRGITEMKVTVESSSNPGFPSTLQISKNDLARRKVFDVQPNVWGHC
DVLAKGAGLSVIQMDVSYNVDRDFLLVPPAYEAFELTLQPHFSGRNRSHINIKSCVRWTL
TNMSEASGAAVLELAIPTGYLNYRPTLDAYVKSRVVPRLRMAKVAPRTAVFMFEYLTNEW
SCVDFLIQRWYPVANSTRYLKAKVYEYNTPENYKETIWENYDLFVLSICEVCGSYQCPYC
PYFSSASSISLSWVLMFSTALLCQELYRKVTQ

MCR2 (IsAM 9)

IsAM9> ISCW007141-RA cdna:NOVEL_protein_coding

ATGCCGGCGGTGGTGGCGTTGCTGGTGGTGGGGCTGCTGTCGCTGTCATCTGCACAGTAC
GCTGGCTACACGGACAACAGGATAGACAGCGGGCCCATTCACCACCAGCAGCCGAACAAG
CGGGTGGAAGACATGCTGCGGGTGACCCAGTCGGTGACCTACGTGAGTGGTGGTGCAGGA
GGCGGTCAGATGCTGAACCCGGTGCCCACACCCGTCTCGGGGTCCCTCGGCATTTGGGAG
GTAGTCCTGGAATCTACGCCGTCTTCGAGTGACTCCTCCTCGGTTAACGCTGTTAGGGCC
ATCAGGCTCGAGGCGGATTTCTATGACGCCAACTACGGGCAGGTTCGGGCCAGCCTTGTG
GCGTACTCATCTTATTCACCCACCAACCACCACATTCAAGTGATGACCAGCACAAAGAAC
CCAAAAGTCGGCGAGTACATCATCTTTCACGTGCGGTCCAACTACTACGTGGAATGCTTT
TCTTACATCGTCATCTCGAAAGGAATCATTCTGCTTTCGGGCCAAGAGAAGATGACTTCC
AGCATCAAGACATTTGCTGTGACCCTATCGCCTGAGATGGCACCCACATCCACTGTGATC
ATTTACGACTTGGCACACGGCAACGAAATCGTGGCAGACAGTCTCACATTCCCTGTTGAT
GGAATATCAAGAGACAAATTCAACATGACTCTGAACAACAGGAAGGACAAAACAGGAGAC
ACGATAGAGGTGGCCATTTATGGTGACCCTGGCACCTACGTTGCTCTCTCAGCAGTAGAC
CGCACATTGTACAACATGCAAGCAGGCACAGAGATCAGCTACTCTGAGATCAAGCCTGGG
AAGTCAGCAGTGGTGTACATGCCGATTGTAGCCATGCGTATTGGCACAATCAACGTGACT
GTCCTGTCGAAAACCCAGATTGCCAAAGACATGGTCACACGCTCGATTCTAGTAGAGCCT
GACGGCATCCCCCAAGCCCGCCACACTTCTCTGCTTCTGGACCTCACTCAAGGGGCCTAC
TTGATCAAATACCTCGACACAAATATCACCGAGACACCAATTCTGCCTTTTCGGCAGGAC
CGACTTTATATTTTTGGCAGCAACAAGGCTACCCTATCAATTGTTGGTGATGTGGTGGGA
CCGGCCTTTCCAACCATGCCTGTCAATGCCACCAGCCTCTTATCCAAGCCCTTCTACTGT
GGGGAACAGAACATGTTCAGCTTTGCTGCCAACTTGTACACGTTGTTGTACTTGCGGCTC
ACTAACCAGCGTGACGTTTCCATCGAGAAGCAGGCCTTCAAGTACCTAAACTTGGGCGGC
ATGAGGTACTGGTCTCGCAGCGACCTGCCGGCGCCTCCTGTCCTCATAGAGAACAACCGG
CCCTACCTGTACCCGCGCCTGCCCTTCACGAACGACGCCTCCAACGTGGAGACCACATCC
TACGGGCTGCTGGTGCACGTGGCTCGTCAAGCGGTCGTGCAGAAAGAGATTGTCGAGTGG
CTCAACACACAGAGGCTCTCGCACGGTGCCTGGGCGTCCACTCAGGACACCCTGATGGCG
ATGCAGGCACTGACCGAGTTTTCGGTGCAATCTCGCTCGAGGGATGTGACGGATATTACG
GTTACTGTTGAGGCCCCCTCCACTCCGGGCTTCACCAGGCAATTGCACATCGGCAGGGAC
AATCTGTCCAAGCTGCAAACACTCTCTATGGTGTTCTACTTCTGA

IrAM9 cDNA - partial sequence

TGTTGGTGATGTGGTGGGACCGGCCTTTCCAACCATGCCTGTCAATGCCACCAGCCTCTT
ATCCAAGCCCTTCTACTGTGGGGAACAGAACATGTTCAGCTTTGCTGCCAACTTGTACAC
ATTGTTGTACTTGCGGCTCACTAACCAACGTGACGTTTCCATCGAGAAGCAGGCCTTCAA
GTACCTAAACTTGGGATACCAAAGACAACTCAGTTACCAAAACGACGATGGGAGCTTCAG
TGTGTTTCGGTGGCACAGCCAGCCAAGTGTCTGGTTAACATCCTTTTGCGCCCGGGTGTT
TCACAAGGCAACGTTTCAGGAGTGGGAGCACTTTCTGTATATAGATCCCACCATCATCCA
GAAGGCCATAGGGTGGCTACTAGACCGCCAATCTCCCGAAGGCTCGTTTCACGAAACATC
CTTTTTCGCCTATGACCGCAAGATGTCTGCTTCGTCGGAGAATCCCGATGATCCGGTGCG
CTTCCGCAACGTGTCTCTAACCGCGCACGTGCTCATCACACTGGCCGAAGTTAGGGATAT
CCGAGGAGAAATCGGCTCAAGGGCAGCCACGGCCCGCAGGTCAGCTGCACGCTACCTGGA
GCGCATGCTGCACGATATCGAGAAGTTGGAGGACCCTTACGAACTGGCCATTGTGGCGTA
TGCCCTCACCCTGGTCAACAGCGTGGAAGGGGAGACCGCATTCAACCGACTGAGCGAGAA
GTTGAGAGAGACAAGCGGCATGAGGTACTGGTCTCGCAGCGACCTGCCGGCGCCTCCTGT
CCTCATAGAGAACAACCGGCCCTACCTGTACCCGCGCCTGCCCTTCACGAACGACGCCTC
CAACGTGGAGACCACATCCTACGGGCTGCTGGTGCACATGGCTCGTCAAGCGGTCGTGCA
GAAGGAGATTGTCGAGTGGCTCAACACACAGAGGCTCTCGCATGGTGCCTGGGCGTCCAC
TCAGGACACCCTGATGGCGATGCAGGCACTGACCGAGTTTTCGGTGCAATCTCGCTCGAG
GGATGTGACGGATATTAC

RT-PCR-primers
RNAi primers

IsAM9>ISCW007141-RA peptide:ISCW007141-PA pep:KNOWN_protein_coding
MPAVVALLVVGLLSLSSAQYAGYTDNRIDSGPIHHQQPNKRVEDMLRVTQSVTYVSGGAG
GGQMLNPVPTPVSGSLGIWEVVLESTPSSSDSSSVNAVRAIRLEADFYDANYGQVRASLV
AYSSYSPTNHHIQVMTSTKNPKVGEYIIFHVRSNYYVECFSYIVISKGIILLSGQEKMTS
SIKTFAVTLSPEMAPTSTVIIYDLAHGNEIVADSLTFPVDGISRDKFNMTLNNRKDKTGD
TIEVAIYGDPGTYVALSAVDRTLYNMQAGTEISYSE **missing exon** IKPGKSAVVY
MPIVAMRIGTINVTVLSKTQIAKDMVTRSILVEPDGIPQARHTSLLLDLTQGAYLIKYLD
TNITETPILPFRQDRLYIFGSNKATLSIVGDVVGPAFPTMPVNATSLLSKPFY**CGEQ**NMF
SFAANLYTLLYLRLTNQRDVSIEKQAFKYLNL **missing exon** GMRYWSRSDLPAPP
VLIENNRPYLYPRLPFTNDASNVETTSYGLLVHVARQAVVQKEIVEWLNTQRLSHGAWAS
TQDTLMAMQALTEFSVQSRSRDVTDITVTVEAPSTPGFTRQLHIGRDNLSKLQTLS
missing exon MVFYF

IrAM9-partial sequence
VGDVVGPAFPTMPVNATSLLSKPFY**CGEQ**NMFSFAANLYTLLYLRLTNQRDVSIEKQAFK
YLNLGYQRQLSYQNDDGSFSVFRWHSQPSVWLTSFCARVFHKATFQEWEHFLYIDPTIIQ
KAIGWLLDRQSPEGSFHETSFFAYDRKMSASSENPDDPVRFRNVSLTAHVLITLAEVRDI
RGEIGSRAATARRSAARYLERMLHDIEKLEDPYELAIVAYALTLVNSVEGETAFNRLSEK
LRETSGMRYWSRSDLPAPPVLIENNRPYLYPRLPFTNDASNVETTSYGLLVHMARQAVVQ
KEIVEWLNTQRLSHGAWASTQDTLMAMQALTEFSVQSRSRDVTDI

missing exons alternatively predicted using GenScan

GENSCAN_predicted_peptide_ region **DS779097** (69270-53752)1|527aa
PDIPTQWMLSAYGMGESSGFGILSNSISFSSAKPFYMNVEMPTKIRLGEQLGIRVTVFNY
RVYETEVLITLASSPDYKFVSVGALGRVNSYAPETFFGEHQHLIFIKPGKSAVVYMPIVA
MRIGTINVTVLSKTQIAKDMVTRSILVEPDGIPQARHTSLLLDLTQGAYLIKYLDTNITE
TPILPFRQDRLYIFGSNKATLSIVGDVVGPAFPTMPVNATSLLSKPFY**CGEQ**NMFSFAAN
LYTLLYLRLTNQRDVSIEKQAFKIPKTTQLPKQRWELQCVSVAQSAKCLKLEDPYELAIV
AYALTLVNSVEGETAFNRLSEKLRETKISKSSKCPAFVTVVKFTTQLMALTNNGARGRAE
IPGERCVNRDGGMRYWSRSDLPAPPVLIENNRPYLYPRLPFTNDASNVETTSYGLLVHVA
RQAVVQKEIVEWLNTQRLSHGAWASTQDTLMAMQALTEFSVQSRSRDVTDITVTVEAPST
PGFTRQLHIGRDNLSKLQTLSIPNAWGVIIVRAQGSGLAIVQLHVEY

used for construction of the phylogenetic tree
overlapping sequences Ix. scapularis Ix. ricinus
overlapping sequences ISCW007141 gene with exon prediction using GenScan

Sequences used for phylogenetic analysis in Fig. 1A.

α_2-macroglobulin group: *Homo sapiens* (HuA2M: NP_000005); *Mus musculus* (MoA2M: NP_783327); *Cyprinus carpio* (CarpA2M: BAA85039); *Limulus* sp. (LiA2M, BAA19844); *Ornithodoros moubata* (OmA2M: NP_000005); *Ixodes ricinus* (IrAM: ACJ26770); *Ixodes scapularis* (A_2M1, A_2M2°, A_2M3: this work - Text S1);

C3/C4/C5 complement group: *Homo sapiens* (HuC3: NP_000055, HuC5°: AAA51856); *Mus musculus* (MoC3: NP_033908); *Carcinoscorpius rotundicauda* (CrC3, AAQ08323); *Ixodes scapularis* (C3-1, C3-2, C3-3: this work - Text S1);

TEP group: *Anopheles gambiae* (AgTEP1: AF291654, AgTEP3°: XM_315149, AgTEP4: XP_318493, AgTEP15: XM_317088); *Drosophila melanogaster* (DmTEP1: CAB87807, DmTEP2: NP_523506, DmTEP3: CAB87809, DmTEP4: CAB87810); *Ixodes scapularis* (TEP: this work - Text S1);

MCR-like group: *Anopheles gambiae* (AgTEP13°: XP_317044); *Drosophila melanogaster* (DmMCR°: NP_524688); *Ixodes scapularis* (MCR1°, MCR2: this work - Text S1);

Alignment of sequences used in Fig. 1A

>**HuA2M**
PDTITEWKAGAFCLSEDAGLGIS-STASLRAFQPFFVELTMPYSVIRGEAFTLKATVLNY
LPKCIRVSVQLEASPAFLAVPVEK----------------EQAPHCICANGRQTVSWAVT
PKSLG--NVNFT-VSAEALESQELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNS
LLCPSGGEVSEELSLKLP-------PNVVEESARASVSVLGDILGSAMQNTQN------L
LQMPYGCGEQNMVLFAPNIYVLDYLNETQQL-----TPEIKSK---AIGYLNTGYQRQLN
YKHYDGSYSTFGE-----RYGRNQGNTWLTAFVLKTFAQAR------AYIFIDEAHITQA
LIWLSQ-RQKDNGCFRSSG--SLLNNAIKGG----------VEDEVTLSAYITIALLEIP
LTVTHPVVR---NALFCLESAWKTAQEGDHGSHVYTKALLAYAFALAGNQDK-RKEVLKS
LNEEAVKKDNSVHWERPQKPKA---------PVGHFYEPQAPSAEVEMTSYVLLAYLTAQ
PAPTSEDLTSATNIVKWITKQQNAQGGFSSTQ--DTVVALHALSKYGAATFTRTGKAAQV
TIQSSGTFSSKFQVDN--NNRLLLQQVSLP---ELPGEYSMKVTGEGCVYLQTSLKY
>**MoA2M**
PDTITEWKAGAFCLSNDTGLGLS-PVIDFQAFQPFFVDLTMPYSVIRGEAFTLKATVLNY
LQTCIRVGVQLEASPDFLATPEEK----------------EQKSHCICMNERHTMSWAVI
PKSLG--NVNFT-VSAEALDSKELCRNEVPVVPERGKKDTIIKSLLVEPEGLENEVTFNS
LLCPTGAEVSEQISLKLP-------SDVVEESARASVTVLGDILGSAMQNTQD------L
LKMPYGCGEQNMVLFAPNIYVLDYLNETEQL-----TQEIKTK---AITYLNTGYQRQLN
YKHRDGSYSTFGD-----KPGRSHANTWLTAFVLKSFAQAR------RYIFIDESHITQA
LTWLSQ-QQKDNGCFRSSG--SLLNNAMKGG----------VEDEVTLSAYITIALLEMS
LPVTHPVVR---NALFCLDTAWKSARRGASGNHVYTKALLAYAFALAGNQDT-KKEILKS
LDEEAVKEDNSVHWTRAQKPRV---------PADLWYQPQAPSAEVEMTAYVLLAYLTTE
LVPTREDLTAAMLIVKWLTKQQNSHGGFSSTQ--DTVVALHALSKYGAATFTRAKKAAHV
TIQSSGAFYTKFQVNN--DNQLLLQRVTLP---TVPGDYTAKVAGEGCVYLQTSLKY
>**CarpA2M**
PDTITSWDTEAFCLSS-KGLGLA-PPAKLTVFQPFFLELSLPYSIIRGEIFELKATVFNY
LSKCIMVKVTPAPSTDYTLKASSD----------------DQYSSCLCANGRKTFKWILT
PSVLG--VLNIT-VSAEAESSQTVCDNEIVSVPERGRIDTVTRSLLVQAEGTEKTETYSW
LLCPKGDTLSEEVDLTLP-------KDVIEGSARSSVSVIGDILGRALTNLHG------L
LQMPYGCGEQNMAILSPNIYILQYLENTEQL-----TSAIRER---ATAFLKSGYQRQLN
YRHTSGAYSTFG---------HGDENTWLTAFVLRSFGKAQ------KYIFIDPQIIQRA
KEWLIS-RQDSDGCFIQQG--RLFNNRMKGG----------VNDNVTMTAYITASLLELE
TPVTDLVVS---KGLSCLKSVVKDVEN------TYSTALLAYTFSLAKDTDT-RQQLFKK
LEDVAISDGSHLHWSQSG------------------SVDSDSLAVEISSYVLLAVLTAD
SL-TSADLGFANRIVSWLVKQQNAYGGFSSTQ--DTVVALQALSLYATKVFS-SDGSSTV
TVQS-AADTHRFDLNQ--DNKLLYQEKQLQ---NVPAKYSIEVKGSTCVSVQVAQFY
>**LiA2M**
PHTITEWVGSAICISEETGLGVS-EAATVKGFQPFFVSFTLPYSVIRGEKVPIIVTVFNY
LSECLPIKLSLEQSDKFEMQNDTNSYTSCVC-----GGKSDTTRWMIKPRSLGQVNLTVY
GASLPNEAICGN-QDYSTVTARDAATRQLLVEPE-GFPKEDTWSTFACPKD-QNGKFTAT
SDLLLPEDLVED------------------SARGYVSITGDLMGPAIKNLDH------L
VRLPTGCGEQNMVKFVPNIFVLDYLTATGSI-----TDSIKEK---ALNNMRKGYARQQN
YRHPDGSYSAFGN-------RDKQGNLFLTAFVYRSFAQAER------FILINKNKLNET
ENWILNRQR-SNGCFRKIG--KLFNSALKGGI-------------SSNDETPAPLTAYV
--LISLLEAGYKNE-TVIDQGISCLEALSNP-STYSLALFAYATSLAGHPSA-KDYLAKL
EERAITEGGKTFWKSPSSGRYY----------------WGNSIGVEIAGYAVLTLLQHG
GA---SNLAKVTPIIRWLAKQQNYRGGFYSTQ--DTVIALQAMSKFATIIYK-DELDLEV
GVESSGFEKKIMLTKDNSILMQTFRLQTVP------SPVDFEATGSGCGLVQTSLRY
>**OmA2M**
PHTVTEWVGSAVCINNQDGIGVS-DPARIKAFQPFFASFSLPYSVIRGEVFPVTLSVFNY
LDKCLPVELTLAESEDFEFL-EERTKTLCVC-----GSK-VVEKFSVKPKTIGEVNVTVF
AVGSENSEVCGD-KPVEKVVAKDAVTQPLLVEAE-GFPKEETRSVFICSQ--GEAGEKPQ
FELALPEDVVEG------------------SARAYVAVSGDIMGPAIKNLDS------L
VQVPTGCGEQNMVKFTPNVYVLDYLKATGKQ-----DADIEKK---AVENLKTGYQRQQK
YRHSDGSYSAFGT-------NDRQGSLFLTAFVIRSFKQAER------YIPIDEKMLQQS
VNWVLNKQIPVNGCFNNVG--RVLSSGLKG---------------KVNESNPGPLTAYV
--LAALLEGGLAHS-NLTEGALHCIDAQKNP-SPHNLALSVYATALAGQDVS--AKLEAL
ESLAVHDGALTHWR--NGG--------------------ASADVETAAYAVLTYVKLG
GQ---ENLNKAQPIIKWMATKRNSRGGFSSTQ--DTVLGLQALSAFSSQLSK-DPVDLAV

KVSGEQVEESYDLKEDSKLVLQQRKVVNLP------NTLTGETTGTGCALISTTLKY
>**IrAM**
PHTITEWVGSTVCINSQDGVGVS-DPAKIKAFQPFFASFSLPYSVVRGELVPVKVSVFNY
LEKCLPIGLALAESEDYTIQ-DSASTTLCVC-----GSKSLTHKFLVRPTTIGEVNFTVS
AAGSTSDTVCGD-QKVEKVVARDAVTRPLIIEAE-GFPKEETKSVFVCPKDVTEGDGKNE
FDLVLPDDLVEG------------------SARAYVSVTGDIMGPAVQNLDS------L
VRVPTGCGEQNMIKFTPNVYVLDYLKATGKH-----EEDIEKK---AVENLKTGYQRQMK
YRHPDGSYSAFGT-------SDSTGSMFLTSFVVKSFKQAEK------YVPIDAANLKES
IKWVTTKQK-TNGCFQNVG--RVLSSGLRG---------------KVNETAPGALTAYV
--LVALLEGGLAEP-KVVESALNCIAAQKNP-SPHNLAVSAYAAALAGHSSA-KDYVEKL
EAVATHKGGLTYWS--NAARKG----------------SSASADIETAAYAVLTYVKLG
DK---ENLGKAQPIVRWMATQRNSRGGFSSTQ--DTVLGLQALSAFATHVSK-DPVDISV
KVAGTDVDESYDLKEPTKLVIQEKKVTNLP------NKLAVETTGSGCALISTTLKY
>**A2M1**
PHTITEWVGSTVCINSQDGVGVS-DPAKIKAFQPFFASFSLPYSVVRGELVPVKVSVFNY
LEKCLPIGLTLAESEDYTIQ-DSASTTLCVC-----GSKSLTHKFLVRPKTIGEVNFTVS
AAGSNSDTVCGD-QKVEKVVARDAVTRPLIIEAE-GFPKEETKSVFVCPKDVTEGDGKNE
FDLVLPDDLVEG------------------SARAYVSVTGDIMGPAVQNLDS------L
VRVPTGCGEQNMIKFTPNVYVLDYLKATGKH-----EEDIEKK---AVENLKTGYQRQMK
YRHPDGSYSAFGT-------SDSTGSMFLTSFVVKSFKQAEK------YVPIDAANLKES
IKWVTTKQK-TNGCFQNVG--RVLSSGLRVI--------------TINEKVEGTLMHTM
RDFCHGLERGVRRPHFITERRYRYVSATKNIGRPHKLGLRAVKTVLA-KKTT-QLVRHNI
RQLFYSTGGLTYWS--NAARKG----------------SSASADIETAAYAVLTYVKLG
DK---ENLGKAQPIVRWMATQRNSRGGFSSTQ--DTVLGLQALSAFATHVSK-DPVDISV
KVAGADVDESYDLKEPTKLVIQEKKVTNLP------NKLAVETTGSGCALISTTLKY
>**A2M2**
PDTITRWEGSALCLHPEAGFGIS-QLANVTGFQPLFVSLTLPQFMKRGEVANVILTAFSY
VDKCVAVRVHLESVGNLEVGSSPNTTDALVCP-----GGSASFTYGVRATKLETARLRAT
VATRPDAQSDYPGTDLYNVNSSDTVLQTIQVRPE-GFPVREVDTYLLCASDEAGSNAPNS
LKISLPTPNALVED----------------SEKVVLVATGDILALEVKDLSVP------
-KLVFTSAEGTLAVLASSAYLLRYLEATGAD-----TPDLRSQ---LLSRIQQAYQSQYG
FRSSDGSYGPYSS-------SEYPRSVFLSAFAVKALTAAKP------YIGSVDSEIQRS
IQYVLQQRDRNNGCFQTLSPSGPFNGNYKN-------------GADLSLVVANSLLEGG
YNDSTVYKA-------VLECVDADNLPSN-----HTLALNAYFSALIGEDAR-ATNTLNK
LLQQADKNGGLTTWD--------------------------DGKTDTAGYAILTMKALG
QN-----LGAAQPIVRWLMQVFARYS-FSYSQ--AYSVAVQGLTEYSRVAFATPTDLTVT
VEDSQSGATPPETFAVSEQNKLVYQEKLLNKRQSYDLEATLNKGSKGCAAVQVKYYY
>**A2M3**
PHSVTQWQAGALCLHPTRGVGLS--NAALNALQPFFAQLTLPAVAKRGELVPVTATLFSY
LQACVPVKLSLNADSACMKLLGEP----------------QKRDCLCGNESIVLRVQVR
PLCLGAINITLH-ALGLAENKGLCDEGKPLETRQARDSLRKSLLVTVSPSWSHWLVFAGS
GEGPQKHEFPLELPRNVVS----------GSSRGVFTLSGNVGSPVSVDRLD-----KL
VRLPTGCGEQNLALLAPNVFVLDYLNSSGER-----GHPLESK---LKENIAKGYQRQLN
YRHAEGGYSAFGS-------QDPEPSLWLTAFAVRTFGRSR------RFMPIDEAELSGS
IRWILS-NQYDNGCFPSVG--RVLNSRLKGGLEG--------HSLAPLTAYVLISLLEAG
AEIPQVSRVG------AVRCLLQELQQQQQ--DSHTMALAAYAFSLFEDSK--ASELLAS
LRDEAQPGNGESIFFFFLS-----------TLHWHKNVSTAVAVETASYVVLASLKLG
G---RAAAKSVLPVVRWVLEQRNHDGGFVSTQARDTVVALQVLAEYAKATSS-SDTRLQI
RVSSEGLGS---TLTVNRENALLKQELFLP---VVPTVLHIEATGTGCAFIQATVKY
>**HuC3**
KDSITTWEILAVSMSDKKGICVA-DPFEVTVMQDFFIDLRLPYSVVRNEQVEIRAVLYNY
RQNQELKVRVELLHNPAFCSLAT-----------TKRR-HQQTVTIPPKSSLSVPYVIV
PLKTGLQEVEVK-AAVYHHFISDGVRKSLKVVPE-GIRMNKTVAVRTLDPERLGREGVQK
EDIPPADLSDQVPDTES---------------ETRILLQGTPVAQMTEDAVDAERLKHL
IVTPSGCGEQNMIGMTPTVIAVHYLDETEQW-----EKFGLEKRQGALELIKKGYTQQLA
FRQPSSAFAAFV---------KRAPSTWLTAYVVKVFSLAV------NLIAIDSQVLCGA
VKWLILEKQKPDGVFQEDA--PVIHQEMIGGLRNNN------EKDMALTAFVLISLQEAK
DICEEQVNSLPGSITKAGDFLEANYMNLQ---RSYTVAIAGYALAQMG-------RLKGP
LLNKFLTTAKDKNRWEDPGKQL--------------------YNVEATSYALLALLQLK
------DFDFVPPVVRWLNEQRYYGGGYGSTQ--ATFMVFQALAQYQKDAP--DHQELNL
DVSLQLPSRSSKITHRIHWESASLLRSEET---KENEGFTVTAEGKGQGTLSVVTMY

>**HuC5**
PDSLTTWEIQGVGISN-TGICVA-DTVKAKVFKDVFLEMNIPYSVVRGEQIQLKGTVYNY
RTSGMQFCVKMSAVEGICTSESPVIDHQG-------TKSSKCVRQKVEGSSSHLVTFTVL
PLEIGLHNINFS---LETWFGKEILVKTLRVVPE-GVKRESYSGVTLDPRGIYGTISRRK
EFPYRIPLDLVPKT-----------------EIKRILSVKGLLVGEILSAVLSQEGINIL
THLPKGSAEAELMSVVPVFYVFHYLETGNHWNIFHSDPLIEKQK--LKKKLKEGMLSIMS
YRNADYSYSVWKG---------GSASTWLTAFALRVLGQVN------KYVEQNQNSICNS
LLWLVENYQLDNGSFKENS--QYQPIKLQGTLPVEAR-----ENSLYLTAFTVIGIRKAF
DICPLVKIDT--ALIKADNFLLENTLPAQS---TFTLAISAYALSLGDKTHPQFRSIVSA
LKREALVKGNPPIYRFWKDNLQHK---------DSSVPNTGTARMVETTAYALLTSLNLK
------DINYVNPVIKWLSEEQRYGGGFYSTQ--DTINAIEGLTEYSLLVKQ-LRLSMDI
DVSYKHKGALHNYKMTDKNFLGRPVEVLLN-----DDLIVSTGFGSGLATVHVTTVV
>**MoC3**
KDSITTWEILAVSLSDKKGICVA-DPYEIRVMQDFFIDLRLPYSVVRNEQVEIRAVLFNY
REQEELKVRVELLHNPAFCSMAT-----------AKNR-YFQTIKIPPKSSVAVPYVIV
PLKIGQQEVEVK-AAVFNHFISDGVKKTLKVVPE-GMRINKTVAIHTLDPEKLGQGGVQK
VDVPAADLSDQVPDTDS---------------ETRIILQGSPVVQMAEDAVDGERLKHL
IVTPAGCGEQNMIGMTPTVIAVHYLDQTEQW-----EKFGIEKRQEALELIKKGYTQQLA
FKQPSSAYAAFN---------NRPPSTWLTAYVVKVFSLAA------NLIAIDSHVLCGA
VKWLILEKQKPDGVFQEDG--PVIHQEMIGGFRNAK------EADVSLTAFVLIALQEAR
DICEGQVNSLPGSINKAGEYIEASYMNLQ---RPYTVAIAGYALALMN-------KLEEP
YLGKFLNTAKDRNRWEEPDQQL--------------------YNVEATSYALLALLLLK
------DFDSVPPVVRWLNEQRYYGGGYGSTQ--ATFMVFQALAQYQTDVP--DHKDLNM
DVSFHLPSRSSATTFRLLWENGNLLRSEET---KQNEAFSLTAKGKGRGTLSVVAVY
>**CrC3**
PHSITTWVVQAVGISNTGGMCIA-EPLKITTFKSIFVQLNIPYSVVRNEQVEIQATVFNN
HAHQSVRASVYMYGVKGLCSGAE-----------EGQRTERKVLDIGRSSAKSVSFPVV
PLKVG--EFPVR-VVVFTVHGSDFIEKKLNVVPE-GAKDSKLISLQLDPTNQQKRQKRSI
HEKYYIDSIDPEKKMQISIVELQPPPNYVPDTAKCLVSVIADRFGPVVETALE--NTEKL
IQHPRGCGEQTMLFMAPTLYTVKYLKVTGQL-----NANTEKN---GYKFIRDGYSRELT
FRKNDGSYAAWQ---------NRPSSTWLTAFVMRVFCQAQ------KLIEIDEKVICSG
MQWLVQ-RQKPDGSFVDEK--PVIHQEMIGGVKG----------ALPMTAFVLMALHECS
CTTVPGLK---LAKIRAAAYLEIKVPHIQ---DPYIMSLVAYSLSLAGNNA--KVEANRK
LLSMATFQADKNYHYWGDPNSP--------------------RAIETAGYGLLVQILNN
------DIEYANSIVNWLNSKRTLSGAFKSTQ--DTVIALYALSEYSILAKK-PETDLQC
NVTLNNDPSFFKELHFKESTANILQQFQIS---NLGGHLIFNTTGYGMGQLAVELKY
>**C3-1**
PDSITTWEVNAVSTAPLGGICAS-EPLEIVAFKNVFVEINVPYSVRKNEQVEIPATVYN-
YGQKAIKARVALRGTKDICSGTR-----------EGERSAIHRIDVPSGHGRTVIFPVI
PLATG--ERYIE-VIAVSSSGSDSARVKLRIEHN-GAPRNESFNVPLNPTDVKKRQQRSI
FHEHYT--------------------------------GDKLGPALETMVK--NPGSI
MSMPTGCGEQTMISLAPTLYAYQYLRAVGSI-----GGPYEDH---ALGFIREGYKRILT
YRKPDGSFAVWT---------DHPSSLWLTAFVLRNLCEAR------KSTMIDEAVITSG
LRYIMT-QQQQNGSFKDAY--HLHHKELLGGVDG----------PVPLSAYVLLTLQECI
KDG---
---VRGTAYALMAFLSER
E-----NRDYVDGYVRWLNGKMQPTGALSSTQ--DTVVALQALAKYATVSKD-DNIDLTC
QVTVSKPREFKEVVRIKRDNAHQLTRIPIP---SEGDKIFVDVRGSGSAHMYFLYKY
>**C3-2**
PHSITTWSIQAVSVSPTGGVCVP-PSKEVRAFQDIFLQVSIPYKVVRNEQIEVLATVYN-
YGSRSLLGNVYIYGAEGLCTGAP-----------VGQRSERRPIQVNATSATSVTFPVI
PLKEG--EFVVK-IHVKSTRGEDIVEKVLNVVPE-GVTVEKSISIPIDPTNERRRKTRSI
RGDRYQDSLDTAAKVQVIAVNTRLPPDAVPDTKHCSLSVIGNKIGPSVQTTLQ--NIENL
IAMPTGCGEQNMMLMAPTLYTLEYLKHKGVL-----NATLEEK---AYRYVREGYEQELS
FRKPDGAFSAFK---------HRDSSVWLTAFVMRVFCKAR------QYASIDPEVIKSG
MLWLAS-RQEIDGSFKERK--PIMHKVMLGGVKG----------SVPMTAFVLLTFYECQ
SPSDTED----KTKSNAEEYLNRHVHDIH---EPYVAALVAYALSLGNNPE--KHTAMDV
MKDELLYDHALNTRSTGEEATP--------------------LVVEGTSYALLAFLEHN
------DLESSSSIVNWLNTHRSASGSFVSTQ--DTVVALQALTEFALKARE-SYLDLMC
NVTLSNQRNFKKSIRLKRENAAILQQLDIP---DVSGKMFVSASGTGSGLLSVKIKY
>**C3-3**

PHSITKWSVQAVSVSPKGGICVA-EPAEVTAFRQVFLQVDLPYKVVRNEQVEVLVTVYN-
YGSKLLYVTVFLYGVPGVCTGAR-----------HQLRPDQKPVEVKAQSAASVTFPVI
PTLEG--KHTIR-ILVNTSQGIDSVEKILNVVPE-GITVEKNISIVLDPTNQQQRKDYRV
KGDFFTDFLDPKSKRQNIKIDTQLPLEAVPNTGVLSLGVMGNQMESTAESTIA--NVESL
ISLPRGCGEQNMMLMAPTLYALEYLKHKNSQ-----NTAVMEK---AYRYIQQGYEQELA
FRNDDGSFSTFK---------QRKGSLWLTAFVLRVFCKAT------KVINIDHRVLHSG
VSWLAK-QQRADGDFEDES--PLMHGQMLGGVNG----------RVPMTAFVLLTLYECG
SRTTVDQQTMLKVTARAENFLNERINVTK---QPYVAALVAYALSLDKGEK--QQEAFQV
LKDHLLYDEEMNELSTGNDAAA--------------------LDVEGTSYALLAYLRHG
------DVEGAARLVNWLNRHRSASGSFTSTQ--DTVVALQALTESGLKVRD-SSPDLMC
NITANRPKNIFHSFRINRRNAFILQEVHIK---DIGGKLLLSVSGEGTGVLTARLRY
>**AgTEP1**
PDTTTSWYLTGFSIDPVYGLGIIKKPIQFTTVQPFYIVENLPYSIKRGEAVVLQFTLFNN
LGAEYIADVTLYNVANQTEFVGRP----------DTDLSYTKSVSVPPKVGVPISFLIK
ARKLGEMAVRVK-ASIMLGHETDALEKVIRVMPE-SLAQPKMDTSFFCFDDYKNQTFP--
---FNLDINKKADNG---------------SKKIEFRLNPNLLTMVIKNLDN------L
LAVPTGCGEQNMVKFVPNILVLDYLYATGSK-----EQHLIDK---ATNLLRQGYQNQMR
YRQTDGSFGVWEK---------SGSSVFLTAFVATSMQTAS-----KYMNDIDAAMVEKA
LDWLAS-KQHSSGRFDETG--KVWHKDMQG----------GLRNGVALTSYVLTALLEND
I-AKVKHAV---VIQNGMNYLSNQLAFIN---NPYDLSIATYAMMLNGHTM--KKEALDK
LIDMSISDNN----------------------KKERYWG-TTNQIETTAYALLSFVMAE
K------YLDGIPVMNWLVNQRYVTGSFPRTQ--DTFVGLKALTKLAEKISP-SRNDYTV
QLKYKKNTKYFNINSE--QID-VQNFLEIP---EDTKKLEINVGGIGFGLLEVIYQF
>**AgTEP3**
PDTTTSWYLTGFSIDPVYGLGIIKKPIEFITVKPFYIVDSLPYSIKRGEAAVLQFTLFNN
LEAEYIADVTLYNVANQTEFIERP----------DKDLSYTKSVSVPPKVGVPISFGVK
ARKLGEMVVRIK-ASIMTGKETDAMEKVIRVIPE-NIMFEKTETRFFSMDEYGKQEFN--
---MQLDIPKNIS-----------------TVQIKCRISSNLLSPVIHNLDS------L
LDVPSASGAPSMINFIPPLVVLDYLKAVSST-----TTHLIEK---ATGLLRNGYQLELK
YRQRDGSFGNWRD---------SKGSVFVTALVGTSLEAAS-----KHITEVDLTLVDRL
FEWLAA-KQHSSGRFDEEQ--PITYYSLQG----------GSRNGIALTSFVLIAFLQNT
K-ASAQHRS---IIEKGIQYVANQLESIA---DVYDLSLATYALMLADHRQ--KSSALNK
LIELGIATN-----------------------ETRYWPRDTASIETTAYALLSLVHAK
R------YADGLMVMHWLVNQQSATGSFPRTQ--DTFVGIRALAALSEAIAP-QKNDYTA
IVLHGKARKVYKVAAS--EAD-QEYHDVLP---GDSKLVRFSANGRGFGMFTVAFQY
>**AgTEP4**
PDTITAWHLTGFSIDPVYGLGIIKQPLQLTTVQPFYIVPNMPYSIKRGELVELQFIVFNN
FPKKYKASVTLFSVDNQTEFVGRP----------ATDT-----------GVPVAFLIK
ARKLGEMTVRVD-ASIEP--AKDSIESVIRVIPE-SLVKREMISRFFCHNTYQNQSFV--
---LGLDFDRKADAG---------------TRKIDFILTPNILTSVMDNLES------L
LSVPTGCGEQNMMRLVPIVLVLDYLTSIGSA-----DKQLTAK---AIGLLRAGYQNQMR
YRQPDGSFGLWEK---------SGGAVFLTAFVGKTLATAA-----KYISEIEPSMVEQA
FDWLAA-RQHSTGRFDEVG--PVFHRDMQG----------GLRQGIALTSFVLIALLEQP
K-VATKHRA---AIEKGIDYVTQTLGSIE---DSYDLAIATYALLLQKHSS--GERFLEK
LIGLSTVQQN----------------------GTERFWARDAHGIETTAYGLLSFVLAE
K------YVDGTSIMRWLVKQRYTPGSFPRTQ--DTFVGLKALTKLAEKISP-SRNDYSV
QLRHAGRKKEFRVTSQ--DIGTLQNAQQGV---DETAQLELHVAGIGFGLLQVVYEY
>**AgTEP15**
PDTITSWIITGFSVNPIYGLGLTQQPRKLNVFLPFFVSTNLPYSVKRGEVVAIPIVVFNY
MEDDQTAEVVLHNDEQEFEFADVENEVVESN----KVELFRQKRLDIASNTGKSVSFMVK
PKKLGHITIKVT-AKTKI--AGDAVERQLLVEPE-GLPQFINKAAFIDLR--AAPELT--
-KTFEVEIPKNAVPD---------------STRIEVAVIGDVMGSTIQNLDS------L
IRMPYGCGEQNMLNFVPNIVVLDYLKATNKL-----TANIEAK---AKKFMEAGYQRELG
YKHRDGSFSAFG-----END--KSGSTWLTAFVARSFKQAA-----NHI-TIDEGVIDKS
LEWLSD-HQAPNGSFPEVG--VVSHKDMQG----------GSGSGVALTAYTLIAFLENI
N-LVDKYKN---TINKAIDYVYRNTESLD---DTYALALAAYALQLADHSS--KGLILSK
LDTKATTDSDSKWWHKPIP----------ETEQKNPWYSRPNSVNVEMSAYGMLAFLEAG
------LDTDALPIMKWLIGQRNDKGGFQSTQ--DTVVGLQALAKLAAKITS-PNNDVTL
TAKINENQEKRMTVNA--ENGMILQKFELP---SAARNIEIQATGSGFAVVQLSYKY
>**DmTEP1**
PDTLTSWVITGFSLSPQSGLAVTRNPSRIRVFQPFFITTNLPYSVKRGEVIAIPVIVFNY

LGMDVKAKVLMDNSDGQYEFIETTNKNVSQY----LRGVRRKKTLWIPANTGRGISFMIR
PKKVGLTTLKIT-AISKY--AGDRLHQILKVEAD-GVQKYVNKAVLINVQRLNRRSLAPP
EKTIIIEKADNVIEG----------------SETVEFEVCGTSQAPQLEHLDD------L
VHLPCGCGEQNMFNFVPSILALSYLKAKNRQ-----DQEIENK---AKRYVETGYQIELN
YKRNDGSFSAWG-----QHD--ALGSTWLTAYVIRSFHQAA-----KYI-DIDKNVLVAG
LDFLVS-RQSTDGKFKELG--MVIHNSHG-------------SPLALTSFVLLTFFENE
E-YMPKYKH---VIDRAVEFVVTEVHQSN---EPYDLAIAALALSLARNRN--AYKVLDK
LDKLATRRGDHKWW--------------TGSD------KCKSSEVETTSYVLLALLEHN
------ISDEPKPIVDWLISKRNSNGGFVSSQ--DTVVGIMALTKYELQSHA-STEAIDI
EFWHLNEDKKHVRVTK--ENEFKVQTHQLP---ENTNEVKLLAKGQGRAQVQLTYRY
>**DmTEP2**
PDTITSWVVTGFSLNPTSGIALTKNPSKIRVFQPFFVSTNLPYSVKRGEVIAIPVVIFNY
LDKTLDADVVMDNSDQEYEFTEATNEVLEKA----IDEVRRVKRVTIPANSGKSVSFMIR
PKNVGFTTLKIT-ATSAL--AGDAIHQKLKVEPE-GVTLFENRAVFINLK--DQPEMS--
-QSLDADIPNEVVPQ----------------SEFIEFSVVGDLLGPTLQNLDN------L
VRMPYGCGEQNMVNFVPNILVLKYLEVTGRK-----LPSVESK---ARKFLEIGYQRELT
YKHDDGSYSAFG-----KSD--ASGSTWLTAYVMRSFHQAG-----TYT-DIDPKVITAG
LDFLVS-KQKESGEFPEVG--KLFDNANQ-------------NPLALTSFVLLAFFENH
E-LIPKYQS---AIKKAVRYVAEEADKTD---DQYSLAIAAVALQLAKHPQ--SEKVIAK
LESVARKENDRMWWSKATE---------STGEDGRVFHWKPRSNDVEITSYVLLALLEKD
------PAEKALPIIKWLISQRNSNGGFSSTQ--DTVIGLQALTKFAYKTGS-GSGTMDI
EFSSAGESKNTIKVNP--ENSLVLQTHDLP---KSTRKVDFTAKGTGSAMVQLSYRY
>**DmTEP3**
PSEMTSWVVSAFALDPVNGLGLSPPNGKLEAYKEFYISTELPYSIKRDELIAIPFVVHNN
RDSDLNVEVTFYNSALDFDFPQLDPKATNQP----KVELYRRRSLQVPGRSARSVSFIVT
PKRVGPLLVKAM-AASSQ--AGDTVEQNLLVEHP-GAMERINRGFLFELN--SNAQNR--
-RNVTIAVPRNAIPE----------------STRIEVSAVGDLIGSLVGNLDS------L
ILLPTGCGEQTMVNFVPNLIVLRYLGRLRQL-----TPEVELR---ATNNLAIGYQRILY
YRHENGAFSAFG-----LDI--KRSSTWLTAYVARSLRQAA-----PFT-QVDSNVLQKA
LTYLGS-VQSANGGFEERG--DVFERFGD-------------DGISLTAFVTLALMENV
D-LYPEYRN---NINKALDFITRGLDGSS---NLHAMAIGTYVLSRANHNA--KAAFLQR
LDSMATNKDGLKWWNKTAP----------AGEQQSPWYNATRSVNIEISAYAALALLENN
------LVGDALPVLNWLMDQRNPKGGFVASQ--DTVVGLQALLMFAERFSS-QGNNLQI
GFHYGEGAETIINVNA--ENSLALQTVELP---NNLKNLSVSATGRGMALAQVSYTY
>**DmTEP4**
PDTITNWVVTGFSLHPQKGLGVTNDQTNIKTFQPFFVSVRLPYSVKRGEVINVPALVFNY
LPKTLDVELTLDNEDQEYDFVDASNEVIG--------DQKRTQNIRVGANEAAGASFLIR
PKVIGNILLKFK-AISPL--AGDAIHKPLKVVPE-GITQYQNRAFFINLK--DTGEFK--
-NTFELEVPEDVVPD----------------SERVEFGLVGDLLGPVVKNLEN------L
LRLPSGCGEQTMSKLVPNYLVRDYLKSIKKL-----TPALDTR---IKRNLQDGYQHMLH
YRHDDGSFSSFGPTKWRQEDPVRNGSTWLTAYVLRSFSKIK-----DII-DLDEHILAKG
YEFLLT-RQAENGSFTEHG--EYFYSSQR-------------SLLTLTANSLLALLEEE
----KPNQA---AIDKAVAYLSANTAESI---ELLPKSIAIYALQKAKAPE--AAKQVAS
LKSLAKHEDDRTWWTEDLDK-L------RASKNCGRWWCWIWSQDVEITSYALLSLLDSD
QE----TADSVLNTVRWLIAQRNGFGGFASSQ--DTVVGLTALIKFAEKSGY-EAAKWEV
TVSNKGKREKTEKLNTSEENDLLLQTVEFP---QGTKSLEFEAKGTGAAMVQISYQY
>**TEP**
PDTITSWVISAFALDSLTGLGIAPSQAKVTVFRPFFVTASLPYSILRGESVAIQCVVFNY
NNKPVQARVTLENAKSEFVFTSLSNDVGGE-----QSKDRRSKEVTVPAQDGVAVSFLIT
PTKLGYIDIHVS-ATSSL--AGDSILKKLLVKPE-GSKQHFNRAVLVDRRNPSAPPTS--
-TNISIPIPKNAVPG----------------SERISVSAVGDLLGPHVNNLDQ------L
LVMPHGCGEQNMLDFVPNVVVLDYLRRANRL-----SPAVRGK---ALRNLEDGYQRQLT
YKRDDNSFSAFG-----NTD--RSGSTWLTAFVLKSFVQAV-----PYT-SVDPAVLENA
TRWLVE-RQKPDGSFEEPG--EVIYKPMQS----------GAGSGAALTAYVLIALLENK
VGFQHALRF---AASAAEEFLLKELRTQS---DPYVVAVVTYALHLSGHRA--RDGAFQK
LLSLATREDDMVFWKDPGVAPV------NTTDKQSDFFFKAHFKDVEMTAYALLTLMERG
------DVSAAIPVMRWLVSKQNSNGGYSSTQ--DTVIGIQALARLAASVVS-QTIAVDA
SVKYGDGRKRTLKIHS--GNALVLQRIELP---SDLKYVEIESSGFGVAIIQVSWSF
>**DmMCR**
PDRPAYWMVSAFSVSPSKGFGMMNKALEYVGVQPFFINVEMPEACRQGEQVGIRVTVFN-
YMITPIEAIVVLHDSPDYKFVHVEEDGIVRSYNPRTSFGEHQFFIYLEAQGTTVVYVPVV

PQRLG--NVDVT-LHVATLLGTDTITRTLHVESD-GLPQYRHQSVLLDLSNRAYVLEYMH
VNVTQTPEIPYQ-VDRYFVYG----------SNKARISVVGDVVGPIFPTMPV--NASSL
LSLPMESGEQNAFSFAANLYTIMYMRLINQR-----NKTLEKN---AFYHMNIGYQRQLS
FMRPDGSFSLFRS-----DWNNSDSSVWLTSYCLRVFQEAS-FYEWENFIWIDATIIEKN
MRWLLQ-HQTPQGSFFEVT--WLP-DRKMNRTNF--------DKNITLTSHVLITLATVK
DISGTLGSRVALATQRALAYIERNMDFLRHQAQPFDVAITAYALQLCNSPI--AEEVFAI
LRRQARTIGDFMYWGNQEIPQPPRKLENQKWFSLPRLPYEYDSLNIETTAYALLVYVARR
-------EFFVDPIVRWLNSQRLNDGGWASTQ--DTSAALKALVEYTVRSRLREVSSLTV
EIEASSQGGKTQTLYIDDTNLAKLQSIEIP---DAWGTIKVQAKGAGYAILQMHVQY
>**AgTEP13**
PQVPALWSVSAFGISGTRGYGMIRKPIEYVGIQPFFINVEMPTACHQGEQVGIRVAVFN-
YQTVDIEATVVLHSSPDYQFVHVEEDGIVRSYNPRTSFGEHQFYIYLNAQDSTNVYLPIV
PTRLG--EIEVT-IHASTLLGAHQISRKITVEAD-GLPQYRHQSILLDLRNRAYLVQFMH
VNVTETPIIPYE-IDRYYVFG----------SNRARISVVGDVVGAIFPTMPI--NTTSL
LELPMDAAEQNMFSFAANFYTIKYMRASTLR-----DKRTEKQ---AFHFMNILYQRQLS
YLMEDGGFSLFRA-----DWNQSAPSVWLTAYCAQVFGEMAGLYEYENFIFIDPYMIQKN
MHWLLR-HQKEDGSFWEET--WLP-DRKANSSAFFSRNDVVREKNVTLTAHVLITLTTVN
LPAGRLAARVALSQQRALQYLQRNLATIKESGSTYEIAIVAYALMIAKAPK--AEAAFTM
LSAKMRSIGEFNYWGEEEVPLPPTKLENQRYFSLPRLPYKYDSLNIQTTAYALLTYVSRQ
-------EIHVDPIVAWLNAQRLTDGGWASSQ--DTGMAMKALTEYSTRNRVSNVTQLAI
KVEATSLPGETKQLYITRKSLAQQQFLDVP---NAWGTVRVEATGVGYAILQMHVQY
>**MCR1**
PKPPTNYMFNAIAVSRKYGFAIIDKPIYHNSMRPFYMTYEAPSTAVIGEQIGIRVVLFN-
YQSYLIQAELRVLGSDDYRFVQVGPLGRVGAYNPVTTKGEIQHIVYIQPYQHIIIHVPIV
SVKIG--DVEVN-LVATTQVAREEATISITFLPD-GVPLRMHTSLLMDLRAQAYNLKFLD
LNVTEDPIIPFESQYRRYLFG----------SPAAHVSVIGDVVGTPLEGNVE--PEDFG
FSAATKSGEHAMFGFAYNVLRLTYLRLTDQL-----TRDIAKP---IFEKLNKAYVYQSS
YFKN-GAFTMFK----------RQPSVWLTAFSIRMY-ELALFPDWENFIFIDPRLISQG
VTFLLS-HQQPNGAFYETT--KHPWNRRMNEKVL-GRDGRYLNRNVTLTAQVVLALSKVT
-LTGDIRQQATTARAAAVKYLERQLAQLK---DAYAISITTYALLEAGSNE--AEYGYNL
LESIKRDAEGAIYWSSVPIPPPVIISQSQRPFLMPRFPHPDDSLAVEATSYALIIYLKQG
-------GLFQDQIVRWLNRMRTTDYGFIGTQARDTIAALEALTQYSFRTHVRGITEMKV
TVESSSNPGFPSTLQISKNDLARRKVFDVQP--NVWGHCDVLAKGAGLSVIQMDVSY
>**MCR2**
PDIPTQWMLSAYGMGESSGFGILSNSISFSSAKPFYMNVEMPTKIRLGEQLGIRVTVFN-
YRVYETEVLITLASSPDYKFVSVGALGRVNSYAPETFFGEHQHLIFIKPGKSAVVYMPIV
AMRIG--TINVT-VLSKTQIAKDMVTRSILVEPD-GIPQARHTSLLLDLTQGAYLIKYLD
TNITETPILPFR-QDRLYIFG----------SNKATLSIVGDVVGPAFPTMPV--NATSL
LSKPFYCGEQNMFSFAANLYTLLYLRLTNQR-----DVSIEKQ---AFKYLNL-YQRQLS
YQNDDGSFSVFR-------WH-SQPSVWLTSFCARVFHKAT-FQEWEHFLYIDPTIIQKA
IGWLLD-RQSPEGSFHETS--FFAYDRKMSASSE-NPDDPVRFRNVSLTAHVLITLAEVR
DIRGEIGSRAATARRSAARYLERMLHDIEKLEDPYELAIVAYALTLVNSVE--GETAFNR
LSEKLRETSGMRYWSRSDLPAPPVLIENNRPYLYPRLPFTNDASNVETTSYGLLVHVARQ
-------AVVQKEIVEWLNTQRLSHGAWASTQ--DTLMAMQALTEFSVQSRSRDVTDITV
TVEAPSTPGFTRQLHIGRDNLSKLQTLSIP---NAWGVIIVRAQGSGLAIVQLHVEY

Table S1. The oligonucleotides used in this work and comparison of *I.scapularis* genome and *I. ricinus* cDNA sequences

	Amplicon	Forward primer 5'-3'	Reverse primer 5'-3'	Expected size (*I. scapularis* - genome) [bp]	Real size (*I. ricinus* - cDNA) [bp]	Nucleotide identity[b] [%]	Remark (related to *I. scapularis* – genome)
RT-PCR	A2M1[a]	**TGATGCCGCCAACCTGAAAGAAAG**	**CCACTGTGAACCCGGAGACCAACT**	-	921	-	false exon
	A2M2	**AACTCCAAATGCCCTCTGAGAAGA**	**GGAGTATCGTGCAAAGACCTGTT**	832	832	96.2	
	A2M3	**GGTCTCTGGATCTTCAAGGG**	**GGACGTATGCTGTCAGTGG**	503	503	95.4	
	TEP	**CTACGTGGTGGCAGTGG**	**GGTTGAGGAAGAAGGCAGG**	587	587	92.9	
	C3-1	**CATCAGCTCACTAGGATTCCG**	**CTGGACTGTATCTGCCCG**	500	497	90.6	
	C3-2	**ACGAGATCACGAAAGCC**	**TGCTTGACCTGTCGTGC**	366	366	92.4	
	C3-3	**GCCAACCGCCCGAAAAAT**	**AATCCGCTGAACATCCCTACCTC**	-	509	-	
	MCR1	**CCATCTATGTAGCAGTGACC**	**GCAAGAGCTTCTGTCTCG**	***328***	***244***	98	addit. exon
	MCR2	**TGTTGGTGATGTGGTGGG**	**GTAATATCCGTCACATCCCTCG**	***498***	***1038***	99	missing exons
RNAi[c]	A2M1[a]	*ATGGGCCC***AACCCGAGTCCCCACAAC**	*ATTCTAGA***GCGTCACCGCAGCTCAAATCC**	-	574	-	false exon
	A2M2	*ATGGGCCC***TTCAGCAGGCCGATAAG**	*ATTCTAGA***TTCAAGGTCGTAGGACTGG**	***368***	***386***	93.8	missing codons
	A2M3	*ATGGGCCC***TTGGAAGGTCATTCCCTGG**	*ATTCTAGA***CCAGGCTGAGCCTCGTCACG**	236	236	95.4	
	TEP	*ATGGGCCC***CTACGTGGTGGCAGTGG**	*ATTCTAGA***GGTTGAGGAAGAAGGC**	587	587	92.9	
	C3-1	*ATGGGCCC***GAGTTTGTCTGCGATAAGGTG**	*ATTCTAGA***GAGAATTCCCTGATGAACC**	362	362	89.3	
	C3-2	*ATGGGCCC***CACGAGATCACGAAAGCC**	*ATTCTAGA***AGTGCTTGACCTGTCGTGC**	368	368	92.4	
	C3-3	*ATGGGCCC***TCGGCAGCGATGAAAGAGG**	*ATTCTAGA***GACAATCTCGCTCCTGGTGG**	186	186	96.3	
	MCR1	*ATGGGCCC***CCATCTATGTAGCAGTGACC**	*ATTCTAGA***ACAGCAAGAGCTTCTGTCTCG**	***331***	***247***	98.8	addit. exon
	MCR2	*ATGGGCCC***CTTCGAGTGACTCCTCCTCG**	*ATTCTAGA***TGCATGTTGTACAATGTGCG**	538	538	97.2	

[a] primers designed according to the IrAM sequence
[b] aligned by Jotun Hein Method (false or missing exons are excluded from the alignment)
[c] In italics - the forward and reverse RNAi primers contain ApaI and XbaI restriction sites, respectively

Table S2: Overview and designation of thioester proteins identified in the genome of *Ixodes scapularis*

Tick α_2M family name (original)	0.5 preliminary genome release[a]	1.0 genome release	Gene(s) ID in 1.0 genome release	The best matching score for BlastP search	E-value	Thio-ester	Cleavage motif [c]	Catalytic residue[d]	Conserved domains
A2M1 (IsAM1)	VBpre_T005181	DS970697	ISCW023777	**ACJ26770** alpha-2-macroglobulin splicing variant 1 precursor [Ixodes ricinus]	0.0	yes	**KR**	**S**	pfam01835 - A2M_N pfam07703 - A2M_N_2 pfam00207 - A2M cd02897- A2M_2 pfam07677- A2M_recep
A2M2 (IsAM2)	35256.m000030	DS790028	ISCW019882 ISCW019883 ISCW019887	**AAN10129** alpha-2-macroglobulin splicing variant 1 precursor [Ornithodoros moubata]	1e-139	**no**	**KR**	**S**	pfam01835 - A2M_N (ISCW019882) pfam07703 - A2M_N_2 pfam00207 - A2M cd02897 -A2M_2
A2M3 (IsAM4)	VBpre_T004236	DS716413	ISCW003923	**BAA19844** alpha-2-macroglobulin [Limulus sp.]	0.0	yes	no	**N**	pfam01835 - A2M_N pfam07703 - A2M_N_2 pfam00207 - A2M cd02897- A2M_2 pfam07677- A2M_recep
TEP1 (IsAM3**)**	35419.m000025	DS837598	ISCW020822	**XP_317088,** TEP15 thioester-containing protein [Anopheles gambiae]	0.0	yes	**RRRRR**	**Y**	pfam01835 - A2M_N pfam07703 - A2M_N_2 pfam00207 - A2M cd02897- A2M_2 pfam07677- A2M_recep
C3-1 (IsAM5)	35417.m000042	DS814846	ISCW020813 ISCW020811 ISCW020810 ISCW020809	**AAQ08323**, complement component 3-like protein [Carcinoscorpius rotundicauda]	1e-123	yes	?	**H**	pfam01835 - A2M_N (ISCW020813) pfam07703 - A2M_N_2 (ISCW020811) cd00017- ANATO (ISCW020810) pfam00207 - A2M (ISCW020810) cd02897- A2M_2 pfam07677- A2M_recep cd03574, NTR_complement_C345C
C3-2 (IsAM6)	VBpre_T003199	DS909780	ISCW022535	**BAH02276**, complement component 3 [Tachypleus tridentatus]	0.0	yes	**RRRR**	**H**	pfam01835 - A2M_N pfam07703 - A2M_N_2 cd00017- ANATO pfam00207 - A2M cd02897- A2M_2 pfam07677- A2M_recep cd03574 - NTR_complement_C345C
C3-3 (IsAM7[b])	VBpre_T003755	DS959833 + DS765537	ISCW023129	**BAH02276**, complement component 3 [Tachypleus tridentatus]	0.0	yes	**RRRRR**	**H**	cd00017- ANATO pfam00207 - A2M cd02896 - complement_C3_C4_C5 pfam07677- A2M_recep cd03574, NTR_complement_C345C
MCR1 (IsAM8)		DS687147	ISCW003089	**NP_524688** macroglobulin complement-related [Drosophila melanogaster]	0.0	**no**	no	?	pfam01835 - A2M_N pfam07703 - A2M_N_2 pfam00207 - A2M cd02896 - complement_C3_C4_C5 pfam07677- A2M_recep
MCR2 (IsAM9[b])		DS779097	ISCW007141	**NP_524688** macroglobulin complement-related [Drosophila	0.0	yes	no	?	pfam07703 - A2M_N_2 cd00112 - LDLa

				melanogaster]					pfam00207 - A2M cd02897- A2M_2 pfam07677- A2M_recep

[a] 0.5 preliminary version of *Ixodes scapularis* genome released in Vector Base. For the corresponding sequences see the online suppl. text S1.
[b] IsAM7 and IsAM9 sequences were predicted using an alternative exon/intron prediction using a GenScan program (http://genes.mit.edu/GENSCAN.html) and sequencing of corresponding *I. ricinus* cDNAs
[c] The putative arginine/lysin-rich cleavage sites important for post-translational processing of IsAM precursors
[d] The catalytic residue important for binding specificity of thioester proteins