



Supplemental Material to:

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**Symbiophagy and biomineralization in the “living fossil”
*Astrosclera willeyana***

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A FASTA formatted file of all ATG8 protein sequences used in our phylogenetic analysis.

>Cln XP_002129578.1 gi1198417572|ref|XP_002129578.1| PREDICTED: similar to predicted protein [Ciona intestinalis]
MKRKYEHFQKRTGEGEKIKKYDVRVPIVEKAKARIGLDLKKKYLVPDQVYFLIKRKHLPEDALFFVNNVPPSTMQLYQEHIEEDFFLYIAYSDESVYGA

>Cln XP_002129622.1 gi1198435488|ref|XP_002129622.1| PREDICTED: similar to microtubule-associated protein 1 light chain 3 alpha [Ciona intestinalis]
MPDRTKQFSDYKDRVQVSEI8KEPKPKPIVTERYQEQQLPVLDKTKFLVPMHSMKDLVRIIRRLQLSPSQAFLLVGHGMSVSDAVSEIYSEQQDEGFLYMYASQETFGT

>Nw_165338 |gi|Nwem11653381|gi|Nwem11653381|est|Ext_ggp_C_590022:1-116 [Nematostella vectensis]
MKREYKEHPFKRAEGEKIKKYDVRVPIVEKAPKARIGLDLKKKYLVPDQVYFLIKRKHLPEDALFFVNNVPPSTMQLYQEHIEEDFFLYIAYSDESVYGCDD

>Nw_181063 |gi|Nwem11810631|gi|Nwem11810631|est|Ext_GenewiseL1_C_258015:1-116 [Nematostella vectensis]
MKRAFKHSLDSRCQESSKIKRKYDVRVPIVEKAPKSTIQDIDKRFLLVPSDLVQAQMYIIRKRIQLPPEKAMFLFNKVLPTTSSMGSYEYEHKDEGFLYIAYSSENTFGH

>Nw_241851 |gi|Nwem112418511|gi|Nwem112418511|est|Ext_fmehs1_pg_C_520094:14-127 [Nematostella vectensis]
MADLDSRSGTFKPKFVSRDEVAGIAPKPKPIVTERYKEXDLPLDKTKFLVQDQLTMSQFVIIRNMGSLSTQAFYLLVNNKSLASMGTMALVEYEEKDEGFLYMYASQESGRULLESRPS

>Nw_121733 |gi|Nwem11217331|gi|Nwem11217331e_gp_182_87:1-199 [Nematostella vectensis]
PTASRRRDESETITQYVQKIPVIERLTKENLPLDKIKYLVPSDLTMSLASSIKRKLQGTQAFLLVNEKNMSESTTVGEVYRDERDEGFLYMYASQESFG

>Hmg_XP_002170100.1 gi1221000727|ref|XP_002170100.1| PREDICTED: similar to predicted protein [Hydra magnipapillata]
MKREYKEHPFKRSGEGEKIKKYDVRVPIVQZFYLIKRIHLRAEDALFFVNNVPPSTMQLYQEHIEEDFFLYIAYSDESVYGV

>Hmg_XP_002163079.1 gi122111900|ref|XP_002163079.1| PREDICTED: similar to predicted protein [Hydra magnipapillata]
MSRAELMTGSRVGGVMEQCQESTKISKYDVRVPIVEKAPKSTIQDIDKRFLLVPSDLVQAQMYIIRKRIQLAPEKAMFLFNKVLPTTSSMGSYEYEHKDEGFLYIAYSSENTFGSI

>Hmg_XP_002163175.1 gi1221121766|ref|XP_002163175.1| PREDICTED: similar to predicted protein [Hydra magnipapillata]
MNDKSKYKPFKQKSFASRRDEVAGIAPKPKPIVTERYKELKALMLDKTKFLVQDQLTMSQFVIIRNMGSLAPTQSYLLVNNKSLASMTTLQEVYKDEKDEGFLYMYASQEMFGF

>Ami_APG8 (GABARAPL2) [Astrasciera williyana]
MKREFNIFEVRCAEAGIKRKYDVRVPIVEKAPKSTIQDIDKRFLLVPSDLVQAQMYIIRKRIQLAPEKAMFLFNKVLPTTSSMGSYEYEHKDEGFLYIAYSSENTFGI

>Adu_XP_002384394.1 gi1340371223|ref|XP_002384394.1| PREDICTED: gamma-aminobutyric acid receptor-associated protein-like 2-like [Amphimedon queenslandica]
MKREFNIFEVRCAEAGIKRKYDVRVPIVEKAPKSTIQDIDKRFLLVPSDLVQAQMYIIRKRIQLAPEKAMFLFNKVLPTTSSMGSYEYEHKDEGFLYIAYSSENTFGT

>Adu_MP134BL3C gi1340374092|ref|XP_002385572.1| PREDICTED: microtubule-associated proteins 1A/1B light chain 3C-like [Amphimedon queenslandica]
MSTSEVPMFQKSFASRRDEVAGIAPKPKPIVTERYKELKALMLDKTKFLVQDQLTMSQFVIIRNMGSLAPTQSYLLVNNKSLASMTTLQEVYKDEKDEGFLYMYASQEFFG

>Adu_MP134B3B gi1340373992|ref|XP_002385523.1| PREDICTED: microtubule-associated proteins 1A/1B light chain 3B-like [Amphimedon queenslandica]
MPSLNSHPKSFVEASRRDEVAGIAPKPKPIVTERYKELKALMLDKTKFLVQDQLTMSQFVIIRNMGSLAPTQSYLLVNNKSLASMTTLQEVYKDEKDEGFLYMYASQEFFG

>Adu_GABA_RAP2 gi1340371721|ref|XP_002384393.1| PREDICTED: gamma-aminobutyric acid receptor-associated protein-like 2-like [Amphimedon queenslandica]
MSKMKAYKDFKPEVLAASKREKPEVPIVEKAPKSTIQDIDKRFLLVPSDLVQAQMYIIRKRIQLAPEKAMFLFNKVLPTTSSMGSYEYEHKDEGFLYIAYSSENTFGI

>Adu_GABA_RAP gi1340376326|ref|XP_002386684.1| PREDICTED: gamma-aminobutyric acid receptor-associated protein-like [Amphimedon queenslandica]
MAFQTKYKQKSFQRRDEGQRLKINPKSVPIVGVKWSGLPDIDKRFLLVPSDLVQAQMYIIRKRIQLAPEKAMFLFNKVLPTTSSMGSYEYEHKDEGFLYIAYSSENTFGI

>Tad_37981 |gi|Tfad1137901|est|Ext_GenewisePlus_C_61165 (Hsa_GABA_A_RAP hit) [Tricoplax adharens]
MKRKYEDFPFKRSGEGEKIKKYDVRVPIVEKAPKARVQIDKIKYLVPAALTVQGFHFLIKRKHLPEDALFFVNNVPPSTMQLYQEHIEEDFFLYIAYSDESVYGL

>Tad_35852 |gi|Tfad1135852|est|Ext_GenewiseL_C_40895 (Hsa_GABA_A_RAP hit) [Tricoplax adharens]
MKRFQKEHITLGRQEGSAKIDAYDVRVPIVEKAPKSTIQDIDKRFLLVPSDLVQAQMYIIRKRIQLAPEKAMFLFNKVLPTTSSMGSYEYEHKDEGFLYIAYSSENTFGT

>Tad_19802 |gi|Tfad1119802|e_gp_L1_2269.1 (Hsa_GABA_A_RAP hit) [Tricoplax adharens]
MSKDYVSKGRSFCVKRQDQEIERYKPIVVERLHTEKHLPLDKNKLVPEDLTMSQFVIIRKRIQLAPEKAMFLFNKVLPTTSSMGSYEYEHKDEGFLYIAYSQETFGT

>Tad_57027 |gi|Tfad1157027|fgeneshTAd_pg_C_scaffold_600000? (Hsa_GABA_A_RAP hit) [Tricoplax adharens]
MSFLVWPGQNFQKQSFARKAIVENYHFNKIPVTERYKELKALMLDKTKFLVQDQLTMSQFVIIRNMGSLAPTQSYLLVNNKSLASMTTLQEVYKDEKDEGFLYMYASQEMFGF

A Clustal formatted alignment file of all ATG8 protein sequences used in our phylogenetic analysis.

CLUSTAL W (1.7) multiple sequence alignment

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Scer_ATG8      -----MKS--TFK---S--EYFPEKRAKES
Spon_ATG8      -----MKS--QFK---D--DFSEKRTKTES
Hsa_GABA_A_RAP -----MKF--YVK---E--EHPFEKRSSEG
Hsa_GABA_A_RAP1 -----MKF--QYK---E--DHPFEYRKKEG
Hsa_GABA_A_RAP2 -----MKW--MFK---E--DHSLEHRCVES
Hsa_MAP1A1B3   -----MPSEKTFK--Q--RRTEFQRVEDV
Hsa_MAP1A1B3A -----MPSDRPFK--Q--RRSFADRCREY
Hsa_MAP1A1B3B -----MKWRFSFGCG--KAADPDRARCEY
Hsa_MAP1A1B3C -----MPSEKTFK--Q--RRTEFQRVEDV
Hsa_MAP1A1B3D -----MPPPOKIPSVRPFK--Q--RKLATRQEEV
Mmu_GABA_RAP   -----MKF--YVK---E--EHPFEKRSSEG
Mmu_GABA_RAP1 -----MKF--QYK---E--DHPFEYRKKEG
Mmu_GABA_RAP2 -----MKW--MFK---E--DHSLEHRCVES
Mmu_MAP1A1B3   -----MPSEKTFK--Q--RRSFQRVEDV
Mmu_MAP1A1B3A -----MPSDRPFK--Q--RRSFADRCREY
Btau_GABA_RAP  -----MKF--YVK---E--EHPFEKRSSEG
Btau_GABA_RAP1 -----MKF--QYK---E--DHPFEYRKKEG
Btau_GABA_RAP2 -----MKW--MFK---E--DHSLEHRCVES
Btau_MAP1A1B3 -----MPSEKTFK--Q--RRSFQRVEDV
Btau_MAP1A1B3A -----MPTPKQSPSLRPFK--Q--RKLATRQEEV
Btau_MAP1A1B3B -----MPSEKTFK--Q--RRSFADRCREY
Btau_MAP1A1B3C -----MKF--YVK---E--EHPFEKRSSEG
Sko_predpro1   -----MKW--QFK---E--EHSIDQRRAEA
Sko_GABA_RAPa -----MKW--EYK---E--EHPFEKRSSEG
Sko_predpro2   -----MVDKDKYQYFK--Q--RKSFATRKEEV
Sko_MAP1C3a    -----MTT-KTKF--D--RRSFAQRTKQV
Lgig_105301    -----MKW--QYK---E--EHPFEKRSSEG
Lgig_122374    -----MKW--QYK---E--EHPFEKRSSEG
Lgig_122409    -----MKW--QYK---E--EHPFEKRSSEG
Lgig_209102    -----MHSKMTFK--E--RRTSQREKQV
Lgig_194601    -----MKSELQESLQTKFK--Q--RKSFATRKEEV
Ctel_21814     -----MKW--EYK---E--EHPFEKRSSEG
Ctel_4205     -----MKF--MFK---E--EHPFEKRSSEG
Ctel_2981     -----MPENDISVGRFKF--Q--RKSFAQRCREY
Ctel_128947    -----MLI--TFE--I--ILSTGTRKKQV
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Dmel_ATG8b     -----MNTV--QYK---E--EHPFEKRSSEG
AmeL_GABARAP  -----MKF--YVK---E--EHPFEKRSSEG
AmeL_MAP1A1B3A -----MNLTPKSKFK--E--RRSFAQRCREY
Spu_XP_782118_2 -----MKW--LTK---E--EHPFEKRSSEG
Spu_XP_786800_2 -----MKW--DVA--Y--DMWHRITSES
Spu_MAP1C3B    -----MK--SFK---E--RRSFAQRCREY
Spu_GABA_RAP_1like MNCRLMKELRFLGLATLVLVNRRVQDQVLRIEAKMKW--GFK---E--EHSIDQRRAEA
Spu_GABA_RAP_1like2 MKW--EYK---E--EHPFEKRSSEG
Spu_MAP1A1B3C -----MGTDKTTEAEKDAVYKFK--Q--RKTFSQRKEEV
Dre_GABA_A_RAP -----MKF--MFK---E--EHPFEKRSSEG
Dre_GABA_A_RAP1 -----MSS--QYK--R--SVLEVRRAEG
Dre_GABA_A_RAP1_iso1 -----MKF--QYK---E--EHPFEKRSSEG
Dre_GABA_A_RAP2 -----MKW--MFK---E--DHSLEHRCVES
Dre_MAP1A1B3a -----MPSDRPFK--Q--RRSFADRCREY
Dre_MAP1A1B3b -----MPSEKTFK--Q--RRTEFQRVEDV
Dre_MAP1A1B3c -----MPPPEKTPHPKPFK--Q--RKLATRQEEV
Dre_MAP1A1B3c_like -----MPPPEKSMVMPFK--Q--RKLATRQEEV
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Cin_XP_002129578_1 -----MKF--QYK---E--EHPFEKRSSEG
Cin_XP_002129622_1 -----MPGRTFK--Q--RRSFEDRVKQV
Nve_165338     -----MKW--EYK---E--EHPFEKRSSEG
Nve_181063     -----MKW--QYK---E--EHPFEKRSSEG
Nve_241851     -----MADLDSRSTFKFKF--Q--RKSFAQRCREY
Nve_121733     -----PTASRRRDS
Hnog_XP_002170100_1 -----MKW--EYK---E--EHPFEKRSSEG
Hnog_XP_002163079_1 -----MSRAELDMTSRAGY--DQWESRQKES
Hnog_XP_002163175_1 -----MNDSSSTPKFKF--Q--RKSFAQRCREY
Awi_AP68      -----MKW--EYK---E--EHPFEKRSSEG
Agu_XP_003384394_1 -----MKW--EYK---E--EHPFEKRSSEG
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Agu_MAP1A1B3B -----MPSSSNPKSTVESRQSTFVAKNFKF--E--RRTEFQRVEDV
Agu_GABA_RAP2 -----MSMKW--ANY--D--EKPEYVLAAEA
Agu_GABA_RAP  -----MAFQVTKYKQV--KPFQRRLEG
Tod_37901     -----MKW--QYK---E--EHPFEKRSSEG
Tod_35852     -----MKW--QYK---E--EHPFEKRSSEG
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Scer_ATG8      ERTRDRFKNRIPVTEKAEKSD--IPEDIKRKYLVPAIDLTVGQFVYVIRKRIMLPPEKAI
Spon_ATG8      QRIRKYPDRIPVTEKAEKSD--IAADIKRKYLVPSDLTVGQFVYVIRKRIHLRRAEDALF
Hsa_GABA_A_RAP EKIRKYPDRIPVTEKAEKAPAR--IGDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Hsa_GABA_A_RAP1 EKIRKYPDRIPVTEKAEKAPAR--VPDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Hsa_GABA_A_RAP2 AKIRKYPDRIPVTEKAEKASQ--IVDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Hsa_MAP1A1B3   RLIREQHPKTPVIERYKGEKQLVLDKTKFLVPHVHMSLWIKIRRLQLNMQAFFF
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Hsa_MAP1A1B3C RLIREQHPKTPVIERYKGEKQLVLDKTKFLVPHVHMSLWIKIRRLQLNMQAFFF
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Mmu_GABA_RAP1 EKIRKYPDRIPVTEKAEKAPAR--VPDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
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Btau_GABA_RAP1 AKIRKYPDRIPVTEKAEKASQ--IVDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
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Btau_MAP1A1B3A RLIREQHPKTPVIERYKGEKQLVLDKTKFLVPHVHMSLWIKIRRLQLNMQAFFF
Sko_predpro1   SKIRKYPDRIPVTEKAEKASQ--IPDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Sko_GABA_RAPa EKIRKYPDRIPVTEKAEKAPAR--IGDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Sko_predpro2   AKIRKFPNKPVIVRYEETFLPDLKTKFLVQELTMTQFLSIRSMWLRTEAFY
Sko_MAP1C3a    EKIRKYPDRIPVTEKAEKAPAR--VGDLDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Lgig_105301    SKIKTKYPERIPVTEKAEKASQ--IQDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
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Lgig_209102    ESTIDQHPKTPVIERYKGEKQLVLDKTKFLVPHVHMSLWIKIRRLQLNMQAFFF
Lgig_194601    GQIRKFPNKPVIVRYEETFLPDLKTKFLVQELTMTQFLSIRSMWLRTEAFY
Ctel_21814     EKIRKYPDRIPVTEKAEKAPAR--IGDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
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Spu_MAP1C3B    EEIRKHPKTPVIERYKGEKQLVLDKTKFLVPHVHMSLWIKIRRLQLNMQAFFF
Spu_GABA_RAP_1like EKIRKYPDRIPVTEKAEKASQ--IVDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Spu_GABA_RAP_1like2 SKIRKYPDRIPVTEKAEKASQ--VPDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
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Dre_GABA_A_RAP1 EKIRKYPDRIPVTEKAEKASQ--IVDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Dre_GABA_A_RAP2 AKIRKYPDRIPVTEKAEKASQ--IVDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Dre_MAP1A1B3a QQIRDQHPKTPVIERYKGEKQLVLDKTKFLVPHVHMSLWIKIRRLQLNMQAFFF
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Dre_MAP1A1B3c_like SKIITKYPDRIPVTEKAEKASQ--IQDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Cin_XP_002128871_1 EKIRKYPDRIPVTEKAEKAPAR--IGDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Cin_XP_002129578_1 EKIRKYPDRIPVTEKAEKASQ--IVDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Cin_XP_002129622_1 EKIRKYPDRIPVTEKAEKAPAR--IGDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Nve_165338     SKIRKYPDRIPVTEKAEKASQ--IQDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Nve_181063     SKIRKYPDRIPVTEKAEKASQ--IQDIDKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Nve_241851     AKIRKFPNKPVIVRYEETFLPDLKTKFLVQELTMTQFLSIRSMWLRTEAFY
Nve_121733     EKIRKYPDRIPVTEKAEKAPAR--IGDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Hnog_XP_002170100_1 EKIRKYPDRIPVTEKAEKAPAR--IGDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Hnog_XP_002163079_1 EKIRKYPDRIPVTEKAEKAPAR--IGDLKDKKYLVPDQTVGQFVYVIRKRIHLRRAEDALF
Hnog_XP_002163175_1 AKIRKFPNKPVIVRYEETFLPDLKTKFLVQELTMTQFLSIRSMWLRTEAFY

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Awt_AP68 AKIRGKYQDRIPVIVEKVPKSS--IPDIDKKKFLVPADLVAQFMVYIIRRRINLPSEKAMF
Agu_XP_003384394_1 AKIRGKYQDRIPVIVEKVPKSS--IPDIDKKKFLVPADLVAQFMVYIIRRRINLPSEKAMF
Agu_MAP1A1B3C ASLIVKFKFNVKVPVVEKVEKQKPLDLDKTKFLVPEELTISQGFVTLIRNKKLSTQAFY
Agu_MAP1A1B38 DEIVRKHQPQKPLVIERARTEKHLPLDLDKTKFLVPEELTMSQLTATIRKRMQLSEQAFY
Agu_GABA_RAP2 SKIREKHPERVPVIVEKVSQ--IADLDKRYKLVPGDLTVAQFMVLRQRQLGATESTY
Agu_GABA_RAP QRTLNKHPKVPVIVEKVKHSG--LPDIDNKFLLLPSSKVSQVIVYMNKLRPSHAPLY
Tod_37901 QKIRKRYKQDRIPVIVEKAPKAR--VQDIDKKKFLVPADLVAQFMVYIIRRRINLPSEKAMF
Tod_35852 AKIRAKYKQDRIPVIVEKAAKSS--IPDIDKKKFLVPADLVAQFMVYIIRRRINLPSEKAMF
Tod_19802 QETREKYPDKVVEKRLHEKHLPLDLDKTKFLVPEELTMSQFINIRKRLVLPNTQAFY
Tod_57027 ENIHRFPNKEPVEVYKRYKPLDLDKTKFLVPEELTMSQFVSIIRNMSLTPSQAFY

Scer_ATG8 IFVND-ILPPTAALMSAIYQEHKDDGFLVYVYSGENTFGK-----
Spon_ATG8 IFIDE-ILPPTAALMSTIYEKSDGFLVYVYSGENTFGYVFF-----
Hsa_GABA_A_RAP FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Hsa_GABA_A_RAP1 FFVNN-TIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Hsa_GABA_A_RAP2 LFVVK-TVPOSSLTMQLYQEKDEDFLYIAYSDETFG-----
Hsa_MAP1A1B3 LLVNGHMSVSTPISEVYEKDEDFLYIAYSDETFQKLSV-----
Hsa_MAP1A1B3A LLVNGHMSVSTPIADIEYQEKDEDFLYIAYSDETFG-----
Hsa_MAP1A1B3B LLVNGHMSVSTPIADIEYQEKDEDFLYIAYSDETFG-----
Hsa_MAP1A1B3B2 LLVNGHMSVSTPISEVYEKDEDFLYIAYSDETFQKLSV-----
Hsa_MAP1L32 LLVNNKLSVMSATMAEYRDKDEDFLYIAYSDETFGGLESAAPRGGSL-EDRPN
Mmu_GABA_RAP FFVNN-TVPPSATMQLYQEHDEDFLYIAYSDESQYK-----
Mmu_GABA_RAP1 FFVNN-TIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Mmu_GABA_RAP LFQNN-VIPPTSATMQLYGN-----TEHLR-----
Mmu_GABA_RAP2 LFVVK-TVPOSSLTMQLYQEKDEDFLYIAYSDETFG-----
Mmu_MAP1A1B38 LLVNGHMSVSTPISEVYERDEDFLYIAYSDETFGAMV-----
Mmu_MAP1A1B3A LLVNGHMSVSTPIADIEYQEKDEDFLYIAYSDETFG-----
Btau_GABA_RAP FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Btau_GABA_RAP1 FFVNN-TIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Btau_GABA_RAP2 FFVNN-TIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Btau_MAP1A1B3C LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Btau_MAP1A1B3B LLVNGHMSVSTPISEVYEKDEDFLYIAYSDETFQKLSV-----
Btau_MAP1A1B3A LLVNGHMSVSTPIADIEYQEKDEDFLYIAYSDETFG-----
Sko_predprot1 LFIER-VLPPTSATMQLYQEHDEDFLYIAYSDETFG-----
Sko_GABA_RAPa FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Sko_predprot2 LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Sko_MAP1C3a LLVNEKMSVSTPISEVYERDEDFLYIAYSDETFGANN-----
Lgig_105301 FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Lgig_122374 LFVVK-TVPPSATMQLYQEHDEDFLYIAYSDETFG-----
Lgig_122409 LFVVK-TVPPSATMQLYQEHDEDFLYIAYSDETFG-----
Lgig_209102 LLVNHMSVSTPISEVYERDEDFLYIAYSDETFG-----
Lgig_194601 LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Cte1_21814 FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Cte1_4205 LFVVK-TVPOSSLTMQLYQEHDEDFLYIAYSDETFG-----
Cte1_2981 LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Cte1_128947 LLVNSRMSVSTPISEVYERDEDFLYIAYSDETFG-----
Dme1_ATG8a FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Dme1_ATG8b FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Ame1_GABARAP FFVNN-TIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Ame1_MAP1A1B3A LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Spu_XP_782118_2 FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Spu_XP_786800_2 LFVVK-TVPOSSLTMQLYQEHDEDFLYIAYSDETFG-----
Spu_MAP1C3b LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Spu_GABA_RAP_1like LFVNE-VTPAASSTLAEVDAEHRDQDFLYIAYSDETFG-----
Spu_GABA_RAP_1like2 LFVVK-TVPOSSLTMQLYQEHDEDFLYIAYSDETFG-----
Spu_MAP1A1B3C LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Dre_GABA_A_RAP FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Dre_GABA_A_RAP1 FFVNN-SLPPSSPLSAVYEHDEDFLYIAYSDESQYK-----
Dre_GABA_A_RAP1_iso1 FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Dre_GABA_A_RAP2 LFVVK-TVPOSSLTMQLYQEHDEDFLYIAYSDETFG-----
Dre_MAP1A1B3a LLVNGHMSVSTPISEVYERDEDFLYIAYSDETFG-----
Dre_MAP1A1B3b LLVNGHMSVSTPISEVYERDEDFLYIAYSDETFG-----
Dre_MAP1A1B3c LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Dre_MAP1A1B3C_1like LLVSKMSCLASMSGYSQFRDQDFLYIAYSDETFG-----
Cin_XP_002128871_1 FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDETFG-----
Cin_XP_002129578_1 FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Cin_XP_002129622_1 LLVNGHMSVSDAVSEYQEKDEDFLYIAYSDETFG-----
Nve_165338 FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Nve_181063 LFVVK-TVPPSATMQLYQEHDEDFLYIAYSDETFG-----
Nve_241851 LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Nve_121733 LLVNEKMSVSTPISEVYERDEDFLYIAYSDETFG-----
Hmgg_XP_002170100_1 FFVNN-VIPPTSATMQLYQEHDEDFLYIAYSDESQYK-----
Hmgg_XP_002163079_1 LFVVK-TVPPSATMQLYQEHDEDFLYIAYSDETFG-----
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Awt_AP68 LFVVK-TVPPSATMQLYQEHDEDFLYIAYSDETFG-----
Agu_XP_003384394_1 LFVVK-TVPPSATMQLYQEHDEDFLYIAYSDETFG-----
Agu_MAP1A1B3C LLVNNKLSMSMTLAEYRDKDEDFLYIAYSDETFG-----
Agu_MAP1A1B38 LLVNGHMSVSTPISEVYERDEDFLYIAYSDETFG-----
Agu_GABA_RAP2 VMVDG-ITPPTSTMTAIVYQKDDGFLYIAYSDETFG-----
Agu_GABA_RAP LYVNDVLGATDSTLRLYQRESDYFLYCYEYGTASSDRES-----
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Tod_35852 LFVVK-TVPPSATMQLYQEHDEDFLYIAYSDETFG-----
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Tod_57027 LLVNNKLSVMTTLLTEVYRDEKDDGFLYIAYSDETFG-----

Scer_ATG8 --
Spon_ATG8 --
Hsa_GABA_A_RAP --
Hsa_GABA_A_RAP1 --
Hsa_GABA_A_RAP2 --
Hsa_MAP1A1B3 --
Hsa_MAP1A1B3A --
Hsa_MAP1A1B3B --
Hsa_MAP1A1B3B2 --
Hsa_MAP1L32 PL
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Mmu_GABA_RAP1 --
Mmu_GABA_RAP --
Mmu_GABA_RAP2 --
Mmu_MAP1A1B38 --
Mmu_MAP1A1B3A --
Mmu_MAP1A1B3B --
Btau_GABA_RAP --
Btau_GABA_RAP1 --
Btau_GABA_RAP2 --
Btau_MAP1A1B3C PL
Btau_MAP1A1B3B --
Btau_MAP1A1B3A --
Sko_predprot1 --
Sko_GABA_RAPa --
Sko_predprot2 --
Sko_MAP1C3a --
Lgig_105301 --
Lgig_122374 --
Lgig_122409 --
Lgig_209102 --
Lgig_194601 --
Cte1_21814 --
Cte1_4205 --
Cte1_2981 --
Cte1_128947 --
Dme1_ATG8a --
Dme1_ATG8b --
Ame1_GABARAP --
Ame1_MAP1A1B3A --
Spu_XP_782118_2 --
Spu_XP_786800_2 --
Spu_MAP1C3b --
Spu_GABA_RAP_1like --
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Spu_MAP1A1B3C --
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Dre_GABA_A_RAP1 --
Dre_GABA_A_RAP1_iso1 --
Dre_GABA_A_RAP2 --
Dre_MAP1A1B3a --
Dre_MAP1A1B3b --
Dre_MAP1A1B3c --
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Cin_XP_002129622_1 --
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Nve_121733 --
Hnog_XP_002170100_1 --
Hnog_XP_002163079_1 --
Hnog_XP_002163175_1 --
Aw1_APG8 --
Agu_XP_003384304_1 --
Agu_MAP1A83C --
Agu_MAP1A83B --
Agu_GABA_RAP2 --
Agu_GABA_RAP --
Tod_37901 --
Tod_35852 --
Tod_19802 --
Tod_57027 --

A Nexus formatted alignment file of all ATG8 protein sequences used in our phylogenetic analysis consisting of only highly conserved domains as selected by G-Blocks.

INEXUS

begin data;
dimensions ntax=73 nchar=96;
format datatype=protein missing=? gap=;

matrix

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Hsg_GABA_A_RAP1 FEYRQKEGEKIKRKYDRIKIPVIEKAKAEKIDKIKKYLVPALTVGQFVYVZKRIKMLPPEKAIFFPTAALMSATYQEHKDDGFLVYTSGENTFG  
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Lg1g_209102 FSQRKEVSEISNKGPKIPVIEERYKGPDKLTKFLVPHVNMSELIXI2RRRLQLMNAQAFVYSVSTPSEVYESEKDDGFLVYTSGENTFG  
Lg1g_214601 FATRKEVAGIRAKFPIKIPVIEERYKGPDKLTKFLVPHVNMSELIXI2RRRLQLMNAQAFVYSVSTPSEVYESEKDDGFLVYTSGENTFG  
Ctel_21814 FEKRAEIEKIKRKYDRIKIPVIEKAKAEKIDKIKKYLVPALTVGQFVYVZKRIKMLPPEKAIFFPTAALMSATYQEHKDDGFLVYTSGENTFG  
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Ctel_2081 FADRCIKVQIIRQDQPKIPVIEERYKGPDKLTKFLVPHVNMSELIXI2RRRLQLMNAQAFVYSVSTPSEVYESEKDDGFLVYTSGENTFG  
Ctel_128947 TGTRKDDVQIIRQDQPKIPVIEERYKGPDKLTKFLVPHVNMSELIXI2RRRLQLMNAQAFVYSVSTPSEVYESEKDDGFLVYTSGENTFG  
Dml_AT68      FEKRAEIEKIKRKYDRIKIPVIEKAKAEKIDKIKKYLVPALTVGQFVYVZKRIKMLPPEKAIFFPTAALMSATYQEHKDDGFLVYTSGENTFG  
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Spu_GABA_RAP_11ke FEYRQKEGEKIKRKYDRIKIPVIEKAKAEKIDKIKKYLVPALTVGQFVYVZKRIKMLPPEKAIFFPTAALMSATYQEHKDDGFLVYTSGENTFG  
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end;