

Figure S1. List of amino acid sequences of the 3 animals (*Saccharomyces cerevisiae*, *Homo sapiens* and *Crassostrea gigas*) collected during the identification of the autophagy proteins in *C. gigas*. All sequences are in FASTA format. The species name of the sequence is highlighted in yellow.

A. MTOR (mechanistic target of rapamycin kinase)

```
>tr|K1PYM7|K1PYM7_CRAGI Serine/threonine-protein kinase TOR OS=Crassostrea
gigas OX=29159 GN=CGI_10010427 PE=3 SV=1
MDLYRFVVTLEMPSEYHTTFMDKFNHFIFEMVSSSDMNERKGGILAIIVSLTGVDVGN
STRISRFSNYLRNLLPSNDVSVMEMAARAVGWLAYSSGSYAAEYVEHEVKRALEWLTSR
QESKRLAAVLVLKELAVNTPFFFFQQVQQFFDCIFNAVRDPKPNIREGAVAALRAALAVT
SQRESKATQKAQWYRQCYDEAVKLYDELQGREKKLSRDDWAHGSLIMNELLRCSNIEGE
RLRMEMEDITNQYQHERTLKEMSKTHKSPSSSLALQQFQHKAFPINNFMNGNRHNMQKI
SFESRTCKQLVESHFDKVCALLLRHKNSKSVHIQLILQVIFPRLAAFKPHEFSRLYLDDT
INFLGSLKTTTRDKTSTFQAIGLLAISVQDNIVRYLPGILEVIRASLPPKDLPAKKQKNM
VVDPSVFTCSIMLARAVGPAMIKDVRDLLDSMFATGLSPALTAALRDLAIQIPQLKKEIQ
EGLLNLSLILMGRQLRHPGAPKSPLOFPMSASLTNLADIQDATSITLALKTLGSFDFE
GHSLTQFVQHCAEQYLSSDHKEIRMEAVRTCARLLTPLLQLLANSQGOISIAAMNTVAEV
LHKLLVVGITDTGELEEGVIINIRTELEYSVGRNKEQAAKMLGHLVANAARLVRPYMEP
ILNALIPKLKEPDPNPNTISVLVAIGEQAQVSGTEMRKWMDELLPLILEMLQDSSSLQK
REVALWTLGQLVESTGYVIEPYKRYPSLLEVLNLFKTEQATGIRREVIRVLGLLGALDP
HKHKMNQGMIQRNESNSVSASDTKSSDSTQPENTSEMLANMTASTTLEEIYPAIAIATL
MRIIRDPSLSQHHTMVVQAITFIKSLGIKCVPIIQQVIPAYLAVIRSADQTFREFLFQQ
LGVIIAIVKQHIRNYLNDIFTIIEKEYWSPNSTMQNTIINLVEQIVTALGTEFKIYLPQII
PQILKVFQMDDNRAVTKGLLNALQLFGANLDDYLHLLLPVVKLFDSPDVPLSVKRIA
LETVDKLTLLDLTEFASRIHPLVRTLDSVPELQTAAMDTLCAMVMQMGPKFTIFIPMV
QRVIQKHKIAHQRYFILMARILKASTIAEEEDDPILLKHKRKNRGKATESSESMA DTAVIK
KLHVSFINLQKALEAGRKESKEDWMEWLRRLSIELLKESPSPALRSCWALAQTYN SLAKD
LFNAAFVSCWTELTEAQQDELILSLEQALTSQEIPEITQTLNLAEFMEHCDKGPLPLDT
SLLGSRAMRCRAYAKALHYKEEEFHRGPTTATLESLSINNKLQQPESASGVLYAQNHR
TDVKVQESWYEKLEHWNKALEAYEKKQEEKPEDFNLTLMRMRCLALAEWGHHLHQIACEK
WGTSSDENRTDMARMAASAAGLQWDSMEEYMCLIPRNSYNGAFYRAVFALHTENYQLA
QQCIDKARDILDTELTAMAGESYNRAYGAMVNVQMLSELEEVMOFKLVPERQEAIKHMWW
DRLQGCQRVVEDWQKIIQVRSLVVSPLEDMKTWLKYASLCRKSGRLLALSQKTLVMLLGM
PAKNC DKPIPTTNPQVTFAYLKHMMWKSSQKKEAYGKLQHFVQHSLOTRALQLITPEDTQQ
RTQLNKLLARCYLKLGDWADMLYGVNEESVTQILEYYSLATEYDKYWKAWHGWALINYE
AVLFYKQSEKSGNQPPSPGDIGPPGRGDAPLSPKTDTSVSTASKMHKYCVLAVQGGFRSI
SLSQNKSLQDTRLRLTLMFYDYGQWLEVYEAALNDGLKTIQVENWLQVIPQLIARIDIPRPL
VSRLISQLLIDIGKAHPQALIYPLTVASKSNVPARQTAANKILKNMCEHSNTLVQQAMLV
SEELIRVAIILWHELWHEGLEEASRLYFGERDIKGMFSTLEPLHNMVERGPOTLKETSFNQ
AYGRDLMEAQEWCRKYQRSENVKDLTQAWDLYYHVFRRI SKQLPQLTSLELQYVSPKLLR
CQDLELAVPGKYEPNVQPIVKIKRCQSSLOVITSKQRPKLSIFGSNGKEFQFLKGHEDL
RQDERVMQLFGLVNLLENPETFRRLNLTQIRFSVPLSTNSGLIGWVPHDTLHSLIRD
YREKKILLNIEHRLMLRMAPDYDHLTLMQKVEVFEHALHTQGGDDLAKILWYKSPSSEV
WFDRRTNYTRSLAVMSMGYVVLGGLDRHPSNLMLDRTSGKVIHIDFGDCFEVAMVREKFP
EKIPFRLTRMLINAMEVTGIDGNYKMTCESVMEVLRHKDSLMAVLEAFVYDPLLNRMLM
DTTAKGKTKTKDSYSGGSQEADMLENVDINQTAHKRSAPEAASSVSGDNFQAEVINKKA
LSIINRVRDKLTGRDFSQGDPI DVPTQVDLLIKQATSHENLCQCYIGWCPFW
```

```
>XM_020068652.1 PREDICTED: Crassostrea gigas serine/threonine-protein
kinase mTOR (LOC105331599), transcript variant X3, mRNA
ATGACACAACATCTGCAAGAAATTATAACCCAGTTTGTGACAGGGTTAAAAAATAAAAAATGAAGATGTTA
GAAATAAGTCTGCCATGGATTTATAACCGCTTTGTGGTCACTGAGTTACGGGAAATGCCCTCCGAGTACCA
CACAACCTTCATGGATAAATTCAACCATTTTCATTTTTGAAATGGTATCCAGTTCAGATATGAATGAGCGC
AAAGCGGAATATTGGCCATAGTTAGTCTCACTGGAGTTGATGTAGGGAACACCTCCACCAGAAATAAGTA
GGTCTCTAATTACCTTCGGAATCTTCTGCCGTCCAATGATGTATCAGTCATGGAGATGGCTGCTCGGGC
AGTGGGCTGGCTGGCTACTCCTCAGGCTCCTATGCTGCAGAGTACGTGGAGCATGAAGTGAAGCGTGCC
TTAGAGTGGTTAACTAGTGATCGACAGGAGAGCAAGCGACTAGCTGCTGTTCTGGTGTGAAAGAACTTG
CTGTAATAACACCAACATTCTTCTTTCAACAAGTGCAGCAGTTTTTTGATTGTATTTTCAATGCTGTGAG
AGATCCGAAGCCCAACATCAGAGAAGGAGCTGTTGCAGCCCTGAGGGCCGCTCTGGCGGTAACCTCACAG
CGAGAGAGCAAGGCCACTCAGAAGGCTCAGTGGTACAGGCAATGTTATGACGAGGCTGTGAAACTGTATG
```

ATGAGTTGCAGGGAAGAGAGAAAAAATTATCTCGAGATGACTGGGCTCATGGATCCCTTCTCATAATGAA
TGAAGTGTGAGATGTAGTAATATTGAGGGAGAGAGGCTAAGAATGGAAATGGAAAGATATAACTAACCAG
CAGTATCAACATGAAAGGACTCTTAAGGAGATGTCAAAGACCCACAAATCACCTCCAGTTCTCTAGCCC
TGCAGCAGTTCCAACACAAAGCATTCCCCATCAACAACCTTTATGTCTGGCAATCGGCATAACATGCAGAA
AATCAGTTTTGAAAGCCGAACCTTGTAACAGCTTGTGCGAAAGTCATTTTGATAAGGTGTGTGCCCTACTT
TTGAGACACAAGAACAGCAAGAGTGTTCACATCCAGCTGATTCTACAAGTTATCTTTCCACGTCTTGCCG
CCTTTAAACCACATGAATTCTCCCGACTGTACCTGGATGATACAATCAACTTCTGTGGGGTCACTGAA
AACACACGTGACAAGACCTCCACATTCCAGGCCATTGGACTACTGGCCATTTCTGTCCAGGACAACATT
GTCCGATACCTTCCCGGGATCCTGGAGGTTCATCAGGGCTTCCCTCCCTCCCAAAGACCTACCAGCCAAGA
AACAGAAGAATATGGTGGTGGATCCATCAGTTTTTACCTGTATCAGCATGCTGGCCAGAGCTGTAGGCC
AGCCATGATTAAGGATGTGAGAGATCTGTTAGACTCCATGTTTGGGACTGGTCTGAGTCTGTGCTTTGACT
GCAGCCCTTCGTGATCTGGCCATACAGATCCCACAACATAAGAAAGAAATTCAGGAAGGGCTGTGAAGA
ACCTCTCACTCATCTTAATGGGGAGACAACCTCCGCCACCCTGGGGCCCCAAAAGTCCCTACAGCCTTT
CCCTATGTGAGCCTCTTTAACAAATTTGGCAGACATCCAAGATGCCACAAGCATAACACTGGCATTAAAA
ACTCTGGGAAGCTTTGATTTTGAAGGCCACTCTTTGACCCAGTTTGTCCAGCATTGTGTGAGCAGTACC
TGTCAAGTGACCACAAGGATACGCATGGAAGCCGTCCGTACCTGTGTGCTAGGCTGTGACACCTCCT
ACAGTTGCTTGCCAATAGTCAAGGACAGATCAGCATAGCGGCCATGAATACAGTGGCTGAGGTGTTACAT
AAGCTGCTGGTAGTGGGCATCACAGACACAGATTCTGACATCAGATACTGTGTTCTGGTCTCTATGGATG
ACCGTTTTGATCCTCATCTAGCCCAAGCAGAGAATCTGTCCGCTTTGTTTGTGGCCCTGAATGATGAGGT
GTTTCGAGATTCGTGAGCTGGCAATTTGTATCATTGGTCGACTTAGCAGTAAAAACCAGCATATGTCATG
CCTTCTTTGAGGAAAACACTTATTTCAGATCAGAACAGAGTTGGAGTACAGTGGGGTGGGAAGAAAACAAAG
AACAAAGCCGCTAAAATGCTTGGCCACCTGGTGGCTAATGCTGCCCGCTGGTGGCCCGTACATGGAACC
CATATTGAACGCCCTGATCCCCAAACTGAAGGAGCCCGACCCTAACCCCAACGTACCATCAGTGTACTG
GTCGCCATAGGAGAACAGGCACAGGTCAGTGGTACAGAGATGAGAAAGTGGATGGATGAGTACTTCCCT
TGATCTTGAAATGTTACAAGACTCGTTCGTCTTACAGAAAAGAGAGGTTGCACTGTGGACCCTGGGACA
GCTGGTTGAGAGTACAGGATACGTGATCGAGCCCTACAAACGCTACCCCTCATTGCTGGAAGTACTCCTT
AACTTCTTGAAAACAGAGCAAGCTACAGGAATTAGAAGAGAGGTGATCCGTGTGCTTGGTTTTGCTTGGAG
CTCTTGATCCACACAAAACATAAGATGAACCAGGGAATGATTTCAGAGGAATGAATCCAACCTCTGTGAGTGC
ATCGGACACAAAGCTATCCTCTGACAGCACCCAGCCTGAGAACACAAGTGAATGTTAGCCAACATGACC
GCTTCTACCCTCTGGAGGAAATCTATCCAGCCATTGCCATAGCAACACTGATGCGGATAATCCGTGATC
CATCTCTCTCACAGCACACACAATGGTGGTCCAGGCCGATCACCTTCATCTTCAAGAGTCTGGGAATTA
GTGTGTCCCCTGATCACCAGCAGGTGATCCCAGTTACTTACCTGGCGGTTATCCGGTCCGCGGATCAGAGCTTT
AGAGTNTCTTTGATTTCCAACAACACTGGGAGTCATCATTGCGATCGTGAAGCAACACATCAGGAACCTCA
ATGATATTTTTACCATTATAAAGGAGTACTGGAGTCCCAACAGCACTATGCAGAACACAATCATTAACT
GGTGGAGCAGATTGTGACGGCCCTGGGGACAGAGTTCAAGATCTACCTCCCCAGATCATCCCCAGATC
CTCAAAGTCTTCATGCAGGACTCCAGCGACAACCGGGCAGTACCCGGCAAGTTACTGAATGCCCTACAGT
TGTTTTGGAGCTAACCTTGATGACTACCTCCATCTACTTCTCCCTCCTGTGGTGAAGCTGTTTTGACAGCCC
AGATGTCCCTCTCTCAGTCAAAGGATTGCCTTGGAACTGTAGATAAATTGACCTTGACCTTGACCTG
ACAGAGTTTGCTTCCCGGATCATTTCATCCCTTGTGAGAACCTTGGACTCTGTGCCTGAGTTACAGACAG
CCGCCATGGATACACTGTGTGCCATGGTGTGATGCAGATGGGTCCAAAGTTCACTATCTTCATTCCGATGGT
CCAGCGTGTGATACAGAAACACAAGATAGCTCACCAGCGATACTTCATTCTTATGGCAAGGATCTCAAG
GCATCAACCATTGCTGAGGAAGAAGATGATCCTATTTTTATTGAAGCACAGAAAGAATCGTGGGAAGGCAA
CAGAATCTAGTGAATCGATGGCAGACACAGCTGTGATTAAGAAGCTTCATGTGAGCTTTATAAATCTCCA
AAAGGCTTTGGAAGCTGGGAGAAAGGAATCCAAGGAAGACTGGATGGAGTGGCTGAGGAGACTGAGTATA
GAGCTCCTGAAAGAGTCCCCATCCCCCGCCCTCAGGTCTGTGGGCTCTGGCACAGACCTACAACCTCGC
TGGCCAAAGATCTGTTCAATGCTGCCTTTGTGTCTGCTGGACTGAACTTACAGAAGCTCAGCAAGATGA
ACTCATTCTTAGTCTCGAACAAGCCCTCACATCTCAGGAAATACCCGAGATCACTCAGACTCTTCTTAAT
CTGGCAGAATTCATGGAACACTGTGATAAAGGGCCCCCTGCCTTTAGATACTCACTATTGGGATCTCGGG
CGATGAGGTGCCGAGCGTATGCCAAGGCTCTACACTACAAGGAAGAGGAGTTCCACCGGGGACCCACCAC
AGCCACTCTCGAATCTCTGATCAGTATTAACAACAAGCTTCAGCAGCCCCGAGTCAGCCTCTGGTGTGCTA
CAGTACGCACAGAATCACAGGACTGATGTGAAAGTACAAGAAAGCTGGTATGAGAAGCTTCATGAGTGGAA
ATAAAGCTCTAGAGGCCTACGAGAAAAAACAGGAGGAGAAACCTGAGGATTTCAACCTGACTCTGGGCAG
AATGAGATGTCTAGAGGCATTAGCAGAGTGGGGTACCTTCATCAGATTGCCTGTGAGAAGTGGGGGACC
AGTAGTGATGAGAATCGCACTGACATGGCGAGAATGGCTGCTTCAGCTGCCTGGGGACTGGGTGAGTGGG
ACAGTATGGAGGAGTACATGTGTCTGATCCCCAGGAACAGTTACAATGGGGCATTCTACCAGCTGTGTT
CGCTCTCCATACAGAGAACTACCAGTTAGCACAAACAGTGCATTGACAAAGCCAGAGATATTCTGGACACA
GAGCTGACAGCTATGGCAGGGGAGAGCTACAACAGAGCCTATGGGGCCATGGTCAATGTCCAGATGTTGT
CGGAGCTTGAGGAGGTGATGCAGTTTTAAACTGGTTCCCGAAAGACAGGAGGCCATCAAGCACATGTGGT
GGACCGCCTCCAAGGCTGTCAGCGCGTGGTGGAAAGACTGGCAGAAGATCATCCAGGTCCGCTCCCTGGTT
GTGTGCCCCCTGGAAGACATGAAAACATGGCTGAAGTACGCCAGTCTGTGCAGGAAGAGTGGAAAGACTGG
CCTTTTCCAGAAAGACTCTGGTGTGTTGTTGGGAATGGACCCTGCTAAGAACTGTGATAAGCCTATTCC
TACCACCAACCCTCAGGTACCTTTGCTTACCTCAAACACATGTGGAAGAGCAGTCAAGAAAGAAAGCT
TATGGTAAATTGCAACATTTTGTCCAACATTCACTTCAAACCTCGGGCTCTCCAACCTGATAACGCCTGAGG

ATACTCAACAAAGAACTCAACTGAACAAGTTGCTTGGCTAGGTGTTACCTGAAGCTTGGAGACTGGGCGGA
CATGTTGTATGGAGTGAACGAGGAATCAGTGACCCAGATTCTAGAGTACTACAGCCTGGCCACAGAGTAC
GACAAATACTGGTACAAGGCGTGGCATGGATGGGCTCTAATCAACTATGAAGCGGTCTTATTTTACAAAC
AATCAGAGAAGTCGGGCAATCAGCCCCAGTCCCCTGGAGATATTGGCCCTCCGGGGAGAGGAGACGCGCC
CCTCTCACCAAAGACGGACACCAGTGTCTCGACTGCCTCCAAGATGCATAAAATACTGTGTTCTAGCTGTA
CAGGGATTCTTTAGGTCCATCTCTCTGTCCCAGAATAAAAGTTTACAGGACACACTCAGGTTGTTGACGC
TGATGTTTTGACTATGGTCAGTGGTTAGAGGTATACGAGGCATTGAATGATGGACTGAAAACCATAACAGGT
GGAGAACTGGCTGCAGGTGATTCCCTCAACTGATTGCCAGGATTGACATTCCACGCCCTTGGTCAGTCGT
CTCATCAGTCAGCTCTTGATCGACATCGGCAAGGCTCACCCCTCAGGCCTTGATTTACCCCTTACTGTGG
CCTCCAAGTCTAACGTTTCTGCCCCGCAACAGCAGCCAACAAAATCCTGAAGAACATGTGTGAACACAG
CAACACTTTGGTACAACAGGCCATGCTGGTGAGTGAGGAGCTGATCCGGGTGGCCATTCTATGGCATGAG
TTGTGGCATGAGGGACTAGAGGAGGCCTCCAGGCTATACTTTGGGGAGAGGGACATCAAGGGCATGTTCT
CTACCCTGGAGCCGCTACATAACATGGTGGAGCGCGGCCCCAGACCCTCAAGGAACTTCATTTAATCA
GGCGTACGGCCGTGACCTGATGGAGGCCAGGAGTGGTGTAGGAAGTACCAGAGGTCAGAGAACGTCAAG
GACCTGACCCAGGCCTGGGATCTCTACTACCATGTGTTCCAGGAGGATCTCTAAACAGCTGCCACAGTGA
CATCCCTGGAGCTTCAGTATGTTTTCTCCTAAACTTCTTCGCTGTCAAGATCTGGAGTTAGCTGTCCTGG
GAAGTATGAACCAACCAACCAATCGTCAAAATCAAACGCTGCCAGAGTTCAGTCAAGTCATTACCTCA
AAGCAGAGGCCAGAAAACCTCAGCATATTTGGTTCCAATGGGAAGGAGTTCAGTTCCTGCTGAAGGGAC
ACGAGGACCTGCGACAAGACGAGCGAGTCATGCAGCTCTTTGGACTAGTCAACTCTCTCTGCTGGAAAA
TCCAGAGACCTTCCGAAGGAACCTTACGATTACAGCGTTTCTCCGTTATCCCCCTGTCGACAACTCCGGC
CTGATTGGCTGGGTACCACACACCCGACACCCTACACTCCCTCATCCGTGACTACCGAGAGAAAAAGAAAA
TTCTGCTCAACATAGAGCACAGGCTGATGCTCAGAATGGCACCAGGACTATGACCATTTGACCCTGATGCA
GAAGGTGGAGGATTTTGGAGCATGCTCTGGAGCACACCCAGGGAGATGACCTGGCCAAGATCTTGTGGTAC
AAGAGTCTTAGCTCAGAGGTGTGGTTCGATAGACGTACAAACTACACTCGCTCCCTGGCTGTTATGTCTA
TGGTGGGCTATGTGTTGGGTCTTGGAGACAGACATCCTTCCAATCTAATGTTGGATCGTACTAGTGCCAA
AGTCATCCATATCGACTTTGGTGACTGCTTTGAGGTTGCCATGGTGAGAGAAAAGTTTCCCGAGAAGATT
CCATTCCGCTTGACTCGCATGTTAATCAATGCTATGGAGGTGACAGGTATCGACGGTAACTACAAGATGA
CCTGTGAGAGTGTGATGGAGGACTGAGGGAACACAAGGACAGTCTGATGGCCGTGCTCGAGGCCTTTGT
GTACGACCCTCTCCTCAACTGGAGGCTCATGGACACAACAGCCAAAGGGAAAAACAAAGACCAAGATTCA
TACTCTGGTGAAGTCAGGAACAGGCGGACATGTTGGAGAACGTGATATCAATCAGACCCGCCACAAAC
GCTCCGCCCTGAGGCCGCAAGTTCAGTCAGCGGGGACAATTTCCAGGCAGAGGTATCAACAAGAAGGC
ACTGTCCATCATTAACTCGGTCAGGGACAAACTAGCTCGTACTTCTCTCAGGGGGATCCGATTGAT
GTCCCCACCCAGGTGACCTCCTGATAAAAACAGGCCACTCCACGAGAATCTATGTCAGTGTACATTTG
GGTGGTGTCCATTCTGGTGAAAGGTTCTCGGCTCTGATGTGTGTGCTGTGGTTTTTCCACCTTTAAACAC
TGTGTTATGCATGTCACCTGTGATTTATTAAGTTGGTATGTCTTATATACATATGTACATTAACATGTTG
TTTTTTTTTATTGCAATTATGTATAGATTAATTTGGCAGTTAAATGTGCTGTGTACAGAAAGATAGTTTG
CAAATGCCATTTTGAATCTTATTTACTGATTGTATATTTGTTTATGGATTATTTATGTAGTAGTGACATG
TTTTAGCAATTTGCTAAGCAATGAACAAGTACTGAAAATGACAGAGAATTATGATACATGTACATGTAT
CCTGGGAATCGTTTTACCCTAAATTAGAGACATGAAAGTATCATAAAATTTGGGATCTTAAAGTTTGCTT
CTAAACAAGTTATAAGCTCCACTTTACTTAAATGATTACTGGTAATTATTGACAATGTTACTGCAATTCAG
GTTTTATTTTTTACAATCAAACATTGCTAGTAGCTTTACATGTGCAACCACATGCTTCACAACATTTATAT
ATGAACATTCATGCTATGAATGTGTGCGAGGTTCCATATTTTTTATGTGTACAGTATGCTTCTATGAATGTA
CTTACTTGTACATGCAGTCATTACCGGGTAAGTCTGTTTTGTATTGTCTGATGTACATACTAGTGCTGG
CTCTGTTATTTTTGTGCTGACAACAGTTTTTATAAGTGTATGCGGATAAAATCTAAATGTCTTTTTTGTAC
ATGTTAATACACATGTAGTTATTACACATGAACATGTTATCAAGGTATCCGATCCATAATAGGATCTAAT
TTTTCCAACCTTGAATATCCATCATGTATTTAATTCTTTGATACCTAAAGCATTTTAAACAAGAAAAAGA
TTTACTGAGAGAAATTTTCAAAAATATTATTAAGTAAAGCAGTGAATTAATTGATCATAAAGATTGCATTAT
GGTCTATGGGGACAAGCACATTTTTTAAAAATAAAAAAGTAAATTTCTAAGAATATCAATAAATGCTTTGGT
GAAAGATGATTTTTATCATTAGGAATACAAAAACTATTGAAAATCAATTTTACACTATATAGATTTTTT
AAAATGAATTTTTATAGAATAAAAGCAAAGGGCGCAATTTTAAAAAAAAGGAAAAGGTCATTAATTAGG
ACTCATTCCACTCTTACATATTGATACTTAAACATGAAAATTTATGTCCAAGTATACTGAGTATTAAAGCC
ATACATATCTGTTATGCACCAAATTCATTGAACCTGGGGCTATTATAGATCGGATACCTTAACGAACATT
CATGTTGATGATTTACTCTTTAAACCATGCTTATTAGATTTGACAAAAATATTCTTGTGATATTTCGCTG
TGTTATGGAAATGGAGCTATATGTACAATTGTCATGAAAACCTTTACATCTACAAATATGCATATTGAGTA
TGTTAATTATGAGGCAGAAATCTTTTTTTTTTTTATTTGACTCGCAAATTCAGAGAAAAAAATCGCAAAAT
ATGAATACTTGAATAAAAAACACAAAATTTGTAGATTTTTTAAAGTTATCAACCTATTCTTTTATGAGGG
AAGTATTGGGGTAATTCAAAGAGTTTTTGTAAATATACAGTGCATGTACCAACATTGTACCGTACATGTA
TGAAGCATTATAATTGTGTCTATAAATGAATACTGTTATGTATTACAAATATACTGTTAAAAATGTCTT
TAAAGTAATATTGTTTGTGACAATAAATTAAGATAAAATGTTAATTCACA

>XM_005263438.2 PREDICTED: *Homo sapiens* mechanistic target of rapamycin kinase (MTOR), transcript variant X2, mRNA
CGGGGAAGGCGGGCGGTGGGGCAGGGGCCTGAAGCGGCGGTACCGGTGCTGGCGGCGGCAGCTGAGGCC

TTGGCCGAAGCCGCGCAATATTAAGGAAACTTCTCTCTAAAGAACCTCAGGGCAAGATGCTTGGAAACC
GGACCTGCCGCCGCCACCACCGCTGCCACCACATCTAGCAATGTGAGCGTCTGCAGCAGTTTGCCAGTG
GCCTAAAGAGCCGGAATGAGGAAACCAGGGCCAAAGCCCAAGGAGCTCCAGCACTATGTCACCATGGA
ACTCCGAGAGATGAGTCAAGAGGAGTCTACTCGTCTTATGACCAACTGAACCATCACATTTTTGAATTG
GTTTCCAGCTCAGATGCCAATGAGAGGAAAGGTGGCATCTTGGCCATAGCTAGCCTCATAGGAGTGGAAAG
GTGGGAATGCCACCCGAATTGGCAGATTTGCCAACTATCTTCGGAACCTCCTCCCTCCAATGACCCAGT
TGTCATGGAAATGGCATCCAAGGCCATTGGCCGTCTTGGCCATGGCAGGGGACACTTTTACCGCTGAGTAC
GTGGAATTTGAGGTGAAGCGAGCCCTGGAATGGCTGGGTGCTGACCGCAATGAGGGCCGGAGACATGCAG
CTGTCTGGTTCTCCGTGAGCTGGCCATCAGCGTCCCTACCTTCTTCTTCCAGCAAGTGAACCCCTTCTT
TGACAACATTTTTGTGGCCGTGTGGGACCCCAAACAGGCCATCCGTGAGGGAGCTGTAGCCGCCCTTCGT
GCCTGTCTGATTCTACAACCCAGCGTGAGCCGAAGGAGATGCAGAAGCCTCAGTGGTACAGGCACACAT
TTGAAGAAGCAGAGAAGGGATTTGATGAGACCTTGGCCAAAGAGAAGGGCATGAATCGGGATGATCGGAT
CCATGGAGCCTTGTGATCCTTAACGAGCTGGTCCGAATCAGCAGCATGGAGGGAGAGCGTCTGAGAGAA
GAAATGGAAGAAATCACACAGCAGCAGCTGGTACACGACAAGTACTGCAAAGATCTCATGGGCTTCGGAA
CAAACCTCGTCACATTACCCCTTACCAGTTTCCAGGCTGTACAGCCCCAGCAGTCAAATGCCTTGGT
GGGGCTGCTGGGGTACAGCTCTACCAAGGCCCTCATGGGATTTGGGACCTCCCCCAGTCCAGCTAAGTCC
ACCCTGGTGGAGAGCCGGTGTTCAGAGACTTGATGGAGGAGAAATTTGATCAGGTGTGCCAGTGGGTGC
TGAAATGCAGGAATAGCAAGAACTCGCTGATCCAAATGACAATCCTTAATTTGTTGCCCCGCTTGGCTGC
ATTCCGACCTTCTGCCTTACAGATACCCAGTATCTCCAAGATACCATGAACCATGTCTTAAGCTGTGTC
AAGAAGGAGAAGGAACGTACAGCGGCCTTCCAAGCCCTGGGGCTACTTTCTGTGGCTGTGAGGTCTGAGT
TTAAGGTCTATTTGCCTCGCGTGTGGACATCATCCGAGCGGCCCTGCCCCAAAGGACTTCGCCATAA
GAGGCAGAAGGCAATGCAGGTGGATGCCACAGTCTTCACTTGCATCAGCATGCTGGCTCGAGCAATGGGG
CCAGGCATCCAGCAGGATATCAAGGAGCTGCTGGAGCCCATGCTGGCAGTGGGACTAAGCCCTGCCCTCA
CTGCAGTGTCTACGACCTGAGCCGTGAGATTCCACAGCTAAAGAAGGACATTCAAGATGGGCTACTGAA
AATGCTGTCCCTGGTCTTATGCACAAACCCCTTCGCCACCCAGGCATGCCCAAGGGCCTGGCCCATCAG
CTGGCCTCTCCTGGCCTCACGACCCCTCCCTGAGGCCAGCGATGTGGGCAGCATCACTCTTGCCTCCGAA
CGCTTGGCAGCTTTGAATTTGAAGGCCACTCTCTGACCCAATTTGTTGCCCACTGTGCGGATCATTTCTT
GAACAGTGAGCACAAGGAGATCCGCATGGAGGCTGCCCCGACCTGTCTCCCGCTGTCTCACACCCTCCATC
CACCTCATCAGTGGCCATGCTCATGTGGTTAGCCAGACCCGAGTGAAGTGGTGGCAGATGTGCTTAGCA
AACTGCTCGTAGTTGGGATAACAGATCCTGACCCTGACATTGCTACTGTGTCTTGGCGTCCCTGGACGA
GCGCTTTGATGCACACCTGGCCCAGGCGGAGAACTTGCAGGCCTTGTGTTGGCTCTGAATGACCAGGTG
TTTGAGATCCGGGAGCTGGCCATCTGCACTGTGGGCGACTCAGTAGCATGAACCCCTGCCTTTGTCTATGC
CTTTCTGCGCAAGATGCTCATCCAGATTTTGACAGAGTTGGAGCACAGTGGGATTTGGAAGAATCAAAGA
GCAGAGTGCCCGCATGCTGGGGCACCTGGTCTCCAATGCCCCCCGACTCATCCGCCCTCATGGAGCCCT
ATTCTGAAGGCATTAATTTTGAAGACTGAAAGATCCAGACCCCTGATCCAAACCCAGGTGTGATCAATAATG
TCCTGGCAACAATAGGAGAATTGGCACAGGTTAGTGGCCTGGAAATGAGGAAATGGGTTGATGAACTTTT
TATTATCATCATGGACATGCTCCAGGATTCCTCTTTGTTGGCCAAAAGGCAGGTGGCTCTGTGGACCTG
GGACAGTTGGTGGCCAGCACTGGCTATGTAGTAGAGCCCTACAGGAAGTACCCTACTTTGCTTGGAGTGC
TACTGAATTTTCTGAAGACTGAGCAGAACCAGGGTACACGCAGAGAGGCCATCCGTGTGTTAGGGCTTTT
AGGGGCTTTGGATCCTTACAAGCACAAAGTGAACATTGGCATGATAGACCAGTCCCGGGATGCCTCTGCT
GTCAGCCTGTGAGAATCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG
TGGGAAACTTGCCTCTGGATGAGTTCTACCCAGCTGTGTCCATGGTGGCCCTGATGCGGATCTTCCGAGA
CCAGTCACTCTCTCATCATCACACCATGGTTGTCCAGGCCATCACCTTCATCTTCAAGTCCCTGGGACTC
AAATGTGTGCAGTTCTGCCCCAGGTCATGCCACGTTCTTAAAGTCAATTCGAGTCTGTGATGGGGCCA
TCCGGGAATTTTTGTTCCAGCAGCTGGGAATGTTGGTGTCTTTGTGAAGAGCCACATCAGACCTTATAT
GGATGAAATAGTACCCTCATGAGAGAATTCTGGGTGATGAACACCTCAATTCAGAGCACGATCATTTCTT
CTCATTGAGCAAATTTGGTGTAGCTCTTGGGGGTGAATTTAAGTCTACCTGCCCCAGCTGATCCACACA
TGCTGCGTGTCTTATGCATGACAACAGCCAGGCCGATTGTCTCTATCAAGTTACTGGCTGCAATCCA
GCTGTTTTGGCCCAACCTGGATGACTACCTGATTTACTGCTGCCTCCTATTGTTAAGTTGTTTGTATGCC
CCTGAAGCTCCACTGCCATCTCGAAAGGCAGCGCTAGAGACTGTGGACCCGCTGACGGATCCCTGGAT
TCACTGACTATGCCTCCCGGATCATTACCCTATTGTTTGAACACTGGACCAGAGCCCAGAATGCGCTC
CACAGCCATGGACACGCTGTCTTCACTTGTTTTTTTCAGCTGGGGAAAGAGTACCAAATTTTCATTCCAATG
GTGAATAAAGTTCTGGTGCACACCCGAATCAATCATCAGCGCTATGATGTGCTCATCTGCAGAATTTGTCA
AGGGATACACACTTGTGATGAAGAGGAGGATCCTTTGATTTACCAGCATCGGATGCTTAGGAGTGGCCA
AGGGGATGCATTGGCTAGTGGACCAGTGGAAACAGGACCCATGAAGAAACTGCACGTGACACCATCAAC
CTCCAAAAGGCCTGGGGCGCTGCCAGGAGGGTCTCCAAAGATGACTGGCTGGAATGGCTGAGACGGCTGA
GCCTGGAGCTGCTGAAGGACTCATCATCGCCCTCCCTGCGCTCCTGCTGGGCCCTGGCACAGGCCTACAA
CCCGATGGCCAGGGATCTCTTCAATGCTGCATTTGTGTCTGCTGGTCTGAACTGAATGAAGATCAACAG
GATGAGCTCATCAGAAGCATCGAGTTGGCCCTCACCTCACAAGACATCGCTGAAGTCAACAGACCCCTCT
TAAACTTGGCTGAATTCATGGAACACAGTGACAAGGGCCCCCTGCCACTGAGAGATGACAATGGCATTGT
TCTGCTGGGTGAGAGAGCTGCCAAGTGCCGAGCATATGCCAAAGCACTACACTACAAAGAACTGGAGTTC
CAGAAAGGCCCCACCCTGCCATTCTAGAATCTCTCATCAGCATTAATAATAAGCTACAGCAGCCGGAGG
CAGCGGCCGGAGTGTTAGAATATGCCATGAAACACTTTGGAGAGCTGGAGATCCAGGCTACCTGGTATGA

GAAACTGCACGAGTGGGAGGATGCCCTTGTGGCCTATGACAAGAAAAATGGACACCAACAAGGACGACCCA
GAGCTGATGCTGGGCCGCATGCGCTGCCTCGAGGCCTTGGGGGAATGGGGTCAACTCCACCAGCAGTGCT
GTGAAAAGTGGACCCTGGTTAATGATGAGACCCAAGCAAGATGGCCCGGATGGCTGCTGCAGCTGCATG
GGGTTTTAGGTCAGTGGGACAGCATGGAAGAATACACCTGTATGATCCCTCGGGACACCCATGATGGGGCA
TTTTATAGAGCTGTGCTGGCACTGCATCAGGACCTCTTCTCCTTGGCACAACAGTGCATTGACAAGGCCA
GGGACCTGCTGGATGCTGAATTAAGTGCATGGCAGGAGAGAGTTACAGTCGGGCATATGGGGCCATGGT
TTCTTGGCCACATGCTGTCCGAGCTGGAGGAGGTTATCCAGTACAAACTTGTCCCCGAGCGACGAGAGATC
ATCCGCCAGATCTGGTGGGAGAGACTGCAGGGCTGCCAGCGTATCGTAGAGGACTGGCAGAAAAATCCTTA
TGGTGGCGGTCCCTTGTGGTGCAGCCCTCATGAAGACATGAGAACCTGGCTCAAGTATGCAAGCCTGTGCGG
CAAGAGTGGCAGGCTGGCTCTTGTCTATAAAACTTTAGTGTGCTCCTGGGAGTTGATCCGTCTCGGCAA
CTTGACCATCCTCTGCCAACAGTTACCCCTCAGGTGACCTATGCCTACATGAAAAACATGTGGAAAGAGTG
CCCGCAAGATCGATGCCTTCCAGCACATGCAGCATTGTGTCCAGACCATGCAGCAACAGGCCAGCATGC
CATCGCTACTGAGGACCAGCAGCATAAGCAGGAAGTGCACAAGCTCATGGCCCGATGCTTCTGAAACTT
GGAGAGTGGCAGCTGAATCTACAGGGCATCAATGAGAGCACAATCCCCAAAGTGTGCAGTACTACAGCG
CCGCCACAGAGCACGCCAGCTGGTACAAGGCCTGGCATGCGTGGGCAGTGCATGAACTTGAAGCTGT
GCTACACTACAAACATCAGAACCAAGCCCGCATGAGAAGAAGAACTGCGTCATGCCAGCGGGCCAAAC
ATCACCACGCCACCCTGCCGCCACCACGGCCGCCACTGCCACCACCCTGCCAGCACCAGGGGAGCA
ACAGTGAGAGCGAGGCCGAGAGCACCCGAGAACAGCCCCACCCCATCGCCGCTGCAGAAGAAGGTCATGA
GGATCTGTCCAAAACCTCCTGATGTACACGGTGCCTGCCGTCCAGGGCTTCTTCCGTTCATCTCCTTG
TCACGAGGCAACAACCTCCAGGATACACTCAGAGTTCTCACCTTATGGTTTGATTATGGTCACTGGCCAG
ATGTCAATGAGGCCTTAGTGGAGGGGGTGAAGCCATCCAGATTGATACCTGGCTACAGGTTATACCTCA
GCTCATTGCAAGAATTGATACGCCCAGACCCTTGGTGGGACGTCTCATTACCAGCTTCTCACAGACATT
GGTGGTACCACCCAGGCCCTCATCTACCCACTGACAGTGGCTTCTAAGTCTACCACGACAGCCGGC
ACAATGCAGCCAACAAGATTCTGAAGAACATGTGTGAGCAGCAACACCCTGGTCCAGCAGGCCATGAT
GGTGAGCGAGGAGCTGATCCGAGTGGCCATCCTCTGGCATGAGATGTGGCATGAAGCCTGGAAGAGGCA
TCTCGTTTTGACTTTGGGGAAAGGAACGTGAAAGGCATGTTTTGAGGTGCTGGAGCCCTTGCATGCTATGA
TGGAACGGGGCCCCAGACTCTGAAGGAAACATCCTTTAATCAGGCCTATGGTCGAGATTTAATGGAGGC
CCAAGAGTGGTGCAGGAAGTACATGAAATCAGGGAATGTCAAGGACCTCACCCAAGCCTGGGACCTCTAT
TATCATGTGTTCCGACGAATCTCAAAGCAGCTGCCTCAGCTCACATCCTTAGAGCTGCAATATGTTTCCC
CAAACCTTCTGATGTGCCGGGACCTTGAATTGGCTGTGCCAGGAACATATGACCCCAACCAGCCAATCAT
TCGCATTAGTCCATAGCACCCTTGTGCAAGTCAATCAACAGAGGCCCCCGAAATGACACTT
ATGGGCAGCAACGGACATGAGTTTGTGTTTCTTAAAGGCCATGAAGATCTGCGCCAGGATGAGCGTG
TGATGCAGCTCTTCCGGCTGGTTAACACCCCTTCTGGCCAATGACCAACATCTCTTCGGAAAAACCTCAG
CATCCAGAGATACGCTGTATCCCTTTATCGACCAACTCGGGCCTCATTGGCTGGGTTCCTCCACTGTGAC
ACACTGCACGCCCTCATCCGGGACTACAGGGAGAAGAAGAAGATCCTTCTCAACATCGAGCATCGCATCA
TGTTGCGGATGGCTCCGGACTATGACCCTTGACTCTGATGCAGAAGGTGGAGGTGTTTGGAGCATGCCGT
CAATAATACAGCTGGGGACGACCTGGCCAAGCTGCTGTGGCTGAAAAGCCCCAGCTCCGAGGTGTGGT
GACCGAAGAACCAATTATACCCGTTCTTTAGCGGTGATGTCAATGGTTGGGTATATTTTAGGCCTGGGAG
ATAGACACCCATCCAACCTGATGCTGGACCGTCTGAGTGGGAAGATCCTGCACATTGACTTTGGGGACTG
CTTTGAGGTTGCTATGACCCGAGAGAAGTTTCCAGAGAAGATTCCATTTAGACTAACAAGAATGTTGACC
AATGCTATGGAGGTTACAGGCCTGGATGGCAACTACAGAATCACATGCCACACAGTGCATGGAGGTGCTGC
GAGAGCACAAGGACAGTGTGCATGGCCGTGCTGGAAGCCTTTGTCTATGACCCCTTGTGAACTGGAGGCT
GATGGACACAAATACCAAAGGCAACAAGCGATCCCGAACGAGGACGGATTCTACTCTGCTGGCCAGTCA
GTCGAAATTTTGGACGGTGTGGAACCTGGAGAGCCAGCCATAAGAAAAACGGGGACCACAGTGCAGAAAT
CTATTCACTTTTTCATTGGAGACGGTTTTGGTGAACCCAGAGGCCCTAAATAAGAAAGCTATCCAGATTAT
TAACAGGGTTCGAGATAAGCTCACTGGTCCGGACTTCTCTCATGATGACACTTTGGATGTTCCAACGCAA
GTTGAGCTGCTCATCAACAAGCGACATCCCATGAAAACCTCTGCCAGTGCATATTTGGCTGGTGCCTT
TCTGGTAACTGGAGGCCAGATGTGCCCATCACGTTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTC
CACTAAACTGAAACCATGGTGAAGAAAGTTGACTTTGTTAAATATTTTGAATGTAATGAAAAGAACTA
CTGTATATTTAAAGTTGGTTTGAACCAACTTTCTAGCTGCTGTTGAAGAATATATTGTCAGAAACACAAG
GCTTGATTTGGTTCCAGGACAGTGAACATAGTAATACCACGTAAATCAAGCCATTCAATTTGGGGAAC
AGAAGATCCATAACTTTAGAAATACGGGTTTTGACTTAACTCACAAGAGAAGTCAATCATAAGTACTTGCT
GATGGAAGAATGACCTAGTTGCTCCTCTCAACATGGGTACAGCAAACCTCAGCACAGCCAAGAAGCCTCAG
GTCGTGGAGAACATGGATTAGGATCCTAGACTGTAAGACACAGAAGATGCTGACCTCACCCCTGCCACC
TATCCCAAGACCTCACTGGTCTGTGGACAGCAGCAGAAATGTTTGAAGATAGGCCAAAATGAGTACAAA
AGGTCTGTCTTCCATCAGACCCAGTGCATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGTA
GGGAGGTTTATTAGATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGATCACTGTGCAGTGGGA
CCACCCTCACTGGCCTTCTGCAGCAGGGTCTGGGATGTTTTAGTGGTCAAAATACTCTGTTTAGAGCA
AGGGCTCAGAAAACAGAAATACTGTGCATGGAGGTGCTGAACACAGGGAAAGGTCTGGTACATATTGAAAT
TATGAGCAGAAACAAATACTCAACTAAATGCACAAAGTATAAAGTGTAGCCATGTCTAGACACCATGTTGT
ATCAGAATAATTTTTGTGCCAATAAATGACATCAGAATTTTAAACATA

>sp|P35169|TOR1_YEAST Serine/threonine-protein kinase TOR1 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=TOR1 PE=1 SV=3
MEPHEEQIWKSKLLKAANNMMDMDRNVPLAPNLNVNMMKMNASRNGDEFGLTSSRFDGV
VIGSNGDVNFKPILEKIFRELTSDYKEERKLASISLFDLLVLSLEHELSEIEFQAVSNDIN
NKILELVHTKKTSTRVGAVLSIDTLISFYAYTERLPNETSRLAGYLRGLIPSNDVEVMRL
AAKTLGKLAVPGGYTSDVFVEFEIKSCLEWLTASTEKNFSSSKPDHAKHAALLIITALA
ENCPYLLLYQYLNLSILDNIWRALRDPHLVIRIDASITLAKCLSTLRNRDPQLTSQWVQRLA
TSCEYGFQVNTLECIHASLLVYKEILFLKDPFLNQVFDQMCLNCIAYENHKAKMIREKIY
QIVPLLASFNPQLFAGKYLHQIMDNYLEILTAPANKIPHLKDDKPQILISIGDIAEYEVG
PDIAPYVKQILDYIEHDLQTKFKFRKKFENEIFYCIGRLAVPLGVPVLGKLLNRNILDLMF
KCPLSDYMQETFOILTERIPSLGPKINDELLNLVLCSTLSGTFPIQPGSPMEIPSFSSRERA
REWRNKNILQKTGESNDDNNDIKIIIQAFRMLKNIKSRFSLVEFVRIVALSYIEHTDPRV
RKLAAALTSCEIYVKDNICKQTSLSLHSLNTVSEVLSKLLAITIADPLQDIRLEVLKLNLP
CFDPQLAQPDNLRLLFALHDESFNIQSVAMELVGRLLSSVNPAYVIPSIRKILLELLTKLKF
STSSREKEETASLLCTLRSSKDVAKPYIEPLLNVLVLPKFQDTSSTVASTALRTIGELSV
VGGEDMKIYLLKDLFPLIKTFQDQNSFKREAALKQLAASSGYVIDPLLDYPELLGI
LVNLIKTENSQNIIRQTVTLIGILGAIDPYRQKEREVTSTTDISTEQNAPPIDIALMQG
MSPSNDEYYTTVVIHCLLKILKDPSSLSSYHTAVIQAIMHIFQTLGLKCVSFLDQIIP
TILDVMRTCSQSLLEFYFQQLCSLIIIVRQHIRPHVDSIFQAIKDFSSVAKLQITLVSVIEAI
SKALEGEFVKRLVPLTTLTFLVILENDKSSDKVLSRRVLRLLLESFGPNLEGYSHLITPKIV
QMAEFTSGNLQRSIIITIGKLAQDVDFEMSSRIVHSLRVLSSSTTSDELKVMIMNTLSL
LLIQMGTSFAIFIPVINEVLMKKHIQHTIYDDLNRILNNDVLPKILEANTTDYKPAEQ
MEAADAGVAKLPINQSVLKSAWNSSQORTKEDWQEWKRLSIQLLKESSPHALRACSNLA
SMYYPLAKELFNTAFACVWTELYSQYQEDLIGSLCIALSSPLNPPEIHQTLNLLVEFMEH
DDKALPIPTQSLGEYAERCHAYAKALHYKEIKFIKEPENSTIESLISINNQLNQTDAAIG
ILKHAQQHSLQLKETWFEKLERWEDALHAYNEREKAGDTSVSVTLGKMRSLLHALGEWEQ
LSQLAARKWKVSKLQTKKLIAPLAAGAAWGLGEWDMLEQYISVMKPKSPDKEFFDAILYL
HKNDYDNASKHILNARDLLVTEISALINESYNRAYSVIVRTQIITEFEEIKYKQLPPNS
EKKLHYQNLWTKRLLGCKQKNVDLWQRVLRVRSVLIKPKQDLQIWIKFANLCRKSGRMRLA
NKALNMLLEGGNDPSLPNTFKAPPPVVAQKLYIATGAYKEALNHLIGFTSRLAHDGL
DPNNMIAQSVKLSASTAPYVEEYTKLLARCFLKQGEWRIATQPNWRNTNPDAILGSYLL
ATHFDKNWYKAWHNIWALANFEVISMVQEEKTLNNGKNDDDDDTAVNNDNVRIDGSILGSG
SLTINGNRYPLELIRHVVAIKGFFHSISLLETSCLODTRLRLLTLLFNFGGIKEVSOAM
YEGFNLMKIENWLEVLPLQLISRIHQPDPTVSNLLSLLSDLGKAHPQALVYPLTVAIKSE
SVSRQKAALSIEKIRIHSPVLVNQAELVSHELIRVAVLWHELWYEGLEDASRQFFVEHN
IEKMFSTLEPLHKHLGNEPQTLSEVSFQKSFGRDLNDAYEWLNKYKSKDINNLNQAWDI
YYNVFRKITRQIPQLQTLDLQHVSPQLLATHDLELAVPGTYFPGKPTIRIAKFEPLFSVI
SSKQRPRKFSIKGSDGKDYKYLKGHEDIRQDSLVMQLFGLVNTLLKNDSECFKRHLDIQ
QYPAIPLSPKSGLLGWVNSDTFHVLIREHRDAKKIPLNIEHWVLMQAPDYENLTLQK
IEVFTYALDNTKGQDLYKILWLKSRSSSETWLERRTTYTRSLAVMSMTGYILGLDRHPSN
LMLDRITGKVIHIDFGDCFEAAILREKYPEKVPFRLTRMLTYAMEVSGIEGSFRITCENV
MRVLRDNKESLMAILEAFALDPLIHWGFDLPPQKLTEQTGIPLPLINPSELLRKGAITVE
EAANMEAEQQNETKNARAMLVLRRITDKLTGNDIKRFNELDVPEQVDKLIQQATSIERLC
QHYIGWCPFW

>sp|P32600|TOR2_YEAST Serine/threonine-protein kinase TOR2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=TOR2 PE=1 SV=3
MNKYINKYTPPNLLSLRQRAEGKHRTRKKLTHKSHSHDDEMSTTSNTDSNHNGPNDSGR
VITGSAGHIGKISFVDSLELDTTFSTLNLIIFDKLKSQVDPQERASGANELSTTLTSLAREVS
AEQFQRFNSLNKIFELIHGFTSSEKIGGILAVDTLISFYLSTEELPNQTSRLANYLRV
LIPSSDIEVMRLAANTLGRLLTVPGGTLTSDVFVEFVRTCIDWLTTLTADNNSSSKLEYRR
HAALLI IKALADNSPYLLYPVNSILDNIWVPLRDAKLIIRLDAVALGKCLTI IQDRDP
ALGKQWFQRLFQGCTHGLSLNTNDSVHATLLVFRELLSLKAPYLRDKYDDIYKSTMKYKE
YKFDVIRREVYAILPLLAAFDPAIFTKKYLDRIHVHYLRYLKNI DMNAANNSDKPFILVS
IGDIAFEVGSISPYMTLILDNIREGLRTRKFKVRKQFEKDLFYCIGKLACALGPAFAKHL
NKDLLNMLNCPMSDHMQETLMILNEKIPSESTVNSRILNLLSISLSGKFIQSNQYDF
NNQFSIEKARKSRNQSFMKKTGESNDDITDAQILIQCFKMLQLIHHQYSLTEFVRLITIS
YIEHEDSSVRKLAALTSCLDFIKDDICKQTSVHALHSVSEVLSKLLMIAITDPVAEIRLE
ILQHLGNSFDPQLAQPDNLRLLFMALNDEIFGIQLEAIKIIIGRLSSVNPAYVVP
SLRKTLLLELLTQLKFSNMPKKKEESATLLCTLINSSEVAKPYIDPILDVILPKCQDASSAVASTA
LKVLGELSVVGGKEMTRYLKELMPLIINTFQDQNSFKRDAALTTLGQLAASSGYVVG
PLLDYPELLGILINILKTENNPHIRRGTVRLIGILGALDPYKHREIEVTSNSKSSVEQ
NAPSIDIALMQGVSPSNDEYYPTVVIHNLMKILNDPSLSIHHTAAIQAIMHIFQNLGLRCV
SF

LDQIIPGIILVMRSCPPS QLDFYFQQLGSLISIVKQHIRPHVEKIYGVIREFFPIIKLQI
TIISVIESISKALEGEFKRFVPETLTFFLDILENDQSNKRIVPIRILKSLVTFGNLEDY
SHLIMPVVRMTEYSAGSLKKISITLGLRLAKNINLSEMSSRIVQALVRILNNGDRELTK
ATMNTLSLLLLQLGTDFVVFVVPVINKALLRNRIQHSVYDQLVNKLLNNECLPTNIFDKE
NEVPERKNEYEDEMQVTKLPVNQNILKNAWYCSQOKTKEDWQEWIRRLSIQLLKESPSACL
RSCSSLSVSVYPLARELFNASFSSCWVELQTSYQEDLIQALCKALSSSENPEIYQMLLN
LVEFMEHDDKPLPIPIHTLKGKYAQKCHAFKALHYKEVEFLEEPKNSTIEALISINNQLH
QTDSAIGILKHAQQHNELQLKETWYEKLRWEDALAAAYNEKEAAGEDSVEVMMGKLRSY
ALGEWEELSKLASEKWGTAKPEVKKAMAPLAAGAAWGLEQWDEIAQYTSVMKSQSPDKEF
YDAILCLHRNNFKKAEVHIFNARDLLVTELSALVNESYNRAYNVVVRAQIIAELEEIIKY
KKLPQNSDKRLTMRWTNTRLLGCQKNIDVWQRILRVRSLVIKPKEDAQVRIKFANLCRK
SGRMALAKKVLNLTLEETDDPDHPNTAKASPPVVYAQLKYLWATGLQDEALKQLINFTSR
MAHDLGLDPNNMIAQSVPPQSKRVPRHVEDYTKLLARCFLKQGEWRVCLQPKWRLSNPDS
ILGSYLLATHFDNTWYKAWHNWALANFEVISMLTSVSKKKQEGSDASSVTDINEFDNGMI
GVNTFDAKEVHYSSNLIHRHVIPIKGFHHSISLSESSSLQDALRLLTLWFTFGGIPEAT
QAMHEGFNLIQIGTWLEVLPLQISRIHQPNQIVSRSLLSLSDLGKAHPQALVYPLMVAI
KSELSRQKAALSIIIEKMRIHSPVLVDQAELVSHELIRMAVLWHEQWYEGLDASRQFFG
EHNTEKMFAALEPLYEMLKRGPETLREISFQNSFGRDLNDAYEWLMNYKKSVDVSNLNQA
WDIYYNVFRKIGKQLPQLQTLLELQHVSPKLLSAHDLELAVPGTRASGGKPIVKISKFEPV
FSVSISSKQRPRKFCIKGSDGKDYKYLKGHEDIRQDSLVMQLFGLVNTLLQNDACFRRH
LDIQQYPAIPLSPKSGLLGWVNSDTHVLIHREHREAKKIPLNIEHWVMLQMAPDYDNL
LLQKVEVFTYALNNTGQDLYKVLWLKSRSSSETWLERRTTYTRSLAVMSMTGYILGLGDR
HPSNMLDRITGKVIHIDFGDCFEAAILREKFPEKVPFRLTRMLTYAMEVSGIEGSFRIT
CENVMKVLRDNKGLMAILEAFADFPLINWGFDLPTKKIEEETGIQLPVMNANELLSNGA
ITEEEVQRVENEHKNAIRNARAMLVLRITDKLTGNDIRRFNDLDVPEQVDKLIQQATSV
ENLCQHYIGWCPFW

B. ULK1 (unc-51 like autophagy activating kinase 1)

>sp|075385|ULK1_HUMAN Serine/threonine-protein kinase ULK1 OS=*Homo sapiens*
OX=9606 GN=ULK1 PE=1 SV=2
MEPGRGGTETVGKFEFSRKDLIGHGAFVVFVKGRHREKHDLEVAVKCIKKNLAKSQTLGKEIKILKELKHENI
VALYDFQEMANSVYLVMEYCNGGDLADYLHAMRTLSEDTIRLFLQOIAGAMRLLHSGKIIHRDLKPNILLSNPA
GRRANPNSIRVKIADFGFARYLQSNMMAATLCGSPMYMAPEVIMSQHYDQKADLWSIGTIVYQCLTGKAPFQASS
PQDLRLFYEKNTLVPTIPRETSAPLRQLLLALLQRNHKDRMDFFEFFHHPFLDASPSVRKSPVPVPSYSSGS
GSSSSSSSTSHLASPPSLGEMQQLQKTLASPADTAGFLHSSRDSGGSKDSSCDTDDFVMVPAQFPDGLVAEAPSA
KPPPDSLMCSGSSSLVASAGLESHGRTPSPSPCCSSSPSGRAGPFSSRCGASVPIPVPTQVQNYQRIERNLQS
PTQFQTPRSSAIRRSGSTSPGLFARASPSPPAHAHGGVLRKMSLGGGRPYTPSPQVGTIPERPGWSGTPSPQG
AEMRGRSPRPGSSAPEHSPRTSGLGCRLLHSAPNLSDLHVVRPKLPKPPDPLGAVFSPPQASPPQPSHGLQSCR
NLRGSPKLPDFLQRNPLPPIILGSPTKAVPSFDFPKTPSSQNLALLARQGVVMTPPRNRTLPLDLSEVGPFGHQP
GPGLRPGEDPKGPFGRSFSTSRLLDLLLLKAAFQAPDPGSTEISLQEKPMIAPSAGFGGSLHPGARAGGTSSPS
PVVFTVGSPPSGTPEHTPEIRTRMFSAGPTGSASSARHLVGPSCSEAPAPELPAPGHGCSFADPITANLEGAVTF
EAPDLPEETLMGEQHTTEILRGLRFTLLFVQHVLEIAALKGSASEAAGGPEYQLQESVVDQISLRSREWFQAEQL
VLYLKVAELLSSGLQSAIDQIRAGKLCSSVTKVQVRRNLNELYKASVVSCQGLSLRLQRFFLDKQRLLDRIHSIT
AERLIFSHAVQMVQSAALDEMFQHREGCVPRYHKALLLLEGLQHMLSDQADIENVTKCKLCIERRLSALLTGICA

>sp|P53104|ATG1_YEAST Serine/threonine-protein kinase ATG1 OS=*Saccharomyces cerevisiae*
(strain ATCC 204508 / S288c) OX=559292 GN=ATG1 PE=1 SV=1
MGDIKNKDHTTSVNHNLMSAGNYTAEKEIGKGSFATVYRGHLTSDKSQHVAIKEVSRAK
LKNKKLLENLEIEIAILKIKHPHIVGLIDCERTSTDFYLIMEYCALGDLTFLKRRKEL
MENHPLLRTVFEKYPSPSENHNLHRAFVLSYLQQLASALKFLRSKNLVHRDIKPNLLL
STPLIGYHDSKSFHELGFVGIYNLPILKIADFGFARFLPNTSLAETLCGSPLYMAPEILN
YQKYNKADLWSVGTVVVFEMCCGTPPFRASNHLELFKKIKRANDVITFPPSYCNIEPELKE
LICSLTTFDPAQRIGFEEFFANKVVNEDLSSYELEDDLPELESKSKGIVESNMVSEYLS
KQPKSPNSNLAGHQSMADNPAELSDALKNSNILTAPAVKTDHTQAVDKKASNKYHNSLV
SDRSFEREYVVVEKKSVEVNSLADEVAQAGFNPNPIKHPTSTQNQNVLLNEQFSNNQQY
FQNQGENPRLLRATSSSSGGSDGSRPRLVDRRLSISLNPNSNALSALGIASTRFLFGGA
NQOQQQQQITSSPPYSQTLNLSQLFHELTENIILRIDHLQHPETLKLNTNIVSILES
AKAFVVYSYAEVKFSQIVPLSTTLKGMANFENRRSMDSNAIAEEQSDDAEEDETLKKY
KEDCLSTKTFGKGRTLSATSQLSATFNKLRSEMILLCNEAIVLYMKALSILSKSMQVTS
NWWYESQEKSCSLRVNVLVQWLREKFNECLEKADFLRLKINDLRFKHASEVAENQTLLEEK

GSSEEPVYLEKLLYDRALEISKMAAHMELKGENLYNCELAYATSLWMLETSLDDDDFTNA
YGDYPFKTNIHLSNDVEDKEKYHSVLDENDRIIRKYIDSIANRLKILRQKMNHQ

>NM_001181045.1 *Saccharomyces cerevisiae* S288C serine/threonine protein kinase ATG1 (ATG1), partial mRNA

ATGGGAGACATTAATAAATAAGATCACACAACCTCTGTGAACCATAATCTAATGGCAAGTGCAGGAAAT
ACACCGCTGAGAAAGAAATCGGAAAGGGTTCGTTTGCCACTGTATATAGAGGGCATCTGACATCCGACAA
ATCTCAGCATGTAGCCATAAAGGAAGTATCAAGGGCGAAATTAATAAATAAGAAATTAAGAGAAATTTG
GAAATAGAAATCGCTATCTTGAAGAAAATCAAGCATCTCATATCGTCGGACTTATTGACTGTGAACGAA
CATCAACAGATTTTTTATTTGATCATGGAGTACTGTGCTCTTGGGGACCTAACATTTCTGTTGAAAAGGCG
TAAAGAATTGATGGAGAATCATCTCTACTAAGGACCGTATTTGAAAAATACCTCCACCGAGTGAGAAC
CATAACGGCCTGCATAGAGCGTTTGTCTTGAGTTATTTACAGCAGTTAGCGTCCGCTTTGAAATTTTTGA
GGTCTAAAACTTGGTTCATAGAGACATCAAGCCTCAAACTTACTATTATCTACACCCCTAATTGGATA
TCATGATTCAAAAGCTTCCATGAACTTGGATTTGTTGGGATCTACAACCTTACCCATTTTTAAAGATAGCA
GATTTCCGGTTTGCAAGATTTTTGCCAAACACGTCATTAGCAGAACTCTTTGTGGCTCACCATTATATA
TGGCACCAGAAATTTGAATTATCAAAAATATAACGCTAAAGCAGATCTGTGGTCTGTCTGGTACAGTGGT
ATTCGAAATGTGCTGTGGCACCCACCGTTTAGAGCTTCCAATCATTTGGAGTTATTCAGAAAAATTA
AGAGCAACAGATGTATAACGTTTCTTCCATATGCAATATTGAACCAGAGTTAAAAGAGTTGATATGTA
GTTTATTGACATTTGATCCAGCCCAAGAATAGGATTTGAGGAGTTTTTTGCTAACAAAGTCAACGA
AGACTTGTCTTCTTATGAATTTGGAAGATGATTTACCTGAGTTAGAATCCAAATCAAAAGGTATTGTAGAA
AGTAATATGTTTCGTTTCTGAGTATTTATCTAAACAGCCAAAGAGTCCGAACAGTAATCTTGCAGGTCATC
AATCAATGGCAGATAATCCCGCGGAGCTCAGTGATGCCCTCAAGAACAGCAATATATTAAGTCCCGCAGC
CGTTAAAACAGACCATAACAAAGCCGTAGATAAAAAGGCTTCAAATAATAAATACCATAATAGCCTAGTT
TCAGATAGAAGCTTTGAAAGAGAATATGTGGTGGTAGAGAAGAAATCGGTTGAAGTTAATTCATTGGCAG
ACGAGGTTGCTCAAGCAGGATTCAATCCAAATCTTATTAAGCACCCAACTTCAACTCAAAATCAGAACGT
CTTATTGAATGAGCAATTTCTCTCCAAACAATCAACAGTATTTTCAAAATCAAGGAGAAAAATCCGAGGTTA
CTGAGGGCCACATCATCTTCCAGTGGAGGTAGTGATGGGTCTAGGCGACCATCTTTGGTGGATAGACGCT
TGTCTATATCCTCGCTGAATCCATCTAATGCATTATCAAGAGCCCTCGGTATTGCATCAACGAGATTGTT
TGGTGGTGCAATCAACAGCAGCAACAGCAACAAATCACATCTTCCCCACCGTACAGTCAAACTTTGTG
AATCCCAACTTTTTTCATGAACTTACTGAGAATATAATATTAAGAATAGATCACCTACAGCATCCAGAGA
CACTGAAATTAGATAATACTAATATCGTTAGTATTTTGGAAATCTCTGGCCGAAAAGGCATTTGTTGTTTA
CTCTTATGCAGAAGTGAATTTTTCTCAAATTTGTTCCATTATCAACAACATTAAGGAGGATGGCTAACTTT
GAGAACAGGCGCAGTATGGATAGTAATGCTATTGCAGAAGAACAAGACTCAGACGATGCAGAAGAAGAGG
ATGAAACGTTGAAAAAGTACAAGGAAGATTGCTTATCCACGAAAACCTTTTGGAAAGGGTAGAACTTTATC
TGCCACATCTCAGTTGAGTGAACCTTTCAATAAACTACCACGTTTCGAAATGATCCTTCTATGTAATGAG
GCCATTGTCTTATATATGAAGGCATTATCCATTTTATCAAATCTATGCAGGTAACGTTCAACTGGTGGT
ATGAATCTCAAGAAAAATCATGTTCTCTAAGAGTTAACGTGTTGGTACAGTGGCTAAGGGAAAAATTTAA
TGAATGTTTGAAGAAAGCTGATTTCTGAGATTAATAAATAACGACTTGAGATTCAAGCATGCTTCTGAG
GTAGCTGAAAATCAAACCTTTGGAAGAAAAAGGTAGTTCCGAAGAGCCAGTATATTTAGAAAAGCTATTAT
ATGATCGTGCATTAGAAATATCTAAGATGGCCGCACATATGGAATTAAGGAGGAAAAATTTGTACAACCTG
TGAATTAGCTTATGCAACTTCACTTTGGATGTTAGAACTTCTCTGGACGATGATGATTTTACGAATGCC
TATGGTACTACCCTTTTTAAACTAACATACATCTAAAAAGTAACGACGTTGAAGATAAAGAGAAATATC
ATAGTGTGTTGGATGAAAATGACAGAATAATCATAAGAAAGTATATTGATAGTATTGCAAACAGGTTGAA
AATATTGAGGCAGAAGATGAACCACCAAATTA

C. ULK2 (unc-51 like autophagy activating kinase 2)

>tr|K1PNL8|K1PNL8_CRAGI Serine/threonine-protein kinase ULK2 OS=*Crassostrea gigas* OX=29159 GN=CGI_10015287 PE=4 SV=1

MEVVDYDYESSKDLIGHGAFVVFVKGRHRKRPNHVVAIKSITKKNLAKSQNLLSKEIKIL
KELSDLHHENVALLDCKETTNNHVYLVMEYCNGGDLADYLQAKGTLSEDTIASFLRQIAA
AMQVMNGKIVHRDLKPQNILLCHDGKPNTPSTEMRLKIADFGFARFLNDGVMAATLCGS
PMYMAPEVIMSLQYCAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKHFYEKHAELKPNIP
KDTSPELRDLKMLKRNADRIEFASPVVPPGRASQGCSSSPTPPRCVSAASPLSGKAD
YSTPPSKVVQMVKQVEAEAMQGSTHDEEFLKVDKGPTRNSNSPTEHDFVLVDPGMSDQS
DGS DKGRAPSTEDLQSLGERAQPQVVRVEPQVGSVAYKKDSGDVSSPSRPSLPMQSNQ
SEPIPVPTQVKAYERIRSSSSPLSSPRKCGTEPSPLDSAKLSSQNIKISPPQESKFSAPD
IGSFSPTVKFVSVGTPPNVSTPWRRGSIGSSQGGAIYHPPSNASNSPSRRASMGSSPSGF
NRNFSSPGSLPTILDASPHFELNQEPQFTDNMPTVPVRAFPQSKPKAIPESKGTKRYHP
SEVDRVKNLNMERCNTDPAAGGMSMLSQMKVAYMNQOGLNLLLEGQVVRYTSENENLVSP
NDNTVQMDTQRSGLRRTMSATTPPSNLMFAQSPPNMEGPVAFVAPGLAEETLMGDNHN
EIMAKLSFVNDLADCVMEELAMAKGAPLNTLSESVNWKQEGEPLHGDQMPKFI EAQRLL EQ

LVLVYRSLQLLSSSLQLARREIKDERLQISNALKTLKQMNERYHRCVSVCKHIQQRLGI
TMQNALTPQVVIATADKLIYNYAIEMCQTAALDELFGNPQECFKRYNTAHILLHSLSQQA
RNSNDKQLLDKYKDAVERRLSHIQATQNYYPQFEIS

>NM_001142610.2 *Homo sapiens* unc-51 like autophagy activating kinase 2 (ULK2), transcript variant 2, mRNA

AGTCGCGCGGGAGCGGGTAGCGCGCGGAGGGCGTTGGGGCCGCGCGAGGCGGGGAAGCGGGGCCG
CGGCGGTGCGGGTCTAGGGCGGGCCGTCGCCGTCGAGCAGCGCCCCGAGCGGGGAGGGCCGAGGAG
GCCCCGACGAGCTGGGGATGGAGAGTACCGGGCCCCCTCACTGCCTCAGAGCGCGTGTGCGGCTCTGGGCGC
GCACAGTGACGGTGACGGCACCCCTGGCCCCGGCAGCGCCGAGGCCGCTTCGCCAGACAGCCAGCGGCCG
CGGCAGGCCGGGCCATGAGCGGCAGGGGCCGGGCCGCGCTCGCTGACCCTGGCTCCGCGCGGCAGCTTC
CCCAGTTTTCCGCTCCGGTCTCTCGGCATGAGAGTCCGCCCCGGGCCCGGGGCTGCGGCTGCCCCAGACCCG
CCGCACGCTGGCGCGCTCCGGGCCCGCGGAGCCGCGGTGCTGATACCTGCGCCGCACTGCGCCGCCCGCC
CGTCCGCTGTGTGCCCCGGGGGCGCGGCCATGGAGGTGGTGGGTGACTTCGAGTACAGCAAGAGGGATCT
CGTGGGACACGGGGCCTTCGCCGTTGGTCTTCGGGGGGCGGCACCCGCCAGAAAATGATTGGGAGGTAGCT
ATTAAAAGTATTAATAAAAAGAAGTGTCAAAATCACAAATACTGCTTGAAAAGGAAATTAATAATCTTAA
AGGAAGTTCAGCATGAAAATATTGTAGCACTCTATGATGTTTCAAGGAATTACCAACTCTGTCTTTTTGGT
GATGGAGTATTGCAATGGTGGAGACCTCGCAGATTATTTGCAAGCGAAAGGGACTCTCAGTGAAGACAG
ATCAGAGTGTCTTCATCAGATTGCTGCTGCCATCGCAATCCTGCACAGCAAAGGAATCATCCACAGAG
ATCTCAAACCCAGAACATCTTGCTGTCTTATGCCAATCGCAGAAAATCAAGTGTGAGTGGTATTTCGCAT
CAAAATAGCGGATTTTTGGTTTTGCTCGTTACCTACATAGTAACATGATGGCTGCAACACTGTGTGGATCC
CCGATGTACATGGCTCCTGAGGTTATTATGTCTCAACATTATGATGCTAAGGCTGACTTGTGGAGCATAG
GAACAGTGTATACCAATGCCTAGTTGGAAAACACCTTTTCAGGCCAATAGTCTCAAGACTTAAGGAT
GTTTTATGAAAAAACAGGAGCTTAATGCCTAGTATTCCCAGAGAAACATCACCTTATTTGGCTAATCTC
CTTTTGGGTTTTGCTTCAGAGAAAACCAAAAAGATAGAATGGACTTTGAAGCATTTTTTAGCCATCCTTTTC
TTGAGCAAGGTCCAGTAAAAAATCTTGCCAGTTCAGTGCCTATGATTCTGGTCTGTCTCTGGAAG
CTCCTGTGGCAGCTCTCCATCTTGTGCTTTTTGCTTCTCCACCATCCCTTCAGATATGCAGCATATTCAG
GAAGAAAATTTATCTTCCCACCATTGGGTCTCCCAACTATCTACAAGTTTTCAAAGATTCTGCCAGTA
CTAGTAGCAAGAATCTTCTTGTGACACGGATGACTTTGTTTTGGTGCACACAACATCTCGTCAGACCA
CTCATGTGATATGCCAGTGGGGACTGCTGGCAGACGTGCTTCAAATGAATTCTTGGTGTGTGGAGGGCAG
TGTCAGCCTACTGTGTACCTCACAGCGAAACAGCACCAATTCAGTTCCTACTCAAATAAGGAATATC
AGCGCATAGAGCAGAATCTTACATCTACTGCCAGCTCAGGCACAAATGTACATGGTTCCTCAAGATCTGC
AGTGGTACGAAGTCCAACACCAGCCCCATGGGCTTCCTCCGGCCGGGATCATGCTCCCAGTACCAGCA
GACACAGCACAGACAGTTGGACGAAGGCTCTCCACTGGGTCTTCTAGGCCTTACTCACCTTCCCCTTTGG
TTGGTACCATTCTGAGCAATTCAGTCAGTGTCTGTGTGGGCATCCTCAGGGCCATGACTCCAGGAGTAG
AAACTCCTCAGGTTCTCAGTGCACAAAGCTCAGTCCCAGTCTCTCTTATCGGGTGTAGACTGCAG
AGCGCCCCACCCTCACTGACATCTATCAGAACAAGCAGAAGCTCAGAAAACAGCACTCGACCCCGTGT
GCCATCCCATACTGGGGCTGGGTACAGCTACTCGCCTCAGCCCAGTCGGCCTGGCAGCCTTGGAACTTC
TCCCACCAAGCACTTGGGGTCTCTCCACGGAGTTCTGACTGGTTCCTTTAAAACCTCTTTGCCAACAAATC
ATTGGCTCTCCTACTAAGACCACAGCTCCTTTCAAATCCCTAAAACCTCAAGCATCTTCCAACCTGTTAG
CCTTGGTACTCGTCATGGGCCTGCTGAAGAACAGTCGAAAGATGGGAATGAGCCACGGGAATGTGCCCA
TTGCCTCTTAGTGCAAGGAAGTGAGAGGCAGCGGGCCGAGCAGCAGAGCAAGGCAGTGTTTGGCAGATCT
GTCAGTACCGGAAGTTATCAGATCAACAAGGAAAGACTCCTATATGTCGACATCAGGGCAGCACAGACA
GTTTAAATACAGAACGACCAATGGATATAGCTCCGGCAGGAGCCTGTGGTGGTGTCTGGCACCTCCTGC
AGGTACAGCAGCAAGTTCCAAGGCTGTCTCTTCACTGTAGGGTCTCCTCCACACAGTGGCGAGCCCC
ACTTGTACCCACATGTTCTTGAACAAGAACAACCTCAGTGGGGCCAGCAACTCCGGGGGCTCTCTTT
GTGCCATGAGTGGCCGCGTGTGCGTGGGGTCCCCGCCTGGCCAGGCTTCGGCTCTTCCCCTCCAGGAGC
AGAGGCAGCTCCCAGCCTGAGATACGTGCCTTACGGTGTTCACCCCCAGCCTAGAGGGGCTCATCACC
TTTGAAGCCCCTGAACTGCCGGAGGAGACGCTGATGGAGCGGGAACACACAGACACCTTACGCCATCTGA
ATGTGATGCTGATGTTCACTGAGTGTGTGCTGGACCTGACAGCCATGAGGGGAGGAAACCTGAGCTGTG
CACATCTGCTGTGCTCTTGTACCAGATCCAGGAGAGTGTGGTGGTGGACCAGATCAGTCAGCTGAGCAAA
GACTGGGGGCGGGTGGAGCAGCTGGTGTGTGTACATGAAAGCAGCACAGCTGCTTGGGGCTTCTCTGCATC
TTGCCAAAGCCCGATCAAGTCCGGGAACTGAGCCATCCACAGCTGTGAAACAAGTTGTCAAGAATCT
GAACGAACGATATAAATCTGCATCACCATGTGCAAGAAACTTACAGAAAAGCTGAATCGATTCTTCTCT
GACAAACAGAGGTTTTATTGATGAAATCAACAGTGTGACTGCAGAGAAAATCATCTATAAATGTGCTGTAG
AAATGGTTCAGTCTGCAGCCCTGGATGAGATGTTTTCAGCAGACCCGAAGATATTGTTTATCGCTATCATAA
GGCAGCCCTTCTTTTGAAGGCCTAAGTAGGATTCTACAGGACCCTGCAGATATTGAAAATGTGCATAAA
TATAAATGTAGTATTGAGAGAAGACTGTGCGCGCTCTGCCATAGCACCCGAACCGTGTGAGCAGCAGGCT
CATCCCGTGGACCGGTGGTGGGAACGTGAGGAAGAGGGGAAGGAAGGAAGAGCTTTTCCATTTGGTGTCTC
CAATGTCTCCTGCTGGACCCATCTGCCTAGTGGAAAGCAGCAAAATTTCAAGAAACAGGTGAGGTTGAGC
AGCTTGGTGAACCCCATGGGGCCTGGAGTTGGAGCTCAACAGCAATGGATTTTCAGAGACCACCTGAAA
CTCCCAGTAAAAAGACTTGGGAGACATGTTAATAAACTCAAGCATTGTGATCGACCCA

D. ULK3 (unc-51 like kinase 3)

>tr|K1Q313|K1Q313_CRAGI Serine/threonine-protein kinase ULK3 OS=*Crassostrea gigas* OX=29159 GN=CGI_10009716 PE=4 SV=1
MSRPTSGRPSTAKSVAVIVPKLSGFVFTTEKLGSGTYAVVYKAYRKSGSRQVVAIKCVLKS
SLNKASTENLLTEIELLKKLNHENIVRLEDFQWDDQYIYLIMEYCSGGDLSNFIRSKRTL
PENILKRFLQQIAKAMRYLREFNIAHMDLKPQNILLTSEYNPTLKIADFGFSKHLFKGDE
LHAMRGSPLYMAPEIICKGTYDSRVDLWSIGVIIYECLFGRAPFASRTFKELNKIWDISK
PVEAMILNLQIPYGVNVSENCRDILRLRRDPDERITFDEFFNHPFVDLEHCASNESLS
KAVNIVANAVKDKQNGEYKEAIKLYCDSLGHFMPAIHYEKDERKKEAIRAKVKDYMNRAE
ELKKLMKPKRPPPPVNGVKRTISEDPMEEELTELCKDNEELTAAVTLIRAADTENSQEDYE
QALKHYELALSTFIKFLKEEKPGHRKDLIGKLSRSWMDEAEKIKMFLDVQNLQTEDTSAK
EEENEKKYLYTVREAVGDKTISER

>NM_001099436.4 *Homo sapiens* unc-51 like kinase 3 (ULK3), transcript variant 1, mRNA

GGAACCGCCGCCCCGAGCGAGGAAGCGCCCCGCGGGCGCAGGCGGCGCGGAATGGCGGGGCCCCGGCTGGG
GTCCCCCGCGCCTGGACGGCTTCATCCTCACCGAGCGCCTGGGCAGCGGCACGTACGCCACGGTGTACAA
GGCCTACGCCAAGAAGGACACTCGTGAAGTGGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAG
GCATCGGTGGAGAACCTCCTCACGGAGATTGAGATCCTCAAGGGCATTGACATCCCCACATTGTGCAGC
TGAAAGACTTTTCAGTGGGACAGTGACAATATCTACCTCATCGAGTTTTTCGCGAGGGGGCGACCTGTC
TCGTTTCATCCATACCCGACAGGATTCTGCCTGAGAAGTGGCGCGTGTCTTCATGCAGCAATTAGCTAGC
GCCCTGCAATTCCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCCACAGAACATTCTACTGAGCT
CCTTGGAGAAGCCCCACCTAAAACCTGGCAGACTTTGGTTTTCGCACAAACACATGTCCCCGTGGGATGAGAA
GCACGTGCTCCGTGGCTCCCCCTCTACATGGCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCGC
GTGGACCTCTGGTCCATGGGGGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGT
CGTTCTCGGAGCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGCGGCCCTGCTCTC
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTGCGATCTCCTTCCAGGAC
TTTTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAGTCTGGGGCGAGCAACCGCCC
TGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATTACAGCAGCTGCCTTATCACTCTACTGCAAGGC
TCTGGACTTCTTTGTACCTGCCCTGCACTATGAAGTGGATGCCAGCGGAAGGAGGCAATTAAGCAAAG
GTGGGGCAGTACGTGTCCCGGGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGA
GGCAGGGGACCTCTGCCCGAGACCTGCTCAGAGAGATGGCCCCGGGACAAGCCACGCCTCCTAGCTGCCCT
GGAAGTGGCTTACAGCTGCCATGGCCAAGGAGGAGGCCCGCGGGGAGCAGGATGCCCTGGACCTGTAC
CAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGGCAGCGGAGCCCCGGGCGGAGGCGGGAGCTGCTTC
ACACTGAGGTTTCAAGCCTCATGGCCCCGAGCTGAATACTTGAAGGAGCAGGTCAGATGAGGGAAATCTCG
CTGGGAAGCTGACACCCTGGACAAAGAGGGACTGTGCGAATCTGTTTCGTAGCTCTTGCACCCCTCAGTGA
CCCTAGAAGAATGATTGGACAGATGTGAGCCATCTGGAGCAGAGGGGCACTAACCAGGCTGACGCCAAG
AATGAAGTGGCCACTGCAGCCCTGGCGAGCAGGCTTCTTGGATGGACAGTGTGAGACCCCATATCCC
AGAGTCCCCAGCCTCCCTCAGGTTACTCTGCACCCACAGATGGTTTGTATGGCTGTGCTGTATACTGGAG
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTTCATGAGACCTTTGTTACTCGGTGGTTACTGGGTCC
TGTGCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTTGGCTCCGAGAAGAGGGCAAGGGGCCCC
GCAGGGTACTTCTGTGCTTGCCCTCGCCCTGCCAGCAGGAGCTGTGCCCTGGCCTGCCCTTCCCGGGA
CCCCTTATTCCAACCTCAGCTCCTCTTTGCACTGGAATGGGGCACTCCAACACCCTCAGGGACCACCCTC
CCCACAGTATGCACTCAGCCCCACAGAACCACCAGTCTTTCTGGGAACTCACACCTGCCCGCCATCTTG
GTACTTTAGGTTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTAAGAAGCCCAAGCCTTGTTC
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCCCTTGGTCTCATCTCTCCACCTCCGTCCCTCTGGGC
CCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGGACCTGGGACAGGGAGAGGGAGGCTTGGAGA
CAGTCTGACCCAGTGCCTCTAGGCCACCCACTTCTAGGCCTGCCCTGCCCGCTGGAGCCCTGGGCAAG
CTCTTTCCCTTTTCTGGGCCTGGGTCTCCCCATCTCTTCAATGGGGCTGATACCTTACAGCCCACAGCA
TGGGCACCTTATGAGGACAAAGTGAATTTAACCTGGAAAAGAATGTATTTGAGAGTTTCTTTTAAATAATC
AGCGGGTGTGGTGTATTTGTAGCCCTTCTGCCCTTAAATGCTTCTTGGGCAAGAGCTGTCTGTCTCCC
TGCAGGAGGCTGAGTGTAAAGAGTATCATTATTGTTTCTCTATTAAATTATTTTCTCTA

E. ULK4 (unc-51 like kinase 4)

>tr|K1QQA6|K1QQA6_CRAGI Serine/threonine-protein kinase ULK4 OS=*Crassostrea gigas* OX=29159 GN=CGI_10017902 PE=4 SV=1
MENFVLYEELGRDINSIIYKGRKGTINFVAIHICIEKCRPEVTNTVVRMTHDISHPNVVK
FYEWYETSNHLWLVLVELCTGGSLATLITQDRNLPSSIRSFGIDLVTGIHYIHSGLGILFC

DLRPTKILLDGSGLTKYADFGLSRVEGEILEELFEKFDADAGEMWSNEADLDDNPLSKKYK
TTGAPTYMSPEGFQSQEITILSDLWSLGCVLYEMFTGHPPFLAESFQQLKEKILHKELPP
PKVKGSRFSSKPSPDFHNLLEGLLQKDPDKRMGWPLVNHFSWQGRLSHLAKDLVTSQEV
RSSIVNTTRSSVLEGTASALGRIKTVLKKSMRDPVSTLETEGTRPGSTMGDYMRPKTA
PGNEGGSTLFTLSTRPPTAVPPDEKLAPTQKPTQSPLSTREVRETI GTTGGESQADETKN
EAELELIYHSDFHITPIVDNTKIQKPGAAKFDAKILVPPFTAEKMANMSEKELSKHIKA
IIDGLSINEKGPSPQKRIHLLHYLTGLSTNPQVATALTRNNVLSVLAKVVKETQHLDVKT
KAARVVGLIAGNAEDLDESVTISESIATLTEVIRENVKNGKLGQVLPVAVGELLYFVAQQ
EVKHGKTCDNWSVTSMTYTVITRCCREGEDAVVNHIAAKTVENVVATQSTHAQKFSNEM
GQSLWYIFKHSTVDSLRLITALNALCRITHHNPTVFQSVIDTVGMTTILSALSFGITRIQQ
SIVTMFGALIASGQSLNRVVQDKDFLQKLI RLLDPSVVI RAKAFVVIHEVVKNNDLLL
NSCQSRLVMIERDSRRQTPREGKAPENNGSESVEYLMQCLDLLINHMVDVVPRLFKEIV
TSLDAVMGRKHPNAVQAKQLRSSPLIHFVFLHLVTSQVFRPKIVNEEFIKNLSSVLSHIK
SIELGETNIEGASGSI SPDFVTTTMSVLEGISQHPMIVAEYHQVILESVLPIIADLVVS
QNGETRALSLRLFSEIASVYLNQEYAAAGEKKMNVAGLHKIITERLLPQFEQILLDQEPL
PSYGLKLLLTLLDQNGGFVKQFEQQGLVSVIFQVMMDHQSNPLNSSMQSIAGILNCLVAH
KDTNMKDLYEQGLIDYFTTLFFDVTTACLDTEDHADNKIAHSMQLNLLDTLHSMFKYVSE
VVRKALQNKKAGGEGGNREAEAEQLLLLTNKSLTDLTTILTQLLFCFEDTDIQDFSTKCLS
LLVQLFGGENKDSMTPENMEYYSKALKKSDAKKQKVLRLRIKRLLSTERVHVESMKQHGE
TLANTIRNLVQTASSHADVAISSLAADILKMTVPQEYYSKALKKADAKKQKVLRLRIKRLL
LSTERVHVESMKQHGETLANTIRNLVQTASSHADVAISSLAADILKMTDIVLPGMEAFTM
ADQNDIRVKNQDFVGCYMDQEPRTLNEKMTVSTTMTVDSCRKTCTDLKFKYYGVEYSAQC
FCGNQPLNVRKMREGDCLKPCAGDRTQACGGSWRIAVYENPQNI PKFVGCYMDQQARTLN
EKMTVSTTMTVDSCRKTCTDLKFKYYGVEYSSQCFCGNQLMNVKRMREGDCLKPCDGDRT
QACGGNWRIVAVYENPLYIPKFVGCYVDQTYRTLGEKMTVSTTMTVDSCRKTCTDLKFKYY
GVEYSSQCFCGYDLIHAIKVSEEDCLRPCSGDRTQACGGSWRIAVYENPRYISREYEEEN
NVEFVGCYVDQARTLNGKMTTSTTMTVYNCRKTCTDLKFMFYGVEVKKAGRKGGNQKAE
HMFPTKSLTDMTITLTSWELLFEFCFCGNKLTITTKMRDGDCLKPCTGDKTQACGGDWRI
AVYENPYITPPKFVGCYMDQQARTLNEKKTVSTTMTVDSCRKTCTDLKFKYYGVEVNICR
ICWLLHGSTSQNLERKDDCLYNNDSGQLPKNVYGVSEV

>NM_017886.4 *Homo sapiens* unc-51 like kinase 4 (ULK4), transcript variant 1, mRNA

GTGGACCTGTCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACTGGACTCTTT
TCTTGACTTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATTGTATGTGAGAAGTCGGCCAGAGATGG
AAAACCTTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAGACTGTTGTCTATAAAGGGCAGGAAGGG
ACAATCAATTTTGTAGCCATTCTTTGTACTGATAAGTGCAAAAAGGCCTGAAATAACCAACTGGGTCCGT
CTCACCCGTGAAATAAAACACAAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCT
GGCTAGTGGTGGAACTCTGCACAGGTGGTTCCTTAAAAACAGTTATTGCTCAAGATGAAAACCTCCCAGA
AGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGATTACATCATCTTCATAAACTTGGCATTCTC
TTTTGTGACATTTCTCCTAGGAAGATACTCTTGAAGGGCCTGGCACACTGAAGTTTAGCAACTTTTGCT
TGGCAAAAGTGGAAAGGTGAAAATTTGGAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGA
TAATGGGGAAAATGTCCTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCA
GAAGTTGTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTATGAAA
TGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTATTTT CAGAATTA ACTGAAAAGATCTTATGTGAAGA
TCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCTCAAAGCTTCTTCAGATTTTATTAATTTGCTTGAT
GGGTTACTTCAAAGAGATCCTCAGAAAAGATTGACTTGGACAAGGCTACTGCAGCATTCATTTTGGAAAGA
AAGCTTTTGTGCTGGAGCAGATCAGGAATCAAGCGTCGAAGATCTCAGTCTCAGCAGAAAACACTATGGAGTG
TTCTGGGCCACAAGATTCCAAGGAGCTTTTGCAGAACTCTCAGAGTAGACAAGCAAAAAGGGCACAAGAGT
GGTCAACCACTAGGTCACTCTTTCAGACTAGAAAATCCAAGTACTGAGTTTCGGCCTAAGAGTACTCTTGAGG
GTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCTACTCCCAGAACTAGCACTGCAGTGGAAAGT
AAGTCTGGTGGAGGATGACTCACTGTTCAACCAAGAACTTCTCCTCTGACCAAGATTACAAGTGGGA
CACCTGAGTCAGCAGGACCTGGAATCCAGATGAGAGAGACTTATCTACACGGACTCAGATCTTGTGTCA
CCCCCATTATCGACAATCCAAAGATAATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCT
ACCAACATATTAGTGGATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTGCAACAAGTG
TGCTCGCAGATCGACTCCACTGAGAAGAGCATGGGGGCCTCCCGAGCCAAGCTGAATCTCCTTTGCTATT
TGTGCGTGGTGGCTGGTCAACAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTGTTCCAATTGCTAAT
CCAGCATTTGCGGATAGCTCCAAACTGGGATATACGGGCCAAGGTTGCTCACGTAATTTGGTTACTGGCT
TCGCACACAGCTGAGCTCCAGGAAAATACACCTGTTGTTGAGGCAATTGTTCTTAACTGAATTAATTA
GGGAAAACCTCAGGAACAGCAAATTAACACAGTGCCTTTTACCAACCTTGGGGAGCTGATCTATCTTGT
AGCCACCCAGGAAGAAAAAAGAAACCTTAGAGAGTGTGGGCTGTTCCCTTGGCTGCATACACAGTG
CTAATGAGGTGCCTTCGGGAAGGGGAAGAGCGTGTGTGAATCACATGGCAGCAAAAATATTGAAAATG

TCTGTACCACCTTTTCTGCTCAGTCCCAGGGCTTTATTACAGGAGAAAATAGGACCCATTTTGTGGTACCT
 ATTCAGACACTCCACTGCTGATTCTCTTAGGATAACAGCAGTATCGGCCTTGTGTAGAATCACTCGCCAT
 TCTCCTACTGCCTTCCAGAATGTTATTGAAAAGGTGGGACTGAACTCAGTAATAAACTCCCTGGCCTCTG
 CCATCTGCAAAGTTCAGCAGTACATGTTGACCTTATTTCGCTGCCATGTTGTCCTGTGGGATTCATCTTCA
 AAGACTAATCCAAGAAAAGGGTTTTGTCTCCACAATTATCCGTTTACTTGACAGCCCTCAACATGCATT
 AGAGCAAAGCCTTCCCTGGTTCTTCTATATATTTTTGATTTATAACCGTGAGATGTTGCTGCTCAGTTGCC
 AAGCAAGACTGGTGTATGTACATCGAGAGAGACAGCAGAAAGACCCTCCAGGCAAGGAGCAGCAAAGTGG
 CAATGAATACCTGTCCAAATGCCTGGATCTTCTCATCTGTACATTGTGCAGGAGCTGCCACGAATCCTG
 GGTGACATTCTTAACCTCCTTGGCTAATGTTTCTGGACGTAAACACCCATCAACAGTTCAAGTGAAACAGC
 TGAAGTTGTGTCTCCCCCTGATGCCTGTAGTGCTTACCTCGTAACTTCACAGGTATTTTCGACCTCAAGT
 TGTGACAGAAGAGTTTCTTTTTCAGCTATGGAATATTCTTAGTCATATTAATCTGTAGACTCAGGAGAA
 ACGAACATAGATGGAGCCATAGGACTGACAGCATCAGAAGAATTTATCAAGATCACATTGTCAGCTTTTG
 AAGCAATAATACAGTATCCTATTTTATTGAAAGACTATCGCTCCACGGTTGTTGACTATATACTGCCACC
 CTTGGTGTCTTGGTTCAAAGCCAAAATGTGGAGTGGAGACTCTTTAGCTTGCAGTTGCTCTCAGAAACC
 ACATCTTACTCGTGAACCAGGAGTTTGGGGATGGCAAGGAGAAGGCCAGTGTGATTCTGACAGCAATC
 TTCTGGCTCTCATTGAGATGTCTTACTTCCCAGTATGAGCACATTCTTTTAGAACCTGACCCAGTACC
 AGCATATGCTCTGAAACTGCTAGTCGCGATGACTGAACACAACCCAACTTTTACAAGACTTGTGGAAGAA
 AGCAAACCTGATCCCCTCATTCTTTTGAAGTAACTCTGGAACATCAGGAGAGCATTCTGGGTAATACCATGC
 AAAGTGTGATTGCATTACTCAGCAATCTAGTTGCCTGCAAAGATTGCAATATGGAACTACTTTATGAACA
 AGGACTTGTGAGTACATCTGTAACCTGCTCACTGAAACTGCCACACTGTGCTTGGATGTGGACAATAAAA
 AACAACAATGAGATGGCAGCTCCACTGCTCTTTTCCCTGCTTGATATTTTGCACAGCATGCTGACCTATA
 CCTCCGGTATTGTACGGCTGGCTTTGAGGCCCAGAAGTCTGGCTCAGGAGAGGACCCCTCAGGCTGCAGA
 AGACCTGCTGCTGCTCAACAGACCTCTGACAGACCTGATTAGCCTGCTCATTCCACTGCTTCTTAATGAA
 GATCCTGAGATTTTTGATGTTTTATCCAAGTGCCTGTCTATACTGGTTCAGCTGTATGGAGGGGAAAACC
 CGGACAGCCTCTCTCCTGAAAATGTGGAAAATTTTTGCTCATTTACTGACATCCAAGGAGGACCCAAAAGGA
 GCAGAAGCTTCTGTTAAGGATTCTCAGAAGAATGATCACCTCCAATGAGAAGCACTTGGAGAGCCTCAAG
 AATGCAGGCAGCCTCCTGCGGGCTCTGGAGCGGCTGGCCCTGGGAGTGGTTCAATTTGCCGACAGTGGCG
 TGGCTCCCTTGGCCCTGGAATCCTCCAAGCCGTTGGGCACTAGGCAAGAAGGTGCTTAGCACAAAGCCCG
 CCCTGTGGCCCCAGCCCTCGGATGCATAAGCAAGGTGAGCTCCCAGACACCTTTGCCACATCCCCTCACA
 GCTGTCTTTGGACCTAATAAAGTCACTTAACCCAGAACCTGGTGGCCCAAGTGTCTACTAACCCCAAGG
 CCTAGAAAACCTGACTCAGAATGGACTTCCTTGGTTTCTGTGGAATGCATCTGGGAAGCCAGGTTTGTTA
 GCTGTTCTCAGAAATGTTCTTTCCCTCTCTGTGTGGGCCAGGTGGGCTAAGGTTAGCACTGCCTGTGGTA
 ATAAAGCAGTGGATGCAAAGCACA

F. ATG13 (autophagy related 13)

>tr|K1QIF8|K1QIF8_CRAGI Autophagy-related protein 13 OS=*Crassostrea gigas*
 OX=29159 GN=CGI_10016010 PE=3 SV=1
 MSKLSQQDRKDLKFTKFLIYKSLQIIVQSRGELKIQAKSKPFSSGADWFNLAIKDIVEV
 HNETHKALVSQLTALLSQNVCEISLKTSEGDSMVLETWYIIGLNKETCDVNRARISYTVYNR
 MGIALKTLFISISRVTPAYKLSRQQGANADEYVICYRIFYQGDPOFFMLGDNYQTIKVGSVPT
 TPVGTIYINLAYRTRKLLITPQKSKAIPKIEVKDDHFKKDNSPRRPTTPKPCSLGFRRNST
 SEDLFGDGVQDLCSSTTFDNSPGEAFLLGMTQHGLVPPNIQKKTALKTDNRENNEAPKK
 QENVEKQLSFTSYQKVGAFQNRNSKEINNTDLEDVPPFLNLLQAEGKSEVKMTVQRELQN
 DIESNEQVSSNKSEEEKSLEQALSPSESISNTSAPDDFVMVELKTPFAGADPNQDLGKF
 YRECQGAPQLTMCSETNVEALAEISSQIQMFESNIEGFDDFVTSITESVTVE

>NM_001346354.1 *Homo sapiens* autophagy related 13 (ATG13), transcript
 variant 45, mRNA
 ACTGCCGCTGCCGCGGCTACCTGCGGTTTCATCTCCGCACATTCCACACGCGGCCCAAACGGTCTCTCTCT
 CTCTCTCTCAAACACCGCCTTTCCGTCTTTGTTTTATCTTGTAGTAGCTTAGAAAAGATTGGAGAAGAAAAGC
 TTACGTGGAATGAAAATCAACTTTTATGGATATTTTGGAGACTAAAAGAATAAATAGGGCGTCCGTACTG
 TAGCGAAAGTGCAGCTAAGGTTAGGCATCTGGATTTCCCCCGTAGCCCTCTTTACCCCCCCCCCCCCGGC
 CATTACCGAAGCGGATGAAAACAAACACTAACGATGGCGGCGCCGGGAAGCGACCGGCTGCTGGGCTTAA
 GCGGGGAGTGACCGCTTAACCAGTGAGGGAAGCACTGAAGAGCGCCAGTCGACGTGGGTGCGACAACCTCG
 CGGAGTCTTAGGAGCAAACGTCTGGGGCTGCGAGCCAGGACCTTCTGAAGCCTTAGGTGTCTATCGG
 CGACGTGTACGGTCACTGCAGCTCCGGAGCGCGGAACCCCTCAGCCAGGAGGCGCGGCTGGTCCGTTCCAG
 GTCCCGGCTCCGTAATGAGAGCCCGGAACCACTCTTTGTGCCGAGCTTCGCAGATTCTATAGGCAAT
 GGAAACTGATCTCAATCCCAGGACAGAAAGGACCTGGACAAGTTTATTAATTTTTTGCCTCAAGACT
 GTCCAAGTGATTGTCCAGGCTCGGCTTGGTGAAGAATTTGCACTCGTTTCATCATCTTCTCCAACGGGTT
 CAGATTGGTTCAACTTAGCAATCAAAGACATCCCAGAGGTTACACATGAAGCAAAGAAGGCACTGGCAGG
 ACAGCTGCCTGCAGTCGGGAGGTCCATGTGTGTGGAGATTTCACTTAAGACTTCTGAGGGAGATTCCATG

GAGCTGGAAATATGGTGTCTTGAAATGAATGAAAAGTGTGATAAAAGAAATCAAAGTTTCTACACGGTGT
ACAACAGACTGTCATTGCTGCTGAAGTCCCTTCTTGCTATAACTAGGGTGACACCAGCCTATAGGCTCTC
CAGGAAACAAGGGCATGAATATGTCATATTATACAGGATATATTTTTGGAGAAGTTCAGCTGAGTGGCTTA
GGAGAAGGCTTCCAGACAGTTTCGTGTTGGGACAGTGGGCACCCCTGTGGGCACCATCACTCTTTCTTG
CTTACAGAATTAACCTTGGCATTTCATGTCTACCAGGCAATTTGAGAGGACCCACCTATCATGGGGATTAT
TATTGATCACTTTGTGGACCGTCCCTATCCCAGCTCCTCTCCCATGCACCCCTGCAATTACAGAAGTGT
GGTGAGGACACTGGAGTAATATACCCGTCTGTAGAAGACTCTCAAGAAGTGTGTACCACCTCTTTTCCA
CCTCCCCACCATCCCAGCTGATGGTTCCTGGGAAGGAAGGTGGGGTACCCCTTGCTCCCAACCAGCCTGT
CCATGGTACCCAGGCTGACCAGGAGAGACTGGCAACCTGCACCCCTTCTGACAGAACCCTGTGCTGCC
ACACCCTCCAGTAGTGAGGATACTGAAACCGTATCAAACAGCAGTGAGGGACGGGCCTCCCTCACGATG
TCTTGGAGACCATCTTTGTCCGAAAAGTGGGGGCTTTTGTCAACAAACCCATTAACCAGGTGACCCTGAC
GAGTTTGGATATAACCTTTGCCATGTTTGTCTCCCAAGAATTTGGAGCTGGAGGATACCGATCCAATGGTG
AATCCTCCAGATTCCCCAGAGACTGAATCTCCTCTCCAGGGCAGCCTGCACTCAGATGGCTCCAGCGGGG
GCAGCAGTGGCAATACCCATGATGACTTTGTTATGATAGACTTTAAACCAGCTTTTCTAAAGATGACAT
TCTTCCGATGGACCTGGGACCTTCTATCGGGAGTTTCAGAACCACCTCAGCTGAGCAGCTCTCCATA
GATATTGGAGCACAGTCCATGGCTGAAGACTTGGACTATTACCAGAGAAGCTGGCTGTGCATGAGAAGA
ATGTCCGCGAGTTTGTATGCCTTTGTGGAAACCCTGCAGTAAAAGTATCCTTGAGTCCCAGCAGCACCC
TTTTTGTGGCCCCAGGGCATAAGCAGCCTCCCATGCATCAGCTGCTCCACCCCTCATCTGCTCTGAGC
CAGGTGGAAGGGAGGCTGGCTTCTCCCATGGGGACCCAGAAGTCCCTACTCTTGGACCTCCTGGAGACTC
CGTGGCGGCAGTCAAGCCAGTGGCCAGTTGGAGAAGACTCACGTGCTGGCCTTGGAGATGGGAAGAACC
TTCGTACGAAAAGCCCTCAGCAGGGCCATCTGTGTGCCCTGCCATCACCAACTGCTTCCCAAGGGTGT
CATCCTGTTTCTCTGCTGCCGGCCTCCTGCCTGGGCCTGCCTTGCAGCTGGCCCTTCCCTGCCTGCTG
TCACCATCCACTGTTTGCATTTCCAGCTGGTGGCCAAGAGATTGGTGTGGAGGCAGAAAGAGGAAGGAGA
CAGTGCCAGGAGGAAGAAGGAAGGAGTCCCTTAGCTCTCTTATTGTCCTTTACTTCTGCTATCTTC
TTCTCCTCTTCTCTCTCTTGCCTCTATGCCTGTATTTCTGGCAATATGACAGGCCTGCCACCCAAG
ATCAGAACTCCAAAACCACTCCACCCCTGAAGGTGGGAGGGTCTGAGCAGCCCTGGTGGCTGCCGTG
CTCAGGTCCCTCAGCTCCATGGGAAATAAAAATGGCACCCCTGAATCTCTAGGATTTTGTCACTTGGAGTCA
CAGCAAAGTTCTCTTCCCTCTTGTCCCCCGTTGCTGCTCCTTGGTTATAGAACATGGTAAATATTTATTA
CTTTCAGAGAAACCAGATATTTTATAGAGGAAATATGTTTGGAGTGGTGTGTTTTTCACTTGGAGAAGGC
GGAGGGCTCTTCCCTGGGACGGAGACCTCCTCCTCCGGAGGTATTGAGAATCCGGGCTGCTGCTTTGAGG
ATCTTCCCACCATAACAGACAGCGAGATCCAAGAAGAGGGCTGGCCGGGGGCAAAGTCACTCCAGTGTG
GCTGCAGTGGAACTGACTAAAGGCTTTACCTTGGATAGTTGCGTATTCTGGTGGAGCCTTACATCTCC
CACATTTTCTCAGAGACTGACTGACTCCATTCTGGCAGCCAGGAAGTCTGGGTGCTAAATGTGATGGCC
ACATGTAGTGGTTAGGGGATGTTGTGTGTGCCCAACTGCCTGGGTACTTGTTCCTGATCCCTGGGGC
TGTCCTGTGGAGCTTTTCTCCTGCTTGGGCCTAGCTACCATCTCCCTCTAATCCCAGGTTCTCTACACT
GCCCTGGGGTTTACCAGCTGGATTGGCTTCTGGTTGAGAAATCAAAGCTGGGCGTATGATTGACTTAACC
CTTACAGGTATTGTTACTTGAATAAGTCAAGTGCCTAGCCTCACCCACCTATGATCTGTCTTTCCCAGCC
TCGCTGGTAGTCTGGTCAAGGAGATCTAGGTCTACTCCATTCTCCTGGCCACCTGGGGCATTCACTG
GCAGCAGCTGTGCTTTCAGTGGAGCAGGTGGTTCTCAGCTGCTTGTAGTATACTGCATGTGACTGTTC
CCACATAAAGGCTGACTTCTGAGGATTGGAGCAGGCTCTGGCGGGGACCAGAGCTCTGCGTGTGCTGC
TGCCACCAAGAAGTGTAGCAGAAGCAGTAGCAGCAACTGGCCCTCCTGACTTTGGCCAGAGCACATG
CGTGGCTTGTGAACCCAGGCTCAGGTTTATCCCCAAGGCCCCAGCTTTGAGAAGGGGGAAAGCCCTTG
TAAGTTATTGATGCCCCATATTTAGCTACTGCTCTCTTTCCAAGGCCTTGCATGGAAAGGCCTAGCCA
TTGTCTGAGGCAGCAATCTTTGGCATCTACAGGTGGCAGCAGCCTTTCACCAGGGCTCCATCTGTGAAGA
GTCTCAGCCATGACTTTGAGCTGAGCTTGGGAGAAGTAAAGCAACTGTTAAGGCCAGCCCTTGGCCCTCA
GACCTGCCATGAAAGGAATGAGCCCTAGACTGACTCCTGCAGCACCCCCGGGACAGGCTGGGACCAGCTG
TTTGTCTCCAGGTGTGAGTCCCTCCTCCTCCTCCAACCTCTCCAACCTACTTTGTTTGGAAATACCGA
GCTACACTTCAAATGTATTCAAGGGATTTCCAATAAATTTTTTCTGTACTTTACAGCCTCCTGTCTG
TAGGTTGTCTGAAGACCTCGTAACCCCTTCCCCACCCCTGCCAGTGCAGGTCTGGGAAAGGGGAGAGT
GGTGCCTTGTGAAGCGCAGAAAGACCTCAAGTGTCTGGGCAAGCCTGTTTTGAGTCCGGTGTGGCCCTT
AGGGGCTGTATACCCTGGGGTTTCTGGGTCAGGAAACTTCTTAGTATTTCTCTTTCCCTGGTCCCTTAT
CAGGGGCTTGAATTTGAATATTAGTGGAGAATGCATTTAAAATACACCCATAGTAAAATCTCCATAAA
ATGCAGGCCACCGTTATCAGCTCTTTATTGCTCTTACATAACAACCTCACCCCTGGAGGGAAAAACAACAGT
GCAAGGCAGGGAGTGCAGGGCTCCCCAAGCCATCTGGGGGATTTGTGGCTGAGCAAGCAGAAAGAGA
GCAGGAAGTTAAAGGTCCATGCAAGTTTGTAGCTGCCTTGTACTGACTGGCGGTGCTTGGAGCAGCCAGG
AAGAGTAGAAGAGCCCCGGGGTATGCGTCTGTCTGGCTCCTGGGGCTGGGGCTGCAGGCCTCTCAACC
CGGCCAGGGCCAGCCCCGCTCCTAATTCTCCTAGTTTGTGACCATAGTTAGGGGAGGGAGCTGATTGGT
GGAGACAACATCCCGGAGGTAGGGATGGTTCTAGAGGCAAAAGAGAAGTACAGAACTGGACAGCTGCTG
TCTGGGTTGCTTCCCCACCCGCCTTACAGGCTGAAGCTAGGCCAGGATTAAGGGGCTGGTTAGAAAAGT
CCAAATCCAGCCTATTCTGGAGCCAGGAGCTCCTGATTATTAGTAAACCAGGTGACACTGATCATGTGG
CCAGCCAGGACAGTTGCCCAATACCTGAGTCAGAAGTGACGAAAAGGCTGTTCTGGTGTTCCTTCAA
TCAGGAACCCCAATAACAAAGTTTTTTCAGTTGCCCATGCCAGCAATGGTGTCTTACCTCTTTAAAGCA
TCTCCCTACACTCTACCCTGGAGGCCATCGTTGTTAAGGCCTTGGTAAATTTGGCATTTGAGTCACTCAG

AAACTTAAAGGATGCATCTGTATTACCTGATTTATGCCTGAGTCACGCAAATCAGTTGATGATTATGTTG
CAAATCATAGAAAAGTGTAGATATTAAGCAGAAGTGTACCCTGCCAAAACAAGAACTAGCAAATAACC
TACATGTCAGACTGAAGTGGTGTGCTTTGTAATGCTTCATGCTGATCAAGATGGAGAGAAGTTACAAGC
TTTGCTCCGCCTCGTAATAGAGCTGTTAGAAAGAGTCAAATTTGTTGAAGCTCTTAGTACAGTTCCCTCAG
ATGTACTGCTTAGCTGTTGTTGAGGTTGTAAGAAGAAAAATGTTCAAAAACACTACAGGGAGTGGGCTG
GTGCTTTAGTCAAAGATGGAAAGAGATTATATGAAGCAGAAAAATCAAAAAGGGAATCCTTTGGGAAAT
ATTTAACTCAAAGCCTCGAAAGTTTGACTGTGAACCTCCAGATATTTCAATAAAAGATTTACAGTTTCT
GCAATCATTTTTGTCCTTCGGAAGTTCCAGCCATTCCTCAGGGTTCCCTTACTTTGTGACTTTGAACCTCTA
CACCAGCATGTACTTGCTCTACATAATTTGGTAAAAGCAGCACAAAAGTTTGGATGAAATGTCACAGACCA
TTACAGATCTACTGAGTGAACAAAAGGCATCTGTGAGTCAGACATCCCCACAGTCTGCTTCTTCACCAAG
GATGGAAAGTACAGCAGGAATTACAACACTACTACCTCACCGAGAACTCCTCCACCACTGACTGTTCAAGGAT
CCCTTATGTCCTGCAGTTTGTCCCTTAGAAGAATTATCTCCAGATAGTATTGATGCACATACGTTTGATT
TTGAAACTATTCCCCATCCAAACATAGAACAGACTATTACCAAGTTTCTTTAGACTTTGGATTCAATTAGC
AGAAAGTCTGAATCAGATTTTATGTCTGCTGTGAATGAGTTTGTAAATAGAAGAAAAATTTGTGCTCTCCT
AATCCTATAAGTGATCCACAAGCCAGAAATGATGGTGAATCACTTTATTCAATCAGATTATCAATGCGA
TAGACAGTAGACGAATGCAGGATACAAATGTATGTGGTAAGGAGATTTTGGAGATCATACTTCTCTGAA
TGTCCAGTTGGAAAGATGTAGAGTTGTTGCCAAGACTCTCACTTCAGTATACAAAACCTTAAGGAAGAC
CTTTGCCACTTTAGAACATTTGTACAAAAAGAACAGTGTGACTTCTCAAATTCATTAATAATGTACAGCAG
TAGAAATAAGAAACATTATTGAAAAAGTAAAATGTTCTCTGGAAATAACACTAAAAAGAAAAACATCAAAA
AGAACTACTGTCTTTAAAAAATGAATATGAAGGTAAACTTGACGGACTAAATAAGGAAACTGAAGAGAAT
GAAAACAAAATTAATAAATTTGAAGGGAGAGTTAGTATGCCTTGAGGAGGTTTTACAAAATAAAGATAATG
AATTTGCTTTGGTTAAACATGAAAAAGAAAGCTGTAATCTGCCTGCAGAATGAAAAGGATCAGAAGTTGTT
AGAGATGGAAAATATAATGCACTCTCAAAATTTGTGAAATTAAGAAGTGAAGCAGTCACGAGAAAATAGTG
TTAGAAGACTTAATAAAGCTCCATGTTGAAAATGATGAGAAGTTACAGTTATTGAGGGCAGAACTTCAGT
CCTTGGAGCAAAGTCATCTAAAGGAATTAGAGGACACACTTCAGGTTAGGCACATACAAGAGTTTGAGAA
GGTTATGACAGACCACAGAGTTTCTTTGGAGGAATTAATAAAGGAAAACCAACAAAATAATTAATCAATA
CAAGAATCTCATGCTGAAATTATCCAGGAAAAAGAAAAACAGTTACAGGAATTAATAACTCAAGGTTTCTG
ATTTGTGACACAGAGATGCAAGTTAGAGGTTGAACTTGCGTTGAAGGAAGCAGAAAAGTATGAAAATAAA
AATTTGCTGGAAAGAAAGCAGAGCCCAGCAGAAGGAGACCTTGAAATCTCTTCTTGAACAAGAGACAGAA
AATTTGAGAACAGAAATTAGTAAACTCAACCAAAAGATTAGGATAATAATGAAAATTAATCAGGTGGGCT
TAGCAGAGCTAAGAATTTAATGACAATGAAAAAGATCAGTGTATTTCCGAGTTAATTAGTAGACATGA
AGAAGAATCTAATACTTAAAGCTGAATTAACCAAGTAACATCTTTGCATAACCAAGCATTTGAAATA
GAAAAAATCTAAAAGAACAATAATTTGAATGCAGAGTAAATTTGGATTGAGAATTTGAGTCTCTTGAAA
GACAAAAAGATGAAAAAATTAACCAACAAGAAGAGAAAATACGAAGCTATTATCCAGAACCTTGAGAAAG
CAGACAAAAATTTGGTCAGCAGCCAGGAGCAAGACAGAGAACAGTTAATTCAGAAGCTTAATTTGTGAAAA
GATGAAGCTATTCAGACTGCCCTAAAAGAATTTAAATTTGGAGAGAGAAGTTGTTGAGAAAAGATTATTAG
AAAAAGTTAAACATCTTGAGAATCAAATAGCAAAAAGTCTGCCATTGACTCTACCAGAGGAGATTCTTC
AAGCTTAGTTGCTGAACTTCAAGAAAAGCTTCAGGAAGAAAAGCTAAGTTTCTAGAACAACCTGAAGAG
CAAGAAAAAGAAAGAATGAAGAAATGCAAAATGTTCGAACATCTTTGATTGCGGAACAACAGACCAATT
TTAACACTGTTTTAACAAGAGAGAAAATGAGAAAAGAAAACATAATAAATGATCTTAGTGATAAGTTGAA
AAGTACAATGCAGCAACAAGAACGGGATAAAGATTTGATAGAGTCACTTTCTGAAGATCGAGCTCGTTTG
CTTGAGGAAAAGAAAAGCTTGAAGAAGAAGTCAGTAAGTTGCGTAGTAGCAGTTTTGTTCCCTTACCAT
ATGTAGCTACAGCCCAGAACTTTATGGAGCTTGTGCACCTGAACTCCCAGGTGAATCAGATAGATCCGC
TGTGAAACAGCAGATGAAGGAAGAGTGGATTGAGCAATGGAGACAAGCATGATGTCTGTACAAGAAAAAT
ATTCATATGTTGTCTGAAGAAAAACAGCGGATAATGCTGTTAGAACGAACATTGCAATTTGAAAGAAGAAG
AAAATAAACGGTTAAATCAAAGACTGATGTCTCAGAGCATGTCTTCAAGGCATTTCTGAAAA
GATAGCTATTAGAGATTTTCCAGGTGGGAGATTTGGTACTCATCATCCTAGACGAACGCCATGACAATTA
GTGTTATTTACTGTTAGTCTACTTTATATTTTCTACATTCAGAGTCTCTACCTGCCCTGGATCTCAAC
CAGCTTCAGGTGCATCTAGAAGACCCTGGGTACTTTGAAAAGTAATGGAAAAAGAATACTGTCAAGCCAA
AAAGGCACAAAACAGATTTAAAGTTCTTTGGGGACAAAAGTTTTACAGAGTGAAGCCGTATCATGGAAT
AAGAAAGTATAACTTATGGACAAAAATTAATACATTCATGACATTTTTTTCTGATTTGTCTTCCCTGAGT
CATTCATCACTCCAAAAACAGCAGGCCATCTTTTTATGCAAAAAGTCAGCGTGACAATATACTTCACTGGT
GTACATCGTTTTACTTTTTAACTGGCTTCATTTTTAGGAATAATAAATTCATCAGAATCCTTTGGCTGAATTA
AAATGGTTTTTTGTTTTTTGGTTTTTTTTTTTACCAGACAACCTTAGAAAATGCGGACCAAACTACTTCAT
TTTCTCAAAGGCATACCTTGTGCATTGTGGCTTATGATGAGCCATATTAATGCTTAAATATAACAC
TAGCTTGAACCTTAGATGTTAAATGTTATTATTACCAGCATTTGTCCTTTTGTGAAATCAGTATCAGAATA
CTTGCACTCTTTAACACATTTCTTTATAAATGTATAAATTAATCAGAACTATTTAAAAATAAGAGGAGTG
TTATTGCATGCTGATAATCATTTTTGAGTTTGCCTCAGTAGATACTAAAGCAAATTTGTTTCACTTTTTTA
AATGCCCTTTGATGTTTCAAAAAAAGGAAGTGAATTTGATTGACTGATTTTAAGATCAGCCATAA
GTAATCAGCAATCTTCAAAGCACTTTCAAGTGGATTGGTCATCTGGGTTCTAAAGGGAAGAGTCTGTGCT
ACTAACCATTTCAAATGCAGACTCAAACCTTCCCAACATCTTTATGACTCTAGAATAATCATATTGATGA
AATCGTAATTCATGGTTGAGTTTCCAGAACAAGATATTCAATGACATTAACCATTTAGAGGTCATTTA
AATAACAAAATATTGTATTGTAAAAGAACTGTACAATTTTAAAACAATAAAGATTTGAACCTGTAATGT

GTGTGCCTTTTAAAGAAGGATACATTTTTTAATATATTTGAGTGATTGCTGGGAAGTGTGAAAAATATTGTT
ATGTATCATATCAAAGAGAAACATGTTTATTACAAAAATGTTCTTTAACTATATACTATGTAAACAGGGTA
AACAGTGTATGTAGAATAGAATTGTGTAACTAGATCTTTAGAGAAGTTGCCATTGAGCAAAGTTATTT
AAATGAGTTAGTTGAGTTGGATGAGAATTGTTTGGAGTTTGTGCTAGAGAACAATAATAAAATAATTCT
TTTTTCAGAAAATATTTAATTTCTTCATAAAAATAAGTTAAATATTTTTTTTAAATATGTATATCTAATAGT
ACAAAATGGAATAAACATCATAGTGTATAGAAAACCTGAATTTGACAAGTTAATGAATAAATGAACAAATG
ATTTCA

H. ATG101 (autophagy related 101)

>XM_011449015.2 PREDICTED: *Crassostrea gigas* autophagy-related protein 101
(LOC105342150), mRNA

ATAAATAAATACGACCCGTTTACGGGTAATAAAGGAAAAACAAAGCAGTGAGTCAGATGATAAGATAGAC
GCTGATTTTCAGTGTGTTGCTCGGGTGTATGTGTGTAATTTTAAAGGCGAAAAATGAAAAATGAACGCTCGAT
CACAAGTGTTCGAATTGTCAGTAGAAGGAAGACAGATTGAGGAGACTGTTAGCAGTATATTTTCATACCTT
GTTGCTCCAAAGAACAGTCGGAAAGTTTCACTACAAACAAGAAGGAACATACTCTATTGGCACTGTTGGA
GTGGAGGATGTGGATTGTGACTTTGTAGACTTTACTTATGTGAGAGTGGCTTCTGACACTCTGGATCATA
TGATCAAGAAAGACATAGCTTTATTTCAGGGACACCCTTCGGAGTATGGATAATCCAGGATCAGGACAGAT
TTCCTTGGAGTTTACCAAAAGAAGCGAGGCCGATGCCCTTCCCACCGGAATGTATTCCTGGGAGGTG
TGGACAGTGAACATAGACATCTTAACACTCAATAACGAAAGTGAAGACAAAATTTGCAGGAAAAAATCTG
GAGAAATGTTAGGAGAACGAGTCATCACTATAGCAGACCTGATGAATCGCCATGACTACGTTCCCAAGAT
GCCAAATCAGACAGAATTAGATTTGATATTTGATACAAGCTTGCCAGATGTGCAACCATACTTATTCAGG
ATATCCCATCAGACTACGGGTCCTTCCCAGTCATCTGTCCGAACCACCATGAGGAAGTTTCATCAAGGACA
CACTGGCCCTATGATGCTGCCACAGGGACTGGATCAAAGTCTCTCAGAGGTGGATCCAAGTCCATCAAGG
GTGAATCAAGGCCCTCCTTGGTGGATCAAAATCCTTGAGGGTGGGGATTTATTCAATATAAACTAATG
CAGCACCAGTGAATGGTCAGCTTCGCTTCTACTTGTGTCTTTCACATTGAATTACATGTATTGAATCTGT
ATGTGTCCATTTTGAATATAGCATAACAGTACTAAATTGTCATTTATTCTATATGTGAGCAGTTGTAATAG
CTTTTTTCTGTGTTATAAACGTAAGAATGGTTTTTGGAGTAGTTAAGTAGTACATGTTTCAATGAACACTA
CAGTCATTTTTTTTATTGATTCAGAAATTTTAATACACATTGAAATGCTGTATGTCCCAATGAAAAAAGT
TTTTTTTATAAGAATTTAAAGATCAATTATCAAAAAGTTGTTGTTTTAATAGCAGAACATTTGAAAGTTG
AAATAGTATTAATAAATGTTAAATGCAACCCCATTCATTACTCCTGCGAAAGAATTTTCATAAATGTACAT
GTTGTCAAGAAATAAAGCTGGAAAATGGTAACTATTAATCAATACCCTTTTTTAAATAAGTACCTGGTAC
GGGATAAATTTATAGCAATGATCTTTATTTCTAGTGAAACATCATCTAAAGTAGTTAGAAAAAACCCTCA
GTAATATATATGGATGTCTTTCATGTCAACAGAAATGTGAAGATAACAGAGAGAGAGAGAGAAAGAGAGA
GAAAGAACACGTACAGCAAATATTTTATAATGGAACATGCTCATTGATTTTGATACATTACTGTCAATTT
TATGGTAAGAATCAATCTTCCAATTATTTATGGTATTAGTACATTGTACATTATTTGATATTACTGTACG
TTTTGTTTTCTTGGAAATCTTGATAAAAATTTGATCACCTTATTTTTGTCAACTCATAAACACCATAGTGT
TATATAATCATCATCTACTTATAAATTGCTAATTATACTCATATTTTTCAACAGCAAAAAATATACATACAT
GACATATTC AACCAATCAATTGTGTGCTATATAATGTCTTGTATTTTTTCCACGGAAAAATATGTTGCTG
TAAGTCAGAATAAATTTTTGTATAAACCACA

>sp|Q9BSB4|ATGA1_HUMAN Autophagy-related protein 101 OS=*Homo sapiens*
OX=9606 GN=ATG101 PE=1 SV=1

MNCRSEVLEVSVEGRQVEEAMLAHLVHTVLLHRSTGKFHYKKEGTYSIGTVGTQDVEDCDFI
DFTYVRSSEELDRALRKVVGEFKDALRNSGGDGLGQMSLEFYQKKSRWPFSDCEIPWE
VWTVKVHVVALATEQERQICREKVGEKLCCKIINIVEVMNRHEYLPKMPTQSEVDNVFDT
GLRDVQPYLYKISFQITDALGTSVTTMRRLIKDTLAL

I. ZFYVE1 (zinc finger FYVE-type containing 1)

>tr|K1QVT2|K1QVT2_CRAGI Zinc finger FYVE domain-containing protein 1
OS=*Crassostrea gigas* OX=29159 GN=CGI_10012695 PE=4 SV=1

MNSFSSAQSDHSQHSSIPDICSAGNEMSSLEAQLAESIIDLNDPYDNIGDEDEFIKKLD
CDSNEHVKVVSIFGNTGDGKSFTLNHTFFGGKEVFKTSSHQSSCTVGVWAAAFDPKEKVIV
IDTEGLLGITSNQNRMLLLKILGISDIIYRTRAERLHNDMYQFLCESSAYTKHFSD
ELEATAKRCNKGVDLTPAVIIFQETVNTNVLGSSGTDSAEKFIWNTFRQLECPMHFKDL
TYVGIRTGRPPTDFTQFQRTMSQHLQDKSNRAARQPAIVYKTLKLNLDKFNGEVEKPLYG
TFPDQLFSCSMKCLSCGEGCTRSMNHDTDSKAHETDKRCKYQHOFENKVFLCKSCYLSGK
EHVVIPTKTESRDSAWSGLIKYVWAGEVLECPSCGVIFRSRQNWYGNKEVEEIVHTEIRH
VWPDGKMLQGTNNAARKLIVGFHYIADSIITSVGSKPTKMSIDWMNDRIAPEYWVPSQI
SHCHQCSKELETEQKHHCRACGKGFCDCCSHRRRVPERGWGEMEVVCDKCYGGKKMSD
SNDSTGSNSQVTARKVGEVVTSAISVAASTLNYPIDMIKDTARPGYWTPDEQIKACYVCE

ELFGPKLRIHHCRACGQGVCECSPNKRVPVPLRGWDYPVRI CRKCINKPDRL

>NM_021260.4 *Homo sapiens* zinc finger FYVE-type containing 1 (ZFYVE1), transcript variant 1, mRNA

ACTCCGATCAGCTGATCCCAACTGACAACAGGAGAGGAGGAAGCCCCGGGAGGCAACGAAGGAGGAGGGTG
GCGGAGATGGAGATGAGGATGGATCTGCCGGTGTCTTGAGGAATAGCCTCTGCCCCACTGGCGCCCTGC
GGCCCCCGACGCCGCCTTGCTGCGGGCCGAGCTTCTCAGTGGTATCCCCTGAAATACTGACTTCAGGTCG
AATTATATTGAAAAGCTCCTGACCACTTTCTTTTATTACCAAAAATTTGTAGCTGATGTCCAACCGATGA
ACCCACCACCGTGAACCCATCAGACCTCTCTCAGATAGCCATAAAAAGACCCTTCCAAGTCAATTTTTGACC
ACATCTTTGCTTGCACCTTTATGGAGGATGAAACCATCAAACCAAATCAACGTTGCTGCTAATACAAGAGT
CTTAGAGGCAGCAAATTAATAATTTGAACATTTGTTTGTGAAGAACTATAACAGGACATGAAAGGTGTTT
TTTTTTAAAGTGTTCAGAACCCTGTGGAAGTTTCGTGCAGTCTTCAGACTCAAATCTTCGTCTTCACCCC
CGGGGCAAGCTCAGTGACTATTATATGGTGGGTGTGTTTCCCTTACCAGCGTGAGTATGAGTGCCAGACT
TCCCCAGCAGAGAAGGGCCTGAATCCGGGGCTGATGTGCCAGGAAAGTTACGCTTCAGCGGGACTGATG
AAGTATCTTTGAGTGTGATGAGTGTGCAGTCTGCAGTGTCTCCGCTGCGAGGAGGAGCTCCATCGGCA
GGAGCGCTGAGAAACCATGAGCGGATAAGACTCAAACCTGGCCATGTCCTTACTGTGACCTCTGCAAG
GGTCTCAGTGGGCATTTACCAGGTGTTAGGCAGAGGGCAATAGTGAGGTGCCAGACCTGCAAAAATTAAC
TGTGCCTGGAGTGCCAGAAGAGGACTCATTCTGGGGGTAACAAAAGGAGACACCCTGTTACTGTGTACAA
TGTCAGTAATCTCCAGGAGTCACTGGAGGCAGAAGAGATGGATGAGGAGACCAAGAGGAAAGAAGATGACT
GAGAAGGTTGTGAGTTTCCCTCCTAGTAGACGAAAATGAAGAAATTCAGGTAACAAAATGAAGAAGACTTTA
TTAGAAAATTGGACTGCAAACCTGATCAGCATCTGAAAGTGGTTTTCCATTTTTGGAAAATACTGGTGATGG
AAAGTCTCATACTCTCAACCACACTTTCTTTTTATGGTTCGTGAAGTCTTTAAAACCTCCCCGACCAGGAG
TCCTGCACTGTGGGAGTGTGGGCAGCCTATGACCCAGTTCACAAAGTAGCAGTGATCGATACGGAAGGGC
TCCTGGGGGCCACCCTGAATCTAAGCCAGAGAACACGGCTGCTGCTTAAGGTCTGGCCATCTCAGACCT
CGTCATCTATCGAACTCATGCAGACCCGGCTGCATAACGACCTCTTCAAATTCCTTGGGGATGCCTCAGAA
GCTTATCTGAAGCACTTACCAAGGAGCTCAAGGCCACCCTGCTCGCTGTGGCCTGGATGTCCCTTTAT
CCACACTGGGCCCTGCAGTTATCATCTTCCATGAGACCCGTGCACACCCAGCTACTGGGCTCTGATCATCC
CTCAGAGGTGCCAGAGAAGCTCATCCAGGACCCGTTCCGGAAGCTGGGCCGTTTTCCCTGAAGCCTTTAGT
TCCATTCATAACAAGGGAACGAGGACTTACAACCCCTCCCACGGACTTTTTCTGGGCTTCGGCGTGCTTTGG
AGCAGCTACTAGAGAATAACACCACCCGTTCTCCCCGGCACCCGGGAGTCATCTCAAAGCCCTGAAGGC
ACTAAGTGACCGCTTCAGCGGTGAGATCCCCGATGACCAGATGGCGCACAGCTCCTTTTTTCCAGATGAG
TATTTACCTGCTCCTCTCTGTGCCTCAGCTGTGGGTTGGATGTAAGAAAAGCATGAATCATGGGAAGG
AAGGAGTGCCTCATGAAGCCAAGAGCCGCTGCAGATACTCCACCAGTATGACAACCGAGTGATACCTG
CAAGGCCTGCTATGAGAGAGGCGAGGAAGTCAGTGTAGTGCCCAAAACATCTGCTTCCACTGCTCCCC
TGGATGGGTCTCGCAAAATATGCCTGGTCTGGGTATGTGATCGAATGTCTTAAGTGTGGCGTGGTCTATC
GTAGTCGGCAGTACTGGTTTTGGAAACCAAGATCCTGTGGATACGGTGGTGGGACAGAGATTGTGCATGT
GTGGCCTGGAAGTATGGGTTTTCTGAAGGACAACAACAATGCTGCCAGCGCCTGTTGGACGGGATGAAC
TTCATGGCTCAGTCGGTGTCCGAGCTTAGCCTTGGACCCACCAAGGCTGTGACTTCCCTGGCTGACAGACC
AGATCGCCCCTGCCTACTGGAGGCCCAACTCCCAGATTCTGAGCTGCAACAAGTGTGCGACGTCCTTTAA
AGATAACGACACTAAGCATCACTGCCGAGCCTGTGGGGAGGGCTTCTGTGACAGCTGTTTATCAAAGACT
CGGCCAGTGCCTGAGCGGGGCTGGGGCCCTGCGCCAGTGCGGGTCTGTGACAAGTGTACGAAGCCAGGA
ACGTCCAGTTAGCTGTTACCGAGGCACAAGTGGACGATGAAGGTGGAACGCTCATTGCTCGGAAGGTGGG
CGAGGCCGTGCAGAACACTCTGGGAGCCGTGGTGACAGCCATTGACATAACCACTAGGTCTGGTAAAGGAC
GCGGCCAGGCCTGCGTACTGGGTGCCTGACCACGAAATCCTCCACTGCCACAAGTGCCTGGGAGGAGTTCA
GCATCAAGCTCTCCAAGCACCCTGCCGGGCCTGCGGACAGGGCTTCTGTGATGAGTGCTCCCATGACCG
CCGGGCTGTTCTTCTCGTGGCTGGGACCATCCCGTCCGAGTCTGCTTCAAAGTGAATAAAAAGCCCGGT
GACCTTTAACCCAGCCCCCTCTCCGAGTCTTACAAATTCCTTAGGTTCTCAGGGTTAGAAAACAGTCTT
GCGAGGTAGGCCCTCTCCAGTCACTGCTGTGGTGTGTGCTCTCTCTCTCCGATCCAGGGCCACTT
TCCCTCAGTGGGGGTGAGCCTGGCGGCAGGCCCCGAAGTTGTGGACCCCTCAGGGCAGGGGACCTTGCAAC
TTATCGCAAAGGGGAATGAACCTGAATCCGTTGCATTTATTTTTCAGTTAAAAATAATGAATATATATGTGT
ATATCTCTCTCATATATACATATGAAAGGCACTCGGGGCGTATCGAGGCTGCTGCTGGCTGTGAAGAC
TTCGCACAGTCTCCTCCGCACAGGGTGAAGTGGCAGTGGCAGCACGCTTCTCATGAGCCGAGCCAGGT
CCATGGCCACCACGTGGCTGGCCCCCTTCCCTCTGCTGCTCTTGGAGCCTTGGAAAGCCTCTCCTGTCTTGG
CTCTTCCCTCCATGCCTGTGAGCTGCCTGGGGAGTGAAGCTCCCTGGTCTTCTGCTGCTGAAAACAGCCTG
AAGGGAATTCTCCCTAGGTCTCCTGGGAGTCGAGTCCCAATTCCTTGGCTTAAAGCCTGTTTTAGTCAGAGA
CCACCCAACTTAGCGTGCAGGTACCCGGAGTGGGTGGAGGGTCAGAGGTCCGGTCTTCGGCCCTGAGAAG
TAGAAATGCAGGGGCCGTGCTGTCCCTGGTCCCCAGGGAACAGCAAGGAAGGAAGTGAAGCTTCTCCAG
CAGGGCTTCTGTCCCAGTGTCTTCTGTCTCCACTCGGCTTTCCCAAAAGGCGGCACCCAGCTCCTCAATC
GAAGCATCTGCCTCCCACCCCTCGGCCCCCTCAAGCCCACCCTGCTTCTGAGTGTGCGACTAGGATTT
TCATTGCTTATTTTTAAAGTGTCTTAATCCTTTGTTCCCAGACACACAACCCCTCTAGCTCTCGGAGGGC
GATCATGAGAAACCTTCCAGGGAACTGAGCACAGGATGAACTGTTAGTTGTTTTTAAAGTCTATATAA
ATATTTCAACAGATCGTAAAGAAAAAATTTATCTCTTTGGTCCCTTGCAAGAGAAGTCAAAGGAACTTTTG
TTTCTCCTCAAGAGCCTGGACATCTCTGTCTGTGATGACTGGAAAGGGCCGTTGTGCTGAAATCTTATC

ATCATGGTGGATTTGATCTTCAGTGGCCAAACACGAATTAAGTATAAATCTTAACTGAACTGGTGGGTG
GGTTGAGCTTTAGGGAAGTATATGGCGGTCATTCCCTGGTGCCTATCGGTGTGACATGAGCCCTGGAGT
GTGTCGTCCCTCTCAGCCCTGCTCCTCCTGCCTCCTGGGGTCCAGTGAAGTGGGACCCTACTCTAGAAGT
TGTACCATCCAATTCGCCATCATAAAGGAATCTTCTGCA

J. ATG9A (autophagy related 9A)

>XM_011418747.2 PREDICTED: *Crassostrea gigas* autophagy-related protein 9A
(LOC105320700), mRNA

GAAGTACACAGAACTGGACATATAACCACTGGATACTCAGGTTCAAAAACACATGATTGCCATGGAGAGGT
AATCCTTACTTCCATTTAAACATAGCATTCCCTTAATGGGAGAATGTGCTTTCTACAGCATTGGATTGAA
ATGCAATCAGGATTTCTTGTCTTCTGGGGTCCCTGGTCCACCTTTTGGAGAATTACTGGAAGTTGAAGGAT
GAATTCAAAATTTATCATAAAAGAAAACAATTGGCAGAAGAGTTGTCTAAGAAAAGTTCTATGGATCGGCA
TTGCAAACCTTTGCCCTTAGTCCACTCATTCTACTATGGCAGATCTTATACTCCTTCTTTAGATATGCAGA
TACACTTAAAAGAGAACCTTCAATGTTAGGATCAAGAAGATGGTCAAATTTATGCGAGACTTTATTTACGG
CATTATAATGAGCTTGATCATGAATTTGATGCAAGGCTGAATAGAGGCTATAGATTAGCCAACAAAATACA
TGGATATCTTTACTTCACAACCTTATAGTTATATTAGCCAAGAATGTGGCATTCTTTGCTGGTTCTGTGCT
GGCTGTGCTGGTTGTGCTGACTGTGATTGATGAGGATGTGCTGGCTGTGGAGCACGTGCTGACCTCCATG
ACAGTTGTCTGGTCTGATTGTGACAGCATGTAAAGTCTTTATAACCAGATGAGCATTAAAGTACTGCCCTG
AGATTTCTGATGAGGAACATCTTGGCCCATGTCCACTACATGCCTCCTGATTGGTCAGGACATGCCACAC
ATCGAAAGTCCGCAATGAATTTCCATATTTTTCCAATACAAAGTTGCATACTTATTCGAGGAGCTTTTA
AGTCCCCTTGTTACCCCTATAGTACTCTGCTTTTTCCCTGCGTCACAAATCGATGGAGATTGTGGATTTTT
TCCGTAACCTTTACGGTTCGATGTTGTGCGGAGTGGGGGATGTGTGTTTCTTTGCACAACCTGGATGTCCGCAA
GCGAGACAACAAATGGATGATAGGGAGGAGGAGGAAGAGCCTCAACCATCCCTGAGGACCAACATGTTT
ACTCCAGACCAGAGCCCTCACAGGAGGGCAAGATCCAGATGTCCCTCATGCACTTCCACCTTACAAAAC
CAGAGTGGAAACCTCCAAAGGAATGCAGTCTGTTTCAATGACATCAAAGAAAAAGCCAATAGAAACAC
TACTTCTCTAAGCATCTTTAACCCTGTGACCCAGAATATGGTGTGATGTCATCTCAGGGGTCCCTTACAGGG
TATCTTTCTGGACTACAGCCAGCGGAGCAGGAGCCCTGGGGGAAAGTGAACAGACCAGTACACCAGCC
TAGCGTCAAGCATCGCCATACAGAGTGGCATGTACCCCCAGTCTACTCAAGTGTCCATGGCCCCAGTGT
GAGTGGGGTTACCACAGGCTCCGGGGGGCCATATCCACCCTGAAGGACCCCTGGAACGGTCCATCGGT
GGACCAGTGGGAACCATGCAGGGCTCGACCAGCATGATCGGCAGTGGGTGGGGGGATACCACTCCATAG
GAAGCTCCAAGCCGAGTGTGGACGAGGGCTCACTTGAAGTGTGTCACATGACATGAGTGTGACGCGCT
GTACCTACACGACCTTCAGTCTCGCAAACAGAGAGGTCAAGGTCAAATGGGATATGAAAATATAGAGGAA
ATGCGGGCTAGGAACCTGTGGCAGAGACAGGACAGTAACCAAGGCCAGTGCATGCTGGGATGCCTAATA
TACAGGAGAAGAGGGAAGAGGAGGAGAAAGATAGTGGAAACACGGAAACCATTGCTAAATCTGTCTAGTG
CCAACAAAACCTCCACAATGCATAGCTTTTTGCTGGCAGCCAGTTATTGTAACATAACATCTCTTTGTG
TGAGTGTGTGCTGTGACTTATATATATACAGCATCTGATTGCTATATCATGTGGCATTACATGT
ACTTTACCATTGTGTTAATCTCATGAACCTGTTGGATTTTATTATTGACATTTACTTTTATTGCA
TTCAGATAGACATGTACGTACACATGATGTATAATATAAGGCACATTAACCAAAAAATACATGTATAATG
TGTATTTTGTCTCTAAAGAGGACATGAGGACTTTTTCATGTAAACAAAAGCTGAATTGTTTATCTTGATAT
GTAGAATTGATCAGATGTGCTTTGTGAGTATCAGTTATCAGTATGAACCGGAATGAATGATCAGATCTCG
GGAGTTTTTTTTTTGGCTTTTTTTGTTACATACACATGTACATGTATTATGAAGTATATAGATACTTCAA
ATAAACCTGAATAATTGTAGAAAGTAGAAGAACATTATTTAAGCAC

>sp|Q7Z3C6|ATG9A_HUMAN Autophagy-related protein 9A OS=*Homo sapiens* OX=9606
GN=ATG9A PE=1 SV=3

MAQFDTEYQRLEASYSPPGEEEDLLVHVAEGSKSPWHHIENLDLFFSRVYNLHQKNGFT
CMLIGEIFELMQFLFVVAFTTFLVSCVDYDILFANKMVNHSLHPTEPVKVTLPDALFLPAQ
VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTW
QEVQARIVQTQKEHQICIKRELTELDIYHRILRFQNYMVALVKNKSLPLRFRPLGLGEA
VFFTRGLKYNFELILFWGPGSLFLNEWLKAHEYKRGGQRLELAQRLSNRILWIGIANFLL
CPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRHFNELEHELQSRNLNRGYKP
ASKYMNCFLSPLLLAKNGAFFAGSILAVLIALTIYDEDVLAVEHVLTVTLLGVTVTV
CRSFIQDQHMVFCPEQLLRVILAHIHYPDPHWQGNHRHSQTRDEFQQLFQYKAVFILEEL
LSPIVTPILILIFCLRRALREIIDFFRNFTVEVVGVGDTCSFAQMDVRQHGHPQWLSAGQT
EASVYQQAEDGKTELSLMHFAITNPGWPPRESTAFLGFLKEQVQRDGAASLAQGGLLP
ENALFTSIQSLQSESEPLSLIANVVAGSSCRGPPLPRDLQGSRRHRAEVASALRSFSPLQP
GQAPTGRAHSTMTGSGVDARTASSGSSVWEGQLQSLVLSEYASTEMSLHALYMHQLHKQQ
AQAEPEHRVWHRRRESDESSESAPDEGGEGARAPQSI PRSASYPCAAPRPGAPET TALHGG
FQRRYGGITDPGTVPRVPSHFSRLPLGGWAEDGQSASRHPEFPVPEEGSEDELPPQVHKV

>sp|Q12142|ATG9_YEAST Autophagy-related protein 9 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG9 PE=1 SV=1
MERDEYQLPNSHGKNTFLSRIFGLQSDEVNPSLNSQEMSNFPLPDIERGSSLLHSTNDSR
EDVDENDLRVPESDQGTSTEEEDVDEEQVQAYAPQISDGLDGDHQLNSVTSKENVLETE
KSNLERLVEGSTDDSVPKVGQLSSEEEEDNEFINNDGFDDDTPLFQKSKIHEFSSKKSNT
IEDGKRPLFFRHILQNNRPQRDTQKLFSTSSNAIHHDKDKSANNGPRNINGNQKHGTYKFG
SATQPRFTGSPLNNTNRFTKLFPLRKPNNLSNISVLNNTPEDRINTLSVKERALWKWANV
ENLDIFLQDVYNYLGNFYCIILEKILNICTLLEFVVFVSTYMGHCVDYSKLPSTSHRVSD
I I I D K C Y S N S I T G F T K F F L W M F Y F F V I L K I V Q L Y F D V Q K L S E L Q N F Y K Y L L N I S D D E L Q T
L P W Q N V I Q Q L M Y L K D Q N A M T A N V V E V K A K N R I D A H D V A N R I M R R E N Y L I A L Y N S D I L N L S
L P I P L F R T N V L T K T L E W N I N L C V M G F V F N E S G F I K Q S I L K P S Q R E F T R E E L Q K R F M L A G F
L N I I L A P F L V T Y F V L L Y F F R Y F N E Y K T S P G S I G A R Q Y T P I A E W K F R E Y N E L Y H I F K K R I S
L S T T L A N K Y V D Q F P K E K T N L F L K F V S F I C G S F V A I L A F L T V F D P E N F L N F E I T S D R S V I F
Y I T I L G A I W S V S R N T I T Q E Y H V F D P E E T L K E L Y E Y T H Y L P K E W E G R Y H K E E I K L E F C K L Y
N R I V I L L R E L T S L M I T P F V L W F S L P S S A G R I V D F F R E N S E Y V D G L G Y V C K Y A M F N M K N I
D G E N T H S M D E D S L T K K I A V N G S H T L N S K R R S K F T A E D H S D K D L A N N K M L Q S Y V Y F M D D Y S
N S E N L T G K Y Q L P A K K G Y P N N E G D S F L N N K Y S W R K Q F Q P G Q K P E L F R I G K H A L G P G H N I S P
A I Y S T R N P G K N W D N N N N G D D I K N G T N N A T A K N D D N N G N N D H E Y V L T E S F L D S G A F P N H D V
I D H N K M L N S N Y N G N G I L N K G G V L G L V K E Y Y K K S D V G R

K. ATG9B (autophagy related 9B)

>sp|Q674R7|ATG9B_HUMAN Autophagy-related protein 9B OS=*Homo sapiens* OX=9606
GN=ATG9B PE=2 SV=1
M V S R M G W G R R R R L G R W G D L G P G S V P L L P M P L P P P P P S C R G P G G G R I S I F S L S P A P H T R
S S P S S F S P P T A G P P C S V L Q G T G A S Q S C H S A L P I P A T P P T Q A Q P A M T P A S A S P S W G S H S T P
P L A P A T P T P S Q Q C P Q D S P G L R V G P L I P E Q D Y E R L E D C D P E G S Q D S P I H G E E Q Q P L L H V P E
G L R G S W H H I Q N L D S F F T K I Y S Y H Q R N G F A C I L L E D V F Q L G Q F I F I V T F T T F L L R C V D Y N V
L F A N Q P S N H T R P G P F H S K V T L S D A I L P S A Q C A E R I R S S P L L V L L L V L A A G F W L V Q L L R S V
C N L F S Y W D I Q V F Y R E A L H I P P E E L S S V P W A E V Q S R L L A L Q R S G G L C V Q P R P L T E L D I H H R
I L R Y T N Y Q V A L A N K G L L P A R C P L P W G G S A A F L S R G L A L N V D L L L F R G P F S L F R G G W E L P H
A Y K R S D Q R G A L A A R W G R T V L L L A A L N L A L S P L V L A W Q V L H V F Y S H V E L L R R E P G A L G A R G
W S R L A R L Q L R H F N E L P H E L R A R L A R A Y R P A A A F L R T A A P P A P L R T L L A R Q L V F F A G A L F A
A L L V L T V Y D E D V L A V E H V L T A M T A L G V T A T V A R S F I P E E Q C Q G R A P Q L L L Q T A L A H M H Y L
P E E P G P G G R D R A Y R Q M A Q L L Q Y R A V S L L E E L L S P L L T P L F L L F W F R P R A L E I I D F F H H F T
V D V A G V G D I C S F A L M D V K R H G H P Q W L S A G Q T E A S L S Q R A E D G K T E L S L M R F S L A H P L W R P
P G H S S K F L G H L W G R V Q Q D A A A W G A T S A R G P S T P G V L S N C T S P L P E A F L A N L F V H P L L P P R
D L S P T A P C P A A A T A S L L A S I S R I A Q D P S S V S P G G T G G Q K L A Q L P E L A S A E M S L H V I Y L H Q
L H Q Q Q Q Q E P W G E A A A S I L S R P C S S P S Q P P S P D E E K P S W S S D G S S P A S S P R Q Q W G T Q K A R
N L F P G G F Q V T T D T Q K E P D R A S C T D

L. WIPI1 (WD repeat domain, phosphoinositide interacting 1)

>sp|Q5MNZ9|WIPI1_HUMAN WD repeat domain phosphoinositide-interacting
protein 1 OS=*Homo sapiens* OX=9606 GN=WIPI1 PE=1 SV=3
M E A E A A D A P P G G V E S A L S C F S F N Q D C T S L A T G T K A G Y K L F S L S S V E Q L D Q V H G S N E I P D V
Y I V E R L F S S S L V V V V S H T K P R Q M N V Y H F K K G T E I C N Y S Y S S N I L S I R L N R Q R L L V C L E E S
I Y I H N I K D M K L L K T L L D I P A N P T G L C A L S I N H S N S Y L A Y P G S L T S G E I V L Y D G N S L K T V C
T I A A H E G T L A A I T F N A S G K L A S E K G T V I R V F S V P D G Q K L Y E F R R G M K R Y V T I S S L V F
S M D S Q F L C A S S N T E T V H I F K L E Q V T N S R P E E P S T W S G Y M G K M F M A A T N Y L P T Q V S D M M H Q
D R A F A T A R L N F S G Q R N I C T L S T I Q K L P R L L V A S S G H L Y M N L D P Q D G G E C V L I K T H S L L
G S G T T E E N K E N D L R P S L P Q S Y A A T V A R P S A S S A S T V P G Y S E D G G A L R G E V I P E H E F A T G P
V C L D D E N E F P P I I L C R G N Q K G K T K Q S

>sp|P43601|ATG18_YEAST Autophagy-related protein 18 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG18 PE=1 SV=1
M S D S S P T I N F I N F N Q T G T C I S L G T S K G F K I F N C E P F G K F Y S E D S G G Y A I V E M L F S T S L L A
L V G I G D Q P A L S P R R L R I I N T K K H S I I C E V T F P T S I L S V K M N K S R L V V L L Q E Q I Y I Y D I N T
M R L L H T I E T N P N P R G L M A M S P S V A N S Y L V Y P S P P K V I N S E I K A H A T T N N I T L S V G G N T E T
S F K R D Q Q D A G H S D I S D L D Q Y S S F T K R D D A D P T S S N G G N S S I I K N G D V I V F N L E T L Q P T M V
I E A H K G E I A A M A I S F D G T L M A T A S D K G T I I R V F D I E T G D K I Y Q F R R G T Y A T R I Y S I S F S E
D S Q Y L A V T G S S K T V H I F K L G H S M S N N K L D S D D S N M E E A A A D D S S L D T T S I D A L S D E E N P T

RLAREPYVDASRKTMRMIRYSSQKLSRRAARTLGQIFPIKVTSLLESSRHFASLKLPEVE
TNSHVMTISSIGSPIDIDTSEYPELFFETGNSASTESYHEPVMKMPVIRVVSSDGYLYNFV
MDPERGGDCLILSQYSILMD

M. WIPI2 (WD repeat domain, phosphoinositide interacting 2)

>tr|K1QZR2|K1QZR2_CRAGI WD repeat domain phosphoinositide-interacting
protein 2 OS=*Crassostrea gigas* OX=29159 GN=CGI_10011163 PE=4 SV=1
MNLATKTGDEQSDLLFVNFNQDCTSLAVGTRTGYKLFSLSSVDKLEQIYDNESEDICIVE
RLFSSSLVAIVLSLSPRKLKVFCHKKGTETICNYSYSNSILAVRLNRQLIVCLEESLYIH
NIRDMKVLHTIRDTPPNPHGLCAL SINNDNCFLAYPGSNQIGEVQIFDITINLRVAVAMIPA
HDNPLASLAFNAQGTKLATASEKGTVIRVFSIPDGQKMFEFRRGVKRCVSIYSMAFSADS
LFLSASSNTETVHIFKLEVPKDRPAEQEPQGWMGYFGQALKSSATYLP SQMTEMFNQGRA
FATARLPNSGMHNVCALATI QKVPRQLVVSQDGYLYIYNLDPNEGGECCMLLRQHRLDGRA
GDSPVPEVTPDRPLTHPTSGTSYASSVKKPESSVVPESQPYQELEQGSTGEGEGTGLG
HLRLDDDNFPPMTHKSD

>NM_001033518.2 *Homo sapiens* WD repeat domain, phosphoinositide interacting
2 (WIPI2), transcript variant 3, mRNA

GTACCGGGTGCCCCGGCTCTGGAGCATAAACAAGAGCGGGGACGGGATGAGGCGGCGGTTGATCCCAGGG
TGGCGAGTGGCGGCGACCGAGGCGGCGAGCGGGGCCGCGCCGACCGCTGAGTGCAGCCTGACCCGCCCT
CGCGCGCGGCCCTCCCCGGCCGGGCCACTCGCCGCGCGCCAGCCATGAACCTGGCGAGCCAGAGCGG
GGAGGCCGGCGCCGGCCAGCTGCTCTTCGCCAACTTCAACCAGGACAACACAGAAGTGAAAGGGGCATCA
AGAGCAGCTGGTCTTGGCCGTCGCGCTGTTGTCTGGTCCCTAGCTGTTGGTAGTAAGTCCGGTTATAAAAT
TTTTCTCCCTTTCTTCTGTGGATAAGCTGGAACAGATCTATGAATGCACCGATACGGAAGATGTGTGCAT
TGTAGAGAGATTGTTCTCCAGCAGCCTAGTGGCCATCGTCAGCCTTAAAGCACCAAGGAAGCTAAAGGTT
TGCCACTTTAAGAAGGGAAGTGAATCTGCAACTACAGCTACTCCAACACGATTCTGGCTGTGAAGCTCA
ACAGGCAGAGGCTGATAGTATGCCTGGAGGAGTCCCTGTACATCCACAACATTCCGGGACATGAAGGTGCT
GCATACGATCAGGGAGACGCCTCCAAACCCTGCAGGCCTGTGTGCGCTGTCAATCAACAACGACAACCTGC
TACTTGGCGTACCCAGGGAGCGGACCATCGGAGAGGTGCAGGTCTTCGATACCATTAAATTTGAGAGCTG
CAAACATGATTCCGGCTCACGACAGTCTTTAGCGGCACTGGCCTTTGACGCAAGTGGAACTAAACTTGC
CACGGCTTCGGAGAAGGGGACCGTGATTAGGGTATTTTTCCATTCCAGAAGGACAAAAACTCTTTGAGTTT
CGGAGAGGAGTAAAGAGGTGCGTGAGCATCTGCTCCCTGGCCTTCAGCATGGACGGCATGTTCTCTCCG
CCTCCAGCAACACTGAGACCGTGCACATCTTCAAACCTCGAGACTGTGAAAGAAAAACCCCGAGAGGCC
CACCACCTGGACCGGTACTTCCGGGAAAGTGTCTATGGCCTCCACCAGCTACCTGCCTTCCCAAGTGACA
GAAATGTTCAACCAGGGCAGAGCCTTCGCCACGGTCCGCTGCCATTCTGCGGCCACAAAAACATCTGCT
CGTACAGCCAAATTCAGAATCCCGCGGTTGTTGGTGGGTGCCGCGGACGGGTACCTGTACATGTACAA
CCTGGACCCCAAGGAGGGCGGCGAGTGTGCCCTGATGAAGCAGCACCAGGCTGGACGGCATCTGAAACG
ACCAATGAGATCTTGGACTCTGCCTCTCACGACTGCCCTTAGTCACTCAGACATACGGCGCAGCTGCAG
GAAAAGCCTACACAGACGACCTGGGTGCTGTGGGTGGCGCCTGCCTGGAGGACGAGGCCAGCGCCCTGCG
CCTGGATGAGGACAGCGAGCACCAGCCCATGATTCTTCGGACTGACTGAACTTGACCTGTGACCTCTGAC
CCGGGAGCAGAGAACACTGGCTTCACAGAGGACTTTGTGCATTGCTGCTATGAACTTTGACCTGAGTCG
GGGAGAGGATGGCAGAGACTTTATTAATAAAAAAAAAAAGATTGTAGTGGTAGTCTAACTCCATAACGCT
GAGGAAATACATCATTTTCACTTCAGTGGCTTTTAAATCCTGCTTATGAATTTTAGCTTTTTGTTGTTT
GTTTTCTTTTTTGCCAAAATTAAGTGTGTTGGTGAAGCCCGCAAACCTCCTCGCTTTCATATCTGT
GTCCAAGCCAGCATAGGGGAGCTAGAAGCCACTTTCAGCCACCTGCCGTTGGGTTTTTTCATATCTGT
ACATAATGCCGAGTGCCTAAGGAAACCGTGGCGTCCGCGCACAGTGGGTCTGCTTGTCAAGGCCAGTTCG
CAGTGACAGGCCAGGGGCTGCCACCAGGTGTGCTGGGCAGACTTCAGCTGGGACAGAAGTCCGATCTC
CCTAGGGCCCCACCTGGACCATTTTCCCTCCGTTTTATTTTGTAAATTAATTTCTTTCCAAATTTGGATCG
CTCTGGGATTTCTTCCATGGTGGACTTTTGTCTGATCTTGTCTTCCCTGTGGATATTGGAGGACAGCG
AGGTTCTTTCTGATACTAAAAACCTTTCTTTCAGGCAGCAAATGAACTTGAAAGGTTGCCTGGACTCGCT
GGAGCAAAGGAAAGCGATTTTGTGTTGATAATTAATGATCTGTTCTTCTACTTCACTCTTCTGTTGAA
AAACTGTGTGATTTTTTTTTTTTTTTTAAAGTAAAGTTTGTAGCTCCTCCCATGCCAGGAAAGCACAGAAC
TCAAGTGTGGTGGCTGAGCTGTCCCTTTCGCTGGCCCCGCTGTCGCGAGGGGCTTCTACCTGTGTG
AGAGGTCGTAGCGGAGACAGCAACAGAGAGTAGGCGGCTGGGCCACGTCCTTTCACAGGGCGTCAATGTG
CTTTCTATTTTTCATCTTAGAAAATTTCTCAGCAAACCGATGAGAGATTGTGGTTGCAAGCTTCAGTATT
TGCCCTCGCTTCCCTTCCCTTTTTCATATTTACAGAATTAACAACCTCAAGTACCTCAGACTCTGCATTC
CAAACCAAGGCACCCAGCAGCCAAAGTGTGAGGGCATTAAAGTGGCATTAATGGCAGGAGAGATGGTTTT
TAGAATCTATGGAGTGGTGAAGTTACGGATAGAAGGAAAAGGCAAAAATTTTACCTGCCTTTGCA
GGCTGGGGTTTTTGAACCGAGGAAGGCTGGGACGCTGTTTCCAGATGGTTGTGATGGTCACGCTGGGCG
AAGAGCTGGAGGGGAGTTGTCCCTCAGCTGAGCGGCTGCGGTGAAATGCCCCAGTGTCTTGGGTTGGC
TTTACGGCAAACATAATGCAGGGGACGCTGGAGTCCGACTCACCTACACCGGCTTCTCCAGCGCTGG

TGTGCGGCACACACAACATCTGCATTAGGCAGAGGTGCAAGTGGGCTGATTGAACTTTTCCTTCAAAAACC
TGCTTGTCTGTCCTGGACCTTTGATGAAATGGGATCCCCGGTCACGCAGGCTGAGACAGTGGGGACC GCCG
AGGCCAGAGTGGGCTATGCTTGAGCAGGGATGAGAAGGGCCGCGGCAGCACGCAGCCTTGACCCACGCCT
GCGTCTTGTGGTGAAGGCCAGAGGGCTCTCTCTAGAACCTGACCGTGCCTCCATCTCTGGGAGCCAC
TTTTGGCAAGAGTGAAGTGTGGGGGGAAAAAGTGTGCACAAGAGATACGGAACCTGAGCTAGGGTTTCCT
GTCACCAAAGAGTGAAGTGCATTTCCAGTCTGCGTTAAAGTATCGTTTGTCTGGTGCCTGCCTGTGGT
GGTGAATTTGGAGACTCAAATTTCCCTTTGCCAGGTCTCTTTTGTCTTTCTTTGGGATTGGTAGTATAGAAG
ATGCTGGGAATTGTCTTCCCTCGCTCAGCCTCGGCTTCCCAGCTGTAAGATGAGGCAGTTGCAGAGGAGG
CCTCGGACGTCTGTGACCTCGGCCCACACTCCCCCTTGGGTGGCCCTGGCAGGGCTGGCTAGGTGCGT
TCCCTGCAGACCACGGGAAGCCCTGTGCTTGCCTGGGTGAGGGCTAAGCTGTGCGCCCTAGAGGAGGGGAG
GAGGACTGCAGATTCTTGGTTCGAGAAGAATGAAGAGGATTTCTGTGTTTGGTGCAGCCATTGTGGAGG
GTTACCCGCTCCACTTTCCCGTTGCCATTTCACTGCCACCAGCTCCTCTTCTCTGCTCGAACCTATG
AGTCCCAGCCTCACTGGCGGCCTCAGACATGCTCAGGAGTGACGGGGACAGAGGGAGGCCGCTGAGTTGC
CCGTTAGAACTCTTACTGCTGCGCCAGTGACCCAGGTGGAGAGGGACCCTGAACCAAACAGAACGTGTGC
TAATTTTCCGAACCTCAAACCTGTACACTCATATTTTAAATTTAAATTTTCCAAACTTCAAAAAGG
ACGATGAGCGTGGGGGATAGGAAACAAAACCTGTAACGTTGTAATGGGCTCAGTGGACTCTGGGACCA
AACCTTCTGTAATCTCTAAAACAATGGGACCAAGAGCTGGATGGAACCTGGAGTCAAAAAGAAGCTGCTTC
AGTCCCCGCTGTACCGCCTGCCTAGCTGTGGGAGCAGGCAGGGCGCCTGGGAGCCTGCGTTTTCTGGACC
GTTCCATGGGACTCATCCCTACCTCACAGGGCTGTTGTGAGGTGTTGTGTGACTGCGTGTCTTGCAAAACG
CCCAGCTCGGTGCCAGCCAGCGGTGGGCACCCAATAAACGCTACAACATAAATGTGTCTTCTGCAATTA
AA

>NM_001179986.1 *Saccharomyces cerevisiae* S288C phosphoinositide binding protein ATG18 (ATG18), partial mRNA

ATGTCTGATTCATCACCTACTATCAACTTTATTAATTTCAATCAAACCGGAACGTGTATTTCCCTTGGAA
CGTCGAAAGGTTTCAAATATTTCAATTGTGAGCCCTTCGGAATAATTTTATTCAGAGGACAGTGGGGGCTA
TGCTATCGTCGAGATGTTGTTCTCCACCTCGTTACTAGCCCTCGTTGGGATAGGCGATCAACCTGCGCTT
TCACCAAGGAGATTGCGTATAATCAACACAAAAAACATTTCTATTATCTGTGAGGTGACTTTCCCTACTT
CTATTCTGAGTGTGAAAATGAATAAGTCTCGATTGGTGGTACTTTTACAAGAGCAGATTTATATTTATGA
TATCAACACCATGAGACTATTGCATACTATAGAAACAAACCTAACCACAGTGGCCTTATGGCTATGTCT
CCTTCGGTAGCCAACAGCTATTTAGTGTATCCATCACCACAAAAGTTATTAACCTCCGAAATTAAGCTC
ATGCCACCACAAACATATCACATTGTGTCAGTTGGTGGCAACACAGAGACCAGTTTCAAGAGAGATCAGCA
AGATGCTGGCCATAGTACATTAGCGACTTGGACTCAGTATTCGAGCTTTACTAAGAGGGATGATGCGGAT
CCAACAAGCAGTAACCGCGGTAACAGCAGTATAATAAAGAATGGTGTGATGATCGTATTCAACTTGGAAA
CATTACAGCCAACCATGGTCATCGAAGCTCATAAGGGCGAGATTGCTGCAATGGCAATTAGTTTTGATGG
GACACTAATGGCTACCGCCTCTGATAAAGGTACTATCATCAGGGTCTTTGACATTGAAACGGGTGATAAG
ATCTACCAATTCAGGAGAGGGACGTACGCGACAAGAATTTACTCCATATCATTGAGTGAAGATAGCCAGT
ACTTGGCGGTTACCGGCTCTTCCAAAACCGTGCATATCTTCAAATTTGGGGCATTCAATGAGCAACAATAA
ACTAGACAGCGATGATAGCAACATGGAAGAAGCTGCAGCCGATGATTCATCGCTCGATAACCACAGTATC
GATGCGCTGAGTGCAGGAAAACCCGACAAGACTCGCAAGAGAACCATATGTGGATGCATCAAGAAAAGA
CAATGGGTAGGATGATACGTTACTCTTCTCAAAGCTATCCCAGAGCTGCCAGAACATTGGGTGAGAT
TTTCCCCATCAAAGTTACATCGTTGTTGGAATCCTCGCGCCATTTTTCGCTCTTTGAAACTTCCCGTTGAA
ACCAATTTCCATGTAATGACCATATCAAGTATAGGCTCTCCAATAGATATAGACACATCCGAGTATCCGG
AACTCTTCCGAAACTGGCAATTCGCAAGTACAGAGTCTACCATGAGCCTGTTATGAAGATGGTCCCCAT
CAGGGTCGTTTTCTCGGATGGATACCTATACAACTTTGTTATGGACCCGGAGAGAGGGCGGATGCTTA
ATATTGTACAGTATTCCATCTTGATGGATTGA

N. WDR45B/WIPI3 (WD repeat domain 45B)

>tr|K1PZL8|K1PZL8_CRAGI WD repeat domain phosphoinositide-interacting protein 3 OS=*Crassostrea gigas* OX=29159 GN=CGI_10026046 PE=4 SV=1

MDLSLGNISYGNLLYAGWNQDQGCFCAGMETGFRVYNSDPLKEKERQDFADGGIHHIEML
FRCNYLALVGGGKPNPKYPPTKVMVWDDLKPKVIELEFSTEVRSVRLRRDRIVVLDLTI
KVYTFQNPQLHVFETCPNPKGLCVLCPNSNNSLLTFPGRKSGHVQIVDLANTEKSATD
I PAHEAPLSCIAMNLQGTTRLATSSIEKGLIRVFDTHSGLQLHELRRGANSAAHIYCINFNQ
DSSLLCVASDHGTVHIFSTEDLKKKQLGIGSASFLPKYFSSSTWSFSKFQVPGGARCICA
FGADPNSVIVICADGSYYKVFVNQKGECTR DVYAQFLEMTDDRS

>XM_011447404.2 PREDICTED: *Crassostrea gigas* WD repeat domain phosphoinositide-interacting protein 3 (LOC105341093), mRNA

TCCTAATCACTCAAATGTTTATCATCGTATGGGGGTGTGTTGTCTAGTAGCTGAAAATAATGTCACATTT
TGCTCCAAAATGAATGCAAATATTCATCGATAGCAACAACAAGTAAAAAATGGATTTATCCCTCGGTAA

TTCTGATGGCAACGGCTTGTGTATGCGGGTTGGAACCAGGATCAAGGATGTTTTGCTTGTGGTATGGAG
ACGGGGTTCCGGGTTTATAACTCAGATCCACTGAAAAGAGAAGGAACGACAAGATTTTGGCTGATGGTGGCA
TTCATCACATTGAGATGTTGTTTCAGGTGCAATTACCTGGCATTGGTGGGAGGGGGTAAAAATCCAAAGTA
CCCACCTACAAAAGTAATGGTGTGGGATGACCTGAAGAAGAAACCTGTGATAGAACTGGAGTTTTCCACA
GAAGTCCGCAGCGTTGACTGCGACGAGACAGAATTGTGGTGGTGTGATACCTCATCAAAGTGTACA
CGTTTACGCAGAATCCACAGCAGCTTCACGTATTCGAAACTTGCCCCAATCTAAAGGACTGTGTGTGT
GTGTCCAAACAGTAACAACCTCGCTCTTGACTTTTTCTGGGAGGAAGTCCGGCCATGTCCAGATAGTGGAC
CTGGCCAACACCGAAAAATCGGCCACCGATATTCCAGCTCATGAGGCCCGCTAAGTTGTATTGCCATGA
ATCTGCAGGGGACCAGGTTAGCAACAAGCTCAGAGAAGGGTACTCTTATCCGTGTATTTGATACTCATTC
AGGGCTCCAGTTACATGAACTACGGAGAGGTGCTAATAGTGTCTCACATTTACTGCATCAATTTCAACCAG
GATTCAGTCTTCTATGTGTGGCCAGTGACCATGGCACTGTACATATCTTCTCTACAGAGGATCTTAAAA
AGAACAACAGTTAGGGATTGGGTGCGCCAGCTTCTACCCAAGTACTTCAGCTCTACGTGGAGTTTCTC
CAAGTTCAGGTCCCAGGAGGGGCACGGTGCATCTGTGCCTTTGGGGCTGACCCAACTCTGTCAATGTT
ATCTGTGTGATGGCAGCTACTACAAGTTTGTGTTCAACCAGAAGGGCGAGTGTACGAGAGATGTGTATG
CCAGTTCTGGAAATGACGGACGACAGATCCTAAATCATTGTGCATAATTTGTACCCGCGACATGAGCAT
GCAATTATAGAATCAATGTTTTTACAATTTTTCTCACCAACCAGTGTGCAAGTAGCCGATGAAATGCAGC
TTATGCCAGGTTCTTTTGAATATTTTATGTTGATATAACATTGTTACGTTGGTTGATTATTATATTTTTT
TTTTAAACATCTTCTCATTAGAGAGTTTTATTTATGAAGTCATATGATTCTTTATTATGTGCATGGAACT
AATATGCCTGTAATATCGGGAGAAGCAACCCTCATGGATTTTGTATATCTTGTCTTTTAAATTTTCATATAGT
TTTGAATATATAAAATTATAACAAAAAACTGGTGTCTGTAATGTCATAGGCCTATTTCTTGATACAAAAT
AGTGAATCAGGGAATTTAAACGTACTCATGTAAATAA

>KX434429.1 *Homo sapiens* WIPI3 long variant (WIPI3) mRNA, complete cds
ATGGATTCCGGCGCCATGAACCTCCTGCCGTGTAACCTCACGGCAACGGGCTGCTCTACGCCGGCTTCA
ACCAGGACCACGGATGCTTTGCGTGTGGGATGGAAAATGGATTCCGAGTCTATAACACTGATCCACTAAA
AGAAAAAGAGAAACAAGAATTTCTAGAAGGAGGAGTTGGCCATGTTGAAATGTTATTTTCGCTGCAACTAT
TTAGCTTTAGTTGGTGGTGGAAAAAGCCGAAATACCTCCCAACAAAGTAATGATCTGGGATGACCTGA
AGAAGAAGACTGTTATTGAAATAGAATTTTTCTACAGAAGTCAAGGCAGTCAAGCTGCGGCGAGATAGAAT
TGTGGTGGTTTTGGACTCCATGATTAAGGTGTTACATTCACACACAATCCCCATCAGTTGCACGTCTTC
GAAACCTGCTATAACCCCAAAGGCCTCTGTGTCTTTGTCCCAATAGTAACAACCTCCCTCCTGGCCTTTC
CGGGCACGCACACGGGCTATGTGCAGCTTGTGGACCTGGCCAGCACGGAGAAGCCACCCGTGGACATTC
TGCACACGAGGGTGTCCCTGAGCTGCATTGCATCAACCTGCAGGGAAACAAGAATTGCAACTGCATCCGAG
AAAGGCAGCTTTATAAGAATATTTGATACTTTCATCAGGCAATTTAATCCAGGAAGTGCAGGAGATCTC
AAGCAGCCAATATTTACTGCATCAACTTCAATCAGGATGCGTCCCTCATCTGCGTATCCAGCGACCGCGG
CACAGTGCATATTTTTGCAGCTGAAGATCCAAAAAGGAATAAACAGTCCAGTTTGGCCTCAGCCAGTTTC
CTTCCAAAATACTTCAGTTCCAAGTGGAGTTTCTCCAAGTTTTCAGGTTCCCTCAGGCTCTCCGTGCATTT
GTGCCTTTGGAACAGAGCCAAACGCCGTCAATTGCAATTTGTGCAGACGGCAGCTACTACAAAATTCCTGTT
CAACCCCAAGGGGAGTGCATCCGAGATGTCTACGCGCAGTTTCTAGAGCTGACCGATGACAAGCTGTGA

>sp|P43601|ATG18_YEAST Autophagy-related protein 18 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG18 PE=1 SV=1
MSDSSPTINFINFNQTGTCISLGTSGKFKIFNCEPFGKIFYSEDSGGYAIIVEMLFSTSLLA
LVGIGDQPALSPRRLRIINTKKHSIIICEVTFPTSILSVKMNKSRLLVLLQEQIYIYDINT
MRLLLHTIETNPNPRGLMAMSPSVANSYLVPSPPKVINSEIKAHATTNNITLSVGGNTET
SFKRDQQDAGHSDISDLQYSSFTKRDDADPTSSNGGNSSIIKNGDVIVFNLETLPQPTMV
IEAHKGEIAAMAI SFDGTLMATASDKGTIIIRVFDIETGDKIYQFRRGTYATRIYSISFSE
DSQYLAVTGSSKTVHIFKLGHSMSNNKLDSDSDNMEEAADDSLDTTSIDALSDEENPT
RLAREPYVDASRKTMRMIRYSSQKLSRRAARTLQGFPIKVTSLLESSRHFASLKLPE
TNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMKMPVIRVVSSDGYLYNFV
MDPERGGDCLILSQYSILMD

O. WDR45/WIPI4 (WD repeat domain 45)

>XM_011455938.2 PREDICTED: *Crassostrea gigas* WD repeat domain
phosphoinositide-interacting protein 4-like (LOC105347054), mRNA
AAAACGTAAATTAGACATTTGCTAATAAGTTATTAACCACCATACTTTCACTTTATAAAAATGTCAACAA
AAATGTTACGCCACAAAGACTGAACAATAATTGTATCCTTACCAAGTTACCAATGCTGTGAGGGGACGTC
AAGAAATGTCAAGAGGTGACTTTCTTAAAGATTCAACCAAGATCATGGTTGTTTCACTTGTGCAACAGA
AACTGGGCTAAAAATCTACAATGTTGAGCCATTGACCCAAAACTTACCCTAGGGCAAGATGTGGTGGGA
AGTATTGCATCTGCAGAGATGTTGTTTTCGCTCAAACCTTAGTTGCAATGGTTGGAGGGGGAAACCTCACCAA
AATATGACGAGAAAGCAGCGTTGATATGGGATGATACAGCAAAAAAAGTAGTCATGGATGTTTCGTTTAA

CCAGCCAGTGGTGTCAATCAAACCTCAAGTATGACAGATTAATTGTGGTGTGAGAAAATCAAATCCATGTC
TTTAGTTTTCCCAATAATCCTACCTTGTTCATTTCATTTGATACAAGGGATAATCCGAAAAGGGCTGTGTG
ATGTCAGTCCTTTTGGACAAGTGATAGCTTTTCTGGACGAAAATGTGGCAGTGTGCAAATTTGCTGACCT
AGAAACCACCCAGCCAGGGCAGTCCACGTCCCCATCACAATCAGTCCCACCAGGGGGAGTTAGCGTAT
ATTACAGTGAATCAACAGGGCACATTACTGGCTACAGCTTCCAAGAAGGGAACATTGATTCGTGTCTTTG
ACACAACCACAAAGAAGTTGGTGGTGGAGCTACGCAGAGGTGCTGACCCAGCCACACTCTACTGCATTAC
CTTCAGCCATGATTCCTCATTTTTTGTGTGCCTCCAGTGATAAAGGAACTATTCATATTTTTGCTGTGAAA
GACACGAGTCTGAACAGGAGATCGACATTTAAGAAGATGGGGTTTCTGGGCACCTTACGTAGAGTCTCAGT
GGGGCTTGGCCAGCTTCACTGTGGCTGCAGAGTGTGCATGTATCTGTGCCTTCGGACCAGGGCATTTCAGT
GATAGCTGTCTGTGTTGATGGGACCTTTTCACAAGTATGTGTTCACTACTGATGGTAACTGCAATAGGGAA
GCCTATGATGTGACTTGGACATTGGGGATGACTTTGAATGAGAGAAAATAAGTTGATGTACATGTCCAG
TCTATTATTTAACATGTTGTTATAGAAAATCAATTTCTATCAAATTTCTGTTTAAATGCATGTACATGTA
CAATGTATATGTGGAATAATTTTTAAATGTTTGGAGGGTGTACAATGTACACATATTTTATGTTTTATTGG
TGTAACCTTTAAGCAATGGCTGAGGAATTTGGTACATTTGAAGTTATTTAGCCAGTTTTGCCTTGCCAGT
AAGGTACCAGCATAACCAGTACATGCAATTTGAACATTTTGAAGGATTTTCATGTACATTGTCTCATCTGTG
TATACATACTTTTCATATCATTGCTTATTTTGCACCTTTTAAAAAAAATATATTTAAGTACATGCAAATGT
AAAGTTCAATTTTAACTGAATGTAAAAATCAACACAATAAGCATAAAGAGATCTGATTTTATTTATATG
TGATATAAATAAACACAACAATTGTCAA

>sp|Q9Y484|WIPI4_HUMAN WD repeat domain phosphoinositide-interacting
protein 4 OS=*Homo sapiens* OX=9606 GN=WDR45 PE=1 SV=1
MTQQPLRGVTSLRFNQDQSCFCAMETGVRIYNVEPLMEKGHLDHEQVGSMLVEMLHRS
NLLALVGGSSPKFSEISVLIWDDAREGKDSKEKLVLEFTFTKPVLSVRMRHDKIVIVLK
NRIYVYSFPDNPRLKLEFDFTRDNPGLCDLCPKSLKQLLVFPGHKCGSLQLVDLASTKPG
TSSAPFTINAHQSDIACVSLNQPPTVVASASQKGTILRLFDTSKEKLVLELRRTDPATL
YCINFSHSDSSFLCASSDKGTVHIFALKDTRLNRRSALARVGVKVGPMIGQYVDSQWLSASF
TVPAESACICAFGRNTSKNVNSVIAICVDGTFHKYVFTPDGNCNREAFDVYLDICDDDDDF

>sp|P43601|ATG18_YEAST Autophagy-related protein 18 OS=*Saccharomyces
cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG18 PE=1 SV=1
MSDSSPTINFINFNQGTGTCISLGTSGKFKIFNCEPFGKFYSEDSGGYAIIVEMLFSTSLLA
LVGIGDQPALSPRRLRIINTKKHSIICEVTFPTSIILSVKMNKSRLLVLLQEQIYIYDINT
MRLLHTIETNPNRGLMAMSPVANSYLVPSPPKVINSEIKAHATTNNITLSVGGNTEF
SFKRDQDAGHSDISDLQYSSFTKRDDADPTSSNNGNSSIKNGDVIVFNLETLOPTMV
IEAHKGEIAAMAIISFDGTLMATASDKGTIRVFDIETGDKIYQFRRGTYATRIYSISFSE
DSQYLAVTGSSKTVHIFKLGHSMSNNKLDSDSDNMEEAADSSLDTTSIDALSDEENPT
RLAREPYVDASRKTMRMIRYSSQKLSRRAARTLGQIFPIKVTSLLESSRHFASLKLPE
TNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMKMPVIRVVSSDGYLYNFV
MDPERGGDCLLSQYSILMD

P. ATG2A (autophagy related 2A)

>tr|K1RSP2|K1RSP2_CRAGI Autophagy-related protein 2-like protein A
OS=*Crassostrea gigas* OX=29159 GN=CGI_10022068 PE=4 SV=1
MSNFWKISGEELKAGIWRPHTLMFLLLWPVTVSQILVFPDRDVSTKQGHMYSMSHSGAPA
LKAHVKSQVQNKRSQRSSGGPRTEISVNLAKELELDGPLYSFSTQMEDESASDETKIDL
SVNCPVVKLTLRFPIPDRLNGSEVTKLPWWQKNLRDELLILDLEQEARFQTSFSLNQPIQQ
VEVSSRNVLGSRFIDPNQSAVPFAFVSCGIDGQEGFNFPQIIKFTQETISVLDEENPD
SDNSIPMDSLNGACEFAKQDTPFSTKHKMYGKGMESDQATQHVSDVMVPGNREDMADF
QERASANCLTLVQLVPLINLYIPDQKFYEVLYNRISNDLLLWEPMAPIPTQEVGPGS
IQPFDLSCYTHAEDCHGEVGMVVKDANLFFVASSYQGNPLLQYICFYCNKATLYHNAAVPD
KKEEFEIENLDFETIPAHLEKSCIIDRSEPGVLCHQSADVESTVTRDMVSVAVRIKLDSTP
LSDLTRDEKIKEFTVAVGVTGATLRHKMAETDMSWISQILNFLDVKDYDILGYVTPKILT
ELHVHLWDCAVDYRPLHLPTKGVVAANYFSISSNIVANSQTSLLRFVLEDAGMYLSQKKG
RESTVDLKKDYVCVLDVESFELELRSDGKDPKFPKMSDLRLRNTKINMRTCTDSCKALFE
LIRYFANDGDLDVEYEEEPNKRQSLDLEMNKEEASDEDSKKKELSESRLENLSSHLED
AMQESGSGSDNDGSESSKQSPNKTEVFFVAQGERTDAQVPPAGVMRPVITASADSVTSS
AVSERTDIFSDEEEEEEDFCIIDDAGLGITPRDGKPEVKIFTDEPIEIKDNYFSQPHGKT
DLLKAPDHFPAEYRYTLKELTIVWHMYGGSDFSPTVQKQKPVETEVMRSMKMDYGEYV
TETSVRFAASKSSVDRIPTWQRGGVGRDHTLMELQLTKVRFQHERYPGHTEQASRQVLI
ISDAEIRDRLSDSKINKFLYQYSSENLPKQTNMVMYIKALHKRPDPSVKTEECSLRVSL
QPLRLNIDQDSLFFLKKFFTEITGGNVNDNPSDPDPKQRRARSVSGASGAPAVITVGOPEC

PGEERTPQELLMKFDEMQQSLASQGSMMSSASVASSDSRTEQSQPVFIKNFMFSPDVPI
RLDYHGKKVVDREHGTLAGVVLVGLASLNCSELKLRNLNYKHGLLGMDKLQAYCINEWITD
ILKKQLPSILGGVGPMSHFVQIAQGIKDLFWLPEVQYKRDGRFVIRGIRGATSFSTSTAM
AMLELTNRAVQSVQYVAEVTYDMVTPGPSRVRQRRRLRGPADVREGVENAYIAITEVQG
TAQYDLLPDANDRKMDHIELFPAPREKFRVY

>NM_015104.3 *Homo sapiens* autophagy related 2A (ATG2A), transcript variant 1, mRNA

AGTGAACAGCGGAGCCGGACGGGGATCGCCGGCGGGCGGCAAGCGGAGGCGGCCAGGCCCGGGCGGTCTC
CGAGATGTCACGATGGCTGTGGCCATGGTCAAACCTGTGTGAAAGAGCGGGTCTGCCGCTACTTGGCTGCAC
CACTACTTAGGTCACTTCTTCCAAGAGCACCTCAGCCTGGACCAGCTCAGCCTCGATCTGTACAAGGGCA
GCGTTGCCCTGCGAGACATCCACCTGGAAATCTGGTCTGTGAACGAGGTGCTGGAGTCAATGGAGTCACC
GCTGGAGCTGGTGAAGGCTTCGTGGGCTCCATCGAGGTGGCCGTGCCCTGGGCTGCTCTGCTCACCGAC
CACTGCACAGTGCAGCTGGCCCTCATGCATGACCACAAGCCTGCAGCTGGCCCAGGAGTGTCTGCGGGATGG
CCGACTCACAGAGCTGGCCCTCATGCATGACCACAAGCCTGCAGCTGGCCCAGGAGTGTCTGCGGGATGG
GCTACCGGAGCCCTCTGAGCCACCACAGCCCTGGAGGGGCTGGAGATGTTTGGCCAGACCATGGAGACT
GTGCTTCGGAGGATCAAAGTGACCTTCTGACACTGTCTGTGAGGGTGGAGCACTCTCCGGGTGATGGGG
AACGTGGTGTGGCCGTGAGGTCCGTGTGCAGAGACTGGAGTACTGTGATGAGGCAGTGCGGGACCCAAG
CCAGGCGCCGCGGTGGACGTGCATCAGCCGCTGCCTTCTGCACAAGCTGCTGCAGCTGGCAGGGGTC
CGCCTGCACTACGAGGAGCTCCCGGCACAGGAAGAGCCTCCAGAGCCCCCTTGAGATCGGCAGCTGCT
CAGGGTACATGGAGCTGATGGTGAAGTTGAAGCAAAATGAGGCCTTCCCTGGCCCCAAGTTGGAGGTGGC
GGGACAGCTGGGCTCCCTGCACCTGCTCCTGACCCCGAGGCAGCTCCAGCAACTTCAGAACTGCTCAGC
GCCGTGAGCCTTACAGACCACGAGGGCCTGGCTGACAAGCTGAACAAGAGCCGCCCGCTAGGTGCCGAAG
ACCTGTGGCTGATTGAGCAGGACCTGAACCAGCAGCTGCAGGCAGGGGCAGTGGCTGAGCCCCCTCAGCCC
AGACCCCTTACCAACCCCTTCTCAACCTGGATAAACAAGTGCCTTCTTCTCCATGGCTGGCCTCACA
AGCAGTGTGGCCTCAGCCCTCTCTGAGCTCTCCCTCTCCGATGTAGACCTGGCCTCCTCTGTGCGCAGCG
ACATGGCCTCCCGCCGGCTCTCTGCCAGGCCACCCAGCTGGCAAGATGGCCCCCAACCCCTCCTGGA
CACCATGCGCCCTGACTCGCTGCTGAAGATGACCTTGGGGGGTGTGACCCTGACCTTGCTTCCAGACGTCT
GCCCCATCTTCCGGACCACCTGACCTCGCCACGCACTTTTTACCGAGTTTGATGCCACCAAGGATGGGC
CCTTCGGTTCCCGAGACTTCCATCACCTTCGACCACGCTTCCAGAGGGCCTGTCCCTGTAGCCATGTTTCG
GCTAACGGGCACAGCCGTGCAGCTGTCTGGGAGCTGCGGACGGGCAGTCCGGGCGGGCGGACAACCAGC
ATGGAAGTGCATCTCGGGCAGCTGGAGGTGGAGTGTCTGTGGCCCCGGGGCACCTTCGAGCCTGAGT
ACACAGAGACTCTGACCTTCTGTTACGCTGGGCTCCAGGCCTCAGCTCGGCCCTGCGCCCATCTGCG
CCACACACAGATCCTGCGCCGTGTGCCTAAGAGCCGACCCCGCGCTCAGTTGCCTGCCATTGCCACTCA
GAACTGGCCCTGGACCTGGCCAACCTTCCAGGCGGACGTGGAGCTGGGGGCCCTGGACCGGCTGGCCGCC
TACTGCGCCTGGCCACCGTACCTGCTGAGCCTCCAGCCGGCCTGCTGACAGAGCCCCTGCCGGCGATGGA
GCAGCAGACGGTATTTTCGGCTCTCTGCACCCCGGGCCACGCTGCGGCTGCGCTTCCCCATTGCCGACCTG
CGGCCTGAGCCGGACCCCTGGGCGGGCCAGGCCGTGCGGGCTGAGCAGCTTCCGCTGGAGCTGAGTGAGC
CCCAGTTCCGGTCAGAGCTTAGCAGTGGGCTGGTCCCCAGTCCCCACCCACCTGGAACCTCACCTGCTC
CGACCTACATGGTATCTATGAAGATGGAGGGAAGCCACCTGTCCCTTCCCTGCGTGTCTCAAAGCCCTG
GACCCCAAGAGCACTGGGCGCAAGTACTTCTGCCCCAGGTAGTGGTACTGTGAACCCCAAGTCCAGCA
GCACACAGTGGGAGGTGGCCCCGGAGAAGGGAGAGGAAGTGGAGCTGTGAGTGGAGAGTCCCTGTGAGCT
GCGGGAACCTGAGCCCTCGCCCTTCTCCTTAAGAGGACCATGTATGAGACAGAGGAGATGGTGATCCCT
GGAGACCCTGAGGAGATGAGGACGTTCCAGAGCCGGACCCCTGGCACTGTCCCCTGCGCCTGGAAAGTGA
TCCTGCCAGTGTCCACATCTTTCTGCCAGCAAGGAGGTCTACGAGAGCATCTACAACAGGATCAACAA
CGACCTGCTCATGTGGGAGCCTGCAGATCTGCTTCCACCCCGACCCCGCCGCCCAGCCCTCGGGCTTC
CCCGGCCCTCAGGCTTCTGGCACGACAGCTTAAAGATGTGCAAGTCAGCCTTCAAGCTGGCCAACCTGCT
TTGATCTCACCCAGACTCGGACTCGGATGACGAGGATGCCACTTCTTCTCAGTGGGGGCATCAGGTGG
CCCACAGGCCGCTGCCCTGAGGCCCAAGTCTTCACTTCAGAGCACCTTCTTCTACTGGTGACAGTG
CTGAAGGGGCGGATCACAGCCCTCTGTGAGACCAAGGATGAGGGTGGGAAGCGGCTGGAGGCTGTGCAG
GGGAGCTGGTGTGACATGGAGCACGGTACCCTCTCAGCGTCTCCAGTACTGTGGCCAGCCAGGACT
TGGCTACTTCTGTCTGGAAGCTGAAAAGGCAACACTCTACCACCGAGCGGCCGTGGATGACTACCCGCTG
CCCAGTCACCTGGACCTTCCAGTTTTGCTCCCCCGCTCAGCTGGCCCCAACCATCTACCCATCGGAGG
AAGGGGTGACCGAGCGGGGAGCCTCGGGCCGCAAGGGCCAGGGCCGGGGACCCACATGTTGTCCACTGC
TGTGCGCATCCACCTGGACCCCCACAAGAATGTGAAGGAGTTCCTGGTGCACACTGCGGTTGCACAAAGCC
ACCTTGCGCCACTACATGGCCCTGCCCGAGCAGAGCTGGCATTCCCAGTTGTTGGAGTTCTTAGACGTGC
TGGATGACCCTGTGCTGGGCTACCTGCCCCGACGGTACATACCATCCTGCACACACCTGTTCTCCTG
CTCTGTGGACTATAGGCCACTCTACCTCCCAGTGCCTGTCTCATCACCGCGGAGACCTTCACTCTCTCC
AGCAACATCATCATGGACACCTCCACCTTCTGCTCAGGTTTCATCCTCGATGACTCCGCTTGTACCTGT
CCGACAAGTGTGAGGTGGAGACCCTGGACCTGCGGCGAGATTATGTCTGTGTTTTGGATGTTGACCTCTT
GGAACCTTGTGATTAACCTGGAAAGGGAGCACCGAGGGCAAACCTGAGCCAGCCACTATTCGAGCTGCGC
TGCTCCAACAATGTGGTACACGTGCACAGCTGTGCCGACTCCTGTGCCCTGCTGGTCAACCTGCTCCAGT
ACGTAATGAGCACAGGCGATCTGCACCCCCACCCCGGCCCCAGCCCCACGGAGATCGCCGGCCAGAA

GCTCTCGGAGAGTCTGCCTCTCTGCCCTCGTGCCCCCAGTGGAGACGGCCCTCATCAACCAGCGTGAC
CTGGCCGACGCCCTCTGGACACCGAGCGCAGCCTACGGGAGCTGGCCAGCCTTCAGGTGGCCACCTCC
CTCAGGCGTCGCCCATCTCCGTCTACCTATTCCCAGGTGAACGGAGTGGGGCCCCACCCCTTCACCACC
TGTCGGGGGCCCTGCTGGCAGCTTAGGGTCATGCTCAGAGGAGAAGGAAGATGAAAGGGAAGAGGAGGGC
GATGGAGACACCCTGGACAGTGTAGATTCTGCATCCTTGATGCTCCCGCCTGGGCATCCCGCCCCGAG
ATGGGGAGCCTGTGGTGACACAGCTGCATCCCGGCCCATCGTTGTGAGGGACGGTTACTTCTCACGGCC
GATCGGCAGCACGGACTTGCTGCGGGCACCTGCCATTTCCCAGTGCCAGCACTCGGGTGGTGCTACGT
GAGGTCTCCCTCGTCTGGCACCTCTATGGGGGCCGAGACTTTGGCCCCACCCCGGCCACAGGGCAAGAA
CTGGCCTCTCAGGTCCCAGGAGCTCCCCTTCCCGCTGCTCTGGCCCCAACCGGCCCCAGAACTCATGGCG
CACGCAGGGGGGCGAGCGGGGGCGCAGCACCATGTCTCATGGAGATCCAGCTGAGCAAGGTAAGCTTCCAG
CACGAGGTGTACCCAGCGGAGCCAGCCACAGGCCCTGCGGCCCCAGCCAGGAGCTGGAGGAGCGACCCG
TGTCCCGTCAGGTGTTTCATCGTGCAGGAGCTGGAGGTCCGAGACCGGCTCGCCTCCTCCAGATCAACAA
GTTCTGTACCTACACACGAGTGTAGCGGATGCCGCGACGTGCCACTCTAACATGCTCACCATCAAAGCG
CTGCATGTGGCCCCACTACCAACCTGGGTGGGCCTGAGTGTGTCTCCGCGTCTCGCTGATGCCCTGC
GGCTCAATGTGGACCAGGATGCCCTCTTCTTCCCTCAAGGACTTCTTCACTAGTCTGGTGGCCGGCATAA
CCCCGTGGTCCCAGGGGAGACCTCCGCTGAGGCTCGCCCCGAGACTCGAGCCAGCCAGCCCCCTTG
GAAGGGCAGGCCGAAGGCGTAGAGACCCTGGTTCGAGGAGGCCCCAGGAGGTGGACACAGCCCTCC
CTCCTGACCAGCAGCCATCTACTTCAGAGAGTTCGCTTTCAGTCTGAGGTCCCCATCTGGCTGGATTA
CCATGGCAAGCACGTACGATGGACCAGGTGGGCACTTTTGTGGCCTCCTCATCGGCCTGGCCAACTC
AACTGCTCCGAGCTGAAGCTAAAGCGGCTCTGTTGCAGGCACGGGCTCCTGGGTGTGGACAAGGTGCTGG
GCTATGCCCTCAACGAGTGGCTGCAGGACATCCGCAAGAACCAGCTGCCCGCCTGCTGGGAGGCGTGGG
CCCCATGCACTCGGTTGTCCAGCTCTTCCAAGGGTTCGGGACCTGCTGTGGCTGCCATGAGCAGTAC
AGGAAGGATGGCCGCTCATGCGGGGGCTGCAGCGAGGGGCTGCCTCCTTTGGCTCATCCACAGCCTCTG
CCGCCCTGGAAGTCAAGCAACCGGTTGGTACAGGCTATCCAGGCCACAGCTGAGACCGTGTATGACATCCT
GTCCCCGGCAGCCCCCGTCTCCCGCTCCCTGCAGGATAAGCGCTCTGCGCGGAGGCTGCGCAGGGGCCAG
CAGCCTGCCGACCTGCGGGAGGGTGTGGCCAAGGCTACGACACAGTGCAGAGGGGCATCTTGGATACAG
CTCAGACCATCTGTGACGTGGCATCGCGGGGCCATGAGCAGAAGGGGCTGACGGGCGCCGTGGGGGGCGT
GATCCGCCAGCTGCCCCGACTGTGGTGAAGCCGCTCATCCTGGCCACGGAGGCCACGTCCAGCCTGCTC
GGGGGCATGCGCAACCAGATTGTCCCCGACGCCACAAGGACCACGCCCTCAAGTGGCGCTCGGACAGTG
CCCAAGACTGAGCCTGGGGTGCCCGGCACCCAGAGGGTGTGCCACCATGCTCCTGAGCCTCCAAGAG
TGTGACCCCAAGGGCCCGGCCGCTGGCCCTTCAAGGGATGGCCACTGTGAAGGACGCCTTCCAGCC
TGCCCGTGGCAATGCTGTGAGAGGGGGGCTCCCTGCTTGGGGCCTTAGCCCTGGCTCTGCATCTT
TCCTCCGGGGAGAAAGGACACTGCCCTTCCCGGACCTGGGCCACACTGCTGCCCTTCCAGGACGGA
GGCTTTTGGACCCTCGGACCCCATCCCACTCAGCCAAGTGTCTTTCTGTGTCTGGGGGGAGGAGGGGATG
ATATCCGTGTGGTTCGATGTATTATTTTTAAGCTCCGTGAGTGCCTGGGTGAGTGTCTGCATGAAGTGA
ATAAAGTGCCACCGCCA

>NM_001183080.1 *Saccharomyces cerevisiae* S288C Atg2p (ATG2), partial mRNA
ATGGCATTGTTACCTCAAATATACAAAAGCGGCTGCTTCTTTACGTCCTTACGCAAATTCGCTGT
TCTCCAATATAGATTTATCTAAGTGGACGTTTCTATAGGGTCTAAGTACATTTCTCGTCCATGATGT
GAATCTGTCACTTGTATCTCAACATTTCAAACGTCAAATAAACGAAGGCATAGTTGACGAGCTTGTG
TTAAATTAACAGTTTCTGGCGGTGTGGAAATCGATGGGTCTGGTTAAGATTTATCATGACACCTTTAT
ATTCCAGTGGCTCACAGGAACCTCACTCAGATTTTTTGGTTAAAAGCATCCAAGATCTTACGAATTCGAT
GTTACAATTTAGTGATCCATTGACCACATATAATAGGTACAAAGAAGATGACATTAGCTCTTACAGCAGT
AGTAGTGATCTCAACTCTAATATAGAAGCTTCAAACCAGCCGAAATGGTCTTATACTCTTCAAATA
TGCGGAACAAGGCCCTTAATGTAGCCTTAGCGAAATGAAAATAGCATTAAAGGACGTTACCATACGTTT
CATAGTGAATGATAGAGATCCTTCCGATAACATTGTGGAGGTTTCTAGAAAAGCATACAACCTTATTACT
ACAGACGCAAATTTACGACATATAAACATTGAAAATATCACCATTTCTCAATACAAAAACAAGCTGTAC
CCGACTCTCTGTGCATCTTTCAATAATGACGATCTGTACAAAAGCGTTTATTTATCAAAAAATGGAGGC
TACTTCACTTTATATGAGCGCCATGGAAGGCAATCAAATGAAGACCCAGTGAACCCCAAGTTACACAA
GAAGAACAAGAGAATGATAAGTGAAGGAATCTTTAATGGAAATAAATAATTTGAACATAGCTTTAAGG
GTTTATCATCGGTCAATGATCTCAGAATGTCTAATATTGTTATTGATATTCAGGATGTTTATTAGCGAT
ACACAAAATTTGTCGAAATCAAAAACCTCCACTTTGAAGAATATTATAGATATCATTGTTACACATTTGGAT
GCCAATGAAAGCTTTTCTTGCCAGGATTTCCAAAGTCTTACCTGACAAGCAGGAACCATCAGCTCTTT
CTTCTGTTGATATCAAATGTATATACTTAAACTTAGGCCAAGATATCACAGTAATTTTGAAGAGCTTTAA
ATTAGAGCAAAAGGAAAATAATTCATTGGCATTCTTTTAGGCTCATTTTATTCTAATTCGAGTCCATTG
ACAATTAGCCATAAAACTAAGCCATTGCTCACTGGAGAACAACCCCTCAAAGCATCGCATTAATAATGG
GCGACGAACTAGATATTATTATCAGTCATGATGGCATTGCGCATTTCTTTAAAATCTTTCAGTTGTTTC
AAAATGTATGTCCTTTTATCAGAATAAGTCAAAGGGATGATGCCTCAAATAGCATCGGATACTAAAAGG
ACCGTACAACCTTACCTCAAAGCAGTGAAGTTGTGCGCTAAGTTTCCATATTTTTTATTATGTTCCAGG
TTTACCCCTTCAATTTACGACTCTAACCGTGAGTTGTACATTGAGCTTGTAGACGTAATTTAAAAAATACC
TTCTCGGTGCACGAAAATATTGACAATGTGAGCATTACGATCTCGAACTTGCAATCCCCTCTACAACCTG
GGTTCATATGACGATACTTTGAAAGAAGCGCTAATTTATAGTTCTGTCCATGCAATCATCAAAGAAGTGA

TATTTAACGAAGAATATTCTGGAATAGTACAATTAGTCAAGATATTTCTGCGTTTGGAAAACTTTTCAC
GGATTCAAAGAACAGTGAATGTACAGGAAAAGTCTAAAAGCAAGAGAGGCTCCTTTTTGCAGAGAAAGTGC
AGAGTACTTAATTCTTCCAGGTTTCGTTTACAAGCAGAGTTTATCCGCTAATTTTTCTCTCAAGATAGATT
CCATGAAGTTAAAAGTATCAGAAATTATAGGGCCGCAATTTGGTTCTGTGGAAGCATTACTATCAAATAA
TTTTCTTTGCGATTACGGATGACTCTCAAATTGTATATTTTACAAAGAAGTAAAGGTAGAAAAGAAAGACA
CCGTCATTATTAGAGCCACAAGAAATCATGTGAGTAGTTTTGAATAAAGCAGTTAACGAACCTGTACTAT
ATGTTTCATAGAAGGGCGAATGGAAAGTTAAAAGTCATTTTTAACAACATTCGCATACATTACTATGCAAG
GTGGTTAGAAATACTAAAGAAAAACATCGGCCCGGATAATGCCAGTTCAAAGATGAACCTGTTTCACAA
AAGCTTAGTAAAAACAACCGACTTCAGGATTTCCCTGGGAAGTCAAATGTCTGGACTGCTCTTAATTC
TGCACCTTTTCAGATTAAGAAAGTGAATGGTCAATTTGACTTTGACAATCTAACAACTGGTGGAAAGTTCATT
TATTCGCGCAGGCAAAGCTTCTTTCAAAGGCGAATACACTCTTCTTAATAGATGACTATCAGAATTTCAA
ATTCAAAGATAAGAAGTGGCCTAGTTTGATAAATTTTTATGCTGGTCAAGGTTTCTCTGCAATCGGTA
AAATAGATACTTTGAATTTTTTAATAAACAATCCGATGGTGCCTTTTATTGGATTGTAATAAGAACAA
AGTTGGTCTTTTATTATGCGCGGATTCTTTTCAAACCTTTTTGTGAGCTTTGTATTGATTTAAAATATCCT
CAGACGTTTTCTGATGAGGAAAAAATTTAGAACGCAGTTGAAAAATCCTATCGATGTATTCAAAGCATCG
ATTGTGATCTTTTCAATTTCTGCCTTCATCCGGGAGAACAAATCATCAAATGATTACGACTCAGTGCAAT
GGTAGACAGTTTTCTCGACAAAACCTCACGAGTTCAACAATGGTGCCAGAAGTAAACTATCCTCTCAAGGT
TCATATGAAATGGACAGTTTCTCTGGAAGTCCACAGGTTGGTATTTTACTTCCCCATGAGAGTTATCTAG
ACTCTGCTCAGCCAAAAGAAGAAGATACTCCACCAATCGCCTCAAAGAGCAAGAAAGGGATGTGGATAT
AAGGGGTAGTATAGATGTGCAAAAAGTTGTTATAAACTATTTCGATGGGTATGATTGGAAATATACGCGG
AAATTTATCGCTAATACTGTTGAAAAGTGGATAAAGAGCTCAGTAAAGCGGAAGCAAGCAGTTGCAAA
CAAATGTACCCCAATCAGAGGCAAATATTTTTGACTCTATTTATATATCTGCTAACAAAAACAATGTCAC
AGATTTGAGAAGAAATCTTGATGGTGAGATCCAGGGGTTTCAAGATTCCTTCTCTGATGTCTCTAAAGTT
AATTTGCGACCTTCTAAGCATTACAAAGCCCTGATTCAATTGAACAAAGTACATGTCAATTTGAAGAATT
ATCGAGTAGATGAACCCGATGAGTCTAACTCTGATAATTCCACAGATGTTTTGAACCGATGTGTAGTTTC
CATTTACGAATTTGAAATTATCGATAATGTTCCACAGTCCACCTGGAATAAATTTGTAACCTTTGCTAAAG
CACGAACCGTGGCCACACAGTTCTCCGATGTTTTCTTCTGGACCTGGAATTTATCCGGCCGATCGACTTTT
TGCAAGCAGTGGAAATAGTCATGCAATTAATGTTGCGCCTTTACGCTTTCACGTGGATCAAGACACTTT
AGAGTTTCTAATAAGGTTCTTAGGGTTCAAAGATAAAAGATTTGAATTAATTTGATGAGTATCCAGATATT
GTATTTATTTCAAATTTTAGCACTAATTTCAATTAAGTTAAGATTAGATTATAAGCCGAAAAAAGTTGATT
ATGCGGGTTAAGATCGGGCCAACTTCTGAATTTGATGAATTTTTTACCCTTGATGGATCCAAGATTAT
TTTGAAAAGCCTAGTCTGTATGGATTAAATGGATTTCGATGAATTAATAATAAACTGAAAGCCATTTGG
ACGCGGATATTACAAAAGCAGCTGCCTGGCGTTTTGGAAGGACTGGCTCCTGTGATGATGATGATGATG
CGATTGGGTGAGGGTGAAGACCCTAGTCACAGTACTAATGTGAGAATACAGGCAAGAAGGGCATTTTGGG
AAGGAGTCTGAAAAGGGTGGCAATGTCTTCTTGAACACGACAAACGGGAGATTTTGTGAAATTTGGGAGTT
AAATTAACCTCAGGGACACAGGCGATATTGGAGAACACCGAGGAACTATTCGGTGGTGTGGTTCCAATG
GCAGGGTGTACGATGCATCGAAATTTGGCTCCGCTGATGGTGCAGACAGTGATACTGCAGCTGTATTAGA
CTTGATACTTTTATTCGAGGAGGATCAGTTAGTTGGTAGTAAATATTCCAGGATAAGAGATCATGAGCCC
ACGGCAGTAGTCATCGATATGTCTTACCAGGAGATCACAACGAACCCACAATAGTGAGTCTGTACGCAG
ATCAGCCCCTCGACCTGCCACGGGTTTTGAAGGAGGCGTATAGTTTATTAGAAAAGCATATGCATATTGC
GTACGATGCGGTATGGAGGGCAAAGGGACAGATGAAGGATGATAAACGGGGAGGGCCGAGCGCCGAGCA
GTTTATGTTGCTAGAGCTGCACCTGTGGCAATTTATTCGGCCGTTAATTTGGGGCCACTGAGGCAGTGTCTA
AGACTTTACAGGGAATAGCTAATCAAGTGGATAAGACGCATAACGAGCAAATCAATGATAAGTACAAGTC
CAATCGGACTGATTCGTAA

Q. ATG2B (autophagy related 2B)

>tr|K1QL77|K1QL77_CRAGI Autophagy-related protein 2-like protein B
OS=*Crassostrea gigas* OX=29159 GN=CGI_10022070 PE=4 SV=1
MPWTFPWTEFLKKRACRYLLQHLYLQFLKEKLSLDQLSVDLYNLRGSIKDLLELDVEALNE
ALDSSSVPLEIVDGFINQISVSVPWNTLIQSSTEMEIQGLEITVQPKQRMENVGGLETMF
NSMCSMTSSLQIAEDCLKSTSDADQGD LGTFEFGVQKFAQTIDSVLCRVKVTLIDTVVR
VEHLPDSAEGKVALEIKIKRIEYFDDMAKEEGSPVDDSSRRTTWEPAIAHKNLLIDGMQI
LCDEFSPRTHQTPSRMFSDDSYQQTFFMSTTSSPSTPVDNQGGTVPVSEVFSDFVQIAGFT
GKSSLLKVKLQEEGVQPKVEIELEVGLHLLLSPTQFHAVLIDLVNGFLSPKSSNEGRER
ARSKSKPMNEEDYRKVETELQRQLHSDRFHPSHMDTLTATDLQDIMTHSIGDEQYFSLAP
DPMESSVNSNFSLASGRSGSTVTTTRSGPRKDGKAAKDSIQRFLLDDPSAELCRYHLRAVF
FSVALLHENPSQKVDLSSAKANNKNQMKDIAAQYFQKMHSFSAASGGEVKALRAAFAEA
LPQDHLRLIGKPVNIEIVERTAPTHHCLTVDVTVAGFLDVVECLFNRTLQTI EPDYTELAA
QLAHQSGDKFNRTVCEISHF

>XM_011444166.2 PREDICTED: *Crassostrea gigas* autophagy-related protein 2 homolog B (LOC105338878), mRNA

GGAAAAACATCAAACACTACGTGCAAACTGTAAATAAAGAGAAATGTATTGCTCACTTACTGTCAATGTTTA
CGTTTTCTGAGCAATGTAATTCTGTGATATTTGATACAATTTTATATTCAAATGTAAGAAAATGCCTTGG
ACTTTTCCATGGACAGAATTTTTGAAGAAAAGAGCATGTCGATACCTTTTACAACATTATTTGGGACAGT
TTTTGAAAGAGAACTGTCTCTAGATCAACTGAGTGTGATCTGTACAATGGAAGAGGCTCGATCAAAGA
TTTGGAGCTGGATGTGGAGGCTTTGAATGAAGCCTTGGATTCCAGCAGTGTACCACTAGAGATAGTGGAT
GGCTTCATTAACCAAATCTCCGTGTCTGTTCCCTGGACCAATCTGATCCAGAGCAGCACAGAGATGGAGA
TCCAGGGACTAGAGATCACAGTACAGCCAAACAGCGCATGGAAAATGTGGGGGGCCTGGAGACCATGTT
CAACAGCATGTGCAGCATGACCAGCAGTCTACAGATAGCGGAGGACTGCCTCAAGTCCACATCAGACGCA
GACCAGGGCCAGGACCTGGGCACACCTTTTTGAGGGCGTGCAGAAGTTTGGCCAGACCATTGATTCTGTGC
TGTGCAGGGTTAAGGTCACCTTGATTGACACAGTTGTGAGGGTGGAGCACCTCCCTGACTCAGCAGAGAA
GGGCGTGGCACTTGAATCAAATCAAACGAATAGAGTACTTTGACGACATGGCGAAGGAGGAGGGCAGT
CCCGTGGATGATTCTCCAGAACCACGTGGGAGCCAGCAGCCATCGCCACAAGAACCTGCTGATAGACG
GCATGCAGATTCTGTGTGACGAGTTTCAGTCGCCCCACTCATCAGACCCCTCCAGAATGTTCTCGTCTGA
CTCGTACCAACAGACTTTTCATGTCCACTACAAGTCCCCATCCACCCAGTGGACAATCAAGGTGGGACG
GTCCCGGTATCCGAGGTCTTCTGTGACCCGGTACAGATTGCCGGATTACAGGAAAAGTCCAGTCTGAAAG
TCAAACCAAACAGGAGGAAGGCGTGCAGGGGCCAAAGGTGGAGATTGAGCTAGAAGTTGGAGGACTCCA
TTTGTGCTCAGTCCCACACAGTTCCATGCTGTCTTGGACCTTGTCAATGGCTTCTGTGCCCCAAAATCC
AGCAACGAGGGCAGGGAGCGGGCAAGGAGTAAAAGTAAGCCAATGAATGAGGAGGATTACAGGAAGGTGG
AGACGGAGTTACAGAGACAGCTCCACTCGGACCGCTTCCACCCAGCCACATGGACACACTGACTGCCAC
GGATCTCCAAGACATCATGACACATTCCATTGGGGATGAGCAGTATTTTTCACTAGCTCTTGACCCAATG
GAATCATCAGTCAACAGTAACCTTTAGCTTGGCTTCAGGCAGATCTGGAAGCACTGTAACCACCACAGAT
CAGGGCCAAGAAAAGATGGGAAAGCTGCAAAAGATTCTATTACAGCGTTTCCCTGACGACCTTCAGCAGA
GCTCTGTAGGTATCACCTAAGGGCAGTCTTCTTCTGTGCTTCTTCCACGAAAACCCGTCCCAAAAA
GTGGACCTATCTTCCAGTGCCAAAGCCAACAACAAGAATCAGATGAAGGACATTGCAGCCAGTACTTCC
AGAAGATGCACCTTTTTAGTGCGGCGAGTGGAGGAGAGGTGAAGGCCTTACGTGCTGCCTTCGCAGAGGC
ATTGCCTCAGGACCATCTCAGGTTGATAGGTAAACCCGGTGAATATAGAGATTGTTGAGAGAACAGCCCCT
ACCCACCATTGTTTGGCGGTAGACGTAACCTGCTGGTTTTCTAGATGTGGTAGAATGTCTGTTCAACAGAA
CTCTTCCAGACTATTGAGCCAGACTACACTGAGATTCTGGTATTCCCCGAGATGTCTCAACCAAACAGGG
GCACATGTACAGTAGCATGCACCTCAGGTGCACCTGCACCTCAAGGCCCATGTCAAGTCAGTGCAGCAAAAC
AAGAGATCACAGAGGCTTTTCAGGTGGACCCAGGACAGAGATTAGCGTCAATTTGGCCAAACTGGAGTGTG
AATTGGATTGTGCAAAATATAGACAGGATAGGAAGCTGATAAAGCCCTCCTCCACCCCAATCAATGGA
CAGCACTGCAGCCTCACAGGGGGTCCATTGTACAGTTTCTCCAGACGATGGAGGATGAGTCTGCTTCA
GACGAGACAAAGATCGATCTCAGTGTCAACTGTCTGAGGTCAAACCTCACACTCAGATTTCCAATCCCTG
ACCTGAGGAATGGGTGAGAGGTCACTAAGCTGCCCTGGTGGCAGAAGAACCTGAGGGACGAGCTGCTGAT
CTTGGATTTACAGGAGGCCCGGTTCCAGACTTCTTCTGTCTAACCAGCCTATCCAGCAAGTCGAGGTC
TCCAGCAGAAATGTGCTAGGGTCTTTCCGTATTGATCCAAACCAGAGTGCAGTCCCTTTTGCATTTGTTA
GCTGTGAGGGAATTGATGGACAAGAGGGCTTCAACTTCCCACAGATAATAATTAAGTTTACAGAACAGAC
CATCTCTGTTCTGGATGAAGAAAATCCAGACTCAGATAACAGTATTCCTATGGACTCGTTGAATGGTGCT
TGTGAATTTGCCAAACAAGACACGTCACCTTTTTCTACAAAGAAACACATGTATGGGAAGGGGAGATGT
CGGACCAAGCTACTCAGCATGTGAGTGTGAGATGGTGTGATGCCTGGCAACAGAGAGGACATGGCCGACTT
CCAGGAGAGAGCCTCGGCCAACTGCCTGACCCTGGTCCAGCTAGTCTACCCCTCATCAACCTCTACATT
CCAGACCAGAAGTTCTATGAAGTTCTGTACAATAGGATTAGCAATGATCTGTTGCTATGGGAACCAATGG
CACCTGCTCCAATTCGACCCAGGAAGTTGGGCCTGGGTCTATCCAGCCATTTGATCTGAGCTGTTATAC
TCATGCTCTGCAGGAAAATTTTAGTATGGCAAAGTCAGCAATACAGTATGACTCTTCAGATGAGGAGGAA
GATAGTAGTTTTGGTTACTACAGTATTCATGACAACAAGCATCCACGCAGGACATTTGACCAGAAGTCAA
GGCCAAGTAAGATGTGTCTGTCACTCAAGATAGACAAAGGGAAAATCACAGCAAGGACCGACTCAAAGGC
TGAGGATTGCCATGGGGAAGTTATGGGTGTGGTCAAGGATGCCAATCTGTTTGTGGCCTCCAGTTACCAA
GGAAACCCACTGCTTCAGTATATCTGCTTCTATTGCAATAAAGCAACTTTATATCATAAATGTCAGTTC
CAGATAAAAAGGAAGAATTTGAGATAGAGAATTTGGACTTTGAGACAATCCCTGCCACCTGGAGAAGAG
TTGTATTATAGATAGGTCTGAGCCTGGGGTTCTGTGTCAACAGTCAGCTGATGTGAGTCCACGGTCAGG
GACATGGTGTGAGTGGCGGTGAGAATCAAGCTCGACTCCACCCCTCAGTGACCTAACACGGGATGAGA
AAATCAAGGAGTTTACAGTAGCAGTTGGTGTCACTGGAGCAACTCTAAGACACAAGATGGCCGAAAACAGA
TATGAGCTGGATATCTCAAATTTTGAACTTTTTGGATGTGAAGGACTACGACATCCTTGGATATGTCACT
CCAAAATCCTGACCGAGCTACACGTACATCTCTGGGACTGCGCTGTGGATTACAGACCATTGCATCTAC
CAACCAAAGGAGTAGTAGCAGCCAATTACTTCAGTATTTCCAGTAACATAGTGGCCAACCTCCAGACCTC
GCTGCTAAGGTTTTGCTTGGAGGATGCTGGGATGTATTTGTCTCAAAGAAAAGGGAGAGAATCCACTGTC
GACCTCAAAAAGATTATGTATGTGTCCTTGTGATGTGGAAAGTTTTGAATTGGAATTGCGTACAAGTGACG
GAAAAGATCCAAAGTTTCAAAGATGGACTTGCAGCTCCGAACCAACAAGATCAACATGAGGACGTGTAC
CGACTCTTGTAAAGGCTCTGTTTGGATTAAATTCGATACTTTGCTAACGATGGCGACCTCGTGGAGTATGAG
GAGGAGCCCAATAAACGCCAGAGTCTGGACCTAGAGATGATGAATAAGGAGGAGGCTCTAGTGATG
AGGACTCAAAGAAGAAAGAGTTGAGTGTGATCCAGATTGGAAAACCTTTCTCTCATCTGGAGGATGCCAT

GTACTGGCATTAAAGTATCCTATGAACAAAGACAAAAGATCAGCTTCCCGATATTTTAGTACTGATATGTC
CATTGGGCAAATGGAATTTTTGGAGTGCCTATTTCCAAGTATTTTTCATTCTGTTCCCTCCTCACTATAACA
GAGCTTTTAAACGTTCCATTCCAAAGAAGAACTGGTTCCCATTTCCCTGTGTGTCTTCAGCTTCATTATA
AGCATTCTGAGAATAGAGGGCCCCAGGGTAATCAAGCAAGACTTAGTTTTCAGTTCCCTCACAAGGCAGAATT
GCAAATTAATTAATCCAGTGTGTTGTGAGCTGGATATCAGTATTGTGGACAGGTTAAATTCCTTGCTT
CAACCACAGAACTTGCCACAGTAGAGATGATGGCATCCCACATGTATACTTCATATAATAAACATATTA
GTCTGCACAAGGCTTTCACTGAAGTGTCTTAGATGATTACATAGTCCCTGCAAATTTGTCGGATATCAGT
ACAAGTTGCCACACCAGCATTAAACCTTTCTGTTTCGCTTCCCAATACCTGATCTTCGATCTGATCAAGAA
AGAGGACCATGGTTTTAAGAAGTCACTTCAGAAGGAGATCCTTTATTTAGCCTTCACAGATCTAGAATTTA
AGACTGAATTTATAGGAGGATCAACCCCAGAACAAAATTAATTTGGAAGTACCTTTAGAGAACTAATTTGG
ATCGTTCCAGGAAGAGAAAGGAGATCCATCTATTAAGTTTTTCCATGTGTCTAGTGGAGTAGATGGAGAT
ACAACATCGTCAGATGACTTTGACTGGCCACGAATTGTACTGAAAATAAATCCACCAGCCATGCATTTCA
TTTTGGAGAGAATTGCAGCTGAAGAAGAAGAGGAGAATGATGGTCACTACCAGGAGGAAGAGGAAGGAGG
TGCTCATTCTTGAAGATGTTTGTGATCTAAGAAGACCAGCCCCATCTCCTTTTTCTCTCGTAGAGTA
ATGTTTTGAAAATGAACAGATGGTGTGATGCCAGGAGACCCTGTAGAAAATGACAGAATTTCAGGATAAAGCAA
TCAGCAATTTCACTATGTGCTGGAACCTACGTTACCAAATATTTATGTAACACTACCTAATAAGAGCTT
TTATGAGAAGCTTTATAATAGGATCTTTAATGACTTGTACTGTGGGAACCAACAGCTCCTTCACCAGTG
GAGACATTCGAGAATATTTTCTATGGCATTGGGCTTTTTCAGTAGCCAGTCAGCTCATTAATACTTTTCAACA
AAGATAGTTTTTGTGATTTTAAATCTGCAGTTCACTATGATGAGGAAAAGTGGATCTGAGGAGGAGACTTT
GCAGTATTTTTTCCACTGTTGATCCCAACTATCGTTTCTCGCAGGAAAAAAAAAATAGACTCTCAGAACAAG
AACTCTCAGAGTTTTTCTCAGTTCTTCTGAATATTAATCATGGATTAATAGCAGTGTTCACAGATGTGA
AGCAAGATAATGGAGATCTGTTGGAAAACAAGCATGGTGAATTCTGGTTAGAGTTCAATAGTGGTTTCAAT
ATTTTGTGTGACAAAATATGAAGGTTTTGATGACAAGCACTACATTTGCCTTCATTCTAGCAGTTTCAGT
CTGTACCATAAAGGCATAGTGAATGGAGTGTCTTCCCAGCAGAAAACAGACTTCCCAGCTCAACCCGCC
CACACTGGTTGGAACCTACTATTTATTCCTCTGAAGAAGATGGCCTCAGTAAAACCTTCTTCAGATGGAGT
TGGAGGAGACAGTTTGAATATGCTGTCTGTTGCCGTTAAAAATATTGTCTGATAAATCAGAGTCCAATACA
AAGGAATTTCTCATTGCCGTAGGACTGAAAGGAGCCACTCTCCAGCATAGAATGCTTCCCTTCTGGGCTTA
GCTGGCATGAGCAGATTTTATACTTCTTGAATATTGCTGATGAACCTGTTTTGGGATATAATCCTCCAAC
TTCATTTACAACCTTTTCATGTTTCTTTGGAGCTGTGCACCTTGATTATAGACCCCTTTATTTGCCAATC
CGATCTCTTCTTACCGTGGAAACATTCAGTGTTCAGTAGCGTTGCATTGGATAAATCTTCTCTACTC
TCAGAATAATCTGGATGAAGCTGCTTTACATCTATCTGACAAAATGCAATACTGTACTATAAATCTGAG
TAGAGATTATGTTCTGTGTGATGGATATGGGGCTTTTTGGAGTTAACCATAACTGCAGTGAAGTCTGATTTCT
GATGGAGAGCAAACCTGAGCCCCGCTTTGAGTTTACACTGTTCCAGCGATGTTTGCATATCAGAAGCTGCT
CAGACTCTTGTGCTGCGTTAATGAATCTCATTAGTACATTGCAAGCTATGGTGACTTGCAGACACCTTAA
CAAGGCAGATATGAAGCCTGGAGCCTTTCAAAGAAGGTCTAAGGTAGATTCCAGTGGTTCGATCATCCTCA
CGTGGTCCAGTACTTCCCTGAAGCAGATCAACAAAATGTTACGAGATCTGATGAGTGTGCTATGGAGGAGA
TCGACATGCAACAAGGCACCTCGTCAGTAAAACCACAGGCTAATGGTGTTTTTGGATGAAAAATCTCAAAAT
TCAGGAGCCATGTTGTTTCCAGACCTCTTCCCTGTTTCCCTGACGAGAGTGGGAATGTATCCAGGAGTCCGGC
CCCACCTATGCCTCATTCTCTCACCATTTTATCAGTGTGCAATGACAGGTGTGCCACTGAGAATGATG
ACTTTTGCATTCTTTTTGCACCAAAAAGCAGCCATGCAGGAGAAGGAAGAAGAACAGTTATAAAAAATCAT
GGTTGATGATGCAATTGTGATAAGAGACAATTATTTTTCAGTCTGCCCGTTAATAAGACCGATACGAGCAAA
GCCCCCTTACACTTTCCCATTTCTGTGATTCGCTATGTGGTGAAGGAGGTCTCTCTTGTCTGGCATCTTT
ATGGAGGAAAGGATTTTGAATAGTCCCTCCCCTTCTCCGGCTAAAAGTTATATTAGTCCCCACAGTTC
GCCTTCTCACACACCCACGAGACATGGACGTAATACAGTATGTGGGGGAAAAGGAAGGAACCATGACTTT
TTAATGGAAATACAGCTAAGCAAGGTGAAGTTTTCAGCATGAAGTCTACCCGCCATGCAAACTGATTGTG
ATTCCAGCCTCTCAGAACACCCAGTCTCCCGGCAGGTGTTTTCATTGTTTTCAGGATCTTTCAGATTCGAGATCG
TTTGGCAACATCACAATGAATAAATTTTTTATACCTGTATTGCAGTAAAGAAATGCCTCGAAAAGCTCAC
TCCAACATGTTGACAGTGAAGCCTTACACGTGTGTCCAGAATCTGGCAGGTCCCCACAGGAGTGTCTGCT
TGAGAGTGTCTGATGCGCTCCGCCTCAATATTGACCAGGATGCTTTGTTCTTCTTGAAGGATTTCTT
CACAAGTCTTTTCTGAGAAGTAGAGCTTCAAAATGACTCCAGATCCAGAAGTTAAAAGTCTCCTGGAGCT
GATGTCACCTGCAGTTTGGCAAGGCATTTGAGTACCTCAAAGGAGCCAAAATCTGGTTATTTCTTCTCTG
GGCCAAAACAGCCTTCCCAAAATGATAGTGCCAATTCAGTGGAAAGTGGTTAATGGCATGGAAGAGAAGAA
CTTCTCTGCTGAAGAAGCATCTTTTAGGGATCAGCCTGTGTTTTTTAGAGAATTTAGATTCACGTCAGAA
GTTCCCATTGCACTTGATTATCATGGCAACATGTATCAATGGATCAGGGTACGCTAGCTGGGATTTTTGA
TTGGTCTGGCTCAGTTAAACTGCTCTGAACTAAAGCTCAAGAGGCTTTTCTATCGACATGGTTTACTAGG
CGTTGACAAAATATTCTCATATGCAATCACTGAGTGGCTTAATGACATTAAGAAGAACCAGCTACCAGGA
ATCCTGGGAGGTGTTGGACCTATGCATTCAGTACAAATAGTACAAGGCCATAAAGGACTTGGTCTGGC
TCCCAATAGAGCAGTACCGGAAGGATGGCCGCTTGTGAGAGGTTTTCAGAGAGGCGCTGCTTCTTTGG
TACCTCGACAGCGATGGCTGCTCTAGAACTCACAACAGAATGGTTCAAACCATAACAGGCAGCTGCAGAG
ACTGCTTATGATATGGTGTCTCCTGGTACCCTTTCTATCGAGCCCAAGAAGACCAAAAAGGTTTCTCATC
ACCGGTTAGCCCACCAGCCAGTAGACCTGAGGGAAAGGTGTGGCCAAGGCTTACAGTGTGTGAAAAGAGGG
AATCACAGACACGGCTCAGACCATTTATGAAACTGCGGCTCGAGAACACGAGAGCAGAGGGGTGACTGGT
GCCGTGGGCGAGGTTCTGCGCCAGATTCCTCCGGCAGTGGTGAACCTCTGATTGTTGCCACAGAAGCAA

CGTCAAACGTGCTGGGTGGCATGAGAAACCAAATTAGGCCAGATGTCCGGCAAGACGAGTCACAGAAATG
GCGCCACGGGGATGACTGATGGCTTGGAACTGACAGTGTGAAGATAAGGAGAGTGGAAACCAGGAGCTCAG
AGTCCTGACAGCAGCTTCAGAGGAAGCTCGTTAATTTTATTGTGCTCATCTCAGGAACAAAAGCATT
TTAGTTAAATAATTTAACATCAAAACAACATGCAACCAAAACTTCTGACATTTATAGTTGATACTTGCC
TATAGAAATGTTTGGTGGCTGGTGTCAAAGGTCTTAAAGCATTGCTGCCAAGTTAGTGGAAAGGCTCAC
TTTTGTTAAGATGACTGTAATTCTCCTTGTACCAGCAGAGATCATTGGAAGCTGCCTTCTAACACTTT
GTGTAGCTCTGTGGAGTTGGATTTTCTTAAGGTTTAAAAAGAATCACAGCTTCGGAACTTTTAACTGAAA
ATGAGAGACAGAAGCCACAGGGGAAGCAAAGCAAATAGGATTTTCAATATAAAATATCAGTGTGGAAAAAT
AACCTATTCTGTTGAATTTAGTGTTCATGCACTTGAGAACAACATTATTTCCATTTACTCCGAAAAATCCT
TCTGTGGGGGTTTGGAGAAAGTGAATGTTGCAGACATGTTCTGTTGTGTTGCACTTTATCCTGTGTTTATG
TGTATGTGTTTTTAGATTAATTTCAAGTTGTGTGCTATATTTCTTGTATAATTTACAAAAGTTACACAAAAT
ATAAAGAGCAGTAACTTGTCTGAAAGTTTTTGGCAAAGGAAGGTAACCTCAATGTAATAGCTTCTCTTA
AGAGTACAGGAAAATGCATTCTGTAATGAAGTGGGGCCCATGTAATTGTTTATATTTTCAAGTTTAAAGCA
GGTATAGTGCAGGCTTGTAGGAATGTGTGGAAGGGAAGATTGGAAGTGATTTTTCTCTTTTAAAAGTA
AACAAAATTTTCAAATATGCCCTAGTTAACTATTTTACAGTAACTTTTACTTGGTTAACAGTGTACA
TTTTGATAACCTATCAGGAATGAATAAAGTATTTTTTAAAGGTGATATTGTTTTTATGCTTCCATGAA
TATTTTGCTTTTCTTAGAGCATATTCATAGATGCAGTACTGTGATTTACCACAAGATAAATGGGAACACT
TTCTCAAATCGATTTTGGTTAATATCAGGTAAATCATTACCTAGGAGTAAGAGGGAAAATGTTGTCAAT
TCCTGACTTTAGATTGATCCAGCAGAAAAGAAAAGGTGGAACCTTTGTATATATCCACTGTTGAAAAGTTGCA
TGACCTGACTTCTGTTTTCTAAAGTTGGGGGAATATTATTGAACTTCAATTTCAGAACTGCATTTCAAT
TTGGGGCTTGAAAATGTAGTTAAATCAATTTCTGTTCTCTAAATTTTCTAAGCAGGAAAGCAATGTAAAC
CAAAAATCAAAATGTTTAGAATTTATAAAAATGGGGTTATATAGCTTTTAAATTTAGTTTCTTTTACT
GCCAAAAAATTTAAAAGACAACAGCGTAACCACCTGTTTAAAGCACCCTGGGACCATCTCTTATTCGGGT
AGAGCCTGGTCTGGCGACACACTAACAGGAAGGCGTGCTGTGTTACCGGGAAGGCGCCTCTGGCTGTGG
GGTGCCTTCTGACCACCCGCTCAGATGCCAGCATTTCATTTGCCCTTAAAGGAACTTGTCTATGTGTG
TTAACCCAGTTATGATTAGTCAAACCTGGAAAACACTTGATCAAACCTAAAATTTGTAATCTGTCTAACT
TTTAAATATACTTTCCACAGTTGTACTTAAAGTTCAATTAACCTACAGTATAGAGAAAAATAATTTCTCT
TCTTTGCACCCGGAGTTGCAAACAAATTAAGTTTACAAATCTCATTTAAACATATATCTTTGTAATGTAA
TCTCCGCGTTCTTTCTTTGTTCTACCCTCCTGCACCTGTTGTGCGATGTAATCATTTTGGGAACAGAAAC
GTTGTGTCTCAAAAAGATTCTGTTGTCAGTTTACGCAAGATGTTCTTTACCTGAGATTCTGGAAAGATGTT
TATCTATATCGGAACACTTCTACATTATTAATGTCTTAAAGCTTTTTCTTTTTTA

>sp|P53855|ATG2_YEAST Autophagy-related protein 2 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG2 PE=1 SV=1
MAFWLPQNIQKRLLLYVLQQISLFSNIDLSNLDVSIKSKSHFSFHDVNLSDDDLNI PNVQ
INEGIVDELVLKLTVSGGVEIDGSLRFIMTPLYSSGSQELHSDFLVKS IQDLTNSMLQF
SDPLTTYNRYKEDDISSSDSSDLNSNIEASKPAANGSYTLQNMNRKALNVALAKLKIAL
KDVTIRFIVNDRDPSDNIVEVHLESIQLITTDANLRHININENITISSIQKQAVPDSVHP
FNDDLSQSVYLSKMEATSLYMSAMEEQSNEDPSEPQVTQEEQENDKCKESLMEINNLNI
AFKGLSSVNDLRMSNIVIDIQDVHLAIHKIVEIKNSTLKNIIDIVTHLDANESFSCQDS
QSPSPDKQEPSALSSVDIKCIYLNLGQDITVILKSFKLEQKENNSLAFSLGFSFYSNSSPL
TISHKTKPLLTGEQTPQSIALNMGDELIIISHDGHIAHFFKIFQFVSKCMSFYQNKSKGM
MPQIASDTRKTVQLTSKAVKLSLKFYFLLCFQVSPFIYDSNRELYIELVDVFKKLP SRC
TKILTMSSITISNLQSPLQLGSYDDTLKEALYSSVHAI I KEVIFNEEYSGIVQLVEDIS
AFGKLF TDSKNSECTGKSKSKRGSFLQRSVRVLNSSRFVYKQSLSANFSLKIDSMKLVKVS
EIIIGPQFGSVEALLSNFFAITDDSQIVYFTKNLKV ERKTPSLLEPQEIMSVVLNKAVNE
PVLYVHRRANGKLVIFNNIRIHYYARWLEILKKNIGPDNASSKDEPVSQKLSKKQPTSG
FPWELKCLDCSLILHPFRLKSVMVIVLDNLTGGSSFIPOAKLLSKANTLFLIDDYQNFK
IQKDKNWPSLINFYAGQGFSAIGKIDTLNFLINKSDGALLLDCKIEQVGLSLCADSFQTF
CQLCIDLKYPQTFPDEEKFR TQLKNPIDVFKDIDCDLNFNSAFIRENNHQNDYDSVHLVDS
FLDKTHEFNNGARSKLSSQGSYEMDSSSGTATGGILLPHESYLDSAQPKEEDTPPIASKE
QERDVDIRGSI DVEKVVIKLFDGYDWKYTRKFIANTVEKLDKELSKAEASSKSNVPQSE
ANIFDSIYISANKNNVTDLRRNLDGEIQGVQNSFSDVSKVNL RPSKHYKALIQLNKVHVN
LKNYRVDEPDESNDNSTDVNLNRCVVS IYEF EIIDNVPTSTWNKFVTL LKHEPWP HSSPM
FLLDLEFIRPIDFLQAVELVMQLNVAPLRLHVDQDTLEFLIRFLGFKDKRFELIDEYPDI
VFIQKFSTNSIKRLRDYKPKKVDYAGLRSGQTS ELMNFFTL DGSKIILKSVVLYGLNGFD
ELNNKLKAIWTPDITKKQLPGVLEGLAPVRSFMAIGSGVKT LVTVLMSEYRQEGHLGRSL
KKGGNVFLKTTTGDFVKLVGKLTSGTQAILENTEELFGGVG SNGRVYDASKFGSADGADS
DTAAVLDLDTLFEEDQLVGSKYSRIRDHEPTAVVIDMSSPGDHNEPTIVSLYADQPLDLP
TGLKEAYS SLEKHMHIAYDAVWRAGQMKDDKRGGPSAAAVYVARAAPVAIIRPLIGATE
AVSKTLQGIANQVDKTHNEQINDKYKSNRTDS

R. PI3KC3 (phosphatidylinositol 3-kinase catalytic subunit type 3)

>tr|K1PVC2|K1PVC2_CRAGI Phosphatidylinositol 3-kinase catalytic subunit type 3 OS=*Crassostrea gigas* OX=29159 GN=CGI_10006484 PE=3 SV=1
MGEMSDRFHYVYSCDLVDNLQIKIGTLEGERQRPDYKELLDDPMLKFSGVYGEESCSDLYV
TCQVFADGHPLSLSMSTSYKAFSTRWNWNEWITLPVKYSDLPRNAILSLTIWDIYGTNKS
IPVGSTVIPLFGKRGTYRQGMHDLKVWPDMLPDPSSNSTTPGKSKDHKQMSKLAKLSKK
HRDGHMLKVDWLDRLTFREIEMINEKQKRDSKFMYLMIIEFPLIHYEDIEYSVVYFEKDGD
EPLVYKTIIPDLVQVPDPEIDMENLVESKHHRLARSLRSGPTDRDMKPDATRNLLEIVR
YPPTKTLTSEEDLVWKFREFYLCNQKKALTKFLKCVNWKQPQESRQGIELLTRWSPMDVE
DALELLSPAFSHPTVRKYAVSRLRQADDQDLLLYLLQLVQALKYEDFEEIMRYNDSIVDR
KDSVSDTSAPEKTRTTSVLSRASSNESILHALGGSSPSQSESPESKLEREMDLASFLISR
ACNNTSLANYFYWYLSVECVDPNGLDVKDSKVTKMYQHVLKRFQALFKESNESRQRRSM
IARQQTFIGDRLVDLVKIVTRESGNRKKKIERLQALLHQEACKFDFSNFEPLSLPLDPDI
KICGIIPEKATLFKSNLMPCKFVFKMVEGGEYMYKHGDDLQDNLILQIITLMDKLLM
RDNLDLKLTYPYKVLATSCKHGFVQFVESVAVAEVLNQHTGIQSFFKICAPCENTPYGFQF
EVMDFVFKSCAGYCVITYVLGVGDRHFDNLLLTKTGKLFHVDVDFGFIILGRDPKLLPPLMKL
TTEMIDGMGGPNSEHFHDFKLCYTAFLAIRRSSNLIILNFTLMVNANIPIAIEPDKSV
KKVQDKFVLLHLTDEEAVQYMQNVIDGVSAMMPVLLVERFHTIAQASTSQTLYIKYTL

>NM_002647.4 *Homo sapiens* phosphatidylinositol 3-kinase catalytic subunit type 3 (PIK3C3), transcript variant 1, mRNA
ATGTTGTTTTTTCCTGTACCTAAGTTCCTCCGCTGTAGGTGGTACCTTTGCAGACGGTGCGATGGGGGAAGCA
GAGAAGTTTTACTACATCTATAGTTGTGACCTGGATATCAACGTCCAGCTTAAGATAGGAAGCTTGAAG
GGAAGAGAGAACAAAAGAGTTATAAAGCTGTCCTGGAAGACCCAATGTTGAAGTTCTCAGGACTATATCA
AGAGACATGCTCTGATCTTTATGTTACTTGTCAAGTTTTTGCAGAAGGGAAGCCTTTGGCCTTGCCAGTG
AGAACATCCTACAAAGCATTTAGTACAAGATGGAAGTGAATGGCTGAAACTACCAGTAAAAATACC
CTGACCTGCCAGGAATGCCAAGTGGCCCTCACCATATGGGATGTGTATGGTCCCGGAAAAGCAGTGCC
TGTAGGAGGAACAACGGTTTTCGCTCTTTGGAAAATACGGCATGTTTTCGCAAGGGATGCATGACTTGAAA
GTCTGGCCTAATGTAGAAGCAGATGGATCAGAACCACAAAACTCCTGGCAGAACAAGTAGCACTCTCT
CAGAAGATCAGATGAGCCGTCTTGCCAAGCTCACCAAAGCTCATCGACAAGGACACATGGTGAAAGTAGA
TTGGCTGGATAGATTGACATTTAGAGAAATAGAAATGATAAATGAGAGTGAAAAACGAAGTCTAATTTTC
ATGTACCTGATGGTTGAATTTTCGATGTGTCAAGTGTGATGATAAGGAATATGGTATTGTTTATTATGAAA
AGGACGGTGATGAATCATCTCCAATTTTAACAAGTTTTGAATTAGTGAAAAGTTTCTGACCCCCAGATGTC
TATGGAGAATTTAGTTGAGAGCAAACACCACAAGCTTGCCCGGAGTTTAAAGAAGTGACCTTCTGACCAC
GATCTGAAACCCAATGCTGCCACGAGAGATCAGTTAAATATTATTGTGAGTTATCCACCAACCAAGCAAC
TTACATATGAAGAACAAGATCTTGTGTTGGAAGTTTAGATATTATCTTACGAATCAAGAAAAAGCCTTGAC
AAAATCTTGAAATGTGTTAATTGGGATCTACCTCAAGAGGCCAAACAGGCCTTGGAACTTCTGGGAAAA
TGGAAGCCGATGGATGTAGAGGACTCCTTGGAGCTGTTATCCTCTCATTACACCAACCAACTGTGAGGC
GTTATAGCTGTTGCCCGTTGCGACAGGCCGATGATGAGGATTTGTTGATGTACCTATTACAATTTGGTCCA
GGCTCTCAAATATGAAATTTTGTATGATATAAAGAATGGATTGGAACCTACCAAGAAGGATAGTCAGAT
TCAGTGTGAGAAAATGTGTCAAATTTGGAATAAATTTCTGCAGAAAATAGATAGCTCCCAAATTTATAACCA
GCCCCCTTCTTTCAGTCTCTTACCTCCTCCTGCATCAAAAACAAAAGAAGTTCCAGATGGCGAAAAATCT
GGAACAAGATCTCTGTACCTTCTTGATATCGAGAGCCTGCAAAAACCAAACTCAACACTGGCTAATTTATTTATAC
TGGTATGTGATAGTGAAGTGTGAAGATCAAGATACTCAGCAGAGAGATCCAAAAGACCCATGAGATGTACT
TGAACGTAATGAGAAGATTCAGCCAAGCATTGTTGAAGGGTGATAAGTCTGTGAGAGTTATGCGTTCTTT
GCTGGCTGCACAACAGACATTTGTAGATCGGTTGGTGCATCTAATGAAGGCAGTACAACCGGAAAGTGGA
AATCGTAAGAAAAAGAATGAGAGACTACAGGCATTGCTTGGAGATAATGAAAAGATGAATTTGTCAGATG
TGGAACCTTATCCCGTTGCCTTTAGAACCCCAAGTAAAATTAGAGGAATAATTCCGGAAACAGCTACACT
GTTTTAAAAGTGCCCTTATGCCTGCACAGTTGTTTTTTAAGACGGAAGATGGAGGCAAATATCCAGTTATA
TTTTAAGCATGGAGATGATTTACGTCAAGATCAACTTATTCTTCAAATCATTTCACCTCATGGACAAGCTGT
TACGGAAAGAAAATCTGGACTTGAAATTTGACACCTTATAAGGTGTTAGCCACCAGTACAAAACATGGCTT
CATGCAGTTTATCCAGTCAGTTCCTGTGGCTGAAGTTCTTGATACAGAGGGGAAGCATTGAGAACTTTTTT
AGAAAATATGCACCAAGTGAGAATGGGCCAAATGGGATTAGTGCTGAGGTCATGGACACTTACGTTAAAA
GCTGTGCTGGATATTGCGTGATCACCTATATACTTGGAGTTGGAGACAGGCACCTGGATAACCTTTTGCT
AACAAAAACAGGCAAACCTTCCACATAGACTTTGGATATATTTTTGGGTGCGGATCCAAAGCCTCTTCT
CCACCAATGAAGCTGAATAAAGAATGGTAGAAGGAATGGGGGCACACAGAGTGAGCAGTACCAAGAGT
TCCGTAACAGTGTTACACGGCTTTCCCTCCACCTGCGAAGGTATTCTAATCTGATTTTGAACCTGTTTCT
CTTGATGGTTGATGCAACACTTCCAGATATTGCACCTTGAACCAGATAAAAACCTGTGAAAAAGTTTCAGGAT
AAATTCGCTTAGACCTGTGCGATGAAGAGGCTGTGCATTACATGCAGAGTCTGATTGATGAGAGTGTCC
ATGCTCTTTTTGCTGCAGTGGTGGAAACAGATTCACAAGTTTGCCAGTACTGGAGAAAAATGAAACTGGGA
TTGACCCATCAAGATGCTTGGCTCAATAAGAAAACACGTTAGGAGCAACCTTTGTATATTGGAGACTTC

TCTGTTGGTCTAATTTTACCAAATAAACCCTAAATAAGAAGTCTGATTTATCTAAAAATAGAAGTTAACA
TAGCATCCCAGTATTGCCATTCTAAAACCTCTGGCATGTAAATGGGAGAAATGGAAAATAAGCTCAAAATGG
GTAGAGTAACCCATTTCTGCATGAACCATAGAATTTAACTAGAATTTGGCTGGCTCATGCCTGTAATGCC
AGCACTTTGGGAGGCCAAGGCAGGCAGATCACTTGAGCCCAGGAGTTTGGAGACCAGCCGGGCAACATGG
TGAAACTCCATCTCTTCAAAAATATATATTTGTGTGTGTGTGTGTGTGTATGTGCGTGCACAAAAATTAG
CTGAGTGTGGTGGTTTACACTTGTAAATCACAGCTACCTGGGAGGCTGAGGCAGGAGGATTGCTTGAGCCT
GGGAGGCAGAGGTTGCAGTGAGCTGAGATTGCACCATTGCACTGCAGCCTGGGTAATAGAGCGAGACAAC
TCTATCTCAAAAAAAGAATTTCACTAGAATTTATATCTTCAGTGTTCATTAGATTGTCACCAGCACT
ATCTGCCTTGTGACTGTCAGGACTAATCCTTATATCATTATCTTATGTCTTTACCTCAGTTTATGTCT
GTCACCACAAGAAACCCAGACCTCCCTAATCATACCATATGCCCTGGTCTTACCCACATACAGCTCGGTA
CAACTGCATTTCCCAACCTCAGAATCCTTGGGCCATCACTGTGAGAGACATTTGAACTAGAGCAACT
CCATCTTGAGTAGGGACTGGGTATAATGAAGCTGAGACCCACTGGGCTGCATTCCAGGAAGTTAGGCAT
TCTTAGTCACAGGATGAGATAGGAGATTGGCTCAAGATAAGGTCACAAAGACCTTGCTGATAAAACAGTC
TGTGGTAAAGAAGCCAGCCAAAACCCACCAAAACCAAGACGGGAATGAAAGTGACCTCCGGTCATCCTCA
CTGCTCATTATACGCTAGTTATAATGCATTGACATGCTAAGAGACACTCCACCAGCACCATTGACAGTTT
ACAAATCCATAACAACATCAGGAAGTTACCCTATATGGTCTAAAAAGGGGAGGAACCCCTCAGTCTGAG
AATTTCTTGAAAATTCATGAATAATCCACCCCTTGTTTAGCATATGATCAAGAAAATAATCATTAAAAAA
TAGCCAACCAGCAGCTCATGCTGCTGGTCTGCCTATGGAGTAGCCATCCTTTCTTTATTAACCTGCTTTC
ACTTTATGGACTCCCCTGAATTCTTCTGCAGGAGATCCAAGAACCCTCTCTTGGAGTCTTAACCAGGATC
CCTTTCCAGTAACTTACGAGGATCTGTGAGTGCCAGTTTCTTCTGTGGTGCAAACTAGGTGCTAAGT
ACACTTTTTCCCCCTTTCTCTATTTTTAAAAGAACTTTAGCCCTTTTGAAGTGGGTACATTGTCTGG
AGTACATAACCTGGGGTTCATTGTTATAGGAGAATTTAGGACACAGACACACGAGGAGTTTAGGAGCAGA
GGTTAATAGGTAGAAGAGAAGGGAAGAGAAACAGCTTCTCTATAGATGTCTGCACTGACACCGTGGC
TTTAAGGCATGGCCATGATGTGTCTCCGAGTGGAAAAGACTGGTTGGTGGTGAATGCGCCAAATTTTAT
AGTCCGGTTTTGAGGAGGTGGTTTTCTGATTGGTTGCATCATGTATGACGTTTGAAGGTGCATGTGAAGG
CTGGTGCACCCACCTAATCTTATGCAAATGGGCTTTCCAGTTGATTGGGTCCATCTTGTGTAACACGTG
GCTGGCAGAGAAGGGAAGATGAAGCCACCATCTTGAATAATGTCTAGTCCTTAGTTTTCTGCTGGCATTAC
CCATGCAAGCTGCCAGCTTGTCTATGTCTGCAGCTCAACTTTACAGGCTGCTCTTTGTTAGCAAATGATT
TGGAGCTTCTTTTCAATTAAGAAAAAGCCTTACCGAGGACTCCCATACCCCTTGCTTTCTGCTTAAGTGA
TTTCTTCTTAACTCCTATGTCAATTTTATACAGCATGAAATAATGATGTATCTATAAATGAGCCTTTGCA
AGATTACCATTTATCAAAGAAAACAGTGATGTTTAGTTAACTGTTTGTAAAAATAAATGGTTAGTAGAA
TGTCTAATTCATAAATGTTTCATAAATGAGTAAA

>NM_001182127.1 *Saccharomyces cerevisiae* S288C phosphatidylinositol 3-kinase VPS34 (VPS34), partial mRNA

ATGTCACTGAACAACATAACATTCTGTGTCTCACAGGATCTGGATGTTCCCTGAAAAGTGAAAAATCAAGT
CATTGGAAGGACATAAGCCACTGTTGAAGCCATCTCAAAAAATCCTGAACCCTGAATTAATGCTGATAGG
GTCAAATGTATTCCCTTCTAGTGATCTAATTGTATCCTTACAGGTATTTGATAAAGAGAGAAAACAGAAAT
TTAACTCTTCCGATATACACGCCGTATATTCCTTTTCAAGAACTCTAGAACCCTGGGATTATTGGTTGACTT
TGCCCATACGTATCAAACAGCTTACCTTTAGCAGTCATTTACGCATTATTTTGTGGGAATACAATGGATC
CAAGCAAATTCCTTTTTCAATCTAGAAACGAGCATCTTTAACTTAAAAGACTGTACTTTAAAAGAGGG
TTTGAATCCTTAAAATTTCTGTTATGATGTGATTGACCCTGTGAAGTGGTCACTGATAACAAAGATCAAG
AAAATTTGAATAAATATTTTTCAGGGTGAATTCACGAGACTCCCTTGGCTTGCAGAAATCACTATAAGCAA
ATTAAGGAAACAACGGGAAAATAGGACTTGGCCTCAGGGCACCTTTGTCTTAAACTTAGAATTTCCAATG
TTAGAGCTTCCCTGTTGTGTTTCATCGAAAGGGAAAATATGAATACTCAAATGAATATTTCCAATTTGAAGA
ACAATCCTGGACTAAGCACAGACTTACGAGAACCGAATAGGAATGATCCTCAAATCAAAATTTCTTTGGG
GGACAAATATCACTCCACATTGAAGTTTTACGATCCTGACCAACCAACAATGATCCAATAGAGGAAAAAG
TATAGGAGATTGAAAGAGCATCTAAAAATGCAAACCTGGACAAGCAAGTGAAGCCGGACATTA AAAAGA
GGGACTACTGAATAAAATCATCAACTACCCCTGGCACTAAATTAACAGCACATGAAAAGGGTTCAAT
ATGGAAATATAGGTATTATTTGATGAACAATAAAAAAGCTCTTACAAAGTTATTACAGAGTACAAATTTG
AGAGAAGAATCGAAAGAGTAGAGGTTTTAGAACTAATGGACTCATGGGCAGAAATTGATATAGACGACG
CATTAGAACTATTAGGCTCAACTTTTTAAAACCTTTTCAAGTGAATCGTACGCCGTAAATAGGCTGAAGAA
GGCATCAGACAAGGAGCTGGAATTTGACTTATTACAGTTGGTAGAAGCTGTCTGTTTTGAGAACCTGTCC
ACTTTTTCCGACAAATCTAACAGTGAATTCATATTGTGGATGCCGTATCTTCGCAAAAAGCTTTCCGGGTG
ATTCTATGTTACTATCTACATCGCATGCCAACCAAAAATTAATAAGTCCATCTCGAGTGAATCGGAAAC
TTCCGGGACAGAATCGCTACCAATCGTCATTTCTCCCTTGGCTGAGTTTTTTGATTAGGAGAGCACTGGTC
AACCAAGGTTAGGAAGTTTTTTCTATTGGTATTTAAAGTCCGAGTCTGAGGACAAGCCATATTTAGACC
AGATTTTAAGTTCCTTTTGGAGTAGACTGGATAAAAAATCTCGGAATATACTGAACGATCAAGTCAAGCT
AATAAATGTGCTCAGGGAATGTTGTGAAACAATTAAGAGGCTGAAAGATACTACAGCCAAAAGATGGAA
TTACTAGTGCAATTTATTGGAGACGAAAGTCAAGCCTCTTGTCAAAGTACGACCAATTGCTTTACCCTAG
ACCCTGATGTGTTGATATGCGACGTTTTGTCTGAAACTTCGAAGGTATTTAAAAGCTCTTTATCGCCACT
AAAAATAACATTCAAAACGACCTTAAACCAACCATATCACTTAATGTTTAAAGGTTGGCGATGATTTGAGA
CAAGATCAACTGGTAGTACAGATCATAAGTTTAAATGAATGAGTTATTA AAAAATGAAAACGTGGACTTGA

AATTGACACCATAACAAAATTTTGGCAACAGGACCACAAGAAGGTGCCATTGAATTTATCCCTAATGACAC
ATTAGCTAGCATACTAAGCAAATATCACGGTATTCTTGGCTACCTTAAACTCCACTATCCTGATGAGAAC
GCGACATTAGGCGTACAAGGCTGGGTTTTAGATAATTTTGTCAAATCTTGTGCTGGCTATTGTGTTATTA
CATACTCTTAGGTGTGCGCGATAGGCATTTAGACAACCTACTAGTCACGCCAGATGGGCACTTTTTTCA
CGCAGACTTTGGTTATATCTTGGGTCAGGACCCCAACCTTTTCCGCCATTAATGAAATTGCCCCCTCAA
ATTATAGAGGCGTTTGGGGGTGCAGAATCATCAAATTATGATAAATTTTCGAGCTACTGTTTTGTGGCAT
ATTTCGATTTTAAGAAGGAATGCAGGCTTAATCTTAAACCTGTTTGAATTAATGAAGACTTCGAACATACC
TGATATCAGAATAGATCCCAATGGTGTATATTACGTGTAAGAGAGAGATTTAATTTGAATATGTCCGAA
GAAGATGCCACAGTGCATTTTTCAGAATCTAATCAATGATAGTGTAAATGCTTTGCTGCCTATCGTGATTG
ATCATTTACATAATCTGGCACAATACTGGCGGACCTGA

S. PIK3R4 (phosphoinositide-3-kinase regulatory subunit 4)

>tr|K1R976|K1R976_CRAGI Phosphoinositide 3-kinase regulatory subunit 4
OS=*Crassostrea gigas* OX=29159 GN=CGI_10027844 PE=4 SV=1
MGNQLTGIAPSQIQPVDQYLTDIPDYQYENSLGSTRFFKVARARTKEGLAVVKVFIHDP
SLPLTSHRNKLEDIHIRLQGSTSNCLPFQKAIHSDKAALLFRQYVKDSLYDRISTRPFLN
RIEKKWLAFLQLLCALNQCHKIKVCHGDIKAENVMITSWNLLLLTDFASFKPTYLPEDNPS
DFSYYFDTSRRRCCYIAPERFVESGLKNQEGAGQTDLTSNDEVKSGDITPPMDFISAGC
VICELFTEGTPPFDFSQLLAYRNGEYSPWKVLEKIDDNYIRDLVRHMIKKDPSHRLSAEE
YMIQQRGKAFPEYFYTFLLKIYLQQFVSTPLTPPDDRINKIKRDFPRIVKSIQEQEERSED
NIGLVLIISLIISSSRKLHLCNTKLTALQLLLEASKFVTTDIILDRIIPYMLSFANDQFP
RVRAEVIHVVTQCLLDVDSIPRSDANVFPEYIFPNITHLTQDPVVMVRAAYAENIAKLAE
TALRVLEMTQRIDLEETEEEEESVDGLLYQANYDIELLTLQETIQQKVVTLSDPDNSVKR
TLENGITKLCVFFGRQKANDVLLSHMITFLNDKTDWHLRGSFFDNIVGVAAYVGVQSCS
ILKPLLDQGLSDPEEFVHVKTLGALTALTELGLIQKSMLEFLQEVVFPFLAHPGIWIRQG
AIGFISALTRMFNIADVHCKVLPALQPCPKRVLQIDKEIFLLNALQSPIPRPVFDYILR
VSQPDRLFIDILRERQYMRSISRSSHRTTYSELDEAMSQVFKKLNLSFGMDESHEDKILAMK
DYVMKLRHSRAGSVETKHELGDSPGRFCIVGAGKAITRRHAELIKQKDPKQGGADQTTSS
RSSKKVQSKEQSVNMNSEWKSMEFSGNESDSSNASLSPKARTLQKTAESLEKLNLSQTVS
QTSSSSGSFVTMSQSQVSSEGSIRSVTEKGS DKNPITKYHNCKIALRNIVHKKRELYSAE
SKDLLEIAWERRPPPSNWKPKGLLVAHLQEHRAAINRIQVSHDHAFASASNDGTVKLWE
SEKLEGNSVANRSKQTLKNTSLPGEKVKGLVFCEASGPSLSLATFTDLGAINIFKIJETGK
ASWNKDLRVDKPDYGNIVDMTYFDTGAVSVLSYATVNGFLVGHDLRTNKEVWKLKRNPKA
GLITSFVAVHHSQCWLAVGTSSGTHICWDMRFQLPINSIVHPTGARVRRIMHPQEQSWLI
SATQGNNEVSIWDVETGARQKVLWASPTPTLSLNQASHHSVYGLHMAVTDTNVFMILTGS
DMRARFWDLSYPANSFILAGAASDPVQQTGVNRYAKLVDGVEVIQELYTKKPVNTDDAPR
RGPEAPPQGHRDIIISDINLCQASQCMVITGSRDGVIKVWK

>NM_014602.3 *Homo sapiens* phosphoinositide-3-kinase regulatory subunit 4
(PIK3R4), mRNA
GAGGTCAGACCGGTTGCTTTCCCGGGAGTTCGGCGTTTGTGGGGCTGCAGCAGCTGAAGTGTAGTGT
TCTTGGGACTGGCGGTCTGCACTTCTCTCCCGGTTCCATCTCCCCCGCCGGTGGTGGAGCCCTCGAG
GAGGGCTCGGACGGGTGTAGCGATCCGCGCTAGAGGAAGACGAGGCCCGGGAACGCATGTCCCCAGGGC
AGGTTAGGGGGCTGGAGGGGTCAAATCCCGGGTACTTGTGGAGACTCTTTAGCGTGGCTTCTTCTCTCT
GCTGAGACCCCGAGAGCTTTCCAGTTCCTCCAGGACCACCGGGGTTCTGAAGATCGGGACTTTTC
TGCGCCCTCCACCAACAGCCCATCTCCTGTCTATGAAGAAAGACCCTTCGTAGAAACAACCTCCCCGCT
GCTGACGCGTTTTCCCGTCCCGTCCCGGAAGTAGTCTACTATGACCTCGTTGTGAGCCTCTGAACGATTT
TGACACTTTCCCGAGGCCTAGGGTATTATATCCTAACCTTACTAAAGACCACAGAGGTGCTTGCCATTAT
GGGAAATCAGCTTGCTGGCATTGCTCCCTCCAGATCCTTTCTGTAGAGAGTTATTTTTTTCAGATATTCAT
GACTTTGAATATGATAAAAGCCTGGGGAGTACTCGGTTTTTTAAAGTTGCTCGAGCCAAGCACCGAGAAG
GCCTGGTCTGTGGAAGGTTTTTGCAATTCAGGATCCCACATTGCCTTTAACCAGCTATAAAACAAGAGCT
GGAGGAACGAAAATCAGGCTTAATCTGCACACAGATGTGCTACCTTTCCAGAAAGCATCAGAAAAAGCA
TCTGAGAAAGCAGCTATGCTCTTTAGGCAGTATGTCGAGACAATCTCTATGATCGCATCAGTACCCGTC
CATTCTTGAATAACATTGAGAAGCGCTGGATTGCTTTCCAGATCCTGACAGCTGTGGACCAAGCACAA
ATCTGGAGTTCGTATGGGGACATCAAGACTGAGAATGTGATGGTCACCAGTTGGAATGGGTTCTTCTA
ACTGATTTTGCCAGTTTTAAGCCCACTTATCTTCCAGAAGACAACCCGGCAGATTTCAATTTTCTTTG
ACACATCACGGAGGAGAACTTGCTATATTGCTCCTGAACGTTTTGTGATGGTGGGATGTTTGCCACTGA
GTTAGAATATATGAGAGATCCTTCAACTCCGCTTGTAGACTTAAATAGCAATCAGAGAACAAGAGGAGAG
TTGAAGAGAGCAATGGACATCTTTTTCAGCAGGTTGTGTGATAGCTGAGCTTTTTTACAGAAGGTGTACCAT
TATTTGATCTCTCTCAACTTTTGGCTTATAGAAATGGACATTTTTTCCCTGAACAAGTGCTAAATAAAAT
TGAAGATCACAGTATCAGAGAATTGGTAACTCAGATGATTCACCGTGAGCCAGATAAACGTTTAGAGGCA

GAAGATTACTTAAAACAGCAGCGTGGCAATGCCTTTCTGAAATATTTTACACTTTTCTTCAGCCCTACA
TGGCCCAGTTTGCCAAGGAAACGTTTCTTTCTGCAGATGAGCGTATTCTGGTTATACGGAAGGATTTGGG
CAACATTATTACAATCTCTGTGGACATGATCTGCCAGAAAAAGCCGAAGGAGAGCCTAAGGAAAAATGGG
CTGGTTATCTTGGTATCTGTTATAACATCCTGCCTACAGACCCTTAAATACTGTGATTCCAAACTAGCTG
CTTTGGAAGTATTCTTCAATTTGGCTCCAAGATTAAGTGTGAAATCCTTTTGGATCGTATTACTCCATA
TCTTTTGCATTTTCAGCAATGACTCTGTTCTAGGGTGTAGGGCTGAAGCCTTGAGGACGTTGACCAAAGTT
CTTGCTCTCGTCAAAGAGGTTTCTCGTAATGATATCAATATTTATCCGGAATACATTCTGCCAGGCATAG
CCCACCTTAGCCCAAGATGATGCTACTATCGTTAGACTAGCCTATGCTGAAAACATAGCTCTGCTGGCAGA
AACAGCTCTGAGATTCTGGAATTAGTACAGTTAAAAAATCTTAATATGGAAAATGACCCCAATAATGAA
GAAATAGATGAGGTTACACATCCAAATGGAAAATTATGACACAGAGCTCCAAGCCTTACATGAAAATGGTCC
AGCAGAAAAGTTGTTACTTTGCTAAGTGACCCTGAAAATATTGTAAAAACAAACCTTGATGGAAAATGGAAAT
AACACGGCTGTGTGATTCTTTGGACGTCAGAAAAGCCAACGATGTTTTGTTGTCCCACATGATTACTTTC
CTAAATGATAAGAATGATTGGCATCTACGTGGAGCATTTTTTGATAGTATAGTTGGTGTGCTGCCTATG
TTGGCTGGCAAAGCTCCTCAATTTCAAGCCTCTGCTGCAACAAGGTCTTAGTGATGCTGAGGAATTTGT
CATTGTGAAAAGCTCTTTATGCCCTTACTTGTATGTGCCAGTTAGGACTGCTACAAAAACCCCATGTTTAC
GAATTTGCCAGTGATATTGCCCCCTTCTGTGTCTATCCCAATTTATGGATACGTTATGGTCCCGTGGGAT
TTATCACAGTGGTAGCTCGTCAAATAAGTACAGCTGATGTCTACTGTAAACTGATGCCTTATCTTGACCC
ATATATTACCCAACCAATAATACAGATTGAAAGAAAACCTTGTCTGCTCAGTGTTTTTAAAGGAACCAGTA
AGTCGTTCTATATTTGATTATGCTTTGAGGTCTAAAGATATTACTAGCTTGTTCAGACATCTTCACATGC
GTCAGAAGAAACGAAATGGTTCTTCCCGACTGCCCTCCGCCAGAGGATCCTGCCATAGCACAGCTTCT
GAAGAAGTTGCTCTCACAGGGAATGACAGAGGAAGAGGAAGACAAACTTCTGGCACTGAAAGACTTCATG
ATGAAATCTAATAAAGCAAAGGCCAATATAGTGGACCAGAGCCATCTTCATGATAGTAGTCAGAAAAGGTG
TAATTGACTTGGCAGCTTTAGGCATAACTGGGAGACAAGTTGATCTTGTAAAACCAAACAAGAACCAGA
TGACAAACGGGCCAGAAAACATGTAAAACAAGACTCAAATGTAAATGAAGAATGGAAAAGCATGTTTGGG
TCACTGGACCCACCAAACATGCCACAGGCCCTACCTAAAGGGAGTGATCAGGAGGTGATTGACTGGGA
AACCTCCTCGTTCGGAGTCTCTGCTGGCATTGTGTCCCTTTGTCAACTTCTTCACAGGTTCCAGAAGT
GACAACCTGTCCAAAATAAAAAACCAGTAATACCGGTTTTAAGTAGTACAATCTTACCATCCACCTATCAG
ATTCGAATTACAACCTTGTAAAACCTGAACTTCAGCAACTCATCCAGCAAAAAGCGGGGAGCAGTGCAATGCTG
AGAGAATAGCTAAGCAGATGATGGAAAATGCTGAATGGGAGAGTAAACCACCACCACCTGGATGGCGTCC
TAAAGGGCTGTTAGTTGCCCATCTTCATGAGCATAAATCTGCTGTGAATCGAATTAGAGTCTCTGATGAA
CACTCACTTTTTGCAACATGTTCAAATGATGGCACAGTGAATACTGGAACAGTCAAAAAGATGGAGGGGA
AGACCACCCTACCAGATCTATTCTTACATACAGCCGAATTTGGAGGACGAGTCAAGACGCTCACATCTG
CCAAAGGCTCCCCTACTTTAGCCATAGCATCTGATAATGGTGTGCTGTCAGCTTCTTGGAAATGAGGCTTCT
AAGCTGCCCAAGTCTCCTAAAATCCATCCTCTACAAAGCAGAATTCTAGATCAGAAGGAGGACGGTTGTG
TTGTGGATATGCATCACTTCAACTCTGGAGCACAGTCTGTTCTTGCCTATGCCACTGTGAATGGCTCTCT
GGTTGGCTGGGACCTTAGGTCTTCAAGCAATGCGTGGACTTTAAAGCATGATTTAAAGTCGGGCCTCATC
ACTTCTTTGCTGTGGACATCCACCAATGCTGGCTCTGCATTGGTACAAGCAGTGGTACCATGGCTTGT
GGGACATGAGGTTCCAGTTGCCAATTTCAAGTCACTGTCTCCTTCCAGGGCTCGAATCAGACGCTCTC
AATGCACCCTCTGTATCAGTCTGGGTGATTGCAGCTGTTGAGGCAACAACGAAGTGTCCATGTGGGAC
ATGGAGACTGGTGACAGAAGATTTACTCTCTGGGCCAGCAGTGCACCACCCTTCTGAATTACAGCCTT
CTCCTCATAGCGTCCATGGTATCTACTGTAGTCTGTCAGATGGAAATCCTATCCTACTAACAGCTGGCTC
AGATATGAAAATAAGGTTTTGGGACTTGGCTTACCCAGAAAGGTCTATGTTGTTGCAGGAAGTACTAGT
TCCCCATCTGTGCTTACTACAGGAAAATAATTGAAGGCCTGAAGTTGTCCAGGAAATTCAGAATAAGC
AGAAAGTAGGACCAAGTGATGACACCCCTCGAAGGGGCCAGAGTCCCTGCCCGTGGGACATCATGACAT
CATCACTGATGTCGCCACATTCCAGACCACACAGGGCTTCATCGTAACTGCTTCTAGAGATGGGATTTGTG
AAGGTGTGAAAATAAACCTACTGATTTGTATAAATTTAATAGTTATAAATAATAACTATAACTCGAG
AAAAGGCATTTCTAGAGAACAGATTCATTTGCTTAATTTTCAAATTTATGTCTCCATATTACTGTTTCAT
GACTGACTGACTAAATGACACCCAAAATGGTTAAGATGTACTTGACTAGTTTACTTATGCATCTCTTTC
AAGAATCAGCCAGCCAACAATGTCTGGGATTTTTATTGTATATGTTATAGAGGTGAGAAAATGAAAAAT
GAAAATGAATATGTTTTATTTTGTATTGAAAAGATGGTTGAAAAGATGGTTGTAAGCTATTATAGTATAA
ACACATTTTTGCTATTA AAAATGCTATTC AAAGCAGTTAAACTGTA

>NM_001178445.2 *Saccharomyces cerevisiae* S288C ubiquitin-binding
serine/threonine protein kinase VPS15 (VPS15), partial mRNA
ATGGGGGCACAATTACTACTAGTGGTCCAAGCATCACCTTCCATAGCCATTTTTTTCATATATCGATGTCT
TAGAGGAAGTACACTACGTTTTCACAGTTAAACTCATCAAGATTCTTAAAAACATGCAAGGCACTGGACCC
TAACGGCGAAATTGTTATCAAAGTGTTTATTAACCAAAGACCAATATAGCTTACGACCTTTTCTCCAA
CGTATAAGGGCTCAATCGTTTAAAGTTGGGACAACCTACCGCACGTTTTTAAACTACAGTAAATTTGATCGAGA
CAAATAGAGCCGGCTACATGATACGGCAGCACTTAAAAAATAATTTATATGACAGATTGAGTTTGAGACC
TTACTTACAAGACATTGAACTGAAATTCATTGCTTTCCAGTTGTTAAATGCATTAAGGACATTCATAAT
CTGAATATTGTCCATGGTGTATATAAAGACAGAAAATATCCTAGTAACAAGTTGGAATTTGGTGTATATTGA
CAGATTTTGTGCTGATTTATCAAACCCGTATATTTGCCTGAAGATAATCCAGGTGAAATTTTTATTCTACTT
CGACACCTCGAAGAGAAGAACCTGTTATCTAGCCCCGGAGAGGTTTAACTCTAAACTTTACCAAGATGGA

AAATCTAACAAATGGTAGGCTAACTAAAGAAATGGACATATTTAGTCTTGGATGTGTTATTGCAGAAATAT
TTGCTGAAGGAAGACCCATCTTCAACTTATCACAGCTATTCAAATATAAAAAGTAATTCATATGACGTA
CAGGGAATTTCTCATGGAGGAAATGAATTCTACCGATTTAAGGAACTTGGTTCTAGACATGATTCAACTA
GATCCATCCAAAAGACTTTTCATGTGATGAACTACTGAATAAATATCGTGGCATTCTTCCCGATTATT
TCTACACTTTTCAATTTATGATTATTTTCAGAAATTTGGTTACTATGACAACAAGCACACCGATATCAGATA
CACTTGCACCAATAGTACCTTGGAAAGACAATGTAAAACCTTTTAGATGAAACTACGGAAAAAATATACAGA
GATTTTTCCCAAATATGTCATTGTTTGGACTTTCCCTTAATAAAAAGACGGGGGTGAGATTGGTTCAGACC
CCCCAATTTTGGAAATCTTACAAAATAGAGATAGAAATTAGTCGGTTTTTAAACACAAACTTATATTTCCC
CCAAAATTACCATTTAGTCTTACAGCAGTTTACCAAAGTATCCGAAAAGATAAAAATCAGTTAAAGAGGAA
TGTGCCTTACTCTTTATCTCTTATTTGTCTCATAGTATAAGAAGTATTGTTTTCGACTGCTACGAAACTTA
AAAATTTAGAACTATTAGCAGTATTTGCACAATTCGTTTTCTGATGAAAATAAAAATTTGATCGAGTCGTACC
TTATTTTCGTATGTTGTTTTGAAGATAGTGACCAGGACGTCCAGGCCCTATCTTTGTTAACATTAATCCAG
GTACTCACCTCTGTAAGAAAATGAATCAATTGAACGAGAATATATTTGTGGACTACTTACTTCCGAGAC
TGAAAAGATTACTTATTTCCAATAGGCAGAATACCAATTATTTAAGGATTGTGTTTGTCAATTTGTTGAG
CGACTTGGCCATTATCATTAAATAGATTTCAAGAATTTACATTTGCTCAGCACTGCAATGATAACTCAATG
GATAACAACACGAAATCATGGAAAGCAGTACCAAGTATTCAGCAAAAATTTGATCCAAAGTGTCAAGATT
TAACTGTCTCTTTTTTAAACAGATAATGATACTTATGTAAAGATGGCACTTTTTGCAAAACATTCTTCCACT
TTGTAATTTTTTTGGTAGGGAAGAACAACGATATTATACTGAGTCATTTAATAACCTACCTTAATGAT
AAGGACCCAGCATTGCGAGTTTTCTTAATTCAAAACAATATCCGGAATATCAATTCTTTTGGGTACCCTTA
CATTAGAACAGTATATTTTACCATTGTTAATCCAGACCATCACTGATTTCGGAAGAATTAGTAGTGATCAG
TGTTTTACAAAGCTTAAAATCTTTGTTCAAGACTGGGTTGATTAGGAAAAAATATTATATTGATATATCA
AAAACAACATCTCCCTTGTGTTGCATCCTAATAATTGGATAAGACAGTTTACTTTGATGATAAATTATAG
AAATTATTAATAAGTTATCAAAGCCGAAGTGTACTGCATTCTCTATCCAATAATAAGGCCTTTCTTCGA
ATTTGACGTTGAGTTCAACTTCAAATCAATGATAAGCTGTTGCAAGCAACCAGTGTCAAGATCGGTTTAC
AATCTATTGTGTAGTTGGTCTGTTAGAGCGTCAAATCTTTATTTTTGGAAAAAATCATCACAAATCATG
TAGATTCATTCGGAATAATAGAATCGAATTTATAACAAAAAATTACTCAAGTAAAAATTTATGGATTTAA
TAAAAGAGATACGAAATCAAGTTCCCTCGCTGAAGGGTATTAAAAACATCATCCACCGTCTATTTCACATGAC
AACAAGGAAATTCCTTAACTGCTGAAGACAGAAATTTGGATTGATAAGTTCCACATTTATTTGGGCTAACAG
AAAAAGATATTTGGAAAATTTGTGGCTTTGAGGGGTTATGTAATAAGGACAGCGAGAGTTATGGCAGCGAA
CCCTGATTTTCCATATAATAATAGTAATTACCGTCCATTAGTACAGAACTCACCACCTAACCTAAACCTT
ACGAATATTATGCCAAGAAACATTTTCTTTGATGTAGAGTTTGTGTAAGAGTCGACAAGTGAGGGACAAG
ATCTAACTTAGAGAACCAACAGATATATAAATATGATGAAAGTGAGAAAGATAGCAATAAGCTAAATAT
TAACGGTAGCAACAGCTACTACCCTGATGGACATAAATGGATCACTAATATTCAAATAAATGATCCAT
GCCACTACTACTTCTAATTTGAAGAACGTTTTTGTTCAGTTAGAACCAACGTCTTATCACATGCATCTC
CAAATCATGGCTTGAAAGATAATGCAAATGTTAAACCAGAAAAGGAGGTAGTCGTCAGCAACAGCTATGA
AGGCGACGTTGAAAGCATAGAAAAATTCCTATCGACTTTCAAATTTTACCTCCTCTGAGAGATTATAAG
GAGTTTGGGCCTATTCAAGAGATTGTACGGAGTCCAAACATGGGTAATTTGAGGGGCAAGTTGATAGCTA
CTTTGATGGAAAACGAACCAATTTCTATTACGTCTTCTGCTGTTTCTCCAGGAGAAAACACCTATTTAAT
AACAGGTTTCAGATCAAGGTGTAATCAAGATTTGGAACCTGAAAGAGATTATCGTGGGCGAGGTTTACTCT
TCTTCTTTAACTTATGACTGCTCCTCTACCCTAAGTACTCAGATAACCATGATTCCCTAATTTGACGCGTTG
CCGTTTCCAGTAAAGATGGACAAATAATTGTATTAAAGGTTAATCATTACCAACAAGAAAGTGAAGTCAA
ATTTTTGAATTCGAATGCATCAGGAAAATTAACCTGAAGAATTTTGGTAAAAATGAATACCGCAGTGAGA
ATGAGAGCATTGTGAATGAGGAAAAATCTCTACTAGTAGCATTGACGAATTTGTCAAGGGTTATTATAT
TTGATATTAGAACCCTGGAGAGGTTACAAATTATAGAGAATTTCTCCAAGGCATGGTGGCGTTTCAAGCAT
CTGTATCGATGAAGAGTGTGTTGTCTTAATTTGGGGACGACTAGAGGTATTATTGATATATGGGATATC
CGTTTCAACGTGCTGATAAGGAGTTGGTCCCTTTGGGGACCACGCACCAATCACGCATGTGGAGGTTTGT
AGTTTTATGGAAAGAATTCTGTAATTGTTGTAGGAGGTAGTTCAAAAACATTTCTAACAATATGGAAATTT
TGTTAAGGGGCATTGTGAGTATGCTTTTATAAATTTCTGATGAACAGCCATCTATGGAGCACTTTTACCA
ATTGAGAAAGGCTTAGAAGAATTAATTTTTTGTGGAATCAGGCTTTTAAACGCACTAAGCACTATCTCAG
TATCTAATGATAAAATCTTCTTACCAGTGAAGCAACAAGTTCCATTGTTATGTTTACCTAAATGAGCT
TTCTTCTTCTAAAGCAGTAATAAGTCCTTCAAGATTCAGTGACGTTTTTTATTCTTACACAAGTTACGGCA
AATCTCACAATGTTATTGAGAAAAATGAAACGTAAGTACTAGCACTCATTGAGTAGATGATTCTCTATATCATC
ATGATATTATAAATTTCTATATCTACATGTGAAGTTGATGAGACACCTTTGCTGGTTGCTTGTGATAACTC
AGGGCTTATTGGAATCTTCCAATAA

T. BECN1 (beclin 1)

```
>tr|K1QHY7|K1QHY7_CRAGI Beclin-1 OS=Crassostrea gigas OX=29159  
GN=CGI_10027731 PE=4 SV=1  
MATIKVESKSGTTHVSFVCQRQRQPLKLDHSFNLTDRQLLAELSAGPFLTGFSSLLDDV  
EVDENYSKRDIITSTPEPDEDAGDFLLGETSPGNMDNLSHRIRVSSALFDVMSGQSEIDH  
PLCEECTDNLDDQLDNQLKITEDECKDYREFLENLDSNHTEEDGSNLDVELQQLOAEEQS
```

LRQQLQNLETEQEHEALLEKEREISQKLQDEEDKYWKEYNEYKRQVQELEDEQRSVDNQ
LKYAQTQLDKLKKTNVFNNTTFHIWHSGHFGTINNFRGLRPLSVPVDWNEINAAWGQTVLL
LNSLAKKMNLTFRYRLVPPGNHSYIESLSDKSKELPLYGSGGFRFFWDTKFDQAMVAFL
DCLQQFKEEVEKGDGTGFLPYKMEKGIKIEDSSTGTSYSIKIQFNSEEQWTKALKYMLTNL
KWGLAWVSSQFANK

>AF139131.1 *Homo sapiens* beclin 1 (BECN1) mRNA, complete cds
CGGGAAGTCGCTGAAGACAGAGCGATGGTAGTTCTGGAGGCCTCGCTCCGGGGCCGACCCGAGGCCACAG
TGCCTCCGCGGTAGACCGGACTTGGGTGACGGGCTCCGGGCTCCCGAGGGATGGAAGGGTCTAAGACGTC
CAACAACAGCACCATGCAGGTGAGCTTTCGTGTGCCAGCGCTGCAGCCAGCCCCTGAAACTGGACACGAGT
TTCAAGATCCTGGACCGTGTACCATCCAGGAACACAGCTCCATTACTTACCACAGCCCAGGCGAAAC
CAGGAGAGACCCAGGAGGAAGAGACTAACTCAGGAGAGGAGCCATTTATTGAAACTCCTCGCCAGGATGG
TGTCTCTCGCAGATTCATCCCCCAGCCAGGATGATGTCCACAGAAAGTGCCAACAGCTTCACTCTGATT
GGGGAGGTATCTGATGGCGGCACCATGGAGAACCTCAGCCGAAGACTGAAGGTCACTGGGGACCTTTTTG
ACATCATGTCCGGCCAGACAGATGTGGATCACCCTCTGTGAGGAATGCACAGATACTTTTAGACCA
GCTGGACACTCAGCTCAACGTCACGTAATAATGAGTGTGAGAACTACAAACGCTGTTTGGAGATCTTAGAG
CAAATGAATGAGGATGACAGTGAACAGTTACAGATGGAGCTAAAGGAGCTGGCACTAGAGGAGGAGAGGC
TGATCCAGGAGCTGGAAGACGTGGAAGAACCAGCAAGATAGTGGCAGAAAATCTCGAGAAGGTCCAGGC
TGAGGCTGAGAGACTGGATCAGGAGGAAGCTCAGTATCAGAGAGAATACAGTGAATTTAAACGACAGCAG
CTGGAGCTGGATGATGAGCTGAAGAGTGTGAAAACAGATGCGTTATGCCAGACGCAGCTGGATAAGC
TGAAGAAAACCAACGTCTTTAATGCAACCTTCCACATCTGGCACAGTGGACAGTTTGGCACAATCAATAA
CTTCAGGCTGGGTGCCTGCCAGTGTTCCTGGAATGGAATGAGATTAATGCTGCTTGGGGCCAGACT
GTGTTGCTGCTCCATGCTCTGGCCAATAAGATGGGTCTGAAATTTTCCAGAGATACCGACTTGTTCCTTACG
GAAACCATTTCATATCTGGAGTCTCTGACAGACAAATCTAAGGAGCTGCCGTTATACTGTTCTGGGGGTT
GCGGTTTTTCTGGGACAACAAGTTTGACCATGCAATGGTGGCTTTTCTGGACTGTGTGCAGCAGTTCAAA
GAAGAGGTTGAGAAAGGCGAGACACGTTTTTGTCTTCCCTACAGGATGGATGTGGAGAAAGGCAAGATTG
AAGACACAGGAGGCAGTGGCGGCTCCTATTCCATCAAAACCCAGTTTAACTCTGAGGAGCAGTGGACAAA
AGCTCTCAAGTTCATGCTGACGAATCTTAAGTGGGGTCTTGCTTGGGTGTCTCACAAATTTTATAACAAA
TGACTTTTTTCTTAGGGGGAGGTTTGCCTTAAAGGCTTTTTAATTTTGTGTTTGCAAAACATGTTTT
AAATTAATTCGGGTAATATTAACAGTACATGTTTACAATACCAAAAAAGAAAAAATCCACAAAAGCCA
CTTTATTTTAAAATATCATGTGACAGATACTTTCCAGAGCTACAACATGCCATCTATAGTTGCCAGCCCT
GGTCAGTTTTGATTTAAACCCATGGACTCCTTTCCCTTTCTTCTGAAAAAACTAATTTAAATTTG
CTTTTTCTTTTTTAACTAGGTTGAATTTGAGATTTGATGTTTCTGTTTTACTGGATTTTTATCTCTCAACT
CCTGCCTTAAACAATATGAAATAGAACTTTTGTCTTTACTGAGATGAGGATATGTTTGGAGATGCACAGT
TGGGATAATGTGGGAAAATGACATCTAAGCTTTTACCTGGTACCATGTGATGTGATCAGATGCTTGAAAT
TTAACACTTTTCACTTGGTTCTTATACTGAATGCCGACTCTGCTCTGTGTTAGAGATATGAAATGGTGT
TGATACTGTTTGGAGACATTATGGAGAGATTTAATTTTGTAAATAAAAAGATTTGCTGCAGTCTGAAAA

>NM_001183934.1 *Saccharomyces cerevisiae* S288C beclin 1 (VPS30), partial
mRNA
ATGAAGTGCCAAACATGTCACCTTACCCCTGCAACTAGACCCATCTTTAGAAGGTCTTAGTTTAAACCCAAA
GAAATTTGCTACTTTCAAATAATTTCAATTATCACTGCAACGAATGAAAATGTCATCAGCAACAAGGGCAT
CGAAGCCGCAGATAATTGTGGGCTCAAATACCGAAGGAGAGGCTGAGGCGATTAGGGGAGATTCAGAAC
ATAAAAGACTTGAATTTAAAAGATGATAAATTAATCACTGATTCGTTTGTGTTTTCTTAATCACGATGATG
ATGATAATGCTAATATTACGAGTAATAGCAGAGAGGACCAGCGTTATGGAAATGCCAACGGAAATGATAA
TAAAAAGCTAATAGTGATACTTCCGATGGAACCAGTACCTTTCCGAGATCATGACGAAGAGGAAACAAGAA
GCTACGGATGAGGACGAAAACCAACAATAACAATTGAATTTCAAGACTTTGTCCACACAAGTCAACGCAA
TGACTAATGTATTTAACATTCTATCTTCTCAAACAACATAGACTTTTCTATCTGTCAGGACTGCTGTAA
CATCTTGATAACAGACTAAAAAGTGAGTATGATGATGCAATAAAAAGAGAGAGATACTTACGCTCAATTT
TTATCGAAGTTAGAGAGTAAAAACAAGAAATATCAGAAAGCAATAAAGAAAAGCAGTATTCCTCAATC
TTTTCGAAAAAGAAAATTTGAAAAAGGAAGAGGAAAAGACTCTTGGATCAATTATTACGTTTGGAAATGAC
AGATGATGACTTAGATGGAGAAGTTCGTTTACAAGAAAAGAAAAGTTCAACTGGAAAATGAGAAAATC
CAAAAAGTGAAGTATCAGAAATTTAATGGATTTAAATAACATTTCAATTTCAACAAAAATTTACAGTCAATTA
AACTGCAATACGAATTATCCTTGAATCAATTAGATAAGTTGAGGAAAATCAATATTTTCAATGCTACAT
CAAAATCTCACATAGCGGCCCTTTGCCACTATAAATGGATTGAGATTAGGCAGTATACCAGAATCAGTG
GTACCTTGAAGGAAAATCAATGCAGCACTGGGCCAATTGATTCTTTTACTGGCTACCATAAACAAAAACC
TGAAGATAAATTTAGTAGACTACGAATTACAACCGATGGGTTCAATTTCCAAAATCAAGAAAAGAAATGGT
TAACAGTGTGCAATATAATAATTTCCACTACGAACGCTCCCGGTGATTGGTTGATTCTGCCTGTCTACTAT
GATGAGAATTTCAATTTGGGGAGAATCTTCCGCAAGGAAACGAAGTTTGATAAATCATTAGAAAACAACAT
TAGAAATAATAAGCGAAATCACTCGGCAGCTTTCTACGATAGCGTCATCATATTCATCTCAAACACTCAC
AACAAAGCAAGATGAATCTTCAATGAATAACGCAATGACGTTGAAAATAGTACTTCCATTCTCGAGCTA
CCCTATATCATGAATAAGGACAAGATTAATGGATTATCCGTCAAATTCGATGGTAGCAGTCCCAACCTTG
AATGGACAACGGCTATGAAATTTTTATTAAACCAATGTAAAGTGGTTGTTAGCGTTTTCTTCCAATTTACT

ATCCAAGTCAATTACCTTAAGCCCTACAGTGAATTACAATGATAAGACCATCAGCGGAAACTAA

U. ATG14 (autophagy related 14)

>XM_011452143.2 PREDICTED: *Crassostrea gigas* beclin 1-associated autophagy-related key regulator (LOC105344371), mRNA

CTTTTAGAAAACCAATTACGTCATTTCCATTTTTATTATAATGGCGACCTCCAGTTCTTGTGAAAGCAAC
TTAGCTCCAACAGAATTTAACTTGACCAGTTCGATAGAAAGTTCCCCTGGTCTCACTGTCGCCATAGAAC
GATGCCCTTATGCGATGGAAGTAGGCGGTCATTTTCATTGCAGAAAATGTGTCAACGAAGGACTCTTTGT
TCACACGAAAGGAAGCCATCCTGAAAGATACAAAGAAAAGAGATTCAAGCTTGATCATTTCAGAAAAGAA
AGACAAGGAAGGTTGGAGAGGGTACAAGATGCACTGAAACAGCACATGCAAAGAGACAAAACAAATCGGGG
AAATTGAAAATGCAGAGAGAGGATAAACCTGTTAAAAATGGCTCTCACAGCAGCAAAAAGAAAAGAGAG
GAAAAGTAAAGAAATTTTCGACAAGAAAAGAGAGAAAACCTATCTACGGGTGTGTGAAAGGTCGAAAACAT
GAAGAAAAGAAAAGCGCATTATTTCTACATTGAAACAGTGAGAATGTCAAATGAAGAGAAAAAGAGC
TTTGTTTACAGAAAAGAGGCAACTAGCTGCAGAGAGGAAGATACAGGTCCAGAGATTGGTGGAGTTTAT
CTTTCAGGTGGAGGAAGTGGCTCTTATTAGTGAGTCAGACTCGATGGCTGTGAGCACAGTGAGTGCCCTG
CGAGATGCGAGTCACACGGCCTATGTGAGAGGGCAGTGGGTGTACACTGATGGTAGTGGCGAGGCCAGT
ACAGGATCGTGGAGCCCACCTTACCCTGCAGTGGGGACTACTCAGCCTATAATCTGTGGGTGGCTGCTAG
TCAGGAAATGATGGTAAACCCAGACAACAGTTTAAGGAACCCAGGTCACAGAATCAGTGCGGGTTTGTGC
TACGCTAGTCAGTGCAGCCATCCTCAGTCATATATGACATCCGCTGCCAAAGAAAACAGCCTTATA
GCGAGTTTTGTACTAATGAGATCACAGAGCGGCAGTTCAAGCACAGTGTGGCCTCTCTCAACAGAACAT
CCTGTATCTGTGCTTCTCCAGAGTGTGCCAATCCCGAGCGGCTTGACCCCGCAACACCTCCAGAAC
ATCGTGGTGTACTCTCCTGTCTTTATTGGGAAGGAACTCCAACCTTTGAAATTGACAAAAGACCTGATGG
CATCCATTGAAGACTCTATCATATTTCAAGAGGAAGATTCCGGATACTGGAGGAATGGAGGATGAAATGAT
CAATGATTGGGAACAGGTGTGAGAGGATGTGACCTATGTGACAGACGTTCCAGCCCCGATCTGGATATAGC
AGCACTCTATCCAACATCCAGACAATGTCGTATCCAGGTGAGCCTCCGGAACAACACTGACTGCCAGTGGTT
TTGTTACATCTGCAGCCACATCTTTCATGTCAATTATTCAGGGGAGGAGATCACAAAAGCTGACATCAGAG
AATTCTCGAGAAAGATATTAGGAAACGCATTTAAAATAAATCAGTATTTTTATCCATCCCAATCACACAT
GTAAAGAGATAGTACCATAGTGAATTTTTTTTTTTTTTCAAAGTGAATTTTTTTCATGCCAACCAAT
ATTTTTGAACGATGTTTTGACTTCTAAGATCAGCAATTTGGATGCATATTGTTTTTGATTGCTTGAAT
AAACCTTAATGAATTCAACTTAAGTCTTCTACCAATATTTTTGAAGAAAAAACATAACCCTAAAATAT
TCTTGAAGGGTGGCCTGTTATCCCATGGTCATAAGTAGTTGACTGTTACATTTCAAGGTTATTCATGGAG
TTCAAGGTCAAATTTATCAGAGTTAAATGTATTATGATACAGTTTGAACCTGATTTATTTGATGGGATTT
TAAAAGTTCTCTATCATGCTACAAATCCATTTATTGTTAATAACTCCAATTCTAAAGATAACTCAGAAAA
CCATAGCTGTATTAGATAGTGCCTCAATATGCCTTGTGCAATCATTCTTATGATTAAGGCACTGTGAT
ATGAGCTTTAGTGCATTTGTTTATAGCATTGCATGGTGTGATAGCTTCTACTGCAGAGATTAGATAATGCC
ATTTTTTTGGTAAAATTTAAATTTTATACATGTATTATTTGTTATTTTTTTTGGTGAATAATAGAAAT
TTAAATTTTTTTTTTAAATTTGCTTACCTCAAATCACAAAATCATGAATTTTTTTAATGATGCTAAGAAA
ATACCAAATGCATGTCTATTTTTGGTCTCCAGCTGTTCTCAGGGTTGTTTATTTGTTAATGAATGTA
TGTTAACGATTGTATGTTGATATTACTTTTTTTTTCACTAAATTTGGCAAGGCATCCTCCTTGAAATGTTT
AAGAAAAATGTAACATGTTATTGGATGCAATTTTAATATTGGATTTTTTTTTTACTAAAAGAGATAAAGA
ATCATTCTTTGAGTATTATGAAGTGATCAAGAAAGAATAAATGAAGAATGAAATGATAATATTATAAGAC
AGAAATGTATATAAAATTTTGTATTAGTTAATGTTTTTCAAGTCTCCTGAAAACCTGTTAATCATCTCA
TATTGCCCTATATCTTTTCGATAAAATTTGTGCTAAAATTTATGTTTCTGAAACGTTTTTGGTACAACCTT
GATATGTGGTTCATTTTTTGCATTAGTTAATGGTTGCTGCTTTTTTATTGCTATTAGGTACAGTTGG
TTTTAGTGTTCGAAAATCTATTCTGACTTTTTCAATGAGCTTTACCTTGCCATTTCCAAGACAATATGC
AATATTTTTAGCAGATTCCTGTATGGTTACTTTTACCTGTAGTTTTGTTTTATTTTTTCCATTGATAA
ATATATTTATTTACTATATCAGTTTTATATATTTTTTTTTGATTTTCTGTGTCCATTAATAGTCGAAAGGA
AGATATATTTTTAATTATCATGACATACAAGTTTTGCGGTTATAGAACTCGAGACGTATTTAAAAATATTT
TTCTCTACAAAGAACAACCTTTAGCTTAAAAAGAGCTGTTAATTTTTAAAAATATAAAATTTAAAAATTAG
CTTAAGAAAAGGATGAACAAGTTAATCAATAAAATCCAGTGAAGTATTAACATTTGTTTTATGGTGTCTGA
CTTCACTTTTTTGGATTTGATTATTCATGAATTTTTTGCAGCTGATTGAAAAACTCAGCTAGTGTATAT
TAGCCACGGAATGCATGAACCTGATGTGAGAAATCCATGTTTTTTTTACTTCTATATAACAATTAATGTT
AATTATTTTTAAAATCAGCTACCAAATGTTTCGTTTGTAGTAAATGCATTTAGGCTATATGAAA
AAAATTTGAGAAGACGTTTTTATGAAATTTTACCCTTTGAGGACCATTCCATGAAACTAAAATATTTATTA
TTCGAATTTTTTTAAAGCAGCAGTAGGCTTATGTTTTGAATAAGATACCTTTTCTAACGGTTCAAATTTCA
AGAGTTTTTACATTGTATGAACGTCATTGTGATGTCTACAATTCAGACCAATAAAGAAGGAACGGAT

>sp|Q6ZNE5|BAKOR_HUMAN Beclin 1-associated autophagy-related key regulator
OS=*Homo sapiens* OX=9606 GN=ATG14 PE=1 SV=1
MASPSGK GARALEAPGCGPRPLARDLVDSVDDAEGLYVAVERCPLCNTTRRRLTCAKCVQ
SGDFVYFDGRDRERFIDKKERLSRLKSKQEEFQKEVLKAMEGKWITDQLRWKIMSCKMRI

EQLKQTICKGNEEMKNSSEGLLKTKEKNQKLYSRAQRHQEKKEKIQRHNRKLGDLVEKKT
IDLRSHYERLANLRSHILELTSVIFPIEEVKTGVRDPADVSSSESDSMTSSTVSKLAE
RRTTYLSGRWVCDHNGDTSISITGPWISLPNNGDYSAYYSWVEEKKTQGPDMEQSNPA
YTISAALCYATQLVNILSHILDVNLPKKLCNSEFCGENLSKQKFTRAVKKNANILYLCF
SQHVNLQDQPLHLTLRNLMLVSPSSEHLGRSGPFVEVRADLEESMEFVDPGVAGESDESG
DERVSDEETDLGTDWENLPSPRFCDIPSQSVEVSQSQSTQASPPIASSSAGGMISAAAAS
VTSWFKAYTGHR

>sp|P38270|ATG14_YEAST Autophagy-related protein 14 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG14 PE=1 SV=1
MHCPICHHRAHVYCAHCINTSPSLLLKLLKLDLILLKDKENKELNGKVEQILNEAMNYDQL
DIKRMEKKKDPMLNSMLKLDVLRMKNNNLIRHRIEQLNERIYSKRNIHSELKVEIDNYK
CYKVGTTGDKLREQVEISDAKNLAQVSKICESARDYKLNLLNNWFVIOKLQDNFQIPFA
IAFQPLISLKNFRILPLAITNDSINIMWKYISFFSDILMIKLPYTNKICEQPMFEFSDSI
QTVVQRLIKLIINILQICRHLKLVSTPMDIPWLLDQYDQVDFYFNMVVRNKMKCRSVSL
YWTFGMLYSMVLDMNNPQRGHPARRTAPPPTVTGPHDRWYVVG

V. AMBRA1 (autophagy and beclin 1 regulator 1)

>tr|K1QU33|K1QU33_CRAGI Activating molecule in BECN1-regulated autophagy protein 1 OS=*Crassostrea gigas* OX=29159 GN=CGI_10018685 PE=4 SV=1
MTKFNLLSYLSNRERGRVKFKLQKSATLEYLEEKGSKPIINQPCELSGKCRATFLMDFSP
DGTKVASTHGHTVRVSDVATGKCLHILRGHPRTWPCIAFHPTSNQILASGCLGGEVRIW
DLHGFGTEVWRSKDNYEITSLTFHPTDHVLFVSVTNHIYFWDWSQPEPFVCKTNYEYEK
IRWVKFDFPLGQFLYTGIANNTTVRPPSRVSFISGNTHPNTVFNASRTQQLSNVYDSLVEC
FQASRRDRVLRNTEAGQDPQSVSNTQHGASNHQHSVPVHEEGLSLARQYASHITQSSQRSM
QGMSQRPEIPSGASNSSSPDMDGISSPANPVLAMQPPRGASADNDVSGESPPSIVSV
DGESSQTRAVSNHPRSERVPGTLIVTERSPEQTSPPFQSLDTSSGVRIVSEAQSVRGILN
DQVHASTTAFIAIEPEEPAEEVVISLSELTSRGLSEEHLHSSNTDCDRLNCPVCGNFDT
THIRRVCESEMFTQLRARRRSLQNSMNNVSARSASFSPYTYNRHGSLVRPEIHSIQDPSQ
LGEMHEIRRVENPNAGASNMDHVSSNNSAPSNTTEGDARLTQVGDNDICASIENFATIT
ARIEREMNELDRRINLRNFTFNESLRRLQHHRVSFLSAREGDVNGRRPSFIVARHTQQAE
GASSSRPEDSTHSLDRGQHLLLETALRSSRPDRTGSHSHSVPRELDSSHAWQSLERHHLHP
HYSVSILDNTINRPNDPIQTAINRAIADAFMGRGEPVATNIINHTYRIQAWDFSRCNIP
DLTDTKSNIVVQHCKLHNDASCNLSQDGTMLATFVPSHRGFPDDNIMAVYSLEPKTRGQC
LFTKSFQPNASVSLSPGSGYVMVGLAAKQLSWVFTPNQHITDVMHPCDMDIRTHVSVNS
ARWMPGSGEGIVYGTNRGDLHVCPRPGTKKSVAGDNSDDRSIRRNLMHMLRMSGEQDVPRI
NTSTQTPGVRRSASTQTDTDSDM

>DQ870924.1 *Homo sapiens* activating molecule in beclin-1-regulated autophagy (AMBRA1) mRNA, complete cds
ATGAAGGTTGTCCCAGAAAAGAATGCTGTCCGGATACTCTGGGGCGAGAACGGGGTGCTCGGGCCATGG
GAGCTCAGCGGCTTCTGCAGGAGCTGGTAGAAGATAAAAACCGGTGGATGAAATGGGAGGGCAAGAGAGT
AGAAGTCCCGGATAGTCCACGCTCTACCTTCTATTGGCCTTCAGCCCAGACAGGACTCTCTTAGCCTCC
ACCCATGTGAACCATAATATCTATATTACGGAGGTGAAGACTGGCAAGTGTGTTTCAATCCCTGATTGGAC
ACCGCCGACTCCATGGTGTGTCACTTTTCATCCCACCATCTCAGGCCTTATTGCTTCTGGCTGCC TAGA
TGGGGAGGTTAGGATTTGGGATTTACACGGTGGCAGTGAAAGCTGGTTCACAGATAGCAACAATGCCATT
GCCTCCCTGGCTTTCCACCCTACGGCTCAGCTCCTGCTGATTGCCACTGCCAATGAGATCCACTTCTGGG
ACTGGAGTCGACGGGAACCTTTGCTGTGGTGAAGACAGCTAGTGAGATGGAACGGGTCCGCTCTGGTGAG
ATTTGATCCACTTGACACTACTTACTCACAGCAATTGTTAACCCCTCTAATCAACAGGGTGATGACGAA
CCAGAGATCCCATAGATGGAACAGAATTATCCCCTACCGTCAGCGTGCCCTCCTGCAATCACAGCCAG
TTCGCCGGACGCCTCTCCTCCACAATTTCTGCACATGCTGTCTCCCGCTCTTCTGGCATCCAGGTGGG
AGAGCAAGACACAGTGAAGATTCTGTACCCCTCACCCCAACCGCTCCCTCAGCCCTCCACGGAG
CGCCCAAGGACTCCGCTTACATCAGGCTCCGACAGCGGGTCAAGTTACCCACAGCTGAGTGTGCCAGC
ACCTTGGGACTCCTGTGCCTTTGCAGCCGCTGCTCTGGCCTCAGAGTTCCTTCCCTTCTGCCACACAGGA
CAGTGTCCCCCTGCTTCTGCCAGAGCTACTACCCCTTCTTTTCTTTTGTACAGACCGAGCCCTCCAT
CCCCCGGAGCAGGCCTCGTCAACGCAGCAGGACCAGGGCCTCCTGAACCGCCGCTCTGCCCTTCACTACAG
TCCAGAGCAGCACTGCCGGCAACACGCTCCGCAACCTCAGTCTGGGTCTACCCGCGCTCTTTGGGAGG
GCCTCTGTCTAGCCACCCTTCTAGGTATCACCGAGAAATAGCTCCTGGGTGACAGGATCTGAGTGGACC
CGGACAGTACTCAGTCTGAACTCCCGCTCTGAGGCGGAATCCATGCCCCCGCCAGAACCAGTGCCTCTT
CGGTGAGTTTGTCTGTCTGTGCTGAGACAGCAGGAAGGTGGCTCTCAGGCATCTGTGTACTTACAGCCAC
AGAAGGGAGGGGTTTTCCGGCATCAGGGTTGGCAACTGAGTCAGATGGAGGGAATGGCTCCAGCCAAAAC

AACTCGGGCAGCATTGCCATGAGCTTCAGTGTGACCTGAGACGCTTCTTTCTGGAGTATGACCGGCTTC
AGGAGCTGGATCAGAGCCTGAGTGGGGAAGCTCCCCAGACCCAAACAGGCCCCAGGAAAATGCTCAACAATAA
CATTGAATCTGAGAGGCCAGGCCCTTCCCACCAGCCCACCCACACAGCAGTGAACAACACTCCAACCTG
TCCCGTGGCCACCTGAATCGCTGTCGTGCTTGCCACAATCTCCTGACCTTCAACAACGATAACCTGCGCT
GGGAAAGAACCACACCTAACTACTCCTCTGGCGAGGCTAGTTCTCTTGGCAGGTCCCAGCTCCTTTGA
GAGTGTGCCATCAAGTGGCAGCCAGTTGCCACCTCTCGAGCGGACTGAGGGCCAAACGCCAGCTCCAGC
AGGCTGGAGTTGAGCAGCTCTGCTAGTCCGCAGGAGGAGAGGACTGTGGGGGTGGCCTTTAACCAGGAGA
CAGGCCACTGGGAAAGAATTTACACCCAGTCCAGCAGATCTGGAACCTGTGTCACAGGAGGCCCTTACATCA
GGATATGCCTGAGGAGAGCTCTGAGGAGGATTCACTCAGGAGATTATCTCCTGCTGCATACTACGCCCAG
AGGATGATCCAGTATCTCTCACGGAGAGACAGTATTCGCCAGCGCTCCATGCGCTACCAACAGAACCGTC
TCCGTTCTTCCACCTCCTCCTCTTCTCAGACAACCAGGGTCCATCAGTAGAGGGAAACCGACTTGGAAAT
TGAGGACTTTGAGGACAATGGTGACAGATCCAGGCACCGAGCTCCACGCAATGCCCGGATGTCTGCACCT
TCGCTTGGACGCTTTGTCCCAAGGCGTTTCTTGTGCTGAGTACTTGCCTTATGCTGGGATTTTTCATG
AACGTGGACAGCCTGGCTTGGCTACTCACTCTTCTGTTAACAGGGTCTTGGCAGGGGCAGTGATCGGTGA
TGGACAGTCTGCTGTGGCCAGTAACATTGCCAATACTACCTACCGGCTCCAGTGGTGGGACTTCACTAAG
TTTGACCTCCCTGAAATCAGTAATGCTTCCGTGAATGTGCTGGTGCAGAAGTCAAGATCTACAATGATG
CCAGCTGTGACATTTCTGCAGATGGCCAGCTCCTGGCAGCTTTCATCCCCAGCAGCCAGAGGGGCTTTCC
TGATGAAGGCATCCTGGCAGTGTACTCCCTGGCCCCCATAACCTGGGCGAAAATGCTCTACACCAAGCGA
TTTGGTCCCAATGCCATTTTCGGTGAGCCTGTCCCCAATGGGCAGATATGTAATGGTGGGCTTGGCCTCAC
GAAGGATCCTGCTGCACCCCTCCACAGAGCACATGGTGGCCAGGTCTTTCAGGCTGCAACAGGCCCATGG
TGGAGAGACCTCCATGAGGAGAGTTTTCAACGTCCTTTATCCCATGCCTGCCGACCAGCGGAGACATGTC
AGTATCAACTCTGCCCCGTTGGCTGCCTGAGCCAGGGCTTGGCTTGGCCTATGGTACTAACAAAGGAGACC
TGGTGATCTGCCGACCAGAGGCCTTAAACTCTGGTGTGAGTACTACTGGGACCAGCTGAACGAGACGGT
CTTCACTGTCCATTCCAACAGCAGGAGCAGCGAGCGGCCTGGAACCAGCAGAGCCACATGGAGGACAGAC
AGAGACATGGGGCTGATGAATGCCATTGGGCTTCCAGCCCCGGAACCTGCCACCTCAGTGACATCTCAGG
GCACCCAGACTCTGGCCCTTTCAGCTGCAGAATGCCGAAACACAGACTGAGAGGGAGGTGCCGGAGCCAGG
GACAGCCGCTCAGGTCTGGTGAAGGTGAGGGTTTCAGAGTATGGTGCCAGTGGAGAAGATGCGCTCAGC
AGGATCCAGAGGCTGATGGCGGAGGGCGGCATGACAGCCGTGGTGCAGCGGGAGCAGAGCACCACCATGG
CCTCCATGGGCGGCTTCGGCAACAACATCATCGTCAGCCACCGCATTACCCGAGCTCTCAGACGGGCAC
TGAACCTGGTGGCGCCACACCTCCTCACCCAGCCCTCCACCTCTCGGGGACTGCTCCCAGAGGCCGGG
CAACTGGCAGAGCGAGGCCTAAGCCCCGGACAGCTTCTGGGACCAGCCTGGTACCCCTGGGCGGGAGC
CAACCCAGCCAACCTGCCCTCTTCTCCTCCCTGTCCCCATTCTGTTTCCCTTCCCAGCGCTGAGGGACC
AACCTCCACTGCGAGTTGACCAATAACAACACCTTCTGGATGGTGGCAGCAGCAGGGGGGACGCTGCA
GGCCCTAGGGGAGAACCACGGAACAGGTAG

W. UVRAG (UV radiation resistance-associated)

>XM_020069853.1 PREDICTED: *Crassostrea gigas* UV radiation resistance
associated protein (LOC105334521), mRNA
ATGGGATCTCTCTGTGAGAATTATGTTCTTGTGTTATCATGCAGCTGGTCTCTGCTGGTACGAGTCTGGG
TAAAGAACAAGACAAGTACCCGCCTCCTCTTGGACTGGATGGTGGACCTAAACGCCCTGGAATATCTCGC
AGACAAGCTCCAGCAGGATAAAGGCATTAAGTATGCTCCAAACACTCTCATCTTTGGAATGTTTGTATCAA
TTCTTTCAGAGCCCCTGAAGTGAAGCCTGTGGGAGTGGGTGTTGGAGACCAGGAGTTGAGGCAGAAGATG
ATAAATCCAGTAAGTACAACTCTGTGAGCACACAGTGTCTCCTCAAGGTGGAAATAGCCAGCACCAAGAA
GTCTTACACAGCCAGTTCTTTGTCCAGAATATACACCGTCTTAAGAGCAATCAAGCAAACCTCAAGCCTCG
GTACATAAAGTTGCAAGGTCAATTGAGGACAAATTATTGTCTCACAAGAGACAACAAGGAAAAGGGCAG
AGCATGAGGACCTGCTCCTCAAGAGGGAACAACCTGTGTGCAGAAGTGACGTGGAGGACAGCCTCCGTCAA
CAAGATGAAGGACCAGGCAGATCAACTCCACAGGTCCAACCAAGAACAAGAAAACAGCAATGAAAAAGAAAT
AAAGAGAAATTGGAAGAGAAACAGAGAGAACAGGCAGAAAAGAAGGATATGACCAAAACAAGAGAAA
AGCTAATTAAGAGAGTGTCAACTTTTTCATCAGAAGGAAACAGCTGATCCGTGAATTAGCCACCTACAT
TTATCCAATTAAGAGAGTGTCAACTTTTTCATCAGAAGGAAACAGCTGATCCGTGAATTAGCCACCTACAT
CAAGGCAAGGATGACAACATGATAGGAGTTTCCCTGGGCTACACCTGTCATCTGTTGTTGATGATTTCTG
GTATTCTGGACATTCCACTCCGGTACAGCATGACTCATCTAGTGTCCAAATCAGTCATCCGTGACGACAT
CCACAGCAGACTGGAGGACAAAGAAAGGGACTTCCCTTATATTTCCAAGGGCAAGGAACAAAATTTATTC
CGATATGGAGTGTTCACCCTGAACAAAATATCAGTCAAGTATGCGGTTTTTATTTGGGGATGGGAACGGTGG
ACCTGAGAACCCTCTGATGAATATAAAGACGTTGCTGGAGAATAGACTAGGCTTGAAACCAGAGAGTCA
GACTGCACAACCTTCGTCCAGCGAGTGAACCGGGTGCAGACAATACAGTGACTTTGACAGAACAGACACG
CGAAGTTCCCTGGCGTCTATGGTAGGATGGCAGTGGACTTCCGGAGGGAACCTTCTGTGCCGCCACGG
AAGAATCTTCTAGACAATCCTCGCCAAATCTTACAGAGGTGGAGGAAAAGGAGATTTTCCATCCAAGCAG
TGATGACAATTTCTTCAAATTTCAAACCCTGTGTGCGAGAGATTGGCAGATTTTGGAGTGAATCAAT
GGATGTGCACAGGACACAGTGAATTTTTCATAAGCCTTCGGACAATCGCCGGCAGACTTGTGGAACGGTG
TAGGAAGCAATGACTTTAATGCTGGTGTGATCAGCCTGAGGAGGACCATATATATGAAACTGTTAATGTCAG

AAAAGTGCCAAATAAACTCAGAGAGAAGATTTCATCTGAACCAGCAAGTAAAGATATACCAGGGGAGACA
 ACTTTCAGGCAGCCTGTACATGGTCAGTCCCTCATCAACTACCTGTCTTCTCAGGATTTTAAACCTGTG
 CCAATCTAGACAAGGAGAATGCACATTTTCAGCATATCTGAGGCATTGATAGCAGCCATAGAACAAATGAA
 GTGGAACCACGTATAAGTCCGAAGGACCGTGAGGATCCTGAGGAGGAAGACTCGGACGAGGAAATCAAC
 AACTGAAGCAGCGAATCCGCATCCGCAAACAGCAGAACTAAGGGAGAAAGCCAAATTTTCCCTACAT
 CCAGTGATGGACTTACTGAAACGGCTACAACCTAGCAAGAGTCCCTCTTCAGTGTTAAATTTCTTCTGTCA
 AGATAACACAGATAGCAGTAATTCAGACATTGAGGTGGATGAAATCAATCTAACAAATGCAGATTTACAG
 AAAGTGAAGCCAGATAGACAAAGCTCTATGGAGATATCTGACCAATCTGGCATGTCAGCAGAGTCGGTAG
 CCATTTTGTGTTAAAGAAATTTCTCGGAAAAGCAGCTTCCAAAGGCATCCGAGCTGGAGTGGCTGGTACC
 TATATCTGAGGCTCCACAGGAGTTACTTCCCTTACCAAAGTCATATCCAGTATCTCCAGATGATATTGAA
 AATGAGATTGGAGGATTCACAACTCGCTGTTTGGGACATTGAGATTGAGAGGGAAACAATGAATGGGCTC
 CTCCCAGATCACAGATCATCTTTGACATCCATCCATATCAAAGAGAGCTGTTGTTATGGCAAAGCAAAA
 TTTCCGGTGTGCTGGATGTGGAACCCGAGTTGAACAGCCTATATTTAAAGATTCCGATACTGTGAATAT
 CTAGGGAATACTTTTGTGAGTGTGTCATAGAAACGAAATCAACTACATTCGGGGCATATAATCAGGA
 AGTGGGATTTTAAACAGTATCCAGTGTCCAATTTCTCTTGAGATTACTTTCAAGGATTTTAAATGAACC
 TTATTTTAACTAAGTACAATTAATCCATCACTGTTCAAACGAGTGAAGTTGTTGGAGACAGTCCATGCT
 TTTAGAGTGCAGCTCATGTATCTGTGTAATTTCTCAGGATTTGTAATATTCAGAAAGGTGAGTTGAAA
 CCATTGGTTTTACTTTTTCATGTCTCTAATGCCTTTTCATCATCTTTAATAACAAATGCATAGCTGGTGCTT
 TCATCTAAATACATGTATGTAGATGATAAAAAATCTTCCCTATTGGCCTACTATAAAAAATTAACAAGACCA
 CTTTAGCCTCTTGAACCTGACTTAGATTTCATATAGACATAAGTGATAATTTGTATTTCCACATGCAGTTC
 ACATCCCTAAATATGCTACATGTAAAGCATTATTTACATGTAAGTTAGGAAAATAGAAAATAGACATGAT
 AAGGGTATAGTTTTGTTATGCATGATGAAGATGGAGAGTGCATATGGAAAAATAATTTAGATGAGGTAT
 GGGGAAAATTATTGTTTGCATATATTAACATGTGATTAATGCTGAAGCTCTTACTTTTAAATCAGAT
 TGGACTTAAAAATTGCTTGTGAATTTTTCTTGCATCTGTTTGTGTTTAAAGATGGAAAGATTGCCATATA
 TCTTTTCTTCAGAAAGATAGATCTATGAGTCTTATTATATTTTAAATAATATATTGTTTGTGCTGATTTAG
 CACAAGTACATATCGTGAATTTGTACTCTGAAAACTGCATGTTTATTGGTCACAACCTTTATAAGGTATG
 ATACTGAAATATACAAATGATTATATAAATAGGGGTAACAATTGAATTGACAACCTGTGAAAACCATTTG
 TCAACTGATGCGATGAAGAGGGGTGTCAATTTCAACT

>sp|Q92622|RUBIC_HUMAN Run domain Beclin-1-interacting and cysteine-rich
 domain-containing protein OS=*Homo sapiens* OX=9606 GN=RUBCN PE=1 SV=4
 MRPEGAGMELGGGEERLPEESRREHWQLLGNLKTVEGLVSTNSPNVWSKYGGLERLCRD
 QSILYHGLIRDQACRRQTDYWFVKDIRWLSPHSALHVEKFISVHENDQSSADGASERA
 VAELWLQHSLLQYHCLSAQLRPLLGDQRQYIRKFYTDAAFLLSDAHVTAMLQCLEAVEQNNP
 RLLAQIDASMFARKHESPLLVTKSQSLTALPSSTYTPPNSYAQHSYFGSFSLSLHQSVPN
 GSERRSTSFPLSGPPRKPQESRGHVSPAEDQTIQAPPVSVSALARDSPLTPNEMSSSTLT
 SPIEASWVSSQNDSPGDASEGPEYLAIGNLDPRGRTASCQSHSSNAESSSSNLFSSSSSQ
 KPDSAASSLGDQEGGGESQLSSVLRSSFSSEGQTLTVTSGAKKSHIRSHSDTSIASRGAP
 ESCNDKAKLRGPLPYSQGSSEVSTPSSLYMEYEGGRYLCSEGMFRFPSEGQSLISYLSE
 QDFGSCADLEKENAHFSISESLIAAIELMKNMMSQCLEEEEEVEEEDSDREIQELKQKIR
 LRRQQIRTKNLLPMYQEAHGSFRVTSSSSQFSSRDSAQLSDSGSADEVDEFEIQDADIR
 RNTASSSKSFVSSQFSHCFHSTSAEAVAMGLLKQFEGMQLPAASELEWLVPEHDAPOK
 LLPIPDSPISPDGQHADIKLRIRVRGNLEWAPRPQIFNVHPAPTRKIAVAKQNYR
 CAGCGIRTDPDYIKRLRYCEYLKGYFCQCHENAQMAIPSRVLRKWDFSKYYVSNFSKDL
 LIKIWNDFLNVQDINSALYRKVLLNQVRLLRVQLCHMKNMFKTCRLAKELLDSDFTVP
 GHLTEDLHLYSLNDLTATRKGELGPRLAELTRAGATHVERCMLCQAKGFICEFCQNEDDI
 IFPFELHKCRTCEECKACYHKACFKSGSCPRCERLQARREALARQSLESYLSDYEEPAE
 ALALEAAVLEAT

Y. SH3GLB1 (SH3 domain containing GRB2 like, endophilin B1)

>tr|K1Q963|K1Q963_CRAGI Endophilin-B1 OS=*Crassostrea gigas* OX=29159
 GN=CGI_10012647 PE=4 SV=1
 MDANTGLFKMKKFFVSDASTVFNRAVQFTEEKLGSAEKTELDAHFNLLQRADKTKAWTEK
 ILKQTESVLQPNPNIRMEDFVYEKLDKKKRDRVNHHEVLGHVLDVGGNDFGPGTTYGNAL
 VKCGQAQLRIGNAEREFIQTTSNNFLQPLHNFLEGMKTIQKEKKILETKRLDLDAASKNR
 LRKAKSTSQPQSSQNSPQNVLMVVEAEADLRVAQAEFDRQAEITKLLLEGVSSAHAHLR
 CLNDFIEAQLTYAQCQNYISELQQQLGYSHTSGVGNSSNSGAGISSGIPSSVPLQP
 SAPPQINVIATPNIEKKQARVLYDYDAADSELTLADELITVYKTPGLDPDWLMAERG
 PQKGVPTTYLEVLE

>AF263293.1 *Homo sapiens* endophilin B1 mRNA, complete cds

CTAGGATGAATATCATGGACTTCAACGTGAAGAAGCTGGCGGCCGACGCAGGCACCTTCCTCAGTCGCGC
CGTGCAGTTCACAGAAGAAAAGCTTGGCCAGGCTGAGAAGACAGAATTGGATGCTCACTTAGAGAACCTC
CTTAGCAAAGCTGAATGTACCAAAATATGGACAGAAAAATAATGAAACAAACTGAAGTGTATTGCAGC
CAAATCCAAATGCCAGGATAGAAGAATTTGTTTATGAGAACTGGATAGAAAAGCTCCAAGTCGTATAAA
CAACCCAGAACTTTTGGGACAATATATGATTGATGCAGGGACTGAGTTTGGCCAGGAACAGCTTATGGT
AATGCCCTTATTAATGTGGAGAAACCCAAAAAGAATTGGAACAGCAGACAGAGAAGCTGATTCAAACGT
CAGCCTTAAATTTTCTTACTCCTTTAAGAACTTTATAGAAGGAGATTACAAAACAATTGCTAAAGAAAG
GAAACTATTGCAAATAAGAGACTGGATTTGGATGCTGCAAAAACGAGACTAAAAAAGGCCAAAAGCTGCA
GAACTAGAAATTCACAATAAAGCTCAGCTCGCCTTGAAGGAGATAACATTATGATTTGGGCAGAGGAG
TGACAAAATCTGAACAGGAATTAAGAATAAAGCTCAAAGTGAATTTGATCGTCAAGCAGAGATTACCAGACT
TCTGCTAGAGGGAATCAGCAGTACACATGCCCATCACCTTCGCTGTCTGAATGACTTTGTAGAAGCCCAG
ATGACTTACTATGCACAGTGTACCAGTATATGTTGGACCTCCAGAAACAAGCTGGGAAGTTTTCCATCCA
ATTATCTTAGTAACAACAATCAGACTTCTGTGACACCTGTACCATCAGTTTTACCAAATGCGATTGGTTC
TTCTGCCATGGCTTCAACAAGTGGCCTAGTAATCACCTCTCCTTCCAACCTTAGTGACCTTAAGGAGTGT
AGTGGCAGCAGAAGGCCAGGGTTCTCTATGATTATGATGCAGCAAACAGTACTGAATTACTTCTG
CAGTAGGTGATCACTGTGTTTCTGTTGTTGGAATGGATTGACTGACTGGCTAATGGGGGAAAGGGGAAA
CCAGAAGGGCAAGGTGCCAATTACCTACTTAGAACTGCTCAATTAAGTAGGTGGACTATGGAAAGGTTGC
CCATCATGA

Z. ATG12 (autophagy related 12)

>XM_011417800.2 PREDICTED: *Crassostrea gigas* ubiquitin-like protein ATG12
(LOC105320040), mRNA

GTGCTGTCTAATTTGACAGGAAGTAAACAAACATGTCTGATGACGGAAATGAAAGTAGAGACAGTAAAAA
CACAGAACTGAAGAGAAGAGCACACCAGCAAGTCCAAGTCATGTGCGCGAAACAAAAATTGATGTACTT
TTAAACCAGCTGGAGATGCTCCAATTATGAAGAAAAAGAAGTGGGCTGTAGACAGGAATAAACGGATTG
GCTGGGTGGGAGAGTTCATCAAGAAGTACCTAAAGCTTACTGCTCAGGATTCTTTGTTCTGTATGTAAA
CCAGTCTTTTGTCTTACACCTGACACAGAAATTGGCTCTATATTTGATTGCTTTGGGAGTGATGAAAA
CTTGTGTTACATTACTGTAAAACACAGGCCTGGGGTTAACCACAAGAAGCAGTAGCTGGTGTCTTTAAAA
CTGTCTAAGTTATGTAAAAGAAGAAAGGGGGTACTTTTTGTTTTTTGTGATGGGATCAACATTGTGAGCTA
GTGCCTCAACCAAGGATCAGTACAAAGTATTTATGTAAACATATGGGCACAGACATGTTAATGTGGTT
GATGGATGGCTCTTGGTACAAGGTGGTAGTAATAGAAGAAAAATCAACCCAACCATCCTGTAGAGTTTTAA
CTTGTACCTTAACTTTATAGGTCTTTTTTGGAGGGGGGATTTCTAGCTTATTGACCACATGTAGTTGAT
GTTTAAGGGTAATTTACAGGATTAACAACTTTTCAAAACAGATTGAACATTTATTAGAAAAAACCCAGAT
TCATTTAAATGTACTATAAAATGCAACATGTACCTGGCATCAGACTTTTGAATTTTAAACCAGATTTTAA
ACAGTATCATTATGTACATGTGTTAATTCTTACATGATCATCACATTTGATGTGAAATGTACTGTTTGT
TTATTTCCAAGTTCATGAAAAAGTAAAGAATGAAAATTGG

>sp|O94817|ATG12_HUMAN Ubiquitin-like protein ATG12 OS=*Homo sapiens* OX=9606
GN=ATG12 PE=1 SV=1

MAEEPQSVLQLPTSIAAGGEGLDVSPETTTPEPPSSAAVSPGTEEPAGDTKKKIDILLK
AVGDTPIMKTKKWAVERTRTIQGLIDFIKKFLKLVASEQLFIYVNQSFAPSPDQEVGTLY
ECFGSDGKLVLHYCKSAWG

>sp|P38316|ATG12_YEAST Ubiquitin-like protein ATG12 OS=*Saccharomyces cerevisiae*
(strain ATCC 204508 / S288c) OX=559292 GN=ATG12 PE=1 SV=1

MSRILESENETESDESSIIISTNNGTAMERSRNNQELRSSPHTVQNRLELFSRRLSQLGLA
SDISVDQQVEDSSSGTYEQEETIKTNAQTSKQKSHKDEKNIQKIQIKFQPIGSIQQLKPS
VCKISMSQSFAMVILFLKRRLLKMDHVYCYINNSFAPSPQQNIGELWMLQFKTNDELIVSYC
ASVAFG

AA. ATG5 (autophagy related 5)

>tr|K1RAJ5|K1RAJ5_CRAGI Autophagy protein 5 OS=*Crassostrea gigas* OX=29159
GN=CGI_10018604 PE=3 SV=1

MLLPKILISGRKRLHNMGENREIQKGVWEGRIPVAFRLSEEDTDGERPEPVYLMVPRISY
FPLHTEKINKHFLKYASEKESEEIWLHEDNQPLKWHYPVGLLFDLYGSETSLPWTITVHF
KDFPEEELLHCVSKDAVESHFMSI KEADSLKHRGQVINSMQKRDHKQLWTGLLHDKFDQ
FWSVNKKLMESSGDETFKYIPFRLYMVDHRHYMTNLFRLPTEEGHHQSLKHLLLSAVPQFF
NEEEEFQKHVRIHGTEPLLDTPILWLSNFSPDNFLHLVIVSDK

>EU283339.1 *Homo sapiens* ATG5 autophagy related 5-like (ATG5) mRNA, complete cds, alternatively spliced
ATGACAGATGACAAAGATGTGCTTCGAGATGTGTGGTTTGGACGAATTCCAACCTGTTTCACGCTATATC
AGGATGAGATAACTGAAAGGGAAGCAGAACCATACTATTTGCTTTTGGCAAGAGTAAGTTATTTGACGTT
GGTAACTGACAAAGTGAAAAAGCACTTTTCAGAAGGTTATGAGACAAGAAGACATTAGTGAGATATGGTTT
GAATATGAAGGCACACCCTGAAATGGCATTATCCAATTGGTTTGTATTTGATCTTCTGCATCAAGTT
CAGCTCTTCTTGGAACATCACAGTACATTTTAAGAGTTTTCCAGAAAAAGACCTTCTGCACTGTCCATC
TAAGGATGCAATTGAAGCTCATTTTATGTCATGTATGAAAGAAGCTGATGCTTTAAAACATAAAAGTCAA
GTAATCAATGAAATGCAGAAAAAGATCACAAGCAACTCTGGATGGGATTGCAAAATGACAGATTTGACC
AGTTTTGGGCCATCAATCGGAACTCATGGAATATCCTGCAGAAGAAAAATGGATTTTCGTTATATCCCCTT
TAGAATATATCAGACAACGACTGAAAGACCTTTCATTGAGAAGCTGTTTCGTCTGTGGCTGCAGATGGA
CAGTTGCACACACTAGGAGATCTCCTCAAAGAAGTTTGTCTTCTGCTATTGATCCTGAAGATGGGGAAA
AAAAGAATCAAGTGATGATTCATGGAATTGAGCCAATGTTGGAAACACCTCTGCAGTGGCTGAGTGAACA
TCTGAGCTACCCGGATAATTTTCTTCATATTAGTATCATCCCACAGCCAACAGATTGA

>NM_001183963.1 *Saccharomyces cerevisiae* S288C Atg5p (ATG5), partial mRNA
ATGAATGACATTAACAATTACTTTGGAATGGTGAGCTTAATGTGCTGGTATCGATCGATCCTTCATTTT
TGATGAAAGGAAGTCCAAGAGAAATTGCGGTGCTACGAATAAGGGTACCAAGGGAAACATATTTAGTCAA
TTATATGCCCTCATTTGGAACAAGATTAATAAGCTTTCTTTCTTTTGGACCATGACCGACAGTGAGAAG
TATTTCTGGTTTGGACATAATAAGACGCCTATTCCGTGGAATTACCCAGTAGGTGTTTTGTTGACTGCC
TAGCCGAAAAAGCGCTACTTTTACCACCTCTTTTGGAGAACCAGGTAAAGGATGTTCTCACTTTTTTGG
AATTCACCTGGTTATGGGCGATTTCGTTGCCACCAACTATCATTCCCATCGCATCTAGCAAAACGCAAGCG
GAAAAGTTTTGGTTTACCAATGGAAACAAGTTTTGCTTCATACTGAATGGTTCCTCAAAGCTATTATGT
CTTTATCGGTCAACGAAGCTCGAAAATTTTGGGGCAGTGTTATTACGAGAAAATTTCCAAGATTCATTGA
AATATCTAACAAGATAAGTTCATCAAGACCGCGACATATACCGCTCATCATTCAAACCTCAAGGACATCA
GGAACTTTTCGAATATCACAACCAACTATCAGTATGACTGGAGTCAATCCTACGTTGAAGGATATTGAAG
GCGATATTCTGGACGTAAAGGAAGGAATCAATGGTAATGATGTCATGGTTATTTGTCAAGGAATTGAAAT
TCCTTGGCATATGCTCCTGTATGATTTGTATTCTAAATTGCGAAGTTTTGATGGCTTTTTGTACATAACT
CTTGTTCCTATAAAAGGCGGCGATAAAGCTTCTCTGAGCTCTAA

BB. ATG16L1 (autophagy related protein 16 like 1)

>tr|K1RWG6|K1RWG6_CRAGI Autophagy-related protein 16-1 OS=*Crassostrea gigas*
OX=29159 GN=CGI_10012629 PE=4 SV=1
MDPKDLHWKHSLLLEQLRQRDKKEKEPFESLISSHWKHFEASQSLKSKNTQLTWEAEKLKE
ENLGLQIKVEQGGSGNSQALEQKLFKLOEEVTELRHRRRGENTQQIIDLNNALQDKEKEL
QGRDARLNDLLANELALKMEIKNLESTIMELEATNQMLKDEHQALQLTYTGLEEKYRKVE
QDNQQLLERLWIKQAKMADQLNAENDQFMAVRQOKLRQDLEDAARENIQILPENQAGVYV
PTSIPICLSLPTKAQYKFDHADGDVNAVRSWSPGSLFATGGADRKIKLWEVINGKCEC
KGILTGSNAGIMALDFDLEENTILGASNDFASRVWVSLTDHRVRHTLTGHSGKVLAAKFLG
DSFKVVSNGTHRDLKIWDLHSRSCVKTIIFAGSSCNDLVTIHGTNIVSGHFDKRVRFWDSR
VDSNTNEILLQGRLLSLDLSPDKMSLLCCTRDRTLKVLDLRMNQISTTLAHDDEFKVGCDW
SRAVFRHSVIACSWHPVGSYVLSCEKQRKTVLWSDI

>JQ924062.1 *Homo sapiens* autophagy-related protein 16-1 isoform 2 (ATG16L1)
mRNA, complete cds
ATGTCGTCGGGCCTCCGCGCCGCTGACTTCCCCCGCTGGAAGCGCCACATCTCGGAGCAACTGAGGCGCC
GGGACCGGCTGCAGAGACAGGCGTTTCGAGGAGATCATCCTGCAGTATAACAAATTGCTGGAAAAGTCAGA
TCTTCATTCAGTGTTGGCCCAGAACTACAGGCTGAAAAGCATGACGTACCAACAGGCACGAGATAAGT
CCCGGACATGATGGCACATGGAATGACAATCAGCTACAAGAAATGGCCCAACTGAGGATTAAGCACCAAG
AGGAACTGACTGAATTACACAAGAAACGTGGGGAGTTAGCTCAACTGGTGATTGACCTGAATAACCAAAAT
GCAGCGGAAGGACAGGGAGATGCAGATGAATGAAGCAAAAATTCAGAAATGTTTGCAGACTATCTCTGAC
CTGGAGACGGAGTGCCTAGACCTGCGCACTAAGCTTTGTGACCTTGAAGAGCCAACCAGACCTGAAGG
ATGAATATGATGCCCTGCAGATCACTTTTACTGCCTTGGAGGGAAAACCTGAGGAAAACACGGAAGAGAA
CCAGGAGTGGTCCACGATGGATGGCTGAGAAAGCCAGGAAGCCAATCGGCTTAATGCAGAGAATGAA
AAAGACTCCAGGAGGCGCAAGCCCGCTGCAGAAAGAGCTTGCAGAAAGCAGCAAAGGAACCTCTACCAG
TCGAACAGGATGATGACATTGAGGTCATTGTGGATGAAACTTCTGATCACACAGAAGAGACCTCTCCTGT
GCGAGCCATCAGCAGAGCAGCCACGAGACGCTCTGTCTCTTCCCTTCCCAGTCCCCCAGGACAATGTGGAT
GCTCATCCTGGTTCTGGTAAAGAAGTGAGGGTACCAGCTACTGCCTTGTGTGTCTTCGATGCACATGATG
GGGAAGTCAACGCTGTGCAGTTCAGTCCAGGTTCCCGGTTACTGGCCACTGGAGGCATGGACCGCAGGGT
TAAGCTTTGGGAAGTATTTGGAGAAAAATGTGAGTTCAGGGTTCCTATCTGGCAGTAATGCAGGAAT
ACAAGCATTGAATTTGATAGTGCTGGATCTTACCTCTTAGCAGCTTCAAATGATTTTGAAGCCGAATCT

GGACTGTGGATGATTATCGATTACGGCACACACTCACGGGACACAGTGGGAAAAGTGCTGTCTGCTAAGTT
CCTGCTGGACAATGCGCGGATTGTCTCAGGAAGTCACGACCGGACTCTCAAACCTCTGGGATCTACGCAGC
AAAGTCTGCATAAAGACAGTGTTCAGGATCCAGTTGCAATGATATTGTCTGCACAGAGCAATGTGTAA
TGAGTGGACATTTTGCACAAGAAAATTCGTTTCTGGGACATTTCGATCAGAGAGCATAGTTCGAGAGATGGA
GCTGTTGGGAAAGATTACTGCCCTGGACTTAAACCCAGAAAGGACTGAGCTCCTGAGCTGCTCCCGTGAT
GACTTGCTAAAAGTTATTGATCTCCGAACAAATGCTATCAAGCAGACATTAGTGCACCTGGGTCAAGT
GCGGCTCTGACTGGACCAGAGTTGTCTTCAGCCCTGATGGCAGTTACGTGGCGGCAGGCTCTGCTGAGGG
CTCTCTGTATATCTGGAGTGTGCTCACAGGGAAAAGTGGAAAAGGTTCTTTCAAAGCAGCACAGCTCATCC
ATCAATGCGGTGGCGTGGTGCGCCCTCTGGCTCGCACGTTGTTCAGTGTGGACAAAGGATGCAAAGCTGTGC
TGTGGGCACAGTACTGA

>sp|Q03818|ATG16_YEAST Autophagy protein 16 OS=*Saccharomyces cerevisiae*
(strain ATCC 204508 / S288c) OX=559292 GN=ATG16 PE=1 SV=1
MGNFIITERKKAKEERSNPQTDSMDDLIRRLTDRNDKEAHLNELFQDNSGAIGGNIVSH
DDALLNTLAILQKELKSKEQEIRRLKEVIALKNKNTERLNDELISGTIENNVLQQKLSDL
KKEHSQLVARWLKTEKETTEAMNSEIDGTK

CC. ATG16L2 (autophagy related 16 like 2)

>sp|Q8NAA4|A16L2_HUMAN Autophagy-related protein 16-2 OS=*Homo sapiens*
OX=9606 GN=ATG16L2 PE=1 SV=2 REVIEWED
MAGPGVPGAPAARWKRHIVRQLRLRDRTQKALFLELVPAYNHLLLEKAELLDKFSKQLQPE
PNSVTPPTHQGPWEESELDSDQVPSLVALRVKQEEEEGLRLVCGEMAYQVVEKGAALGT
LESELQQRQSRLALEARVAQLREARAQQAQVEEWRAQNAVQRAAYEALRAHVGLREAA
LRRLEQEEARDLLERLVQRKARAAAERNLRNERRERAKQARVSQELKKAARTVSISEKPD
TLGDGMRRERRETLALAPEPEPELEKEACEKWKRPFRSASATSLTSLSHCVDVVKGLLDFKKR
RGHSIGGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFPGNSLLATGGADRLI
HLWNVVGSRLLEANQTLLEGAGGSITSVDFDPSGYQVLAATYNQAAQLWKVGEAQSKETLSG
HKDKVTAAKFKLTRHQAVTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIISGH
NDQKIRFWDSRGPHTQVIVPQGRVTSLSLSHDQLHLLSCSRDNTLKVIDLKRVSNIRQVF
RADGFKCGSDWTKAVFSPDRSYALAGSCDYGALYIWDVDTGKLESRLQGPCHCAAVNAVAWC
YSGSHMVSVDQGRKVVWLWQ

DD. ATG10 (autophagy related 10)

>tr|K1PT50|K1PT50_CRAGI Autophagy-related protein 10 OS=*Crassostrea gigas*
OX=29159 GN=CGI_10025434 PE=4 SV=1
MAAGSISEDEYWDSIIFFLTLSSKIDSKWTIVDTKDGRRFACKTEVFILSTENKESTMND
DVIRNTELMEEQEEDTAAAFQVRGNSDVEVVTYEYHILYSPSYGVPVLYFNAHTQGGKLLA
LEEIWKRVPDAYKERLSEERWTFITQOEHPHLLGRPFYLLHPCHTADLMKNSPVLTDKRHY
IVSWLSAVGPVVGLKLPLEYGKLCVS

>XM_005248611.5 PREDICTED: *Homo sapiens* autophagy related 10 (ATG10),
transcript variant X1, mRNA
CGGTCATAGCTCACTGCAACCTTGAATTCCTAGCCTCAAGTGATCCTCCTACCTCGGCCTTGCAAAGTGT
ACATCAGTTTGTGTAAGAAAGGTCCAAGAAGTGAACAGGCCTGAAAGTTGAAGAAAAGTTATCATTTAACA
TGGAAGAAGATGAGTTCATTGGAGAAAAACATTCCAACGTTATTGTGCAGAATTCATTAACATTCACA
ACAGATAGGTGATAGTTGGGAATGGAGACCATCAAAGGACTGTTCTGATGGCTACATGTGCAAAATACAC
TTTCAAATTAAGAATGGGTCTGTGATGTCACATCTAGGAGCATCTACCCATGGACAGACATGTCTTCCCA
TGGAGGAGGCTTTTCGAGCTACCCTTGGATGATTGTGAAGTGAATGAACTGCAGCAGCGTCCGAAGTGAT
TAAATATGAGTATCATGTCTTATATTCCTGTAGCTACCAAGTGCCTGTACTTTACTTTAGGGCAAGCTTT
TTAGATGGGAGACCTTTAACTCTGAAGGACATATGGGAAGGAGTTCATGAGTGCTATAAGATGCGACTGC
TACAGGGACCATGGGACACTATTACGCAACAGGAACATCCAATACTTGGGCAACCCCTTTTTTGTACTTCA
TCCCTGCAAGACGAATGAATTCATGACTCCTGTATTAAGAATTCCTCAGAAAATCAATAAGAATGTCAAC
TATATCACATCATGGCTGAGCATTGTAGGGCCAGTTGTTGGGCTGAATCTACCTCTGAGTTATGCCAAAG
CAACGTCTCAGGATGAACGAAATGTCCCTTAACAAGATTCTTCTATTGAGTTTAGGAATTCGCGGCACGAA
GAATGCCAAGAGTTTACCTGGCCAGCCCTGGCTTTAATAGGACTGATACCATGGAATATTTTCATCTCACC
AAGATGTGACATGGATTATTTTTCCCTTGGACACAAATGTCTACAGCAACTGGTGTGATAGGCTGAAT
GTTTAGAAGAACAACACTTCAAAGGGATACATCATGACCAGGCATGGTGGCTCACACCTGTAATCCAAGCAC
TTTGGGAGGCCAAGGTGGGAGCATCACTTGATCCTGGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAA
CCCTGTGCGGTACAAAAAATACAAAAATTTGCCTGTTTATGGTGGTGTGTTTCTGTAGTCCCAGCTCCCC

AGGAGGCTGAGGTGGGAGGTTGGCTTTAACCAGGAGGCAGAGGTTGCAGTGAGCTGAGACTGTGCCACT
GCAGTCCAGCCTGGGTGACAGAGCCAGACACTGTCTCG

>sp|Q07879|ATG10_YEAST Ubiquitin-like-conjugating enzyme ATG10
OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG10
PE=1 SV=1
MIPYQEWHSQQLSLYDSQIFHNWALCQDVHLNDEKDGLLLLRLIPTRQLQKNTERIENKLL
NHIELYLTYSKVYNEPLLLLRIWEEKSIDGIPMTKMLPTDIESLLDVQKQFLGLDTII
NLEGSVWYSFHPCDTSCIVGDQAEFMSTYLRRVWSIFIFSWLGYEDS

EE. MAP1LC3A (microtubule associated protein 1 light chain 3 alpha)

>tr|K1R9V4|K1R9V4_CRAGI Microtubule-associated proteins 1A/1B light chain
3A OS=*Crassostrea gigas* OX=29159 GN=CGI_10021322 PE=3 SV=1
MEMQKPFKERRSLTQRLKDVESIRTQHMDKIPVIIERYNGEKSLPMLDKTKFLVDPDNVM
SELVKIIRRRLQLHPSQAFYLVNRRSMVSNTTPIAEVYEQEKDEDEGFLYIVYASQETFG
GSCH

>BT007452.1 *Homo sapiens* microtubule-associated protein 1 light chain 3
alpha mRNA, complete cds
ATGCCCTCAGACCGCCTTTCAAGCAGCGGGCGGAGCTTCGCCGACCCTGTAAGGAGGTACAGCAGATCC
GCGACCAGCACCCAGCAAATCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCT
GGACAAGACCAAGTTTTTGGTCCCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCGC
CTGCAGCTGAACCCACGCAGGCCTTCTTCTGCTGGTGAACCAGCACAGCATGGTGAGTGTGTCCACGC
CCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGACGGCTTCTCTATATGGTCTACGCCTCCAGGA
AACCTTCGGCTTCTAG

>NM_001178318.1 *Saccharomyces cerevisiae* S288C ubiquitin-like protein ATG8
(ATG8), partial mRNA
ATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAGGAAGGCGGAGTTCGGAGAGGATTGCTGACA
GGTTCAAGAATAGGATACCTGTGATTTGCGAAAAAGCTGAAAAGTCAGATATCCAGAGATTGATAAGCG
TAAATATCTAGTTTCTGCTGACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAAGAGAATTATGCTA
CCCCCTGAGAAGGCCATCTTCATTTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATACATTTGGCAG
GTAG

FF. MAP1LC3B (microtubule associated protein 1 light chain 3 beta)

>sp|Q9GZQ8|MLP3B_HUMAN Microtubule-associated proteins 1A/1B light chain 3B
OS=*Homo sapiens* OX=9606 GN=MAP1LC3B PE=1 SV=3
MPSEKTFKQRRTFEQRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVDPDHVM
SELIKIIRRRLQLNANQAFLLVNGHSMVSVSTPISEVYESEKDEDEGFLYIMVYASQETFG
MKLSV

GG. MAP1LC3C (microtubule associated protein 1 light chain 3 gamma)

>tr|K1QLL7|K1QLL7_CRAGI Microtubule-associated proteins 1A/1B light chain
3C OS=*Crassostrea gigas* OX=29159 GN=CGI_10020484 PE=3 SV=1
MPEKGGDITYKTFKQRKSFVRKEEVGIRSKFPTKVPVIVERYYYKEQQLPMLDKTKFLVP
QELSMSQFASIIIRNMSLNSNQAFYLVNKNKSISSMSMTLAEVYRDEKDEDEGFLYMTYAS
QEMFGGC

>XM_005273139.3 PREDICTED: *Homo sapiens* microtubule associated protein 1
light chain 3 gamma (MAP1LC3C), transcript variant X1, mRNA
GATCTGCCCACCTCCGCTCCTAAAGTACTGGGATTACAGGTGTGAGCCACTGCACCTGGTGAATCCTT
GGAATTTTCAAAGTGACACAGCTACTGAGTGAATGCCGCTCCACAGAAAATCCCAAGCGTCAGACCT
TCAAGCAGAGGAAAAGCTTGGCAATCAGACAAGAGGAAGTTGCTGGAATCCGGGCAAAGTTCCCCAACAA
AATCCCGGTGGTAGTGGAGCGCTACCCCAGGGAGACGTTTCTGCCCCGCTGGACAAAACCAAGTTCTG
GTCCCGCAGGAGCTGACCATGACCCAGTTTCTCAGCATCATCCGGAGCCGCATGGTCTCTGAGAGCCACGG
AAGCCTTTTACTTGCTGGTGAACAACAAGAGCCTGGTCAGCATGAGCGCAACCATGGCAGAGATCTACAG
AGACTACAAGGATGAGGATGGCTTCGTGTACATGACCTACGCCTCCAGGAGACATTTGGCTGCCTGGAG
TCAGCAGCCCCCAGGGATGGGAGCAGCCTTGAGGACAGACCCTGCAATCCTCTCTAGCCCATGTCGGGAA

GGATGTGTGCTCTGACAGACGTGTCAGATGCTGGCAGAAGGGATTGGTTTTCTCCTGTGTATACAGTGGA
GGAGTCTGAGAAGCAGGGATGCCTGGGGTGATCAGCTCCAACCAGTGGCAGCAGAGTGGTGGCTCTTCCT
AGTTTAGTTTTTGTGCTCCGTGTTCTTGTGTCCTTCTAAGAAAAATGTGGGCTGCTCTTGAAAGTTATAT
AATTATCATTTTTTTTTTTTTTGAACAGGGTCTTGTCTATTGCCTAGGCTGGAGCACAGTGGCATGATC
TTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGTGATTCTTCTGCCTCCACCCCCGAGTGGCTGGTA
TTACAAGCACATGCCACCACACCAGGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTTGG
CCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCACCTCGGCCTCCCAAAGTGTGGGATTACA
GGCGTGAGCCACTGCATCCAGCCATATAACCGTATTCTAAATAAGAAATGGTTGGCTTGTGTGATGGTTT
TGTGTAATGAGCTAGAGATAATATTTAAGTGTCTTCTGTGGTATATGTGGGAGGGCCATTAAGGAGTGG
GTTTCACTCCCTGCATGTGGGCAGGTGTCCCATCTAGGGCTCGGTAAGTACTAGAGAATCTCTGGCCTGTAGGC
TGTCTCTGTGGAACCCAGTGAAGCCAGCGTGAACAATGGTAAGCTCATCTGGAGGTGCTCTTATCTGTGT
CATTAGAGAGATTATTCGATTTCCCCAGCATTCACTCTATTTAGTTATTTTCTGTCACTTCTTTTTTGTG
TTTCTATACCATAACATATTTATGCCAAAGCTGTAACCTCTCAACATGAAGTCATTTAAACCATGTGCATG
TTTACTATGTGCCAAGCTGTATTCTAAAATAAATATTCTTTATTTT

>NM_001178318.1 *Saccharomyces cerevisiae* S288C ubiquitin-like protein ATG8
(ATG8), partial mRNA
ATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAAGGAAGGCGGAGTCCGAGAGGATTGCTGACA
GGTTCAAGAATAGGATACCTGTGATTTGCGAAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCG
TAAATATCTAGTTCCCTGCTGACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAAGAGAATTATGCTA
CCCCCTGAGAAGGCCATCTTCATTTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATACATTTGGCAG
GTAG

HH. GABARAP (GABA type A receptor-associated protein)

>tr|K1PXH7|K1PXH7_CRAGI Gamma-aminobutyric acid receptor-associated protein
OS=*Crassostrea gigas* OX=29159 GN=CGI_10025849 PE=3 SV=1
MKWEYKEEHSFEKRRAEGEKIRKKYPDRVPVIVEKAPKARVGDLDKKKYLVPSDLTVGQF
YFLIRKRIHLRPEDALFFFVNNVIPPTSATMGSLYQEHHEEDFFLYIAYSDESUYGA

>AF161586.1 *Homo sapiens* GABA-A receptor-associated protein (GABARAP) mRNA,
complete cds
CGACCGGCCCCGTCCCGGCCCCCTGGGTTCCCTCAGCCAGCCCTGTCCAGCCCGGTTCCCGGGAGGAT
GAAGTTCGTGTACAAAGAAGAGCATCCGTTTCGAGAAGCGCCGCTCTGAGGGCGAGAAGATCCGAAAAGAAA
TACCCGGACCGGGTGCCGGTGTATAGTAGAAAAGGCTCCCAAAGCTCGGATAGGAGACCTGGACAAAAAGA
AATACCTGGTGCCTTCTGATCTCACAGTTGGTCACTTCTACTTTGATCCGGAAGCGAATTCATCTCCG
AGCTGAGGATGCCTTGTTTTTCTTTGTCAACAATGTCACTTCCACCCACCAGTGCCACAATGGGTCAGCTG
TACCAGGAACACCATGAAGAAGACTTCTTTCTCTACATTGCCTACAGTGACGAAAAGTGTCTACGGTCTGT
GAAGCTGCTGCCCCGTGAGCTGGAGGGGGTCTCATTCTACAAAGAGAGAGGTGGCCCCCTTTCTTGACC
TCCTCCTCCTTCAAGCTCAAACACCACCTCCCTTATTACAGGACCGGCACTTCTTAATGTTTGTGGCTTTC
TCTCCAGCCTCTCTTAGGAGGGGTAATGGTGGAGTTGGCAACTTGTAACCTCTCCTTTCTCCTTTCTTCCC
CTTTCTCTGCCCCCCTTTCCCATCCTGCTGTAGACTTCTTGATTGTCAGTCTGTGTACATCCAGTGATT
GTTTTGGTTTTCTGTTCCCTTTCTGACTCCGTCAAGGGGCTCAGAACCAGCAATCCCTTCCCTTCACTAC
CTTCTTTTTTGGGGTAGTTGGAAGGGACTGAAATTGTGGGGGAAGGTAGGAGGCACATCAATAAAGAG
GAAACCACCAAGCTG

>NM_001178318.1 *Saccharomyces cerevisiae* S288C ubiquitin-like protein ATG8
(ATG8), partial mRNA
ATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAAGGAAGGCGGAGTCCGAGAGGATTGCTGACA
GGTTCAAGAATAGGATACCTGTGATTTGCGAAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCG
TAAATATCTAGTTCCCTGCTGACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAAGAGAATTATGCTA
CCCCCTGAGAAGGCCATCTTCATTTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATACATTTGGCAG
GTAG

II. GABARAPL1 (GABA type A receptor-associated protein like 1)

>sp|Q9H0R8|GBRL1_HUMAN Gamma-aminobutyric acid receptor-associated protein-
like 1 OS=*Homo sapiens* OX=9606 GN=GABARAPL1 PE=1 SV=1
MKFYKEDHPFEYRKEGEKIRKKYPDRVPVIVEKAPKARVDPDLDRKYLVPSDLTVGQF
YFLIRKRIHLRPEDALFFFVNNVIPPTSATMGQLYEDNHEEDYFLYVAYSDESUYGK

>sp|P38182|ATG8_YEAST Autophagy-related protein 8 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG8 PE=1 SV=1
MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGLYVVTYSGENTFGR

JJ. GABARAPL2 (GABA type A receptor associated protein like 2)

>tr|K1QQ43|K1QQ43_CRAGI Gamma-aminobutyric acid receptor-associated protein-like 2 OS=*Crassostrea gigas* OX=29159 GN=CGI_10027515 PE=3 SV=1
MKFKFREEHTFEQRKAESTKIRDKYPERIPVIVEKDPKSQIQDIDKRKFLVPNDISVAQF
MWIIRKRIQLPSEKAIFLFGVKVLPQSSASMGQVYEEHKDEDGLYIAYSSENTFGQ

>NM_007285.7 *Homo sapiens* GABA type A receptor associated protein like 2 (GABARAPL2), mRNA

AGTCGCCGCCGCTCGCTGCCGCTGCCGCTGCCGCGTTCGTTGTTGTTGTGCTCGGTGCGCTGAGCTCCGCG
GCTCCGCGAGCCGGTTCGGTCCCCTTCCC GCCGCCGCCATGAAGTGGATGTTCAAGGAGGACCACTCGCT
GGAACACAGATGCGTGGAGTCCGCGAAGATTTCGAGCGAAATATCCCACAGGGTTCCGGTGATTGTGGAA
AAGGTCTCAGGCTCTCAGATTGTTGACATTGACAAACGGAAGTACTTGGTTCATCTGATATCACTGTGG
CTCAGTTCATGTGGATCATCAGGAAAAGGATTGCCAGCTTCCTTCTGAAAAGGCGATCTTCCTGTTTGTGGA
TAAGACAGTCCCACAGTCCAGCCTAACTATGCGACAGCTTTACGAGAAGGAAAAGATGAAGATGGATT
TTATATGTGGCCTACAGCGGAGAGAACAACCTTTTGGCTTCTGAGGGCCATTGCTGGGCTAGGTGCACCGTA
ACTGCTTGTGTATCTTGTAATAGCCAGCCATTTTTCAGTTATTATACCAGAACCTCTTCACATAGACCTA
TTAGTGCATTTGTAAGTGGATTTATTTCTTAATATATTGGAAGGTTTTGTTTCTTAGACTAGTAAATTA
TCATACAGAGTTTTATTTTGGAGTTTTTCTTTTTGTGCATTGTCCTCATGCCTGTATTCTCCAGGAACTT
GTCCTTCTGGAATCATATTGAATGATATTTCTATATCGAAGTGAGGTAGGTGCGGTATTAAGTGAAAG
GGAAGGTGATGCATTTATTTCTGGGTTATGCTTGAAGTGTTAGATGGCTAAGTATTAATAATTCCAAAT
AAATCCTTAGCAGTCAGAACACTTGCTTCACTAGAATATGCCAACTGCCAATCATGTTGGACTGAGCTAA
TTTGTTCCTCTTTCTGAAACTATTAAGGTAAATAATTAACAATAAAAATTCTCTTATAAAGGCA

>NM_001178318.1 *Saccharomyces cerevisiae* S288C ubiquitin-like protein ATG8 (ATG8), partial mRNA

ATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAGGAAGGCGGAGTCCGAGAGGATTGCTGACA
GGTTCAGAATAGGATACCTGTGATTTGCGAAAAAGCTGAAAAGTCAGATATTCAGAGATTGATAAGCG
TAAATATCTAGTTCCTGCTGACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAAGAGAATTATGCTA
CCCCCTGAGAAGGCCATCTTCATTTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATACATTTGGCAG
GTAG

KK. GABARAPL3 (GABA type A receptor associated protein like 3 pseudogene)

>sp|Q9BY60|GBRL3_HUMAN Gamma-aminobutyric acid receptor-associated protein-like 3 OS=*Homo sapiens* OX=9606 GN=GABARAPL3 PE=2 SV=1
MKFYKQYKEVHPFEYRKKKEGKIRKKYPDRVPLIVEKAPKARVPDLDRRKYLVPSDLTDGQF
YLLIRKRIHLRPEDALFFFVNNITPPTSATMGQLYEDSHEEDDFLYVAYSNESVYK

>sp|P38182|ATG8_YEAST Autophagy-related protein 8 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG8 PE=1 SV=1
MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGLYVVTYSGENTFGR

LL. ATG7 (autophagy related 7)

>XM_011419559.2 PREDICTED: *Crassostrea gigas* ubiquitin-like modifier-activating enzyme ATG7 (LOC105321294), transcript variant X1, mRNA
CACGTGATATTCAAATGTCTGCGCCCTTGTAAACAAAATGGAACGTAAACAACACTACAGTTTGTGGCAT
TTAATAGTTTTTTAGACTCAGGATTTTGGCATAAGCTCTCCGAAAATAAACTTGATGTTTATGGTTTAGA
TGAAAGCCAAAAGGAGATAAAAGGATTTTACTTCAATGGTGACCCTGTTGGAATGCCTTGCAGAATGAAT
GTTGAGTTTTCTGCATTTGACCAAGATGCCAAAACGCCACAGCGATGCCTGCCCATGCTGGGAGAGTTAC
ATAACACCAATACAGTGGACAAATTCAGGAGTGTGATAAAAAAGAGATGATCAGTGAAGCCGGAAAAA

GATATGGGACTCCGTTGTAAGTGGTAAAGCACTGGACACCCCTGAACTTCTGGCTACTTTCCCTTCTTTTG
ACCTTTGCAGACTTAAAGAAGTACCATTACTATTACTGGTTCTGTTTTCCCTGTCTCTGTCCATCAACTG
ACATCACCTTTGACCAAGAACCAAAGAACTCAAGTACAGGTTGACTGCAGAGGAGATGGAACAGTTTCT
ACAAGCTTATGACACATTCCAAGATGCTCATCCAACATATCAGGGTTTCTTTGTTGCTGTCTTTCTAAA
GGGAACATTGTAATCGAGGATGTAAAATATATGAACAAGTTTAAAATACTCAGGAGGTGACTTTGGAT
TCTGTGATCCCAGTAATATTGAGGACTATCCAGGCTGGCCTCTTAGGAATTTCTGATGTTGATATCCTA
TCATTGGAAGGGAGACCTGCGAGGTGTAAATGTACTGTGTTTGCAGATAGGAGTCGAGACGGGACACGA
GATATATCACACAGTCTTCTGCTGTCCCTTTGTGTCCCGGATATTAAGAATGTGCTAGAATGTCCAAAGT
GTGTGGGTTGGGAGAAAATGAAAAACAAAAGCTGGCTCCAAGATTTGTAAATCTCAGTGCTAGCATGGA
CCCCACAAGACTGGCAGCCTCAGCTGTTGACCTCAATCTAAAGCTGATGAGATGGAGGCTGCTCCCAGAG
CTTGACCTTGACCTTATATCAAAGACAAAATGTCTGCTGCTAGGAGCCGGGACTCTTGATGCAATGTGG
CAAAGTGCCTGATGGGCTGGGGAGTAAGAACCATAACTCTGGTGGACAATGGCCGCGTGTCTTACTCTAA
CCCAGTACGCCAGCCCTTGTTCAGTTTGAAGACTGTGTAAAGGGAGGTAAAGCCAAAAGCGGAGGCTGCT
GCAGAGGCCATGAAGAAGATATTCCCTGGAGTGAATGCAAAAGGGTTGAGTTTATCCATTCTATGCCTG
GACATGCAGTACCTGAGAGTGAATAGAGGGTGTGAAGAAAGACGTTGAAACCCCTCAGGATCTGGTGAA
TTCTCACAGTGCAGTGTTTTTACTGTTGGATACGCGGGAGAGCCGTTGGCTTCTTACATTGATGGCACA
GAAAAACAAAAGATAGTGATATGCTCTGCACTGGGCTTTGACACATATCTAGAGATGCGCCACGGCGTAA
GGTCAGACACAGAGGGAGCTGACCTCGCCCCCTCTGTCTCTTACAGCTCCATCCCCAGGGATCAGCTAGG
CTGCTACTTCTGCAATGATGTAGTGGCACCAGGGAATTTCTTTGAAGGACCGTACTCTGGACCAGCAGTGT
ACAGTATCCAGGCCGGGCATCTCTACATGGCGTCCGCGCTCGCCGTAGAACTCCTTGTGTCCATGCTCC
AACATCCAGAAGTAGGGAAAGCCCCGGCGGATATAAGTGTAGTGTAGCACCCTGAGTAAAGACTTTGT
CTGCCCCCTAGGGCTGGTCCCTCACCAGGTGAGGTCATTGTACTGCTGTCTCCAATGTCAATGAAATGTC
ATACTGGTTCCCTCTGTTTAAATTTACTGATTGAAGTAACTGGAATCTTATGAAGCATGTGATTTTTAGCTA
ACCTGAGCTGCTGAAACCATGCCTTTTTTGCAAAGGTAGTGTAGATTCAAAGTTGTGAAAAAATATGA

>XM_020072211.1 PREDICTED: *Crassostrea gigas* ubiquitin-like modifier-activating enzyme ATG7 (LOC105340241), mRNA
TTTCTTTCCCTCTAGATGGAACAGTTTCTGCAAGCTTATGACACATTCCAAGATGCTCATCCAACATATC
AGGGTTTCTTTGTTGCTGTCTTTCTAAAGGGAACATTGTAATTGAGGATGTAAAACATATGAACAAGTT
TGAAAATACTCAGGAGGTGTACTTTGGATTCTGTGATCCCAGTAATATTGAGGACTATCCAGGCTGGCCT
CTTAGGAATTTCCCTGATGTTGATATCCTATCATTGGAAGGGAGACCTGCGAGGTGTAAATGTACTGTGT
TCCGAGATAGGACTCGAGACTCGAGATATATCACACAGTCTTCTGCTTTCCCTTAAATGTCCCGGA
TATTAGGAATGTGCCAGAATGTCCAAAGTGTGGGTTGGGAGAAAAATGAAAAACAAAAGCTGGCTCCA
AGATTTGTTAATCTCAGTGTAGCATGGACCCACAAGACTGGCAGCCTCAGCTGTTGACCTCAATCTAA
AGCTTATGAGATGGAGGCTTCTCCCAGAGCTTGACCTTGACCTTATATCAAGGACAAAATGTCTGCTGCT
AGGAGCTGGAACCTTGATGTAATGTGGCAAGGTGTCTGATGGGCTGGGGAGTAAGAACCATAACTCTG
GTGGACAATGGCCGCGTGTCTTACTCTAACCAGTACGCCAGTCCCTTGTTCAGTTTGAAGACTGTGTAA
AGGGAGGTAAGCCAAAAGCGGAGGCTGCTGCAGAGGCCATGAAGAAGATATTCCCTGGAGTGAATGCAAA
AGGGTTGAGTTTATCCATTCCCTATGCCTGGACATGCAGTACCTGAGAGTGCAATAGAGGGTGTGAAGAAA
GACGTTGAAACCCCTCAGGATCTGGTGAATTCTCATGATGCAGTGTTTTTACTGTTGGATACGCGGGAGA
GCCGTTGGCTTCTTACATTGATGGCAGCAGAAAAACAAAAGATAGTGATATGCTCTGCCCTGGGCTTTGA
CACATATCTAGTGTGCGCCACGGCGTGAGGTGAGACACAGAGGGAGCTGACCCTGCCCCCTGTCTCT
TACAGCTCCATCCCCGGGGATCAGCTAGGCTGCTACTTCTGCAATGATGTAGTGGCACCAGGGAATTTCT
TGAAGGACCGTACTCTGGACCAGCAGTGTACAGTATCCAGGCCGGGCATCTCCTACATGGCGTCCGCGCT
CGCCGTAGAACTCCTTGTGTCCGTGCTCCAGCATCCAGAACTAGGGAAAGCCCCGGCGGATACAAGCGCT
AGTGATGAGCACCTGAGTAAAGACTTTGTCTGCCCCCTAGGGCTGGTCCCTCACCAGATTCGATGCTTTG
TGTCCCGCTTCCAGCAAGTGTACCAGGCTGTAAAGGCATTTGATAAATGTACAGCTTGTTCAAAAGACTGT
GATAGAACAGTTCAGACGGGACGGCTTTGACTTCTGAGGCGGGCGTTCAATGACCCGTCCTACCTGGAG
GATCTTACAGGCTCACACAGATGCATCAGGAAACCCTCGACGCTGAGGTGTGGGGGTTCAAGTATGACG
AGGAATGTAGCAGCATGGAAGTCTCCAGTCTTGACCCAGTTTTAAATTTGACCCAACTGAAGACTTTT
ATTTTTATTTTATTTATTTACCAATCAGACATTTATCAGTGTATAAGCTTTTCATGGTATTACATGTAA
TGACTTTTGTATTACATGTAATAAGTACATTGTAGCGTAAATTTGTGATATTCCGATTCAGGTTATGAA
TCATTATATTATACAATGAATAATATGACATTAATAAATGCTTTAACTCTGTT

>sp|O95352|ATG7_HUMAN Ubiquitin-like modifier-activating enzyme ATG7
OS=*Homo sapiens* OX=9606 GN=ATG7 PE=1 SV=1
MAAATGDPGLSKLQFAPFSSALDVGFWHELTQKKLNEYRLDEAPKDIKGYYYNGDSAGLP
ARLTLEFSAFDMSAPT PARCCPAIGTLYNTNTLESFKTADKLLLEQAANEIWESI KSGT
ALENPVLLNKFLLLTFADLKKYHFYYWFCYPALCLPESLPLIQGPVGLDQRFSLKQIEAL
ECAYDNLCQTEGV TALPYFLIKYDENMVLVSLKHYSDFFQGRQTKITIGVYDPCNLAQY
PGWPLRNFLVLAHRWSSSFQSVEVVCFRDRMTQGDVAHSII FEVKLPMAFSPDCPK
AVGWENKQKGMGPRMVNLSECMDPKRLAESVDLNLKLMCWRLVPTLDLKVVSVKCLL
LGAGTLGCNVARTLMGWGVRHITFVDNAKISYNSPVRQPLYEFEDCLGGGKPKALAAADR

LQKIFPGVNRGFNMSIPMPGHPVNFSSVTLEQARRDVEQLEQLIESHDVVFLMDTRES
RWLPAVIAASKRKLVINAAALGFDTFVVMRHGLKPKQGGADLCPNHPVASADLLGSSLF
ANIPGYKLGICYFCNDVVPAGDSTRDRTLDDQCTVSRPGLAVIAGALAVELMVSVLQHPEG
GYAIASSSSDDRMNEPPTSLGLVPHQIRGFLSRFDNVLPVSLAFDKCTACSSKVLQYERE
GFNFLAKVFNSSHSFLEDLTGLTLLHQETQAAEIWDMSDDETI

>sp|P38862|ATG7_YEAST Ubiquitin-like modifier-activating enzyme ATG7
OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG7
PE=1 SV=1

MSSSERVLSYAPAFKSFLLDTSFFQELSRLKLDVLLKLDSTCQPLTVNLDLHNI PKSADQVPL
FLTNRSEKHNKRTNEVPLQGSIFNFNVLDEFKNLKDQLFLHQRALECWEDGKIDINKC
VSFVVIISFADLKKYRFYYWLVGVPFCQRPSSSTVLHVRPEPSLKGLFSKQKWFVDVNYSKWV
CILDADDEIVNYDKCIIRKTKVLAIRDSTSTMENVPALTKNFLSVLQYDVPDLIDFKLLI
IRQNEGSFALNATFASIDPQSSSNPDMKVS GWERNVQGLAPRVVDLSSLLDPLKIADQ
SVDLNLKLMKWRILPDLNLDI IKNTKVL LLGAGTLGCVSRALIAWGVKRKIFVDNGTVS
YSNPVRQALYNFEDCGKPKAELAAASLKRI FPLMDATGVKLSIPMIGHKLVNEEAQHKDF
DRLRALIKEHDIIFLLVDSRESRWLP SLLSNIENKTVINAALGFDSYLVMRHGNRDEQSS
KQLGICYFCHDVVAPTDSLTDRTLDQMCTVTRPGVAMMASSLAVELMTSLLQTKYSGSETT
VLGDIHQIRGFLHNFSILKLETPAYEHCPACSPKIVIEAFTDLGWEFVKKALEHPLYLEE
ISGLSVIKQEVERLGNDFEWEDESDEIA

MM. ATG3 (autophagy related 3)

>tr|K1R934|K1R934_CRAGI Autophagy-related protein 3 OS=*Crassostrea gigas*
OX=29159 GN=CGI_10024759 PE=3 SV=1

MQNVINAVKGTALNVAEKFTPVVKESKFKETGVITPEEFVAAGDHLVHHCPTWQWSTGDE
SKVKPYLPKEKQYLITRNVPYKRVKQVDSHKEEQEKVIEADDEDGGWVDTHHFDPGTT
SLQDAVQEMTLDGKGDKRKSSSEEVKRS GDDDDDDDDDEEAMDMEA FEQSGMLDEEDD
AALDPSTLGRQDSESAATESGILQTRTYDLNITYDKYYQTPRLWLFYDENRKLPTVEQM
YEDFSQDHAKKTVTMEAHPLPGPPLASVHPCRHADVMKKIIQMVAEGGGDLGVHVYLM I
FLKVFQAVIPTIEYDFTRDFTM

>AB079384.1 *Homo sapiens* mRNA for Apg3p, complete cds

ATGCAGAATGTGATTAATACTGTGAAGGGAAAGGCACTGGAAGTGGCTGAGTACCTGACCCCGTCTCA
AGGAATCAAAGTTTAAAGGAAACAGGTGTAATTACCCAGAAGAGTTTGTGGCAGCTGGAGATCACCTAGT
CCACCCTGTCCAACATGGCAATGGGCTACAGGGGAAGAATTGAAAGTGAAGGCATACCTACCAACAGGC
AACAATTTTTGGTAACCAAAAATGTGCCGTGCTATAAGCGGTGCAAACAGATGGAATATTCAGATGAAT
TGGAAGCTATTGATGAAGAAGATGATGGTGTGATGGCGGATGGGTAGATACATATCACAACACAGGTATTAC
AGGAATAACGGAAGCCGTTAAAGAGATCACACTGGAAAATAAGGACAATATAAGGCTTCAAGATTGCTCA
GCACTATGTGAAGAGGAAGAAGATGAAGATGAAGGAGAAGCTGCAGATATGGAAGAATATGAAGAGAGTG
GATTGTTGGAACAGATGAGGCTACCCTAGATACAAGGAAAATAGTAGAAGCTTGTAAAGCCAAAATGA
TGCTGGCGGTGAAGATGCTATTTTGC AAACCAGA ACTTATGACCTTTACATCACTTATGATAAATATTAC
CAGACTCCACGATTATGGTTGTTTGGCTATGATGAGCAACGGCAGCCTTTAACAGTTGAGCACATGTATG
AAGACATCAGTCAGGATCATGTGAAGAAAACAGTGACCATTGAAAATCACCTCATCTGCCACCACCTCC
CATGTGTTTCAGTTACCCATGCAGGCATGCTGAGGTGATGAAGAAAATCATTGAGACTGTTGCAGAAGGA
GGGGGAGA ACTTGGAGTTCATATGTATCTTCTTATTTTCTTGAAATTTGTACAAGCTGTCATTCCAACAA
TAGAATATGACTACACAAGACACTTCA CAATGTAATGA

>NM_001183184.3 *Saccharomyces cerevisiae* S288C Atg3p (ATG3), partial mRNA

ATGATTAGATCTACTAAGTAGTTGGAGAGAATATCTTACCCCATACGCACAAATCTACCTTTTTTAA
CCACAGGTCAAATAACTCCTGAGGAGTTTGTACAAGCAGGTGATTATTTATGTCATATGTTTCCACCTG
GAAGTGAACGAAGAGTCGTGAGATATTAGTTACAGAGATTTTTTACCGAAGAATAAGCAGTTTCTGATA
ATTAGAAAAGTTCCCTGTGATAAACGTGCCGAGCAATGTGTCGAAGTTGAAGGGCCAGATGTAATCATGA
AAGTATTTTGCAGAAAGTGGAGATGAAGATGATGTTCTGGAATACATAGGATCTGAACTGAACATGTGCA
AAGTACCGCTGCGGGGGGACCAAGGACTCATCTGATATCGATGATATTGATGAGCTAATAACAAGACATGGA
ATAAAAGAGGAGGATGAAAATGACGATACAGAAGAATTTAATGCTAAAGGTGGCCTAGCCAAAGATATGG
CGCAAGAAAGGTATTACGACCTTTATATTGCGTACTCGACATCTTATAGGGTCCCTAAAATGTATATAGT
GGGGTTTTAATTCTAATGGTTCCACTAAGCCCTGAGCAGATGTTTCAAGATATATCAGCAGATTATAGA
ACAAAGACAGCCACCATTGAAAAGCTACCTTTTTTACAAGAATTCAGTGTATCTGTTTCCATTCATCCAT
GTAAGCATGCTAATGTAATGAAAATATTGCTAGATAAGGTTTCGTGTGGTTAGACAACGAAGAAGGAAAAGA
GCTGCAGGAAGAACAAGAGCTGGACGGTGTGCGGAGACTGGGAGGATTTACAAGACGATATTGATGATTCG
TTACGGGTAGACCAATACTTGATTGTTTTCTTAAAGTTTATTACTAGTGTACACCGAGTATACAACATG

ACTATACCATGGAAGGTTGGTAA

NN. ATG4 (autophagy related 4 cysteine peptidase)

>tr|K1QKP1|K1QKP1_CRAGI Cysteine protease OS=*Crassostrea gigas* OX=29159
GN=CGI_10023225 PE=3 SV=1
MDMTNDVGTTCMVTYESAALGYVDFPLTEEPVYLLGIKYSALYDRDELKGFSLKIWCTYR
KNFPAIGGTGPTCDGGWGCMLRCGQMMMLAQALVVRHLGRDWKWNKNCQDQTYKRILQMFA
DKKSANYSIQQIASMGVSEGKPVGSWFGPNTVAQVLKKLAVYDEWSSIVIHAMDNVTVE
NDIKSVCKDDGKSTCDIIIGVRQLKHESAATGRSKKSSQDSSKQDKNKQNAVDVKSWKPLL
LVIPLRLGLTEINSVYVQSLKAACLSFPQSVGIIIGGKPNHAHWVFGYMSDKLIYLDPHTTQ
LCEDLDSPNFSDESYHCPYPSTMNVMELDPSIALGFYCGTEKEFDLDTQSVQKFFVVGSSK
TPMFELYKDRPPHPYESYTGQTTASASVMTMTGGQDTDEEFELV

>XM_011441099.2 PREDICTED: *Crassostrea gigas* cysteine protease ATG4C-like
(LOC105336676), mRNA

GGAGATTTGTCATGTGAAAGAGAACTTGACGGATGTCACGGATATGTTAATGTTCCGACGTTTCGTACAA
ATTTTGGTTAAAAATGAATTAAGATGAATCGAAAACTCCCAAGAGTTACTCTCGTCGAGTATCTGAGGA
TGTGGCTTCTTTAGATTCGAGTGAAGCTCTGAGTGATGTGTCAACTATAACGGTAAATGATAAA
GGCCATCCTAAGTCTGTAGATTTAAAAGCGAGGAAAACTCTTCTAATAACCGCTTTTATTGAATC
CAGCAAAGTTGGTTTCTCAATCCTCATCGCGAAATGCTGTTTCGGAACAGAAACGAAGAAAGTGGGAGAAG
ATTCGAAGCGAGTAGTTTCGGGACCAAGGCGAAATCCTTCAGAACAAACAGGTGTGAAGTTTGACATCTCT
ACAAGCGATCCCTTTGATATTGACGATGGATCATTTCGATAATATCAACAGTGTGTATTTATCATTGCCTG
AAGGACATGGGGCTTGTCTAAAGGAGTCATATTCCACCATCAGTACCTCGGAAAAATAACCTGGACTATAA
TGACTGTAGTGATTTTTCATAGCCTCCAGATTTAACTGCGGTTAATTCAAAGACACGGACGTATCCCCCT
CACTATGTACACCCAAAATCTTTGCAATATCCAACACAGGGTGAACCTTCGAAAAAGTGAAAAACAAGT
TAATGTCCATGTGGAACAATGTGAAATATGGATGGACGTTGAAGACAAAGACCAGCTTTAGATTTGACAG
TCCAGTCTGGCTTTTGGGAAAATTTTACCATATAAAGCCAAGTGATCTCATAGATGATGATATTCAGAGA
GGAAAAAGAACAAGAGTTGTGCCAAACATTGAAAAGTTCAAACAGGATTTCTCGAGCCTGCTGTGGTTTA
CGTATAGACAAGACTTCCCGGCTATCCCGGGGACCAAGCTGACCTCGGACTGTGGGTGGGGGTGCATGTT
AAGGAGTGGTCAGATGATGCTTGCTAAGGCTCTCACATTACATTACTTAGGACCAGAATGGAATGTGTTT
AGTGACCAACAAGAGAACAGGAAACGTACAGGAAGCAGATAATCCGCTGGTTTGGAGATTACCTCTGTG
ACGAGTCACCGTTCTCTATGCACCGATTGGTGGAGGTTCGGGAAAAATCTTGGCAACAGCCAGGGGAGTG
GTTTGGTCCCGCCTCAGTCGCTCACATACTCAAGGAAACAATGGTGAAAGGACAGAAGACACAGACAGTT
CTGTGATCTCTGTGTATATGTCTCTCAGGACTGCACTGTCTACAAACAGGACATATATGAGCTCTGTT
GTACCGCAGCCGAGGGCGGATACAAAGTTCCACCACTCCACGGAGTCCGAGCATGAATCCAGTCAGGATGC
TTCTCCATCCAGTGAAGCGGGCTGTCGTGATCCTTATTTCGGTTAGACTAGGAGGGGACAGCTTAAT
CCAGTCTACATTCCTTGTGTGAAAGGGCTTCTATCTCAGGACTCCTGTATCGGCATCATCGGAGGGAAGC
CCAAACATTCACTCTACTTTGTAGGATGGCAAGAGGACAAACTGATATATTTAGATCCACACTACTGTCA
GGATGTGGTTGACACAAGGGAGAGACACTTTCCAATCCAGTCTTATCACTGTATGTCGCCCCAGAAAAGT
TCCATTGACAAAATAGACCCTAGCTGTACCATTGGCTTCTACTGCAGAAAACCAGAAAAGATTTGAAAAGT
TTGTACAGCAAACAGAGGAGATGGTGGCACCACCAAAACAAAGGCTTTCTACCCAATGTTTGTGTTTCAG
TGATGGACATAGTAATGAGGTCAAGATAGACACGGCTGAAAAGGACCGCTCCTTCGAGTCAAGCACGTT
CGCCTGGACGAATATGGTCGCATTCGTTCCAGACACTGGATTCTGAGGAATTTGTAGTTTATAAACAC
TATTTATTTGTTGACTTAGCCTTATTATATAATGGAGTGCAGTAGTACAAATTAGCATGTACATGTATGT
TTCTCCTTCTTGAGAGCTATGTTTAAACATTCATACTATGTTAACAATCTTCTAGCATAATGAAGCATAT
CAGTTCTTTGATATCTGAGGCATTACCTTAGCCACTATCTGGAGCATATATTTATAGGGTGTAGTTAAA
ATCCCTGTAAAAGAAAATCTGAGGGAAGGTGATATCTGAGGCATTACCTTAGCAACTATCTGGAGCATAT
ATTTATAGTGTGTTAGTAACATCTGTCCATCTTGTTTAGAAAGTATATAAAGCTCAAATGGATTTGTGTC
CTAACCTTATTTTCGATACGACATATTTACTCCTAGTTGTGTGAAGTTAATCCCAAGCAGTTAAAAAGT
TCAGATTTCAAAGACATCAAAGGGATATGGATCGCGCTTATTTTTAGCCTAGAATAAATACCAGACGTA
CCATACATGTAAGAACTTGACGACAAAATCCAGATGTCTAAGTTATGACAATCAATTACACTTCATGAG
AGTCTTTCCCTGTAAGAAGTGTTCGTCTACATGTATAACAACACTGCTCTACTTTCTTGGTAAATGCACAC
TGTAAAGTCCATCATATTAACCTCACCATGTTTTCATCTGTCTTGTGCAATAGCGAGACTTGCATAAAC
TGTCCCAAATGATGGCAATGTTAATTTTGTGTGAACTCTCTCAAACATCCCGAGTTTATTTTGGCGT
GTTAATTTTGTATTGGATTGAACCTATTTGCCAAGTTGAACAATGTCAAATATTTGACACTTTTAACTT
AATGTGGTGACTTAAGTCTGTACTTCAGTTAGTACGTGATGTTGGTAAATTCAGGTTTCTGAGGATTCAC
ATTTTACTGTATCTCGTATATTCATGATTAATTAATTACCATTGGGCACTAGAATGATTGCTCACATCA
AAGAGTAAAGAGAATTCTCTGGTTACTTTGCATCTTGATATGTAGTATTGGAAAATTTGTTTGCAAAATG
AAGGAATTTAATTTAGAATTTACACTATTTTTGGTGAATTTTTAATCTGCCAGTTTTTCGGTACAGGTA
TTTGAGAATAAGAATTCAAAGAATGTTTTTCATAAGATTACCTCCATGTACATATATATATATAACAAC
TGATTTAGGAGAATAACCAGGATGCATCAAAGAAATCTTAGATAACCTTGAAGAGATCAGCCAAAATTA

CGAACTCTGTACAATGTATACATATGATTTCCAAGCTACATGCTTGTCTTTAAACAAAATAGATGGCTGT
ACATATGAAGAAAGATGTACTGTTATAAAGCAGTTCAGACCTATTTTATTTGTACAAGAATATACATGTA
TGTATATTTTATTGTTAATGTTAATTGTACATAATGGTTAATCATGTACCGTACATTATTTTTGATTTGC
AATATTTGTATATTATGTTAATTTATTTTTTGGCTGTACGATATGAATCAGATGGCAGTAAATGGGAAAT
ATACAAGTGTGTTTTACAAATTGTCTTAGCATAATTTTCGGTCAAGTATGTGATTGTTTTGGGTGACCT
ATTTCTTGAATGTTGTTGTTAATGAATATGAAATAAAATATTGAATTTTACCAAAAAAAAAA

>sp|Q8WYN0|ATG4A_HUMAN Cysteine protease ATG4A OS=*Homo sapiens* OX=9606
GN=ATG4A PE=1 SV=1

MESVLSKYEDQITIFTDYLEEYPDTDELVWILGKQHLLKTEKSKLLSDISARLWFYRRK
FSPIGGTGPPSSDAGWGCMLRCGQMMLAQALICRHLGRDWSWEKQKEQPKEYQRILQCFLD
RKDCCYSIHQMAQMGVGEKSGIGEWFGPNTVAQVLKLLALFDEWNSLAVVVSMDNTVVIE
DIKKMCRVLP LSADTAGDRPPDSL TASNQSKGTSAYCSAWKPLLLIVPLRLGINQINPVY
VDAFKECFKMPQSLGALGGKPNNAYYFIGFLGDELIFLDPHTTQTFVDTEENGTVDNQTF
HCLQSPQRMNINLNDPSVALGFFCKEEKDFDNWCSLVQKEILKENLRMFELVQKHP SHWP
PFVPPAKPEVTTTGAEFIDSTEQLEEFDLEEDFEILSV

>XM_017003638.1 PREDICTED: *Homo sapiens* autophagy related 4B cysteine
peptidase (ATG4B), transcript variant X3, mRNA

TTGTTTGTGATGCAGGATTTTTCTCAGCCACTCTGGCAGCCAGAGACCTCCGGCTGGCGAGGCCCTGCC
CAGGCCTTGCTTGGGTCCAGGCTCGCCGAGGAGATAACCCATCTACTTGGTCCACCGGTGGGCACCTGG
TTTGCACTATGGCACGGATAACCATGGCCACCATGACTGTATGCTCAGCCCCTGGCGGGAGTGGGTGTGTG
GCTACTCTGACCTACGACACTCTCCGGTTTGTGAGTTTGAAGATTTTCTGAGACCTCAGAGCCCGTTT
GGATACTGGGTAGAAAATACAGCATTTCACAGAAAAGGACGAGATCTTGTCTGATGTGGCATCTAGACT
TTGGTTTACATACAGGAAAACCTTTCCAGCCATTGGGGGGACAGGCCCCACCTCGGACACAGGCTGGGGC
TGCATGCTGCGGTGTGGACAGATGATCTTTGCCCAAGCCCTGGTGTGCCGGCACCTAGGCCGAGATTGGA
GGTGGACACAAAGGAAGAGGCGAGCCAGACAGCTACTTCAGCGTCCCAACGCATTTCATCGACAGGAAGGA
CAGTTACTACTCCATTCACCAGATAGCGCAAATGGGAGTTGGCGAAGGCAAGTCCATAGGCCAGTGGTAC
GGGCCAACACTGTGCGCCAGGTCCTGAAGAAGCTTGTGTCTTCGATACGTGGAGCTCCTTGGCGGTCC
ACATTGCAATGGACAACACTGTTGTGATGGAGGAAATCAGAAGGTTGTGCAGGACCAGCGTTCCTGTGC
AGGCGCCACTGCGTTTCTGCAGATTCCGACCCGCACTGCAACGGATTCCCTGCCGGAGCTGAGGTCACC
AACAGCCCGTGCCTTGGAGACCCCTGGTACTTCTCATTCCCTGCGCCTGGGGCTCACGGACATCAACG
AGGCCTACGTGGAGACGCTGAAGCACTGCTTCTATGATGCCCCAGTCCCTGGGCGTCATCGGAGGAAGCC
CAACAGCGCCACTACTTCATCGGCTACGTTGGTGGAGGCTCATCTACCTGGACCCACACCACGAG
CCAGCCGTGGAGCCACTGATGGCTGCTTCATCCCGACGAGAGCTTCCACTGCCAGCACCCGCGTGCC
GCATGAGCATCGCGGAGCTTGACCCGTCCATCGCTGTGGGGTTTTTCTGTAAGACTGAAGATGACTTCAA
TGATTGGTGCCAGCAAGTCAAAAAGCTGTCTCTGCTTGGAGGTGCCCTGCCCATGTTTGGAGCTGGTGGAG
CTGCAGCCTTACATCTGGCCTGCCCCGACGTCCTGAACCTGTCCCTAGATTCTTCTGATGTAGAGCGAC
TGGAAAGATTCTTCGACTCAGAAGATGAAGACTTTGAAATCCTGTCCCTTTGAAAATCCTGGGGTCGGGG
GTGGCACCTGTGAGAGCCTGGGGCTCCTGGTGCCGCTGCGTTTTCATCCATCCCGCCGCTCGCTGCCGA
GGGCTGCGCCCCGTGCTGCCTCCCCCAGAGGGCCACCCGCTGTGCTCGTGGACTGAGGCTGCGCTGCC
GGGAGGCCTTACTGCTTGGTGTGACTGCCCAGCTCAGAGTGCCCGTCCAGGGCCTGTGCATCCGCACGC
GGAGCCGTCTGTTAGGAGCTTCCAGAGTGTCTCTCGACACTGCCAGCCCCGTGTTAGCACCTGGGCCCTC
AGTCCCCTTGTCTCCAGGCGCCGGTTCTGTGGTTGGTTTTGGAATTAAGTCCCTGTTTGAAGTTGTCAGA

>sp|Q96DT6|ATG4C_HUMAN Cysteine protease ATG4C OS=*Homo sapiens* OX=9606
GN=ATG4C PE=1 SV=1

MEATGTDEVDKDKTKFISAWNNMKYSWVLKTKTYFSRNSPVLGKCYHFKYEDEDKTLF
AESGCTIEDHVIAGNVEEFRKDFISRIWLTYREEFPQIEGSALTTDCGWGCTLRGTGQMLL
AQGLILHFLGRAWTWPDALNIENSSESWTSHTVKKFTASFEASLSGEREFKPTPTISLKE
TIGKYSDDHEMRNEVYHRKIIISWFGDSPALFLGLHQLIEYGKKS GKKAGDWYGPVVAHI
LRKAVEEARHPDLQGITIYVAQDCTVYNSDVIDKQSASMTSDNADDKAVIILVPVRLGGE
RTNTDYLEFVKGILSLEYCVGIIGGKPKQSYFFAGFQDDSLIYMDPHYCQSFVDVSIKDF
PLETFHCPSPKKMSFRKMDPSCTIGFYCRNVQDFKRASEEITKMLKFSSKEKYPLFTFVN
GHSRDYDFTSTTTNEEDLFSSEDEKKQLKRFSTEEFVLL

>sp|Q86TL0|ATG4D_HUMAN Cysteine protease ATG4D OS=*Homo sapiens* OX=9606
GN=ATG4D PE=1 SV=1

MNSVSPAAAQYRSSSPEDARRRPEARRPRGPRGPDNGLGSPGASGPALGSPGAGPSEPD
EVDKFKAKFLTAWNNVYKGVVKSRTSFSKISSIHLCGRRYRFELEGDIQRFRQDFVSR
WLTYYRRDFPPLPGGCLTSDCGWGCMLRSGQMMLAQGLLLHFLPRDWTWAEGMGLGPPELS
GSASPSRYHGPARWMPRWAQGAPELEQERRHRQIVSWFADHPRAPFGLHRLVELGQSSG
KKAGDWYGPSLVAHILRKAVESCSDVTRLVVYVSQDCTVYKADVRLVARPDPTAEWKS

VILVPVRLGGETLNPVYVPCVKELLRCELCLGIMGGKPRHSLYFIGYQDDFLLYLDPHYC
QPTVDVSDQADFPLESFHCTS PRKMAFAKMDPSCTVGFYAGDRKEFETLCELTRVLSSSS
ATERYPMFTLAEGHAQDHSLLDDLCSQLAQPTLRLPRTGRLLRAKRPSSEDFVFL

>sp|P53867|ATG4_YEAST Cysteine protease ATG4 OS=*Saccharomyces cerevisiae*
(strain ATCC 204508 / S288c) OX=559292 GN=ATG4 PE=1 SV=2
MQRWLQLWKMDLVQKVSHGVFEGSSEEPALMNHDIYIVLGEVYPERDEESGAEQCEQDCR
YRGEAVSDGFLSSLFGREISSYTKFLLDVQSRVNFYRTRFVPIARAPDGPSPLSLNL
VRTNPSTIEDYIANPDCFNNDIGWGCMI RTGQSLLGNALQILHLGRDFRVNGNESLERE
SKFVNWFNDTPEAPFSLHNFVSAGTELSDKRPGWEFGPAATARS IQSLIYGFPECGIDDC
IVSVSSGDIYENEVEKVF AENPN SRILFLLGVKLGINAVNESYRESICGILSSTQSVGIA
GGRPSSSLYFFGYQGN EFLHFDPHIPQPAVEDSFVESCHTSKFGKQLQSEM DP SMLIGIL
IKGEKDWQWKLEVAESAI INVLAKRMDDFDVSCSMDDVESVSSNSM KK DASNNENLGV
EGDYVDIGAI FPHTTNTEDVDEYDCFQDIHCKKQKIVVMGNTHTVNANLTDYEVEGV LVE
KETVGIHSPIDEKC

>NM_001183061.1 *Saccharomyces cerevisiae* S288C cysteine protease ATG4
(ATG4), partial mRNA

ATGCAGAGGTGGCTACA ACTGTGGAAAATGGATTTGGTACAAAAAGTGTCTCATGGCGTTTTTGAAGGCT
CGTCCGAAGAACCGGCTGCTCTTATGAATCATGATTATATAGTATTAGGGGAAGTATATCCTGAGCGAGA
CGAAGAATCTGGCGCTGAACAATGTGAACAAGACTGTGCATATCGCGGTGAAGCGGTTAGTGACGGGTTT
TTAAGCTCTCTTTTTGGTAGGAAATTTCTTCTTACACAAAGGAATTTCTTTTGGATGTACAATCAAGGG
TCAACTTTACATATCGGACAAGATTTGTTCCCTATAGCAAGGGCGCCAGATGGGCCTTACCTTTAAGTCT
AAATTTATTAGTACGTACAAATCCGATCAGTACAATAGAGGACTATATAGCAAATCCTGATTGCTTTAAC
ACTGATATTGGGTGGGGGTGTATGATAAGGACAGGACAAAGTTTGTGGGGAATGCCTTACAAATCCTTC
ATTTGGGCAGAGATTT CAGGGTAAATGGTAACGAAAGTCTGGAAAGAGAATCAAAAATTTGTAAATTTGGTT
TAATGACACGCCTGAGGCTCCATTTTCGTTACATAACTTTGTTTTCTGCAGGTACAGA ACTCTCTGATAAAA
AGACCAGGTGAATGGTTTGGTCCC GCAGCTACGGCAAGGAGTATACAATCTTTAATATATGGCTTCCCCG
AATGTGGCATCGATGATTGTATAGTATCTGTTTCATCCGGCGATATCTATGAAAATGAAGTTGAAAAAGT
ATTTGCTGAGAATCCAAATAGTAGAATATTGTTCTTGTGGGCGTGAAGCTCGGGATTAATGCGGTAAT
GAGAGCTATAGAGAAAGTATATGTGGTATCTTAAGTTCAACACAGTCAGTAGGCATTGCCGGCGGTAGGC
CGTCTTCATCGTTGATTTTTTTGGTTATCAAGAAATGAATTTTTACATTTTCGATCCTCATATTCCTCA
ACCGGCAGTAGAAGATTCATTTGTAGAGTCGTGCCATACCAGTAAATTTGGTAAATGCAACTATCGGAA
ATGGATCCCTCGATGCTCATTGGTATTTTGATTAAGGGCGAAAAAGACTGGCAACAATGGAAGCTAGAAG
TTGCAGAATCTGCTATTATCAATGTTCTTGCTAAGAGAATGGATGACTTTGATGTGAGTTGTAGTATGGA
TGACGTGGAAGTGTAAGTTCTA ACTCAATGAAGAAAAGATGCAAGCAATAATGAAAATCTCGGAGTACTA
GAGGGAGACTACGTAGATATTGGTGCAATATTCCACACACAAACAAATACAGAAAGATGTAGACGAATATG
ATTGTTTTCAAGATATTCATTGCAAGAAACAGAAGATTGTTGTTATGGGAAACACACACTGTTAATGC
GAATTTAACAGATTATGAAGTAGAAGGCGTCTTGTAGAGAAGGAAACGGTAGGTATTCACAGTCTTAT
GATGAAAATGCTAG

OO. SQSTM1 (sequestosome 1)

>XM_011453843.2 PREDICTED: *Crassostrea gigas* sequestosome-1 (LOC105345634),
transcript variant X1, mRNA

TTGGTTATGCAAAGTCACATGACCATGATGTTGTGAATTTGACAGGTCCTATAAAAAGCCAGACTAAGCCA
TTTGCAACCATTATTGGCCATTTTTGAGATAGAAGGAAGGAAGCTACAAGACAAACGAATATTTCCCGA
AAAGTACATTAGTTGTCAACTAATTTATTTGAAAAGTACGAGATCCAAGATGTC ACTTACTGTAAAAGC
ATTTTTGGTGAAAGGAGGGAATGAGAAGGCCGAAATTCGACGCTTACAGTGCCTCAAGATGTATCCGCA
AGTTTTGATTACCTGCAGAAGAAGATCGCTGACATCTTTCCAGGACTTGCTCGAGGCAACTTTAATTTGT
TTTGAAAGATGAGGATGGTGATCTTATTGCCTTCTCAACTGGAGAGGAGTTGCTTGAGGCTTTGGGAT
TGTGGACAATGGACTTTTCAGAGTTTTTGTAAACCAACATCTCAGTCAAGTGGTGACAAACCAGCAGGA
AATACTCCCATGCAGGAGCATCCTGGAATCATCTGCATGGATGCGAGGGTAAAGTGATCGGAAGACGGT
ACAAGTGTACTGAGTGTCCAGATTATGACCTGTGTCCAGATGCGAGTCCAAAGGAATCCACTCGGAGCA
TAACCTTTATGATGTATGACACCCCTGTCCACCTGGATTTGGATTCCCCTTCTCCTGGCCCCCAAGACC
CAGTGTCCCCCTGGGCCCCGTGGACCTAGTGGCCAAGGACAACCCCCATGTGCCCTCCCCACTTTTTCC
GTTGGATGGAGAGAATGGCAAGGAGACAGCAAAACAGAGATAATGCTGGCTGTCCCAGGAGTGGCCAAAG
GAACGCTGAAGATCAAGGGTCAAATGACACCAGTGGAGAGGGTGCCTACAATCCCGAGGAATTCCTGCAG
AATGTTGGCCAGAGTGTGGCTGCTATGCTTGATCCATTAGGAATTTGATGTTCAAGTGGATGTTGAACATG
GAGGACGTAGATGCCAGCTTGGGGACAGGGTGGAGGATGCAAGGGAAAGAGAAGTGGAAAGTGTGGACA
AGGAAAATGTGGAACAAAGGAGAACAGGAGGAGAAAATGGAGTCTGACAAAGTGGAGACTGAACAGATG
AAGACCCAGAGGAGGCCACTCCAATGGCCACCGACAATGCCGACAAGCTGCAGACAGATGGACCATCCA

CAAGCGCAGAAAATGCCCAAACCCATCTGAAAAGGTCACCAAGGACTTTGAAACCTGGACCTTCATGGA
GGATGGCAATAGATCTGGGAGAAGTCCCTCTCCCCCTGCTCTACCCCAGTACAGCCCCCTCCCACCCAG
CTGATCTATCCCCCACAGATCCAAGAATTGCAGAAGCCCTGCAGCAGATGCTCGGAATGGGATTTTACA
ATGAGGGAGGATGGCTACAGAACCTGTTGGAGCAGAAGGAGGGAAACATCAGCCAGGTGTTGGACGCCAT
CCAGACCAGAGCCAAGACCACCCCTGATGGCGGCTTCATGGCCTAAACCCATGGGAAAGATGGAAATATA
TAGAACTGGAGACAGATTGGACTTTGTCTTGACTTTTAATTTTTTGGTGGATGTTGTAATTTTTTGTAGTT
TGGAACCTTTTCTTATTAATATGAATCACTACCTATAGTGTGTGCTTATTCTGTTTGTGTTTGAATTGTTT
TTTTATTCTAGTATTTTTGGAAACATGACTTGTGTATTTTTATTTTTTTAACCATGTAAACATTGAAATCAAT
CTTGCTTAACACAGACATTATGATTTTTGAAAATGTATATTTAAAAATTGTTAAACCTGTTAACGATAATT
GTGGTACTGCTTTCCCAAATGATAAAATATTTAATTTATAATCAAATAAATGACATAAATGAAACAATT
GCTGTTTCATATTTAACCATATTATGCATGGGTAACCTTGCTTCATCCTGCAAAAAAGTAGTACTGCGGTTA
TAGTGAAGCAGTTTTTATGTCAAATTGCTTTATGAATACATGTAACATCAGTCGGATTTCTGTTGTTGG
GCTGGTTCTAATTAGACTTACAATTTAGAGTTATTTCAAAGATCATGTATGATAACAAGAAGGGATGACC
TATTATTATTTTTAGACAAATTGGGAATTGTTGAATCTTTGATATTTTCAATTTAGTAAATTGTCTATTTTA
ATTTTTTGATCTTACTTAGAACCTACTACATGAAAAATTTTTGTTATGTTATTGTCTTGCCTACTTTTTA
ATGACCAAAATTCATAAAAAAAAAATCATCAAATAATA

>sp|Q13501|SQSTM_HUMAN Sequestosome-1 OS=*Homo sapiens* OX=9606 GN=SQSTM1
PE=1 SV=1
MASLTVKAYLLGKEDAAREIRRFSFCCSPEPEAEAEAAAGPGPCERLLSRVAALFPALRP
GGFQAHYRDEGDGLVAFSSDEELTMAMSYVKDDIFRIYIKEKKECRDRHRPPCAQEAPRN
MVHPNVICDGCNGPVVGTTRYKCSVCPDYDLCSVCEGKGLHRGHTKLAFFSPFGHLSEGFS
HSRWLRKVKHGHFGWPGWEMGPPGNWSPRPPRAGEARPGPTAESASGPPSEDPSVNFKNV
GESVAAALSPLGIEVDIDVEHGGKRSRLTPVSPSSSTEKSSSQPSSCCSDPSKPGGNV
EGATQSLAEQMRKIALESEGRPEEQMESDNCSGGDDDWTHLSSKEVDPSTGELQSLQMPE
SEGPSLDPSQEGPTGLKEAALYPHLPPEADPRLIESLSQMLSMGFSDDEGGWLTRLLQTK
NYDIGAALDTIQYSKHPPL

PP. Atg29 (autophagy related 29)

>sp|Q12092|ATG29_YEAST Autophagy-related protein 29 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG29 PE=1 SV=1
MIMNSTNTVVYIKVKGRRPQGFDPKFEWNGTKERQLWMTMVSNLNYSQDQIDWQNLSKI
FETPEFFLKKRKYKLF AEHLELLQLQLEKKRDLEKYSNDQVNEGMSDLIHKYTPTLQNDN
LLNVSASPLTTERQDSEEVETEVTNEALQHLQTSKILNIHKKTS DSENKPNDKLKDGIN
KEMECGSSDDDLSSLSVSKSALEEALMDRLQF

QQ. Atg 31 (autophagy related 31)

>sp|Q12421|ATG31_YEAST Autophagy-related protein 31 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG31 PE=1 SV=1
MNVTVTVYDKNVKYRLEENIKNNKGPSNDDQPAYNNESKSTDGSDYAMFPTNIKIYIFEDN
NDELVDSSDAALTAGIDKVGDELENIIVQLDESGSLEDITLISDQYELLSHRTNSLSLE
ENQMRTLSSHGDDKSNDEEEELSVDSDFRVDSDIELDVISQFCDLSPFLRDLSLNDLIK
LYVTQNEQLQMLSNSV

RR. Atg20 (autophagy related 20)

>sp|Q07528|ATG20_YEAST Autophagy-related protein 20 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG20 PE=1 SV=1
MSDLNDVQENAKLNSETRNTGKAEPPHGTTEYVAEAEISKNGVGSPPKSPKKGKVGKGDN
NKVETELVHTALLEKDNPFMEEGPTGFTKSALLEIPGMRSHNLKNPNEDYEDDSEGLLPL
NQESNAETCRTSLSGSINSMNGETSASEEPSVSNRKK SARIHILEAKRVSEGQGRAYIAY
VIQFENSTVQRRYSDFESLRSILIRLFPMTLIPPIPEKQSIKNYGKSITGSSSKYLLPSE
GSGSVDLSLSVIHASVNSDEKLIRHRIRMLTEFLNKLLTNEEITKTSIITDFLDPNNHN
WHEFVNSSSTFSSLPKSI LQCNPDPNTTTRIHAMPLIPGSSSQLLLNKESNDKMKDKER
SKSFTNIEQDYKQYENLLDNGIYKYNRRRTTKTYHDLKSDYNEIGEVFAQFAHEQAQVQV
AEQLSYLSNAFSGSSISLEKLVGRLYNINEPLNESVHMATSARELIKRYRKLKYLQNEMI
KKSLNSKRAQLEKLEAQNNYKDVDKIIDNEMSKSHTINLERPNNTGSGGKSYGGKLFN
GFNKLASMVKDSVKYQETDPHTASINLKEIEQLSESLEVTENDLEVISKVIKNDQLPKF
SKEREVDLSEILKHYSRYMRNYARQNL EIWKEVKRHQDFA

SS. Atg24/Snx4 (sorting nexin 4)

>sp|P47057|SNX4_YEAST Sorting nexin-4 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=SNX4 PE=1 SV=1
MTDKGKNDLTSKAKDKARGNPEKPPYWFEEIIVSDPQKRTGDPGSSSGYVSYQISTKTNNT
SFYDNRGDPESIIIVVHRRYSLLLLLHDILLNRFPCTCIIPPLPDKKVFQYIAGDRFSQRFT
QKRCHSLQNFLLRRVSLHPDLSQSKVFKTFLVSKDWESHKVLQDSLQPNKDEVTDAFMNA
FKTVHKQNEEFTEIREKSDKLDRTVTVKIDKLFHKVVKKNDMSSEYTKLGSNLQELQELV
TGENEELAALKLIFNEGVTSYGLQDLTKYLDYEYIVDLKDLEHYIDSMRQLIKLKDQK
QIDYEELSDYLTRSIEKNNLISGYGGSNFFANKLEELAGINQEASRREKINKLEGKITS
LTGELENAKKVADGFEQECLKEIDHFESVKTAEIKKSLGSLADHHIEFYERILEAWEKVD
DSL

TT. Atg23 (autophagy related 23)

>sp|Q06671|ATG23_YEAST Autophagy-related protein 23 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG23 PE=1 SV=1
MELNQVLEKKEQILQYLGTLVGLHEKALSDVNSASQVTSIRKIDITICLNDLCRINDLLVS
HDGLLKREIGSLLRDKQELLELNEREQLLWKERKSWHIKQETDAAPADYVIDKDAIITIS
SHHRTSLNKYIESVGAENTILSNTDDSDAMIEEVQNAESSADQMIRNYKLLQLSHKQAKS
EIIIRLETLLRDFKKNKFIIEELKRQSGRIRSEMGNIDFHLKSKIEESKHQLMKRIGFESP
LTQEKSLSEKIFNLRLSSADEDYNERQTIINMKNFVHMKDIELKIEDLQEQLMRNKNESS
TVLTQRELWLDQCQKVGDLSEKLIKLRSSSNKIPPNEMSEMINSTIQYLNLLDSSDE
KLTTTLISNERDVLKACEELHSESTTAQDGSALPSKPIDIHKSHKGSNASSNLKQPST
PSFLVASKSPPKIGISESVVNANKNDIAISKKVE

UU. Atg27 (autophagy related 27)

>sp|P46989|ATG27_YEAST Autophagy-related protein 27 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG27 PE=1 SV=2
MVSKTWICGFISIIITVVQALSCEKHVDLKKYQVGKFSSTLSTERDTPPSTTIEKWWINVC
EEHNVEPPEECKNDMLCGLTDVILPGKDAITTIIDFDKNIGFNVEETESALTTLTKGA
TWGANSFDKLEFQCNDNMKQDELTSHTWADKSIQLTLKGPSGLKSKDDDKNGDGDNG
KGDGSEGGKPAKKAGGTSWFTWFLYALLFTLIYLMVVSFLNTRGGSFQDFRAEFIQRST
QFLTSLPEFCKEVVSRIILGRSTAQRGGYSAV

VV. Atg19 (autophagy related 19)

>sp|P35193|ATG19_YEAST Autophagy-related protein 19 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG19 PE=1 SV=1
MNNSKTNQOMNTSMGYPLTVYDECNKFQLIVPTLDANIMLWCIGQLSLLNDSNGCKHLFW
QPNDKSNVRILLNNDYDGHFLFKYLQCRKCSVYIIGEGTLKKNYNTISTSFDFNFDLTPSE
EKESLCREDAHEDPVPKAGSEEEIISPSTSNVVVSRECLDNFMKQLLKLEESLNKLELE
QKVTNKEPNHRISGTIDIPEDRSELVNFTELKTVKQLEDVVFQRYHDIYERLSQECDKTE
IASDHSKKEKIEVEPPNERSLQITMNRDNSLYFQLFNNTNSVLGNCKLKFTDAGDKP
TTQIIDMGPHEIGIKEYKEYRYFPYALDLEAGSTIEIENQYGEVIFLGKYGSSPMINLRP
PSRLSAESLQASQEPFYSFQIDTLPDLDDSSIIISTISLSYDGDNEKALTWEEL

WW. Atg17 (autophagy related 17)

>sp|Q06410|ATG17_YEAST Autophagy-related protein 17 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG17 PE=1 SV=1
MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKLSSWQLSISKLNFLIVGLRQQGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKYWQYEITSKVQRDLGIVNELSISEKDDT
DPSKLGDIYISRDVNLNDKLEKVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVDTQK
FQSKFGIDNLMETNVAEQFSRELTDLKDLAEIMNSLTQHFDKTLQLLQDKKIDNDEREEL
FKVVQGDDEKELYNIKTLHEVIDDVDKTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLDISFKNSCTQDIQTTELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQEERQNFIAENGTYPETIWPBKIDDFSSLYTLNKNVKNP

XX. Atg11 (autophagy related 11)

>sp|Q12527|ATG11_YEAST Autophagy-related protein 11 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG11 PE=1 SV=1
MADADEYSTAPTQQEITPLQTTATIINAISGECITTNVDFVSLDKFKQFIARKWKIPPD
QLLILLPYGNKPKSMFKELLINRSFTLNDFYVYDRRLFSLVSKPTPTNLLTSKDSNPMN
SPNSNDLTETLEYLIKNSHISQYQGSDTIMIKPMPSPLEDADVDLSRLNYHSVTSLLTTN
LGWLSALEIDVHYFKSLIPDIIAHIKRIFDGLTVC SQYLKLYCFDVESLYNSNVQFLNQL
VDNGMTSKWEKCFNDTLSKLTALEGDSLQKFINIESLLENEKSVKILNHSINGKLNKIKR
EIDENASFRDIIITVNIDRLRQMFTPNESKFELEDQMAESFEVLVSEMRTRSRNVLDKEEE
EFNSQEFKSMNVMLEKDKKESVKTLFTISQALYSQIGELIDLKKS LQKHAVAILGNIAF
TQMEILGIKRLLLNECNKDLELYKKYEVEFAQVEDLPLIYGLYLIIEKYRRLSWFOQILSF
ISNFNQDLELFKQNELRTRNKWVKNFGSIATVFCEDLLSSSDFKRLNEYHSHTSPPNEDE
EDENENSIANYRQDLVKVVSQAIDNYMTQIKETDVSEPIIDLKSKTLFETKRFHIIYSNFK
NNNNNSSNGNSISPEGSIALKSDDVVKGYKTRIKKLESLLHEFQYSDIGHWPQGVNLNTHL
KPFGRSATSINKKKFLGASVLEPANISEVNIDSVSQANNHQIQELESNVDDLHLQQLL
KEENNRKSMQISEMGKKISDLEVEKTAYRETLTNLNQELARLTNEEQSHRTEIFTLNASF
KKQLNDIISQDNEKIEKLTGDYDDVSKSRERLQMDLDESNNKHEQEVNLLKADIERLGKQ
IVTSEKSYAETNSSSMEKGEKFETIPLAEDPGRENQISAYTQTLQDRIFDIISTNIFILE
NIGLLLTDFNNNNIQIRRVKGLKKGTAQSNILDESTQMLDAHDNSLIKSPVFKLQKDEYE
LIKSVANGSEKDTQQSIFLGNITQLYDNKLYEVAVIRRFKDIETLAKKLTKENKIKRTLL
ERFQREKVTLRNFQIGDLALFLPTRENVNSVGSMSSTSSLSSSFSSVDLSTPPPLDAMS
IQSSPSVIHSNVINQASISGRDKNKLMPWAAFTAFEESTRYFLKDEKGLTKGKEWVGR
IVTLEHFVADSPSNNPFRLPKGSVWFQVTAVVVSYQGV

Figure S2. List of amino acid sequences of the species used to performed phylogeny analysis of ATG7, ATG9A, ATG12 and ULK2. All sequences are in FASTA format. The species name of the sequence is highlighted in yellow.

A. ATG7

```
>MK173046|Ubiquitin-like modifier-activating enzyme ATG7
[organism=Crassostrea gigas] mRNA, complet cds
MSAPLVNKMESKQLQFVAFNSFLDSGFWHKLSSENKLDVYGLDESQKEIKG
FYFNGDPVGMPCRMNVEFSAFDQDAKTPQRYLPMLGELHNTNTVDKFKEC
DKKEMISVAGKKIWDIVTGKALDTPPELLATFLLLTAFADLKKYHYWFC
FPCLCPSTDITFDQEPKLLKDKLTAEEMEQFLQAYDTFQDAYPTYQGFFV
AVLSKGNIVIEDVKHMKNKFENTQEVYFGFCDPNIEDYPGWPLRNFMLLI
SYHWKGDRLRGNVNLCLDRSRDGTDRDISHSLLLSLNVDPDIKNVSECPKCV
GWEKNEKQKLAPRFVNLASMDPTRLAASAVDLNLKLMRWRLPELDLDDL
ISRTKCLLLGAGTLGCNVARCLMGWGVRTITLVDNGRVSYSNPVRQSLFQ
FEDCVKGGKPKAEAAAEAMKKIFPGVNAKGLSLSIPMPGHAVPESAIEGV
KKDVETLQDLVNSHDAVFLLLDTRESRWLPTLMAAEKQKIVICSAIGFDT
YLMRHGVRSDTEGADPAPLSSYSSIPGDQLGCYFCNDVVAPGNSLKDRT
LDQQCTVSRPGISYMASALAVELLVSVLQHPPELGKAPADTSASDEHLSKD
FVCPLGLVPHQIRCFVSRFQQVLPACKAFDKCTACSKTVIEQFRRDGFDF
LRRAFNDPSYLEDLTGLTQMHQETLDAEVWGFSDDEECSSMEVSSS
```

```
>sp|O95352|ATG7_HUMAN Ubiquitin-like modifier-activating enzyme ATG7
OS=Homo sapiens OX=9606 GN=ATG7 PE=1 SV=1
MAAATGDPGLSKLQFAPFSSALDVGFWEHLELTKKLNRYRLDEAPKDIKGYYYNGDSAGLP
ARLTLEFSAFDMSAPTARCCPAIGTLYNTNTLESFKTADKLLLEQAANEIWESIKSGT
ALENPVLLNKFLLLTAFADLKKYHFYWFCCYALCLPESLPLIQGPVGLDQRFSLKQIEAL
ECAYDNLCQTEGVTALPYFLIKYDENMVLVSLKHYSDFFQQRKTKITIGVYDPCNLAQY
PGWPLRNFVLAAHRWSSSFQSVVVCFRDRMTQMGARDVAHSIIFEVKLPEMAFSPDCPK
AVGWEKNQKGGMGRMVNLSGCMDDPKRLAESSVDLNLKLMCWRLVPTLDLTKVSVKCLL
LGAGTLGCNVARTLMGWGVRHITFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAADR
LQKIFPGVNARGFNMSIPMPGHPVNFSSVTLEQARRDVEQLEQLIESHDVVFLMDTRES
RWLPAVIAASKRKLVINAAALGFDTFVVMRHGLKPKKQGGAGDLCNHPVASADLLGSSLF
ANIPGYKLGCFYFCNDVVAPGDSTRDRTLDQQCTVSRPGLAVIAGALAVELMVSVLQHPPEG
GYAIASSSDDRMNEPPTSLGLVPHQIRGFLSRFDNVLPVSLAFDKCTACSSKVLQYERE
GFNFLAKVFNSSSHFLLEDLTGLTLLHQETQAAEIWDMSDDETI
```

```
>sp|Q9D906|ATG7_MOUSE Ubiquitin-like modifier-activating enzyme ATG7 OS=Mus musculus
OX=10090 GN=Atg7 PE=1 SV=1
MGDPGLAKLQFAPFNSALDVGFWEHLELTKKLNRYRLDEAPKDIKGYYYNGDSAGLPTRLT
LEFSAFDMSASTPAHCCPAMGTLHNTNTLEAFKTADKLLLEQSANEIWEAIKSGAALEN
PMLLNKFLLLLTAFADLKKYHFYWFCCYALCLPESLPLIRGPVSLDQRLSPKQIQALEHAY
DDLCRAEGVTALPYFLFKYDDDTVLVSLKHYSDFFQQRKTKITIGVYDPCNLAQYPGWP
LRNFLVLAHRWSSSFQSVVLCFRDRMTQMGARDVTHSIIFEVKLPEMAFSPDCPKAVGW
EKNQKGGMGRMVNLSGCMDDPKRLAESSVDLNLKLMCWRLVPTLDLTKVSVKCLLLGAG
TLGCNVARTLMGWGVRHVTFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAAERLQKI
FPGVNARGFNMSIPMPGHPVNFSDVTMEQARRDVEQLEQLIDNHDIFFLLMDTRESRWLP
TVIAASKRKLVINAAALGFDTFVVMRHGLKPKKQGGAGDLCPSHLVAPADLGSSLFANIPG
YKLGCFYFCNDVVAPGDSTRDRTLDQQCTVSRPGLAVIAGALAVELMVSVLQHPPEGGYAI
SSSDDRMNEPPTSLGLVPHQIRGFLSRFDNVLPVSLAFDKCTACSPKVLQYEREGFTFL
AKVFNSSSHFLLEDLTGLTLLHQETQAAEIWDMSDEETV
```

```
>sp|Q5ZKY2|ATG7_CHICK Ubiquitin-like modifier-activating enzyme ATG7
OS=Gallus gallus OX=9031 GN=ATG7 PE=2 SV=1
MAAVSNESQNPVDPGSSKQLQFAPFSSALNVGFWEHLELTKKLNRYRLDETPKVIKGYYYNG
DPSGFPARLTLEYSAFDINASIPARCCPAFGTLYNTNTFETFKSCDKKSLEKEANEIWE
SIKSGAALENPMLLNRFLLLTAFADLKKYHFYWFCCYALCFDPDGIHVIQKPVCLGDRFSL
NQIQALQKAYDELQTEGVTAFYFLIKYHDNSVVVSPLKWDGFFQDQGGKVTVGVDYD
CNLSHYPGWPLRNFILASHKWNILQSIIEVLCFRDRMTQGVDRDITHSIIFEIKLPQGAF
GPDCPKAVGWEKNQKGGMGRVVNLSGCMDDPKRLAESSVDLNLKLMCWRLVPTLDLEKIV
```

SAKCLLLGAGTLGCSVARTLMGWGVRKITFVDNARISYSNPVRQPLYEFEDCLSGGKPKA
LAAAERLQKIFPGVNSEGYNMSIPMPGHPVNFSEVTMAQARKDVATLEELIDAHDVVFLL
MDTRESRWLPAVIAASKRKLVINAAALGFDTFVVMRHGLKPKQOETGNACFSTAPGPSDL
LGSSLSFNIIPGYKLGICYFCNDVVAPGDSTRDRTLDDQOCTVSRPGLAMIAGALAVELMVSV
LQHPEGGYAVASSSDDRMNEPPTSLGLVPHQIRGFLSRFDNVLVSLAFDKCTACSPKVL
DQYEREGFNFLAKVFNSSHSFLEDLTGLTLLHQETQAAEIWDMSSDDETV

>tr|Q7JY94|Q7JY94_DROME Autophagy-related 7, isoform A OS=*Drosophila melanogaster* OX=7227 GN=Atg7 PE=1 SV=1

MSTEKEIILQFAPWESFVSPTFWHKLAEKLDHDLSDSKRSITGHYTNRNASGCLLEVD
YTAYNRMAKPPKFSHSAIGTIYKNKNTIEEFKALDKLQLLADEGKELLADMCSGGALRDP
LLTRFFVLSFADLKCHSYWFAFPCLPTPTLKLQGAQVQKLRDLNPNSSYIMALKALPTE
SQNFFILYANVEKNIFEARSLSLDDKNVEFCYFGFADPSEYEHPAWIMRNYAAFLQOC
PSFVVGKPLKFLGLRHNQOMNIDDSLWVKVIQTEACDLSQSENIKFGWELNKNKMGPRM
VCMRDSMDPAKLAENSVNLNKLMKWRLVLDLNLLEIIISQTKCLLFGAGTLGCAVARNLLS
WGFKHITLLDSGKVGFSNPVRQONLYTHADAVAGNRMKATTAAQRLKEINPSAETAGYVLE
IPMPGHTIGESLLAQTKHEHLKVIKLVQDHDVIFLLTDSRESRWLPTLLGAAKEKIVINA
ALGFDSYLVMRHGTTRKEAGDDGQIEIQLKINGDQGLGICYFCNDVTAPGNSLKDRTLDDQ
CTVTRPGVSNIAASYAVELLVALLQHPRELAPAYYAQSGRGRSEETEELKVPGLLGLILP
HSIRGMLCNENILPATQKFAQCIACSAAVLNEYKKEGHAFLFKTFETAKFLEDLTGISE
FKRLNSEIIDFDDEEFDMSSDDED

>tr|G5EBK4|G5EBK4_CAEL AuTophagy (Yeast Atg homolog) OS=*Caenorhabditis elegans* OX=6239 GN=atg-7 PE=1 SV=1

MATFVFPVTCCLDTGFWNEVNKKLNDWKLDETPKCISSQLSLHQTEGFKCHLSLSYDSLS
SLESTTGLSMSGTLLLYNTIESFKMVDKSDLIRSEAEKIWESITTRKWLQNPRLLSQFFI
IAFADLKKFKYIYWTCVPALVYPSEIKQEITPLSSLGADHKILFDFYRKNFPIFLYSKQ
SSKMLELSELENNTNPDEICVVDADPSPVAYSAGWMVRNLAVAHLHPTWKHCHIIISLR
SADSIGIKYTWTLPSEADGAQNAVPAVGVWERNANDKLQPI SVDLKSKEFDPKILMER
SVDLNLSLIKWRLHPDIQLERYSQLKVLILGAGTLGCNIARCLIGWVRHISFLDNSTVS
YNNPVRQSLSEFEDARLGRGKAETAQAQAIQRIFFPSIQATAHRLTVMPGHSIDKDVPEL
EKDIAKLEQLVKDHDVFLALDSREARWLPTVLA SRHKKIAISVAIGFDYVIIRHGIGS
RSESVSDVSSDSVPYSQSLCYFCSDVTAPGNSTFDRTLDDQOCTVARPGTSMIASGIAVE
LLSSVLYQPDPLKTPASHDDNTTVLGAAPHQIRGFLGRFQQILPSVKRFDQCVACGDAIA
AQFQQNGWKVFRDVMNSPGRLEEVTGLDELQNSVNAIDIDFEDDED

>tr|W4Y917|W4Y917_STRPU Uncharacterized protein OS=*Strongylocentrotus purpuratus* OX=7668 PE=4 SV=1

MASQEKTDSSQQPLQFAPFSSALDVGFWHKLTKQKLNEYKLDGPKDIYGYYYNGDPDGL
PCRLSLEFNADFQSETTPPHCFSSRGTLVNFNTLDAFKTCDDKALLDVTAEQWLWDDIRQG
SAIQDPSLLSRFRLTTFADLKKYHYCYWFAFPALLAPEGTKLIQPPEKLDKAMDQDKITA
LQAAYDLASQSLGQEPAFFLISTEDDKTVVLPPLTAWDQVTDKSKVMFGYADPCTLEQYPG
WPLRNFLCLISCHWASQLDQVTVVCFRNRTREGIRNSSHSLILRLQVPSTSP EISCPKCV
GWEKNQRNKLARKVDLSSSMDPTRLAETSVDLNLKLMRWRLPSLDLKD KISQTRCLLLG
SGTLGCNVARCLLGGWVRTITFVDNSTVFSNPVRQSLFEFEDSLGGGKPKAQTA AEKIE
KIFPGVKTRGVLSIPMPGHAVGTSDEAIQQTRESVQKLEELIDEHDVVFLLMDTRESRW
LPTVICSSKRKIVMNAALGFDTYLVLRHGMKPARDQPPPDQTPSSSASSGAAGGAEGGAA
GGASCSTSSISLSHIPGDKLGCYFCNDVVAPGDSTRDRTLDDQOCTVSRPGLSMVAAALVV
ELMVSILQHSQAYAAAETS AKDSHLTVDLTSPGLVPHQIRGFLARYHCVLPASLCFDK
CTACCDIVLASYEREGFDLLKVFNKPRFVEDLTGLSQLHLESELIEILDFSDDETMSTS
SQ

>tr|A0A0G2KPR3|A0A0G2KPR3_DANRE ATG7 autophagy-related 7 homolog (S. cerevisiae) OS=*Danio rerio* OX=7955 GN=atg7 PE=1 SV=1

RTPNIIISMAESSLKLQFAPFCSALEAGFWHQLTKQKLNEYRLDESPKNIKGYYYNGDAVG
LPARLTLEFSAFDADGPTPARCCPASGTLYNTNTLEAFKSTDKKALLDKAANEIWSAIQS
GAALEDSSILNKFILLTFADLKKYHYFYWFCCPALCFVEGIQLLRAPLSLEQHFSDKQIS
SLQSAYDNLCASSGTTAVPHFLLKYSEESVEVAPLKEKLSFFPD LKRVIIYSTSHQCGLLP
QHPGWPLRNLLVLLAKKWASQLDVVEVLCFRDRTLQGVRSVQHSIIIFQLRLSDPAPSAAP
TTDINIHWKMIHSIQGNSAFFVSECQGVRLAESSVDLNLKLMRWRLV PALDLEKVVST
RCLLLGAGTLGCNVARTLMGWGVRHITFVDNAKISYSNPVRQPLYEFEDCLSGKSKALAA
VDRLLKIFPGVNAEGFNMSIPMPGHPVNFSDLTVAQAQQDVEQLKKLISEHDVVFLLMDT

RESRWLPTVIAASQRKLVNAALGFDTFVVMRHGLKKPRESEESSPMSASSSSSSSNTPA
ATVTAGSSLSFVSNIPGHRLGCFVNDVVPAGDSTRDRTLDDQCTVSRPGLAMIAGALAVEL
MVSVLQHPGEGYAVASSSDDRMNEPPTSLGLVPHQIVPLLSNVTNVLKYEMFWRKDTRCL
KKVLENYEREGFQFLAKVFNSSSHFLLEDLTGLTLLHQETQAAEVRLTPSISI

>tr|A0A087ZSN9|A0A087ZSN9_APIME Uncharacterized protein OS=*Apis mellifera*
OX=7460 GN=LOC726637 PE=4 SV=1

MSEFVKFTKLRSTTDCTFWAKFVELKIDKFKLDEKSNLWGSYSLQSLNEDNFNPLVLDF
TSFNEDLETINNKSSVICFGHMINTNTFEAFRQINPEQFIDSMGKDIINSIQDGTILQNP
WKLFLVFLVLAISDLKRYFYVVAHPTPLKLPemyyEEIPKSITEEFSEKHVEDLCNNFL
HLDCRTKNYFTVLI SKENKMCIVDLATGINVININNEKQSQDYTEIYFAFYDPCTSSNPG
WPLRNLCLLCWYCPTHYFSKI IKFISIRGNKAQKSLVFKLKTKEYKNYKNIRDNLFLSH
LVGWESNSNDKLGPTIADLSDTMDPTKLSKAINLNLKLMKWRLVPLNDLEKICNLKCLL
LGAGTLGCSVARVLLGWGVNII FVDSSHVSHSNTVRSLYNHQDAIKHKYKAHAADAL
LNIRPSINTEGIVLHIPMPGHVVGQSMLESTKQSLKKLEELIEISDVVFLLLDSREARWL
PTVLC AAKNKITINAALGFDSYTVQRHGTRNFNNQISPDLEVKNPRGMDLGCYFCNDVTQ
PGNSQTDRTLDDQCTVSRPGLSQIAAGLAVELLVALLQHPEGVEAEALVGNRDNINSND
AKLVGLLGCVPHTIRGSLWNYDTQLTITHRFTSCTACSVPIIEYKNRGLSFVLDACNIP
NYLEKLSGLEEILKRPDLDELALDNI SDEDEDDQKM

>XP_022296278.1 ubiquitin-like modifier-activating enzyme ATG7 [*Crassostrea virginica*]

MSAPMERKQLQFVFPSSFLDSGFVHKLSENKLDVYGLDES RKDIKGFYFNGDPVGMPCRMNVEFSAFDLD
AKTPQKCLPMLGELHNTNTIDKFKCEDKEMMTEAGKKIWEAII SGRALVSPNLLASFLILTFADLKKYH
YYYWFCFPCLCLPTDVTNLNQEPIKMKDKFTKEQMDQFLT SYDTFQEEQPCYQGGFFVAAFSQDKFMVKDVK
SLNNFDDTQEVYFGFCDPSTIEDYPGWPLRNFMLLSYHWKGSLENINVL CIRDRSRDGNRDISHSVLLS
LNVDPVKSLEQCPKCVGWEEKNEKQKLAPRFVNL SASMDPARLAASAVDLNLKLMRWRLPELDDLISRT
KCLLLGAGTLGCNVARCLLGWGVRTITLVDNGRISYSNPVRQSLFQFEDCVKGGKPKAEAAAESLKRIFP
GVNATGLSLSIPMPGHAVPDSAIDGVQKDVATLQSLVSDSHDAIFLLLDTRESRWLPTLMAAEKQKIVICS
ALGFDTYLVMRHGVKSDTEEEEDVPLSYHSIPGDQLGCYFCNDVVPAGNSLKDRTLDDQCTVSRPGISYM
ASALAVELLVSVLQHPQGGKAPADTSANDDHL SKDFVCPLGLVPHQIRCFVSRFQVLPACKAFDKCTAC
SKTVIKEFRKEGFGFLRRAFNEPSYLEDLTGLTQMHQETLDAEVWGFSDDEECSSMEVS

B. ULK2

>tr|K1PNL8|K1PNL8_CRAGI Serine/threonine-protein kinase ULK2 OS=*Crassostrea gigas*
OX=29159 GN=CGI_10015287 PE=4 SV=1

MEVVDGYEYSKDLIGHGAFVVFGRHRKRNPHVVAIKSITKKNLAKSQNLLSKEIKIL
KELSDLHENVVALLDCKETT NHVYLVMEYCNGGDLADYLQAKGTLSEDTIASFLRQIAA
AMQVMNGKGI VHRDLKPQNILLCHDGKPNTPSTEMRLKIADFGFARFLNDGVMAATLCGS
PMYMAPEVIMSLQYCAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKHFYEKHAELKPNIP
KDTSPELRDLLLKMLKRNADRIEFASFPVVPGRASQGCSSSPTPPRCVSASPLSGKAD
YSTPPSKVVQMVKQQEVAAEQGSTHDEEFLKVDKGPTPRSNSPTEHDFVLVDPGMSDQS
DGS DKGRAPSTEDLQSLGERAQPQVVRVEPQVGSVAYK KDSGDVSSPSRPSLPMQSNNO
SEPIPVPTQVKAYERIRSSSSPLSSPRKCGTEPSPLDSAKLSSQNIKISPQPESKFSAPD
IGSFSPTVKFVSGTTPNVSTPWRRSIGSSQGGAIYHPPSNASNSPSRRASMGSSPSGF
NRNFSSPGSLPTILDASPHFELNQEPPQFTDNMPTVPVRAPFGQSKPKAIPESKGT KRYHP
SEVDRVKLNL MERCNTDGAAGGMSMLSQOMKVAYMNQQGLNLLLEGQVVRYTSNENLVSP
NDNTVQMDTQRSGTGLRRTMSATPPSNLMFAQSPNMEGPVAFVAPGLAEETLMGDHNH
EIMAKLSFVNDLADCVMEAMAKGAPLNTLSESVNWKQEGEPLHGDQMPKFIEAQRLLLEQ
LVLYVRS LQLSSSLQLARREIKDERLQISNALKTLLKQMNERYHRCVSVCKHIQQR LGI
TMQNALTPQVVIATADKLIYNYAIEMCQTAALDELFGNPPQECFKRYNTAHILLHSLSQQA
RNSNDKQLLDKYKDAVERRLSHIQATQNYYPQFEIS

>sp|Q8IYT8|ULK2_HUMAN Serine/threonine-protein kinase ULK2 OS=*Homo sapiens*
OX=9606 GN=ULK2 PE=1 SV=3

MEVVDGFEYSKRDLVGHGAFVVFGRHRQKTDWEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALYDVQELPNSVFLVMEYCNGGDLADYLQAKGTLSEDTIRVFLHQIAAAMR
ILHSGKGI IHRDLKPQNILLSYANRRKSSVSGIRIKIADFGFARYLHSNMMAATLCGSPMY
MAPEVIMSQHYDAKADLWSIGTVIYQCLVGKPPFQANSQDLRMFYEKNRSLMPSIPRET
SPYLANLLLGLLQRNQKDRMDFEAFSSHFFLEQGPVKKSCPVVPMYSGSVSGSSCGSSP

SCRFASPPSLPDMQHIQEENLSSPPLGPPNYLQVSKDSASTSSKNSSCDTDDFVLVPHNI
SSDHSCDMPVGTAGRRASNEFLVCGGQCQPTVSPHSETAPIPVPTQIRNYQRIEQNLST
ASSGTNVHGSPRSVAVRRSNTSPMGFLRPGSCSPVPADTAQTVGRRLSTGSSRPYSPSPL
VGTIPEQFSQCCCGHPQGHSRNRSSGSPVQAQSPQSLLSGARLQSAPTLTDIYQNKQ
KLRKQHSDPVPCPSHTGAGYSYSPQPSRPGSLGTSPTKHLGSSPRSSDWFFKTPPLPTIIGS
PTKTTAPFKIPKTQASSNLLALVTRHGPAEEQSKDGNPRECAHCLLVQGSERQRAEQQS
KAVFGRSVSTGKLSDQGGKTPICRHQGSTDSLNTERPMDIAPAGACGGVLAPPAGTAASS
KAVLFTVGSPPHSAAAPTCTHMFRLRTRTTSVGPSNSGGSLCAMSGRVCGVSPGPGFGSS
PPGAEAAAPSLRYVPYGASPPSLEGLITFEAPELPEETLMEREHTDTLRHLNVMLMFTECV
LDLTAMRGGNPELCTSAVSLYQIQESVVDQISQLSKDWGRVEQLVLYMKAQAQLLAASLH
LAKAQIKSGKLSPOSTAVKQVVKNLNERYKFCITMCKKLTEKLNRFSDKQRFIDEINSVT
AEKLIYNCAVEMVQSAALDEMFOQTEDIVYRYHKAALLLEGLSRILQDPADIENVHKKYC
SIERRLSALCHSTATV

>sp|Q9QY01|ULK2_MOUSE Serine/threonine-protein kinase ULK2 OS=*Mus musculus*
OX=10090 GN=ulk2 PE=1 SV=1

MEVVGDFEYCKRDLVGHGAFVFRGRHRQKTDWEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALYDVQELPNSVFLVMEYCNGGDLADYLQAKGTLSEDTIRVFLHQIAAAMR
ILHSGKGIHRDLKPNILLSYANRRKSNVSGIRIKIADFGFARYLHSNTMAATLCGSPMY
MAPEVIMSQHYDAKADLWSIGTVIYQCLVGKPPFQANSPODLRMFYEKNRSLMPSIPRET
SPYLANLLLGLLQRNQKDRMDFEAFFSHPFLEQVPVKKSCVPVVPVYSGPVPGSSCSP
SCRFASPPSLPDMQHIQEENLSSPPLGPPNYLQVSKDSASNSKNSSCDTDDFVLVPHNI
SSDHSYDMPMGTARRASNEFFMCGGQCQPTVSPHSETAPIPVPTQVRNYQRIEQNLIST
ASSGTNPHGSPRSVAVRRSNTSPMGFLRVGSCSPVPGDTVQTGRRRLSTGSSRPYSPSPL
VGTIPEQFSQCCCGHPQGHEARSRHSSGSPVQTPAQPSLLLGLARLQSAPTLTDIYQNKQ
KLRKQHSDPVPCPSHAGAGYSYSPQPSRPGSLGTSPTKHTGSSPRNSDWFFKTPPLPTIIGS
PTKTTAPFKIPKTQASSNLLALVTRHGPAESQSKDGNPRECSHCLSVQGSERHRSEQQQ
SKAVFGRSVSTGKLSQVQKAPLGGHQGSTDSLNTERPMDVAPAGACGVMALPAGTAAS
ARAVLFTVGSPPHSATAPTCTHMLVLRTRTTSVGSSSSGSLCSASGRVCGVSPGPGPLGS
SPPGAEGAPSLRYVPYGASPPSLEGLITFEAPELPEETLMEREHTDTLRHLNMMMLMFTEC
VLDLTAVRGGNPELCTSAVSLYQIQESVVDQISQLSKDWGRVEQLVLYMKAQAQLLAASL
HLAKAQVKSGLSPSMVAALKQVVKNLNERYKFCITMCKKLTEKLNRFSDKQRFIDEINSV
TAEKLIYNCAVEMVQSAALDEMFOQTEDIVYRYHKAALLLEGLSKILQDPTDVENVHKKYC
CSIERRLSALCCSTATV

>tr|X1WEA3|X1WEA3_DANRE Unc-51-like autophagy-activating kinase 2 OS=*Danio*
rerio OX=7955 GN=ulk2 PE=4 SV=1

METVGDFFEYSRKDLIGHGAFVVFGRHKKKTDWEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALYDVQETPSSVFLVMEYCNGGDLADYLQAKGTLREDTLRVFLQQAAMR
ILNSKGIHRDLKPNILLSYTGRKKSSINGIRIKIADFGFARYLQSNMMAATLCGSPMY
MAPEVIMSQNYDAKADLWSIGTVIYQCLVGKPPFQANSPODLRMFYEKNKSLVPIPRET
SPQLEDLLLGLLQRNQKDRIDFDFTFFSHPFLEPISTIKKSCVPVVPSCSGLVSDSTCGSS
PSCRYVSPSLPDMQTLPELVLSSPPLGPPNYLQLSKESGGSTSSKNSSCDTDDFVLVPH
LSGEQSYDLPMAVGRRPSSEFLLCGGSPQSTGQTPMVSPRSETTPIPVPTQVRNYQRI
KQNLSSSPTTTLYGSPRSGTVRRSNTSPMGFPKMVSASPSPADTVQTVGRRLSTGSSRPY
SPSPLVGTIPEQLGHCCCGHPQSHEPRSRSSSGGSPVSSQLLGLARLQSAPTLTDIYQSK
QKLHKQLSDPVHPTSSAYPSNHSPQLGRPANLGTSPTKHLGSSPRTSDWLTKSPLPTIIG
SPTKVTAPFKIPKTQASCNLMALADSPIPNKTLMDGRELCAHHTAYPSSRQPAPEASKT
SFGRSVSAGRLSEPPVRLITLGGQPYQGSTDSLNTERPMDTAPAGMCALAAGGSPRTVVF
TVGSPSSSTPPTCSHLASRPRATSVGSNSAGSLCSTSGKVYMGSPPGMTIGSSPPGAE
AGPSSLRYVPYGTSPSLDGFITFEAPELPEETLMEREHTDTLMYLRMMLSFDCVLEIA
ALRAGGPDLGASAASLYPPQDSVVDQISQLSREWGQVEQLVLYMKAQAQLLASSLHLAKA
QIKSAKLNPOSTAVKQVVKSLNERYKSCISLCRRLTDKLNHFFSDKQRFVDEINSVTAEKL
IYNHAVEMVQSAALDEMFOQTEDIAYRYNKASMLLEGLTKILQDPADIENVIKYKASVDR
RISALCYCTVTLYE

>tr|A0A1S3HB46|A0A1S3HB46_LINUN serine/threonine-protein kinase ULK2-like
isoform X1 OS=*Lingula unguis* OX=7574 GN=LOC106153722 PE=4 SV=1

MESIGDFEYKRDLDIGHGAFVVFGRHKKVTHDPVAIKSITKKNLAKSQNLLSKEIKILK
ELSDLHHENVALLDCKETTHVYLVMEYCNGGDLADYLQAKGTLSEDTISGFLRQIAGA
MRALNGKGIHRDLKPNILLTHSGQSPNPQPSDLQLKIADFGFARFLNDGVMAATLCGS
PMYMAPEVIMSVQYDAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKAFYEKNANLAPNIP

SGTSKELRDLLMKLLKRNADRIDDFEFFSHPFVCPAKASSPVPVPPQQRARHPSDSPTLK
TVSSSPLSGNVYPYSPVNTDVQRVQKQEDVSESPQEGADFKVDSKSGSPAEDFVLVNNL
GGESEGSASSGRSKEPKHGRKDSQPSAQRVVRVDTTTEAASFRKGNAGSPSPQDQTS
TRPTSLPVIKQTSPPSQPIPVPTQVEAYQRIQKNSSPKPRTKEAGTHVMSPORELAS
QAVPIPRIASDRMVSVGSFPDIRSVSPSVQFHIGTPPSKNIRRNNSIEVSPGRPNTATPP
NGSPLRKSQAQSNSSPFGPASLPKPSVMSVAQRFTVTNYPAGGRDVVALARTRTVPEGV
QAMTTVAGAAYDPYATWPRRLDITGLAPSQTEPSNLQRTTSSGGHLAPTRIGEQLMKAAGF
QTRGLSNQIPANSVVPYRERNQSESGQRERRDSFQKRDSFTREERQDSTGRERSGSSPP
NSLPYAQSPNMEGPILFEAPELAEETLMDSEHNETVAKLTFVLALVETIIELAQKRSTP
LTQSISSPQRRDGGSEQVKFLSESQRRMEQLVLHVKALQLLSASLQLAKEEIKAGKLMPS
NTVKNILKEMNNHYHRCMGIKQLKSCNINDNELKSFSTTADKLIYNYAIEMCQTAALDE
LFGNPQECFRMYKNAQIILLHALAHQAQHNKDKDMLNKYKEAVEKRLFSLQSQGLNYFQYE
N

>XP_011676911.1 PREDICTED: serine/threonine-protein kinase ULK2 isoform X1
[*Strongylocentrotus purpuratus*]

MEHIDEYEYKNDIIGHGAFIVFRGRERKRPDQTVAIKCKINKKNLSKSKQTFPEKEIEILKELHHGNVVS
LLHFKEETSSLFMVEFCNGGDLADYLHIKGLTSEDTRFFLGQIACAMKAIHEKGIHRDLKPNLLLS
HNSKHKVPHPNEIHLKIADFGFARFLEGMMAATLCGSPLYMAPEVITSQHYDAKADLWSIGTIFQCLT
GSAPFKAANPPELKKLYMKARTLDPNIPPGTSKALKDLLIRLLKRNQKDRIEFDKFFSHDFLGKLNKSTS
TSPMPVPSRTYFSSSDSPGERRSLSVSPLSGHMPISSEPEPSSVCGPRGYSISPLAAPPListDRPS
AAKGLQEKRLRSSGMGSSDLVEDDFVIVQPSIVSELSYETSGASINVQTTTVDVITIRSNSSPIMSSSRGH
SAQPKSSTSPVSGRIMAAVRRKLPSPSERPSSLPISSSPSTSPNTGRHRVSPKQSPSSLISPSRIHAQI
RHSYSSSGSPIGSPSQRRRLSPNQSPSLARHCILAQAGVDNKPPSPVQVTGLSSPGSQYNPGVVHKF
YKFHASPTSPSPPHIIPRVSTDPMSCSQGAGLYRGSSPQSQSGTSPTNIPSPARRKLSPPARSSPQFF
TGSSSLPTIAGSPTKKGFGNEITFTIGTHGISPSEPLNMPFAKSRVRASSCCLEGGDQDIDSDSPGRDA
LIPRSASSRSLSEPLCLKAAFDNLAMNPGSSIEGIPGAI AASPPMHPTSFFIGSQRRNSVLTEGSPSSQ
GSLTFATSPNMEGPISFVAPELPEETLLAAEHTETVDRLNVILGIVEAIVEVAKSRVPLAESIYNQGS
SIFSNSQVCFVSENYRLAEQLVLYTRSLLELLNAALTAKEEFAARLKPSNAVRTVLQELNRVYHLCLIK
SRQLCEGSPQLDIDLNSAMITADKLMYSYAI EQCQSAGMDEMFGNTQECLQRYRTAQMLLHLGLCLQAG
TDHNRNLLKFKNALDQRLFLERQOTPVTPMIGL

>XP_004946752.1 PREDICTED: serine/threonine-protein kinase ULK2 isoform X1
[*Gallus gallus*]

MEVVGDFEYSKDKLIGHGAFVVFKGRHRKKTDEVAIKSINKKNLSKSKQILLGKEIKILKELQHENIVA
LYDVQEMPSSVFLVMEYCNGGDLADYLQAKGLTSEDTRVFLQQIAAAMRILHSGKGIHRDLKPNILLS
YASRRKSSVSGIRIKIADFGFARYLHNSMMAATLCGSPMYMAPEVIMSQHYDAKADLWSIGTVIYQCLVG
KPPFQANSPODLRMFYEKNRNLIPSIIPRETSTYLADLLGLLQRNQRMDFEAFFNHPFLDQISTVKKS
CPVPVPTYAGSVSGSSCGSSPSCRFASSPLPDMQHIQEENLSSPPLGPPNYLQVSKDSASTSSKNSSCD
TDDFVLVPHNISSDHSYDMLPGAAGRASSEFLMCGGQSPLTISGSSGTQVQPSSTSSRSTASGTTNRHC
QPSVSPRSETAPIPVPTQLRNYQRIEQNLSSSTASPVSNPHGSPRAGVRRSNTSPMGFMKMGSCSPIPGD
TAQGVGRRLLSTGSSRPYSPSPLVGTIPEQLGHCCCGQLQGHESSRSRNFAGSPIPPSQSPQSLLMGARLQS
APTLDIYQNKQKLRKQHS DPVCPYAGYGYSHSPQPSRPGSLGTSPTKHMGS SPRSSDWLFKTPLEPTII
GSPTKATTPFKIPKTKQASSNLLALANRQGSIDAPLQPKDITEPRDFSHFHSTQGSEKHAGEQHSKATFGR
SVSTGKLSDDQVKTTLGGQLYQGSTDLSLNTERPMDTAPAGAYGIAVAPPMSMGSGASSRAVMFTVGSPPSS
ATPPTCTHMLVLRTRTTSVGSNSGGSLCSTSGRVYMGSPPGIYMGSSPPGAEAAPSLKYMPYGTSPPSLE
GFITFEAPELPEETLMEREHTDTRLRHLNMLTFTTECVLDTALRGGNPDLCSTSAVSLYQIQESIVVDQIS
QLSKEWGQVEQLVLYMKAQQLLASSLHLAKAQVKLGKLNPNSTAVKHVVKSLNERYKFCIGMCKKLTEKLN
RFFSDKQRFIDEINSVTAEKLIYSCAVEMVQSAALDEMFOQTEDITYRYHKAALLLEGLTKILQDPADIE
NVHXYKSSIERRLSALCCSTVAVYEQ

>XP_022286173.1 serine/threonine-protein kinase ULK2-like isoform X1
[*Crassostrea virginica*]

MEVVGDIYEYSKDKLIGHGAFVVFKGRHRKRPNHVVAIKSITKKNLAKSQNLLSKEIKILKELSDLHHEN
VVALLDCKETTNNHVYLVMEYCNGGDLADYLQAKGLTSEDTRIAAFLRQIAAAMQVMNGKGIHRDLKPNINI
LLCHDGKPNTPSTEMRLKIADFGFARFLNDGVMAATLCGSPMYMAPEVIMSLQYCAKADLWSIGTIVFQC
LTGKAPFQAQTPQQLKHFYEKHAELKPNIPKDTSPELRDLLLKMLKRNADRIEFEDFFKHFPFLKPPGQS
AAASSSPVPVPGRTSQGCSSESPTPPRCVSASPLSGKAEYSTPPSKVVQMVKQVEVAEAMQSSHDEEFL
KVDKGPTRNSPTEHDFVLVPGGMSDQSDGSDKGRVPSSEDLPLGLGERAQPVVRVPEQAGSVAFFKDT
VDVPSRPSLPMQTQNSQSEPIPVPTQVKAYERIRSSSPLSSPRKFGAVEVSPVDPKLLSQNIKMSF
QPESKFSAPDIGSFPPTGTLKFCVGTTPNVSTPWRRSIGSSQGAQYHPPSNASNSPSSRRASMGSSPL
GFNRNFTSPGSLPTILDASPHFELNQEPOITDNMPTVPVRAPFGQSKPKAIPESKGTKRYNPSEVDRVKV

NLMERCNTDPGAAGGLSMLSQQMKVAYMNOQGLNQLLEGQVMRYTSNEQLVSPNENTVQMDTQRSGSNLRR
TMSATTPPSNLMFAQSPPNMEGPVAFVAPGLAEETLMGDNHNEIMAKLSFVNDLADCVMEAMAKGAPLN
TLSESVNWKQGEGLPQGEPMKPFIEAQRLLLEQLVLYVRSLLSSSLQLARREIKDERLQISNALKTKLLK
QMNERYHRCVSVCKHIQORLGITMQNALTPQVVIATADKLIYNYAIEMCQTAALDELFGNPQECFKRYNT
AHILLHSLSQQARNNDKQLLDKYKDAVERRLSHIQATQNYYPQFEIS

C. ATG12

>MK069431|Ubiquitin-like protein ATG12 [organism=*Crassostrea gigas*] mRNA,
complet cds
MSDDGNESRDSKNTETEEKSTPASPSHVAETKIDVLLKPAGDAPIMKKKK
WAVDRNKRIGWVGEFIKKYLKLTAQDSLFLYVNVQSFAPTPDTEIGSIFDC
FGSDGKLVLYHCKTQAWG

>sp|O94817|ATG12_HUMAN Ubiquitin-like protein ATG12 OS=*Homo sapiens* OX=9606
GN=ATG12 PE=1 SV=1
MAEFPQSVLQLPTSIAAGGGLTDVSPETTTPEPPSSAAVSPGTEEPAGDTKKKIDILLK
AVGDTPIMKTKKWAVERTRTIQGLIDFIKKFLKLVASEQLFIYVNVQSFAPSPDQEVGTLY
ECFGSDGKLVLYHCKSQAWG

>sp|Q9CQY1|ATG12_MOUSE Ubiquitin-like protein ATG12 OS=*Mus musculus*
OX=10090 GN=Atg12 PE=1 SV=1
MSEDSEVVLQLPSAPVGGESLPELSPETATPEPPSSAAVSPGTEEPGDTKKKIDILL
KAVGDTPIMKTKKWAVERTRTIQGLIDFIKKFLKLVASEQLFIYVNVQSFAPSPDQEVGTL
YECFGSDGKLVLYHCKSQAWG

>sp|Q9VTU1|APG12_DROME Autophagy protein 12-like OS=*Drosophila melanogaster*
OX=7227 GN=Atg12 PE=3 SV=3
MAETPESQAALSTSSSTPADKDGSKICILLNATGNVPIIKKRTWTVDPNKTVGWIQTFIH
KFLKLDASEQIFLYVNVQTFAPAPDQIIKNLYECHGTNGKLVLYYCKNQAWG

>tr|F1P145|F1P145_CHICK Ubiquitin-like protein ATG12 OS=*Gallus gallus*
OX=9031 GN=ATG12 PE=3 SV=2
MAEAEQAPVSPQSEGRSGAGEEAPERTPESGASLGVGEPATSPAGSPGTEDPAGDAKKK
IDVLLKAVGDTPIMKTKKWAVERTRTIQGLCDFIKKFLKLMASEQLFIYVNVQSFAPSPDQ
EVGTLYECFGSDGKLVLYHCKSQAWG

>tr|Q10931|Q10931_CAEL Ubiquitin-like protein ATG12 OS=*Caenorhabditis
elegans* OX=6239 GN=lgg-3 PE=1 SV=1
METETATPTGNTEPTAAASAEPKSDKVTVRLRNIADAPVLKKNKMVNPTDQVASFIL
KLRKLLNIQANNSFLYIDNTFAPSPDTTFETLSRCYSVKITDKEILELQYSITPAYG

>tr|W4XIA0|W4XIA0_STRPU Ubiquitin-like protein ATG12 OS=*Strongylocentrotus
purpuratus* OX=7668 PE=3 SV=1
MAEAQSTTGAGDETADPGTQNDQISKQTKEGDVVKKKSDKVDILLKATGSAPIMKKKKWA
VDANKKVAWVIDFIHKYLKCDPSQSLFLYVNVQAFAPAPDQEIRNLFECYGS DGRLLIHYC
TSEAWG

>tr|F1Q9E0|F1Q9E0_DANRE Ubiquitin-like protein ATG12 OS=*Danio rerio* OX=7955
GN=atg12 PE=1 SV=1
MSDNAESPTENPKDEHSLQHAVTDHSESSDEKKKIDVLLKAVGDTPIMKTKKWSVERRRT
IQSLAQFISRFLKLEPSEQLFIYVNVQSFAPSPDQEVGVLFECFGSDGKLVLYHCKSQAWG

>tr|A0A1S3ILW0|A0A1S3ILW0_LINUN Ubiquitin-like protein ATG12 OS=*Lingula
unguis* OX=7574 GN=LOC106165540 PE=3 SV=1
MSDEGGSESADLQGGYAVTLEDQSTQLSPVSEPANSPSSGTASPAIKLKSQKVDVLLKA
TGDAPIMKKKKWAVDPSKIGWIIIEFIKKYIKAEPSESVFLYVNVQSFAPAPDVEVGTVYD
CFGSDGKLVLYHCRQAWG

>XP_022317493.1 ubiquitin-like protein ATG12 isoform X2 [*Crassostrea
virginica*]

MSDDGNESRDSKNTETEEKSSPTSPSHAVESKIDVLLKPAGDAPIMKKKKQWAVDRNKRIGWVGEFIKKYL
KLTAQDSVFLYVNVQSFAPTPDTEIGSVFDCFGSDGKLVVHYCKTQAWG

D. ATG9A

>MK069430|autophagy-related protein 9A-like [organism=*Crassostrea gigas*]
mRNA, complet cds

MADYQTQYQPLASCEEDTDENDVPIHESANLMMHVPESTRWNHIENLDD
FFTRVYHYHQGGFVCMVSDVQLIQFIFVVGSTFLLECVNYDILFAN
SKNDTHKVTIPEAVAPFGQCVQEFDFGITVCLLVAFVFWFRLIKVLYNI
FKYWEIRSFYLTALHITTTDLTNMTWHEVQRRLLLEVQKEQQMCIHKQELT
ELDIYHRILRFKNYMIAMERKSLLPFKHSIPLMGECAFYSIGLKYNLDFL
LFWGPWSPFENYWKLKDEFKIYHKRQLAEELSKKILWIGIANFALSPLI
LLWQILYSFFRYADTLKREPSMLGSRWSNYARLYLRHYNELDHEFDARL
NRGYRLANKYMDIFTSQLIVILAKNVAFFAGSVLAVLVVLTVIDEDVLAV
EHVLTMTVAGLIVTACKVFIPEHLVYCEILMRNILAHVHYMPPDWSG
NAHTSKVRNEFSIFFQYKVAYLFEELLSPLVTPIVLCFSLRHKSMEIVDF
FRNFTVDVVGVDVCSFAQLDVRKRDNKMDRRDDEEPPQPSLRTNMFTPD
QSPSQEGKIQMSLMHFHLTNPEWKPPKECSLFINDIKEKANRNTTSLSIF
NPVTQNMVMSQGSGLTGYLSGLQPSGAGALGESATDQYTSLASSIAIQSG
MYPQSTQVSMAPSVMVSGVHRLRGAISTAEGLERSIGGPVGTMQGSTSMI
GSGLGGYHSIGSSKPSVDEGSLELLSHDMSVSALYLHDFQSRKQRGQGM
GYENIEEMRARNLWQRQDSNQGVPVHAGMPNIOEKREEEKDSGNTETIAK
SV

>sp|Q7Z3C6|ATG9A_HUMAN Autophagy-related protein 9A OS=*Homo sapiens* OX=9606
GN=ATG9A PE=1 SV=3

MAQFDTEYQRLEASYSPPGEEEDLLVHVAEGSKSPWHHIENLDLFFSRVYNLHQKNGFT
CMLIGEIFELMQFLFVVAFTTFLVSCVDYDILFANKMVNHSHPTEPVKVTLPDAFLPAQ
VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTW
QEVQARIVQTQKEHQICIHKRELTELDIYHRILRFQNYMVALVNKSLPLRFRPLPGLGEA
VFFTRGLKYNFELILFWGPGSLFLNEWSLKAEYKRGQRLELAQRSLNRILWIGIANFLL
CPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRHFNELEHELQSRNLNRGYKP
ASKYMNCFLSPLLTLLAKNGAFFAGSILAVLIALTIDEDVLAVEHVLTVTLLGVTVTV
CRSFIQDQHMVFCPEQLLRVILAHIHYPDHWQGNHRSTQTRDEFAQLFQYKAVFLEEL
LSPIVTPLILIFCLRPRALEIIDFFRNFTVEVVGVDTCFAQMDVRQHGHPQWLSAGQT
EASVYQQAEDGKTELSLMHFAITNPGWQPPRESTAFLGFLKEQVQRDGAASLAQGGLLP
ENALFTSIQSLQSESEPLSLIANVVAGSSCRGPPLPRDLQGSRRHRAEVASALRSFSPLQP
GQAPTGRAHSTMTGSGVDARTASSGSSVWEGQLQSLVLSYASTEMSLHALYMHQLHKQQ
AQAEPERHVHRRRESDESGESAPDEGGEGARAPQSI PRSASYPCAAAPRPGAPETTALHGG
FQRRYGGITDPGTVPRVPSHFSRLPLGGWAEDGQSASRHPEPVPEEGSEDELPPQVHKV

>sp|Q68FE2|ATG9A_MOUSE Autophagy-related protein 9A OS=*Mus musculus*
OX=10090 GN=Atg9a PE=1 SV=1

MAQFDTEYQRLEASYSPPGEEEDLLVHVAEGSKSPWHHIENLDLFFSRVYNLHQKNGFT
CMLIGEMFELMQFLFVVAFTTFLVSCVDYDILFANKMVNHSHPTEPVKVTLPDAFLPAQ
VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTW
QEVQARIVQTQKEHQICIHKRELTELDIYHRILRFQNYMVALVNKSLPLRFRPLPGLGEV
VFFTRGLKYNFELILFWGPGSLFLNEWSLKAEYKRGQRLELAQRSLNRILWIGIANFLL
CPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRHFNELEHELQSRNLNRGYKP
ASKYMNCFLSPLLTLLAKNGAFFAGSILAVLIALTIDEDVLAVEHVLTVTLLGVTVTV
CRSFIQDQHMVFCPEQLLRVILAHIHYPDHWQGVHLGGVAESHRHTPHSHLLPPPSGPG
DHRLLPQLYGRGRGCRHLLLCSDGRSPAWPSSVAVWRADRLSVPASRGREDRVVAHAL
CHHQSRLAAPS

>tr|F1QCA8|F1QCA8_DANRE Autophagy-related protein 9 OS=*Danio rerio* OX=7955
GN=atg9a PE=3 SV=1

MAHFDTEYQRLEASYSPPGEEENLLVHVPEGSKSPWHHIENLDLFFQRVYNLHQKNGFT
CMLLGEIFELVQLVFFVAFTVFLANCVDYDILFANKFVNHTDSLKVTLPAFLPVDVCSA
RIRDSVPVIFILVISGVFWLHRLVKFIYNICCYWEIRSFIYINALKISMADLPYFTWQEVQ
ARIVEIQKEHQICIHKKELSELDIYHRILRFKNYMVAMVNKSLPLPVRFRPLPVLGDTVFYT

RGLKYNFELIFFWPGSLFENEWSLKSEYKRGGRLELADRLSSRILWIGIANLLLCPVI
LIWQILYAFFSYTEVIKREPGSLGARCWSLYGRFYLRHFNELDHELMSRLSKGYKASSKY
MNCFMSPLLTVVAKNVAFFAGSILAVLIALT IYDEDVLAVEHVLSSITLLGVCITVCRSF
IPDKHMVFCPEQLLKVILAHIHYPDHWQGNARHRYETRDEFAQLFQYKAVFILEELLSPV
ITPFILIFCLRRKSLEIIDFFRNFTVDVVGVGDTCSFAQMDVRQHGHPAWMSAGKTEASI
YQQAEDGKTELSLMHFAITNPHWQPPRESTHFI SLLKEKVHRDAAVGQQGIIAENAGFTS
THSLHNDSEPRSLIANLLMGPPSLASLHLGREGSINHVSIGVSEGASALRSLSPVSTSLH
LRGSYPSARLPRSDHPAVVAGRGMAGSGTDARTISSGSSAWEGQLTSMILSEYASTEMSI
HALYMHMHKQQSRGELSRTWHRQESDESSESVNEDVEAARNFPRSSFTPTTTTSHQEG
AAAQQSGSQRQGGTSDPSSGSFRVQRTPRMAMGGWSEENQTSRHHDPVPEEGSEDELPP
HIHKVT

>tr|A0A0B4KF86|A0A0B4KF86_DROME Autophagy-related protein 9 OS=*Drosophila melanogaster* OX=7227 GN=Atg9 PE=1 SV=1

MSSPHINYRSLAEEAASPFLEHHPSTGQGPSKTQDAKANAAAAHLDPGEGHLEQPLDEH
DTEHEGEDTPRNSGVMIHMPVETGRARWNHIEDLDSFFSRMYQYQKHGFTVIVVDEMLQ
VLEFGFVWLLAFVMHCVRFDVLFGDTPPGGLNPNKTTLSDVMYPTGECLANFTWVYTLV
VFIAAIYLGIRLLKMVYHITQYADIKRFYNSALHIEDSDLDNFTWHEVQQRIRRVQAEQH
MCIDKESLTELDIYHRVLRFKNYLVALMKNQLLPVRFHIPLYGEVVSLSRGMFLNIDFIL
FRGPGSPFQNNWQLRDEFVRSNQTELAQRSLKILGVALLNVLAPVIFVWQLIYFSFS
YANILRKEPGALGLRTWSNYGRLYLRHFNELDHEDARLNRAYDYADRYLNSFSSPLAAV
IAKNLLFISGGLLLLILALGIYEEHVQVEHLLAILAGLGAIGVVCRTLIPDENLVWCPE
QLMTAILAHVHYLPSEWRQQAHTTKVRQEFNSFFQFKAGYLLSEIFSPFVTPFVLI FVFR
PKAIELVRRFFRTFTVSVRGVGNVCSFAQMDVRKHGNPDWQLTSELEEMTRATAQQPQQEP
QQQSLAGGKTEMSLLRFTLNNPEWQMPKEAKQFLRGVREHAVGELVQAKTSMVQENPLTN
SLISFGTMGADYCSIANSVLTAQVTPQQLEISQSLRPGLGPVSGGFVVAASDFRQMLQQN
LSASVGPLDSMRRLRLSRAEGRLEGPTDTLLYGLCGVDPVVGSTPLNVGVADMCLSALYL
HELNQQKRQARQSRIDEAEDERPGTSHWPPRPPAAPSADTGFGRSRTVITSKAAESTPLL
GSIRSXQRPEWI

>tr|E1BVB2|E1BVB2_CHICK Autophagy-related protein 9 OS=*Gallus gallus* OX=9031 GN=ATG9A PE=3 SV=2

MAHLETQYQRLESSTESPPGGDLLVHVPEGAKSPWHHIENLDLFFSRVYNLHQKNGFT
CMLIGEIFELMQFIFVVAFTTFLISCVDYDILFANKAVNHSQHPSEPIKVTLPDAPLPPN
VCSARIQANSFLICILVIAGVFWIHRLVKFIYNICCYWEIHSFYINALRIPMSNLPYYTW
QEVQARIVQIQKEHQICIHKKELTELDIYHRILRFKNYMVAMVNKSLLPVIRFRLPLLGDT
VFYTRGLKYNFELIFFWPGSLFENEWSLKAEYKRAGRLELAEKLSTRILWIGIANFLL
CPLILIWQILYAFFSYTEILKREPGSLGARCWSLYGRCYLRHFNELDHELQSRLSKGYKP
ASKYMNCFISPLLTIVAKNVAFFAGSILAVLIALT IYDEDVLAVEHVLTTVTLGVGITV
CRSFIPDQHLVFCPEQLLRVILAHIHYPDHWQGNARHRYETRDEFAQLFQYKAVFILEEL
LSPIITPLILICLRPKSLDIVDFRNFTVEVVGVDTCFAQMDVRQHGHPAWMSAGKT
EASIIYQQAEDGKTELSLMHFAITNPKWQPPRESTAFIGFLKERVHRDSSVALAQQAVLPE
NALFSSIQSLQSESEPHSLIANVIAGSSVLGFHMGRDQASRHLSEVASALRSFSPQLQA
QQPSGGFQTAGSSAMTASGADARTMSSGSSAWEGQLQSMILSEYASTEMSLHALYMH
KQHAQLEPERHTWHRRESDESGESTHEELDAQRGAPVPLPRSASYPFSSRQPAEETATLQ
TGFQRRYGGITDPGTVHRAPSHFSRLPLGGWAEDGQSARHPEPVPEESSEDELPPQIHKV

>tr|Q3T903|Q3T903_CAEL Autophagy-related protein 9 OS=*Caenorhabditis elegans* OX=6239 GN=atg9 PE=2 SV=1

MAETQNLLQKIDNSSINLIFFQKKTHQMFNSQSKRAYQQIDDDFDDEVLRNSTCTSRFMQ
GWGSSTRSLLFGGASNDEQRNLIASSSSHSHSYHDSPAEPPETHYEQFTATHNHGPPTMA
SSSQLNSRRWDHVLNLDEFFTHIYEHQNGGYLCIVLQKVFSLQFIFVMSFTTFFFTQCV
NYQFLFANTNVTSHGTVNQKRHFGDAVVDNCPAHISIWMIFAILAAIVYWITRVIKHAQ
YIMKMSEIQQFYAHELKIADDQLPNLTWHAIVKRICEAQKKLRLSIHQDNITSIYIYHRI
LRYKNYMTGMINKRILHPVFDVPFLGPIAYLPNNLKHEIERILFTSSTSAWTNGPNLREE
YKHHEQLDMAAKMKEDVINLFLQILRISVARPDASTAPIPDYGIVLLTDGAHKKTRWA
WNEKIQYLLRHFNELDHESARLNRSIIYAAAYMDQFFSPVLEIAAKNITFIAAAVFGVL
TILSAWDEDVLQVEHVITVLTICGIVVLVCRGMIPDENLVWQPEILMTHVTSELHYLPST
WKGKAHTTGVRHEFDQLFQMKWMFFVLELTSPIFTFVLLFWLRPRCSQLANFFHDYTER
VDGLGDVCSFAVMDVGKHDGPKWNHIKELKAIVEDQEDQQQAQSVVTSLNRARDGKTELS
ILHFKTTNPEWQPPKASEKFLRKRNRQLGQEAASMLAPLTSMHLGQQMDRQQQGGKIGRNI
LLESVHSIVPTTSGGISASQVAPGRHPLIGDGLHRIDGVPVGNVAFQGIQGAKLGGGVLAS

LYQEQPRAAESLSNSLRASGVDIDGAGAEMRINALFLRGLHDESIIHSSSRNYGGTTSSF
NMHPTAMQSVFAMPDGFQGPAPAVESSLIDTPTYHRESVQRSAAEHKMEHETPEPLAE
LPDLPGPSSSEHQQRSLVNPNTQHRQINEEEEEEEEEEDNTPPLSFSS

>tr|A0A087ZP33|A0A087ZP33_APIME Autophagy-related protein 9 OS=*Apis mellifera* OX=7460 GN=Atg9 PE=3 SV=1

MKRETVITCVEPNRRAKTMTTVLDGSYQRMEPYDGEEEDGEDDDEHEETPQESGVMIHVV
PEGNKARWNHVEDLDSFFTRMYHYHQKHGFACMILQEALELGQFIFVVFSTFLFHCINY
SLLFKNGKERRKISISDVILSKSECIASMGILITWICILVAAIFWILRLVKVLYHCTQFWDI
KLFFNTALKIEDCDLNLTWHEIQKRVREVQKEQEMCIHKRELTELDIYHRILRFKNYMV
AMINKSLLPIRLKVPIIGEIIFLTRGLKYNMELLLFWGWPSPFENNWHLKEDYKKNLKRQ
ELARALSKHILWVGIVNFLCPLILLWQILYSFFNYGEI IKREPGLGTRMWSLYGRLYL
RHFNELDHELNARLNRAYRPASKYMSMFTSPIMTVIAKNVAFVAGSILAVLLILTVDYED
VLTVEHVLTITITILGAIVAGARAFIPDENLVWCPETLLTAVLAHATHYRPSWRGHAHTQT
TRAEVAQLFQYRAVHLLLEELISPLITPFILCFRMRQRALDIVDFYRNFTIEVTGVGDVCS
FAQMDVRRKHGPNMWQTATQIPVQDRAAKYDNQYATDPEKLQIPIISDQYTQAEDEGKTELSL
IHFTLTNPEWKPPSHAENFVTALRERVKKDVHGGGHEINPLLASLNSLSGLGPGYNDIIS
NIIRSTMINQASGPSTSTMFTNQPCCTTSVCTSGNEMLMNKSDIFPHAVQCGLSKAEGPVH
NEKGLLYGLQQEISNQSLGASVVFSSHEFSTDLSIPVELIAADMSLSTLYLHELHHRQVR
RRGYQELAMRSVWQRSVPVQELATLPEVRQERAPLLLHQDSSIRNNREFKYNLNTRLDSI

>tr|A0A1S3JC03|A0A1S3JC03_LINUN Autophagy-related protein 9 OS=*Lingula unguis* OX=7574 GN=LOC106171792 PE=3 SV=1

MSEFTTSYQPLPASGYEEDEVDTPHMETDVLIVVPEESSKSRWNHNIENLDEFFARVYQY
HQNRNGFFCMVLEDVLQQLQFVVFVILFSSYLIECVKYDVVFDEIYRNNTGHKKVTIAESV
IPLDQCVS SVRPFVAICLLVAAVFVWLRLIKVVYNVLYWEIRAFYLTALKISADELPNL
TWHEVQKRVVEVQEQQMCIHKKELTELDIYNRILRFKNYQVAMVNKSLPLKYRIPFVG
DYVFLSTGLKYNLEMILFWGWPAPFENYWHLKQDFKNYHKRRELADYVVSQRILWLGLANL
ILSPLIFLWQILYSFFRYAEI IKRQPGSLGARRWSLYGRLYLRHFNELDHEFEARLNRGY
KPAEEYMNI FTSPVLVILAKNVVFFAGAVLAVLIILTLIDEDTLQVENILRMMTILGAVV
AVCRAVI PAEHMVFCPEFLMTHILKEVHYI PDSWKGNATHKVRQEFQALFQYKALYLLE
ELISPLVTPILCF SIRHKAYDIVDFYRNFTVEVTGVGDVCSFAQMDIRKHGNPQWVKEE
QTQADLYHQAEDEGKAELSLMHFALTNPEWKPPENC SVFLNDIKDQAVNDANA AVVAPGDN
ALFTSLHTFASALSPGVYNSINISVVPGPSMASAHHSMRPLGTVP GPMSPPGGSHLRGA
GVAAHAEGPLQSGK GILASLHSSGALSGSATGLGSGPTSLDTGHFLSSEVSQELSSAEMS
FSALYIHELHRRRRRQGHRLLEYLDFDGRPHVELQELGTRLTFDLDPMPGHGGVVRGHMSNI
VESPQEEKSEEEEMSNEDAITFVSFDERVTKST

>XP_022310215.1 autophagy-related protein 9A-like isoform X1 [*Crassostrea virginica*]

MSGAAMADYQTQYQALGSCDEDDTDETDAPTHESANLMIHVVP ESTRWNHNIENLDDFFTRVYHYHQGGF
LCMMVSDVLQVLVQFLFVVGSTFLLFCVNYDILFANSKNDTHKVTISEAVTPFGQCQVEFDGFIGITVCLLV
ALAFWIFRTIKVLYNIFKYSEIRSFYLTALHISTAELSNTWHEVQRRLLLEVQKEQQMCIHKQELTELDI
YHRILRFKNYMIAMERKSLPLKHXVPLGECAFYSIGLKYNLDFLLFWGWPSPFENYWKLKDEYKVVYHK
RKQLADELSKILWIGVANFALSPLILLWQILYSFFRYADTLKREPSMLGSRWSNYARLYLRHYNELDH
EFDARLNRGYRLANKYMDIFTSELIVILAKNVAFVAGSVLAVLVVLTVIDEDVLAVEHVLTITMTVAGLIV
TACKVFIPEHVLVYCEILMRNILAHVHYMPPDWTGNAHTSKVRNEFSMFFQYKVAYLFEELLSPIITPL
ILCFYLRHKSMEIVDFFRNFTVDVVGVDVCSFAQLDVRKRDKKTGEVEQEEEEDEPEPSLRTNMFTPVQS
PSQEGKIEMSLMHFHLTNPEWKPPKECSLFLNDVKEKAQRNTASLSIFHPVTQNMVNSSQGLTGYSGL
QPSGAGGLGESSTEQYTSLASSIAIQSGMYPQSTQVSMAPSVSGVHHRLRGAISTAEGPLERSVSGNLGT
LTNMQASSTASMVGSYVMGYHSLGSKNSKPSVDEGSLELMSQDMSVSALYLHDLQSRQRGQGHLYENLED
LRARNLWQRQDSNNPPPGASAGMYNIQEKKEEEEGGREGTSETITKTA